New Directions in Biocultural Anthropology
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This volume is dedicated to the memory of George Armelagos, friend, mentor, teacher, scholar, intellectual, and joker.
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A biocultural tribute to a biocultural scholar: Professor George J. Armelagos, May 22, 1936–May 15, 2014

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The case studies that comprise this volume all share one fundamental theme: the primary authors worked with George Armelagos on a variety of human behaviors and cultural strategies that have resulted in human suffering, in the past and the present. Most of the scholars in this volume obtained their doctoral degrees in anthropology under George, or worked closely and collaboratively with him on research projects, and so the tie that binds these chapters is one man’s vision for how to utilize a particular approach to solving the core problems that humans face in their lives. The problems addressed by everyone working with George are fundamental and inclusive in scope. These include topics such as the evolution of diet, human nutrition, and health; the effects of racism on the health and well-being of generations of African Americans; the meaning and causes of violence; how inequality, poverty, and marginalization affect human biology and well-being, especially of women, children, and minorities – the most vulnerable members of a given society; the effects of economic change and development on human health and well-being, from agriculture to industrialization; how infectious diseases and the pathogens that cause them have adapted to and co-evolved with humans over time and across space, and the dialectics of this relationship; and how indigenous people all over the world have fared throughout time under conditions of climate change or cultural disruptions (see Chapters 19 and 20). How could one person oversee the production of so many different dissertation, postdissertation, and collaborative research projects? We provide a little background to the man, the teacher, and the scholar so that his vision for how engaged and important research should be done might be better understood.

George was born in Detroit on May 22, 1936. He died unexpectedly but peacefully at his home in Atlanta on May 15, 2014 after being diagnosed with pancreatic cancer one week before. At the American Association for Physical Anthropology meetings in Knoxville, TN, a year before (2013), an
afternoon-long session honoring his work by his former graduate students and colleagues paid tribute to the many directions in which his mentoring and interests had taken his students and collaborators. Those presentations form the basis of this volume. In turn, each of George’s former students and collaborators spoke about the importance of having George as a mentor in graduate school, as a colleague and collaborator in continued projects, and as a fiercely loyal friend for decades after leaving graduate school. Grown men had tears in their eyes as they spoke lovingly of George’s generosity and spirit as he guided them in their careers and research.

One constant theme in the presenters’ narratives was what a great teacher George was. They talked about how caring he was and how it was his goal to turn every student on to the joys of seeing the world through an anthropological lens. In particular, speakers recalled his use of the biocultural model and detailed the ways in which this approach was useful to them in their research. As is discussed in greater detail throughout the text, the biocultural approach is an analytical perspective in anthropology that explicitly emphasizes the dynamic interaction between humans and their larger social, cultural, and physical environments. That is when we got the idea to honor George by producing a textbook for undergraduates and graduate students taking anthropology classes that highlighted a wide range of case studies on the theory backing the biocultural approach and how the biocultural approach could be applied.

George had a very distinguished career in biological anthropology. With a BA with Honors in Anthropology from the University of Michigan at Ann Arbor, George entered the Medical School at Michigan. This foreshadowed his life-long commitment to understanding human disease and human variation within a biocultural perspective. He transferred a year later into the Rackham Graduate School in Anthropology at Michigan, and from there he moved into the PhD program at the University of Colorado at Boulder. It was here that he began formulating his early ideas about the biocultural nature of human health and disease, and the forces that shape the emergence and development of disease and human responses to it and experiences of it.

George Armelagos worked within several areas of anthropology in developing and using the biocultural approach (see Chapter 1). Working on human skeletal remains from Sudanese Nubia in the late 1960s for the purposes of his dissertation, George began to piece together the patterns of morbidity, the diseased state, and mortality, or death, that he saw in this skeletal sample and the portion of the ancient population that it represented. As was the custom in the field of paleopathology, the study of ancient disease, at that time, he would only have been expected to publish case studies or single episodes of the more interesting or unusual pathologies. However, George instead drew from the fields of epidemiology and demography to study the patterns of illness and death within a population-level framework (see Chapters 10, 15, and 16). His first published study, “Disease in ancient Nubia” (Armelagos 1969), was holistic and integrative, looking not only at evidence of poor health but also at
the cultural and environmental processes that produce poor health and disease (see Chapters 8, 9, and 12). He was able to empirically demonstrate that the patterns of disease evident in the sample were strongly associated with the age and sex of the skeletal individuals, as well as their dietary practices and patterns of consumption. He further demonstrated that temporal changes in patterns of health and disease were evident in the sample and this corresponded to political, economic, and cultural shifts in the larger region. This classic publication, still used in paleopathology seminars, stands as a mile-marker in paleopathology and the biocultural approach.

As he developed this bioculturally based approach in subsequent research projects and publications, the perspective began to have widespread influence on the development of biological anthropology overall, medical anthropology, and the cultural ecology of disease (see Chapters 2 and 3). What was so innovative and outside the box about this research perspective, specifically with regard to health, well-being, and disease, is that in the approach, disease was conceptualized as a process, involving multiple levels of analysis on single individuals – from histological and chemical to anatomical – that needed to be understood at a population level and across time and space, using comparative and cross-cultural

Figure I.1 George Armelagos with skeletal material from ancient Nubia.
perspectives. This produced a paradigmatic shift in the way that disease in the past and present was analyzed. In paleopathology, it shifted the field from its previous focus on descriptions of isolated cases of pathology to comprehending both the proximate and ultimate causes of diseases and their diverse manifestations at a population level, a regional level, and throughout time (see Chapters 9, 10, and 21). In medical anthropology and studies of the cultural ecology of disease, George argued for – and through his research demonstrated the utility of – a systematic, integrated, biocultural approach that attended to ecological, social, cultural, and political economic aspects of diseases processes (see Chapters 3–5). An example of the broad appeal of his research was when a new journal entitled *Ethnicity and Disease*, a broadly multidisciplinary journal publishing research on causal and associative relationships in the etiology of common illnesses through the study of ethnic patterns of disease, came out in the early 1990s. George published a short overview in the first issue entitled “Human evolution and the evolution of human disease” which comprehensively addressed patterns of human health, disease, and co-evolutionary processes with pathogens throughout human history (Armelagos 1991) – no mean feat.

Another area of great interest to George was diet, disease, and nutritional anthropology. At the same time that George was pioneering the study of disease in broad biocultural terms, he was also making in-roads into how diet and disease interact, how food choices and nutrition structure population health, and the evolution and biological impact of changing diet during the population transformation known as the first epidemiologic transition, the increase in dietary disease and mortality from acute, epidemic infectious diseases associated with the shift from foraging to farming during the Neolithic Transition (c. 10 kya) (see Chapters 12, 13, 14, and 18). In 1980, George co-wrote with Peter Farb a text entitled *Consuming Passions: The Anthropology of Eating*, which explores the anthropological connections between various eating habits and human behavior. This text helped to create the newly emerging field of nutritional anthropology.

Another major contribution that George made to the subdisciplines of both biological anthropology and archaeology was his work with Mark Cohen in bringing together researchers who would address the biological and cultural impacts of this shift from hunting and gathering to agriculture. The resulting edited volume, *Paleopathology at the Origins of Agriculture* (1984), is standard reading in most graduate seminars in biological anthropology, paleopathology, bioarchaeology, and related fields. In the text, researchers systematically investigated archaeological and bioarchaeological evidence for the diverse impacts of the agricultural transition during the Neolithic on human health, patterns of fertility, morbidity, and mortality, as well as social stratification and gender equality. This far-reaching text revolutionized how anthropologists conceptualize the effects of subsistence change and economic growth on human health and, more specifically, how bioarchaeologists employ robust empirical data to assess the biological and social impacts of major cultural changes in the archaeological record. Expanding upon these themes, in 1990, George co-edited,
A biocultural tribute to a biocultural scholar

with Alan Swedlund, another major set of papers in a volume entitled Disease in Populations in Transition: Anthropological and Epidemiological Perspectives. This text employs an interdisciplinary, biocultural approach to explore factors and processes common to the epidemiologic transitions that human societies have experienced throughout time (see Chapters 11, 12, 14, 17, and 18).

George’s contribution to the area of race, racism, and human variation was also biocultural in nature. He has written several of the more important papers on the invalidity of race as a genetic or biological meaningfully category, and as an indicator of behavioral attributes, such as intelligence. These works directly undermine the typological and descriptive work on race and human variation that characterized physical anthropology in the nineteenth to mid twentieth centuries (see Chapter 4 and 5). Instead, they attend to the potency of race – and other forms of social identity – as a social category with great influence on the access to resources, stresses, and well-being that an individual and their community experience throughout the life course (see Chapters 6 and 7). For instance, using empirically derived data from the long chronological prehistory of the Nubians, he demonstrated how in situ adaptive changes in cranial morphology were a function of dietary changes and not due to an intermingling of various Saharan and sub-Saharan “races,” as was being promoted (see Chapters 9 and 12).

Finally, it is safe to say that George was a leader in formulating a biocultural approach in the analysis of human remains and in skeletal biology. George helped to situate the study of ancient and historic human remains within not only a biocultural and ecological context but also an archaeological one. In 2003, he published the article “Bioarchaeology as anthropology” in an edited volume entitled Archaeology is Anthropology, in which he emphasized how bioarchaeology aligned with and embodied the core tenets and objectives of anthropology. Importantly, in this and other works on the subject, he emphasized that bioarchaeological and paleopathological work was most valuable when it addressed issues and generated knowledge that was directly relevant to contemporary populations, whether on the effects of economic and cultural change on health or the multiple purposes for which different kinds of violence were carried out in the past and the varied effects of these behaviors (see Chapters 22 and 23).

In all of these areas – biocultural approaches to race and identity, health and diet, social inequality, disease and evolution, and population dynamics throughout time – George helped to shape fundamentally biocultural research questions that could be answered by robust empirical data. George spent his life building elegant and compelling arguments in research areas which he was passionate about, and the case studies in this text bring these interests to life in an engaging and compelling way. George was a man of the people, he disdained jargonistic and overly technical talk and preferred to capture the complexity of his studies in plain speech. And so, we took that as our mandate to ask each of George’s students and collaborators to craft their case study in a way that keeps undergraduates, graduate students, and all of those new to the biocultural approach in anthropology engaged. The collective sum of all of his work highlights an
original thinker who dedicated himself to his craft and to his students. We dedicate this volume to him and to the legacy of the biocultural approach.

References

CHAPTER 1

Introduction: the development of biocultural perspectives in anthropology

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Introduction

Since the mid-twentieth century, the biocultural approach has acted as a cohering and integrative intellectual approach within anthropology, particularly within the subdisciplines of biological, medical, and sociocultural anthropology (Goodman and Leatherman 1998; Goodman et al. 1988). It has provided an avenue for synthetic research that unites and crosscuts these diverse arenas, helping to prevent fragmentation and schisms in the face of increasing specialization. Further, it enables anthropologists to achieve the core anthropological objectives of explaining human behavior across time and space, comprehending cultural similarity, difference, and complexity across space and time, and applying this knowledge to the solution of human problems (AAA 2012). These objectives are obtained by addressing and answering complex research questions through an array of methods, theory, and data from across anthropology and related disciplines, such as demography, public health, medicine, biology, ecology, and geological sciences, with the biocultural approach providing coherence.

Definitions of the biocultural approach have varied over the past several decades and, to a certain extent, based on the intellectual enterprise to which it is being applied, but it is characterized by several core themes. Overall, the biocultural approach attends to both the intertwined biological and cultural aspects of any given human phenomena (Levins and Lewontin 1985), explicitly emphasizing the dynamic, dialectical interactions between humans and their larger physical, social, and cultural environments. In this approach, human variation is conceptualized as a function of phenotypic plasticity and responsiveness to factors within these larger environments that both mediate and produce each other (Blakely 1977; Dufour 2006; Van Gerven et al. 1974).
We introduce readers to the development, utility, and applications of the biocultural approach. We provide a short history of its origins and development, and unpack the approach and demonstrate how it translates into a model that can be operated to guide research. Further, we demonstrate the diverse theories and explanatory approaches, methods, and data sets that have been incorporated into the biocultural approach, through the course of its development into its contemporary usage, through a short review of the chapters included in this volume, highlighting the unique applications of the biocultural approach found in each. Importantly, each of the chapters contained within this edited volume has a consistent format. Each is centered around a key concept within the biocultural approach, from the causes and meaning of violence to the effects of colonialism on indigenous communities. Each chapter provides a review of relevant theory, methods, and data, and then delves into a case study, grounded in a real-world human problem that demonstrates the applicability of the biocultural approach to each particular concept and the utility of the approach for generating resolutions and solutions to the problem. We highlight each chapter and case study, emphasizing for readers how the biocultural approach can be used to elucidate, think through, and in some cases productively resolve real-world human problems. While some of these are ostensibly far removed from the lives of modern-day students, such as the effects of agricultural intensification during the Neolithic (c. 10 kya) on human health, readers will see many of their own tribulations and trials reflected in these case studies, from an exploration of what cultural factors motivate violence (see Chapters 22 and 23), to the role that the ‘cleanliness’ of modern environments may play in producing high rates of allergies and asthma (see Chapter 18), to the continuing effects of agricultural diets and sedentary lifestyles on modern-day human health and well-being (see Chapters 3 and 14). While the biocultural approach is a deeply useful analytical tool for exploring the diversity of problems that human societies have faced throughout time, it is also very useful for laying bare just how many of these challenges are shared across societies, time, and space.

The origins and development of the biocultural approach

The biocultural approach has a rich and varied history in anthropology, which is discussed in greater detail in Zuckerman and Armelagos (2011). Here, we provide a short survey of its origins and development. The biocultural approach has its origins within biological anthropology, though for much of its history biological anthropology was deeply uninterested in the humanistic, cultural, and historical inquiries that have characterized the other anthropological subdisciplines since their nineteenth-century emergence
Chapter 1: The development of biocultural perspectives in anthropology

(Armelagos and Goodman 1998). Instead, throughout the nineteenth to mid-twentieth centuries, biological anthropologists were devoted to descriptive attempts to establish racial typologies for various regions and cultural contexts, largely through cranial morphology and other phenotypic traits. This focus did not shift until the 1950s, with the Holocaust, eugenic science, and the fall of colonialism, all of which demonstrated to physical anthropologists the disastrous, real-world applications of racial classification and typological thinking (Armelagos and Goodman 1998; Blakey 1987). This paradigmatic shift coincided with the development of the population approach in the biological sciences, which emphasized population-level rather than individual-level analyses and investigation of characteristics in breeding populations. This perspective provided an avenue for biological anthropologists to investigate the mechanics and effects of evolutionary processes in human populations for the first time. This development was augmented by the introduction of Washburn’s (1951, 1953) “new physical anthropology” to the field, which proposed a strategic redirection from typological thinking towards synthetic, theory-driven research, and hypothesis testing based on models of evolution and adaptation.

At the end of the 1950s, Livingstone (1958), in what is widely regarded as one of the first truly biocultural works in anthropology, cohered these trends into an investigation of the complex relationships between the adoption of agriculture in West Africa, the protective effect of sickle cell anemia on malaria, and the ecology of the Anopheles mosquito that carries the plasmodium parasite that causes malaria. This study not only was one of the first to conceptualize the “environment” as more than just external physical conditions, it also struck a wedge into typological thinking about phenotypic and genetic traits as static “racial markers” (Dufour 2006). Livingstone’s use of deep time to unravel the complexities of contemporary health problems is one of the foundational components of the biocultural approach, as is his entanglement of humans with many aspects of their environments, including insect vectors and changing ecologies. Together, these advances mark the beginnings of the development of the biocultural approach (Armelagos 2008).

Between the 1960s and the 1980s, the biocultural approach matured under the influences of ecological anthropology and political economy. Livingstone’s work launched research within biological anthropology exploring human adaptability, which includes genetic adaptation, and non-genetic acclimatization and phenotypic plasticity in response to a wide range of environmental and social stressors (see Chapter 2). This coincided with increasing popular concern in the United States and around the world about environmental issues and ecology; these issues became popular within anthropology and the larger social and natural sciences as well (Goodman and Martin 2002). As part of these studies, anthropologists developed an ecological approach that conceptualized all of the social, cultural, biological, and physical aspects of human environments as an integrated whole that could influence human behavior and biology
New directions in biocultural anthropology

(see Chapter 3). This integrative, ecological approach became fundamental to biocultural studies (Goodman and Leatherman 1998), as is evident in many of the case studies in this volume, from Thomas’s attention to how political conflict can shape the biology of affected communities in Peru to Smith-Guzmán et al.’s holistic, ecologically informed approach to identifying the disease responsible for causing an ancient epidemic, the Hittite plague.

Political economy, and with it, processual ecology, both developed in the 1980s, became critical for developing political economic perspectives within biocultural anthropology. Processual ecology places greater emphasis on mechanisms of change, actor-based models, and on conceptualizing adaptive strategies as being constrained by scarce resources and social and economic hierarchies. A processual approach is one that focuses on methodological study of culture change and variability. Overall, political economy paradigms in anthropology focus on the history of intersections between local and global systems, how these intersections shape social relations and institutions that control access to fundamental resources such as housing, food, and medical care (Goodman and Leatherman 1998). In this way, power – and who has it and who does not – as well as related issues of sex, sexuality, gender, class, race, and ethnicity, are central foci (Roseberry 1988; see Chapters 2 and 3).

In the 1980s and 1990s, these approaches and paradigms – human adaptability, processual ecology, and political economy – became firmly embedded within biocultural anthropology, permanently shaping the approach (Zuckerman and Armelagos 2011). These have made the biocultural approach and its practitioners more socially engaged, action oriented, and activist than previous generations of anthropologists, particularly during the earlier adaptationist paradigm (Buikstra 2006). In particular, it has produced the biocultural approach’s focus on the impacts of power relations and social inequality, such as processes affecting the control, production, and distribution of material resources on human biology in cultural systems throughout history, as well as the reciprocal influence of compromised biologies on these cultural systems (Blakey 2001; Goodman and Leatherman 1998; Leatherman and Goodman 1997). In this way, the biocultural approach is deeply dynamic and diachronic, attending to the dialectical (the interaction of opposition forces) relationships between biology and culture, power and well-being across time and space.

In these first few decades of the twenty-first century, the biocultural approach has forcefully maintained its political economic, ecological, and processual ecological components (Stinson et al. 2012). Foci are diverse and proliferating, but some are highlighted here (see also Chapter 2). Practitioners have intensified their focus on the key variable of poverty and determining the best ways to unpack and operationalize this complex, multifaceted, and culturally and historically contingent or context-dependent concept (Dufour 2006). Political economic perspectives have been applied to better understand how adaptive responses to environmental stress will vary depending on an individual and their community’s relative social and economic status, with attention to the fact
that some overly stressed and extremely poor individuals may find themselves beyond their ability to adapt, making short-term adjustments with long-term detrimental consequences; this reminds scholars, as Thomas and Leatherman et al. discuss (see Chapters 2 and 3), that not all biological responses are adaptive (Bailey and Schell 2007).

Biocultural anthropologists increasingly attend to how components of modern cultural and economic systems, such as environmental degradation and the "Americanization" of the world, in particular through the spread of high-calorie, nutrient-poor "Western diets," have altered the disease risks for certain communities as well as the overall global system, as a product of our contemporary interconnectedness (see Chapters 3 and 14). Many biocultural anthropologists employ the concept of embodiment, drawn from social epidemiology, which contends that humans biologically incorporate their social, physical, and biological conditions, and that bodies therefore can tell "stories" about the conditions of their lives that otherwise might go unrecognized and untold (Krieger 2005). Bioarcheologists and paleopathologists, studying ancient bones to reconstruct past lives and diseases, employ this concept, whether explicitly or implicitly, to reconstruct how humans have adapted, or failed to adapt, to various types of conditions in the past (see Chapters 6–11 and 21). Medical anthropologists use this concept to unpack how different patterns of health, disease, and well-being are found in different communities as populations are largely a product of differential circumstances, such as wealth versus poverty, but more insidiously, life-long levels of exposure to prejudice, social inequality, and stress (see Chapters 3–5).

Overall, practitioners of the biocultural approach seek integrative and engaged methods for broadening the ways in which questions are framed. Researchers consider multiple levels of causality for various conditions, processes, and outcomes, attending to both microenvironmental, proximate or closest causes and the often more complex, ultimate or fundamental causes, which are often political, economic, and social (Goodman and Leatherman 1998). These causes, conditions, processes, and outcomes are addressed and investigated by framing robust hypotheses within political, social, and economic contexts, with attention to such variables as violence, gender, and sexuality and testing them with empirical data (Armelagos 2003). This engagement, producing a broad, cross-cultural, historically situated study of human behavior, is an important scholarly activity because it contributes to explaining the complex human behaviors that underlie the pressing and persistent problems of today.

Locating the history or origins of contemporary problems is productive because it isolates the very specific, historically contingent factors that help to situate and explain human behavior. Often, in order to understand a complex behavior in its specific manifestation, for example, culturally determined age at weaning or the age at which males go off to war, it is useful to look deep into the past to see when those behaviors first appear and what the circumstances were that favored them. Anthropological studies have the potential to situate modern-day problems within a larger temporal and spatial framework.
these cross-cultural and deeply temporal analyses, the biocultural approach contributes to understanding human variation within and across different cultures as well as non-Western ways of dealing with and adapting to challenges.

**Using a biocultural model**

The linking of demographic, biological, and cultural processes within an ecological framework that is found in the biocultural approach is essential for dealing with the kinds of questions that interest anthropologists across the discipline. These include, for example, understanding the diverse purposes for which violence is committed, the relationship between subsistence and economic change and disease, and the relationship between social stratification, differential access to resources, and health. These kinds of problems demand a multidimensional approach because they cross over numerous disciplinary boundaries.

A deceptively simple model (Figure 1.1) provides a very useful framework for integrating information regarding human adaptability and health with larger biocultural and ecological contexts. In this model, the physical environment is viewed as the source of resources essential for survival. If there are constraints on the resources (Figure 1.1, box 1), then the ability of the population to survive may be limited accordingly. Humans’ ability to adapt to these conditions can be enhanced by their cultural system which can buffer the population from environmental stressors (Figure 1.1, box 2) or, when this fails, exacerbate the stressful effects. The technology, social organization, and even the ideology of a group provide a filter through which environmental stressors pass. However, cultural practices can also be the source of stress as well (Figure 1.1, box 3). For example, epidemiological data strongly suggest that the high incidence of chronic

![Figure 1.1](image_url) Biocultural model highlighting the common and important aspects of integration across domains.
inflammatory conditions, such as asthma and allergies, currently afflicting high-income developed nations may be a byproduct of public health interventions, like water sanitation and food pasteurization, that reduced mortality from epidemic infectious disease in the nineteenth century (see Chapter 18).

When thinking about all of the possible ways in which individuals can be physiologically stressed, it is important to acknowledge that the impact of stress will be different depending on the individual’s host resistance factors: their age, sex, and overall health and immunological status (Figure 1.1, box 4). For example, infants and the elderly may be harder hit by a seasonal drought that decreases food supplies than a healthy adult. A female who has lost a lot of blood during a difficult childbirth experience will be hit harder by food shortage or cold stress than a female who has not just given birth. Someone suffering from dysentery will have a lower resistance to contagious infections than someone who is healthy. Thus, host resistance is both biological but also cultural in nature because such things as wealth can buffer some people from dying of disease, while poverty can predispose communities to greater morbidity and mortality.

One excellent example of this is articulated by Kuzawa and Gravlee (see Chapter 5), in which they demonstrate how host resistance is always part of a larger political economy in which some bodies/hosts are of higher value than others, thereby receiving greater access to food, medical care, and other resources. As they discuss, racial inequality and prejudice become literally embodied in the biological well-being of racialized groups and individuals. This kind of reasoning can be extended to other biologically based phenomena such as age and sex across the life history of individuals who also are affected by inequality and differential access to resources (see Chapters 4, 6, and 7).

Human bodies and phenotypes are highly plastic and can physiologically respond to a diverse range of stressors in a variety of ways. Positively, in ways that are neutral to positive for survival and reproduction, the stress response can lead to habituation, acclimation, and adaptation over the course of hours to years. But humans can also physiologically respond in ways that are disruptive and maladaptive, and detrimental to survival and reproduction (Figure 1.1, box 5). Maladaptive responses to stress, particularly chronic stress, can manifest on the phenotype in a variety of ways (Figure 1.1, box 6), with particularly marked effects on young, developing individuals (Shonkoff et al. 2012), older individuals, and those already in a poor state of health (Schneiderman et al. 2005). A robust, burgeoning body of evidence demonstrates that stress experienced by parents, particularly while the mother is pregnant, can influence the health of offspring (e.g., Barker 1997; see Chapter 4), and that these effects can even extend back to the stresses experienced by previous generations (multigenerational effects) (Aiken and Ozanne 2013; see Chapter 5). These negative effects include an impaired immune response, which can lead to greater susceptibility to disease (Khansari et al. 1990) as well as reduced rates of wound healing and tissue repair (Graham et al. 2006), impaired developmental growth (Shonkoff et al. 2012), and predisposition to chronic and degenerative
disease, such as cardiovascular disease and stroke (e.g., Barker 1997). Ultimately, extreme acute stress and prolonged chronic stress and its negative impacts can also cause death. Growth disruption can manifest in a variety of ways, such as through reduced stature, evident both in height of living individuals and stature reconstructed from skeletal metrics, as well as reduced deposition of enamel on teeth, known as enamel hypoplastic defects (see Chapters 6–11 and 21). Human tissue often responds in a generalized and non-specific way to stress, but what often has the greatest explanatory power for understanding human experiences of stress is not the specific disease agent involved, but rather the severity, duration, and temporal course of physiological disturbances (Figure 1.1, box 5). Information from a variety of phenotypic indicators, from birth weight to enamel hypoplastic defects to stature, provides a large body of data to interpret the well-being of individuals during life, from modern to ancient populations.

Although it is crucial to document these physiological changes at the individual level, from an anthropological perspective it is even more important to realize that health and adaptation fit into a larger network of relations that extends beyond the individual to the population and community (Figure 1.1, box 7). For example, undernutrition of individuals can be established by examining their phenotype. This can be extrapolated to community effects; severe or prolonged undernutrition in large numbers of people within a group has the potential to negatively impact work capacity, fertility, and mortality. It is also associated with disruptions to the social, political, and economic structure of single communities and has the potential to destabilize whole regions as well.

Although ecological stress can be sometimes causally related to biological stress, ecological factors are not the only source of stress. For instance, warfare can become pervasive due to shifts in ideology and power and this can be a source of biological stress and mortality as well. The model in its most simplistic form may seem to be largely processual, in suggesting unicausal variables and a simple feedback loop. However, the model can easily accommodate much more complex, and postprocessual, cultural factors as causal mechanisms creating biological stress. The feedback from box 7 back into boxes 1, 2, and 3 represents the ways that cultural and population-level changes can further cause changes in the environmental – both the physical as well as the culturally constructed – systems. During these times, the subcomponents of cultures, including the economic, political, and social systems that are inextricably linked with the ability to respond to stressors, could be further impacted as well.

Although this generalized model may strike some as being static and containing simple factors within boxes, as a heuristic device, it and other similar models are invaluable to biocultural anthropologists. And, with the recognition that conditions are historically contingent, relational, and highly dynamic, the model can be adapted to particular moments in time and space. The biocultural model is only as dynamic and complex as the researcher using it makes it. For instance, when there is a great deal of available evidence on environmental,
social, cultural, and other contexts, the model can be added to in order to integrate and operationalize all of the forces and processes at work.

**Difficulties in using the biocultural approach**

As many scholars have noted, the biocultural approach can be too complicated to apply to anthropological research (Dressler 1995; Dufour 2006; McElroy 1990). For instance, researchers using the biocultural approach typically seek to assess the effects of a culturally defined variable – an independent variable – on some aspect of human biology. These variables can be difficult to operationalize (Dufour 2006), especially when they are composed of multiple, intersecting social, ecological, and economic components. Successfully operationalizing them in ways that are ethnographically or historically accurate and valid and scientifically replicable requires having location- and condition-specific ethnographic, archeological, and/or historical knowledge (Dressler 1995). Sometimes, particularly for the ancient past, this information is no longer available. Researchers must also wrestle with understanding the complex mechanics and effects of concepts and processes such as inequality, poverty, health, and well-being (Dufour 2006). Poverty, as noted earlier, is especially difficult to conceptualize, as it is multidimensional, as well as being a social, economic, material, and even psychological phenomenon. Different aspects of the particular conditions under study, such as nutrition or the dynamics of a given infectious disease, as well as characteristics of the human-built and physical environments, can lead to a great number of research questions and possible approaches (see Narayan 2000).

Lastly, understanding the complex interactions that can occur between various aspects of biology and culture requires researchers to identify, define, and measure – in a scientifically replicable way – many different causal pathways, which can be very challenging in practice (Dufour 2006). However, as this volume demonstrates, these complications, with the assistance of biocultural models such as the one discussed earlier, can be overcome. The authors of all the chapters in this volume and the case studies contained therein make sure to fully explain the theoretical approaches that they employ, be transparent about the methods that they use, and clearly explain how they interpret their results. This shows not only how these challenges can be surmounted, but also the tremendous intellectual rewards and insights that can be gained when they are.

**The case studies in this volume**

The volume is divided into six sections, each addressing a critical topic that is under investigation using the biocultural approach. In the following, we discuss these topics and the chapters addressing them, highlighting the unique insights of each and how they fit into the volume’s synthetic framework.
**Part I: Critical and synthetic approaches to biocultural anthropology**

Contributions in this section demonstrate how the biocultural approach can be used to synergize and integrate diverse variables, processes, outcomes, and mechanisms dealing with the intersection between biological and cultural factors. Thomas (Chapter 2) provides an overview of the development of the biocultural approach during the twentieth and twenty-first centuries, but without the biases that can come from describing a process in the past while knowing the outcome in the present – “hindsight is 20/20.” Instead, with humility and honesty, Thomas describes how changes in his approach to his long-term (more than 20 years and counting) collaborative research project on human adaptability and plasticity in the highland community of Núñoa, Peru, mirror changes in the overall biocultural approach. More specifically, he shows how misunderstanding, trial and error, and analytically running in place to keep up with a constantly changing political and cultural landscape drove changes in his thinking, and how these mirror the same processes in the overall discipline of anthropology as it progressively produced the biocultural approach. This transparency should be highly appealing to students, as it reveals the “human side” of research as well as the dynamic nature of research design, all the while explicitly demonstrating how anthropology and the biocultural approach in particular are exceptionally well suited to prepare students to understand, unpack, and address change and flux in their own communities, nations, and world system.

Leatherman and colleagues (Chapter 3) highlight the dynamic and fundamentally intertwined intersection of local and global systems, ecological, economic, and epidemiological, in their analysis of diet, health, and nutrition in Mayan communities in the Yucatán Peninsula, Southern Mexico. They employ a critical biocultural approach, which is centered on critique and reflexivity; great attention is paid to understanding both how historical and political economic forces shape biological variation as well as how the social context in which the research is carried out shapes the research process itself. As applied here, this approach allows Leatherman and colleagues to identify the nuanced processes through which local diets are shaped by global political forces, specifically the replacement of a local, healthful, indigenous cuisine with the high-calorie, low macro-, and micronutrient “Western diet” that so many readers will be familiar with (for many of you, this is your diet as well), and how these processes are a reflection of more global nutritional, economic, and epidemiological trends.

**Part II: Biocultural approaches to identity**

In this section, contributors tackle issues of identity in a variety of different forms. Goodman (Chapter 4) explores relationships between race and health, grounded in the anthropological understanding that race is not biologically “real” or valid, but that social race has dramatic effects on many aspects of quality of life, especially health. Throughout this fascinating chapter, Goodman identifies, unpacks,
and examines evidence for two primary hypotheses or causal pathways posited as to why race – being “black” or “white” – is associated with a great range of differential health outcomes, from cardiovascular disease to death by homicide. These causal pathways are the “raciogenetics” hypothesis, which posits that racial health differentials are the product of genetic differences between the races, and the “lived experience” hypothesis, which posits that chronic, life-long experiences of racism, prejudice, and reduced access to opportunities and resources cumulatively produce poor health. With a variety of lines of evidence firmly supporting the lived experience pathway, Goodman explores how insidious and hidden the destructive effects of race-based social inequality can be.

Kuzawa and Gravlee (Chapter 5) tackle questions of disparities in health across racialized identities within contemporary populations. Drawing on many biocultural factors that determine access to resources and good health in the United States, they demonstrate how little genetics have to do with illness and death. Taking the longer arc of time as their reference point, they ably demonstrate that political, economic, and historical factors have led African Americans to not have the opportunities for good health and the social context for a stress-free life. Their case study illustrates the pathways by which these differences in lived experience lead to biological differences that operate through wear and tear on the body’s defensive systems or by modifying early growth and development in children.

Continuing in this vein of exploring the ways in which racism gets under the skin and affects health and patterns of death, Blakey and Rankin-Hill (Chapter 6) present an overview of their long-term study which focused on the now famous African Burial Ground in New York City. Using a wealth of biocultural data collected from the skeletal remains of enslaved individuals, they show the innumerable ways in which they were physiologically and biologically beaten down by oppressive treatment, poor nutrition, and being literally worked to the bone, in a larger political and economic context of the commodification of African bodies. What is most unique about the approach taken here is their engagement with the opinions and desires of the descendant community of African Americans. This case study, perhaps more than all others, emphatically demonstrates that biological indicators of disease or early death only tell part of the story. The rest of the story lies in ethnohistoric documents, slave owners’ wills and diaries, demographic records, and medical accounts.

Rankin-Hill (Chapter 7) follows with a vivid biocultural study of burials from the First African Baptist Church that provides another angle to the story about the welfare and health of Africans forcibly brought to the New World. In this nuanced and richly detailed study focusing on diasporic patterns, she demonstrates how historical skeletal samples can yield not only information about health and disease, but that the burials also offer glimpses into the lived experiences and reality of specific locations at specific times in history. Her study also emphasizes that Africans who ended up in the New World represent wildly heterogeneous populations, which is crucial for deconstructing the myth of the homogeneity of African American identities.
Part III: Biocultural approaches to health and diet
In this section, a number of authors tackle the common yet deadly ways in which diet and disease interact to create human suffering in the form of illness, nutritional diseases, stunted growth, and early death. All of these chapters fall under the rubric of “lessons learned from the past” – admittedly an old trope but one that is employed in novel and inventive ways by these works.

Sandberg and Van Gerven (Chapter 8) present the culmination of decades of research on the medieval indigenous communities that thrived along the Nile River in present-day Sudan. Groups from archeologically contemporaneous sites at Nubia, on an island, and Kulubnarti, on the mainland, are compared to assess the differential biological effects, specifically illness and mortality in infants and children, as well as religious, political, and economic social forces, all of which operated differently between the two communities. They argue, as is reflected in their title – “Canaries in the mineshaft” – that when vulnerable infants and children suffer, it is a signal, like the death of a canary in a contaminated mineshaft, that as go the children so too the adults. The authors use a wide variety of biocultural indicators of health to show why and how the groups on the mainland did so much better, health-wise, than those on the island.

The next chapter, by Baker (Chapter 9), maintains this focus on medieval Nubia, here examining how archeological excavations and skeletal samples from the region have been instrumental in development of the biocultural approach, particularly within bioarcheology. Throughout this discussion, Baker emphasizes the unique insights into ancient lifeways, identity, society, and adaptations in Nubia, that the biocultural approach has been used to generate. These include nuanced interpretations of the biological costs of sociopolitical, economic, and environmental change, including state collapse, as well as social changes wrought by immigration and processes of assimilation, putting into practice Thomas’s assertion that the biocultural approach is uniquely well suited to comprehending the effects of large- to small-scale social change, in the past and the present.

Grauer and colleagues (Chapter 10) employ multiple lines of evidence and methods, including historical demography and paleopathology, to produce a holistic, nuanced, and carefully considered reconstruction of life in nineteenth-century Peoria, IL, a bustling riverside industrial community. Importantly, they emphasize the need for a thoughtful approach to the methods and data employed for reconstructions of lifeways in the past, but one that is just as relevant to multifactorial, holistic reconstructions for present-day communities: what can we learn about their lives from these methods and data sets and what can we not? What can we learn from comprehensively studying one individual in a community versus all available members of the community? In particular, they apply this cautious, considered approach to gain profound insights into the effects of urban living and industrialization on Peoria’s most biologically and economically vulnerable residents: children.
Magennis and Clementz (Chapter 11) use the biocultural framework to interrogate the effects of industrialization on one indicator of adequate nutrition and overall health, specifically skeletal robusticity, which is a measure of bone strength relative to body size. Traditionally, studies investigating skeletal robusticity over the long arc of time have suggested that as humans became less mobile and more committed to sedentism and agriculture, their bone robusticity declined. The authors extend this idea by asking if the shift from an agricultural lifestyle to an industrialized one of mechanization and urbanization also affects robusticity. Their findings, only interpretable within a biocultural context, reveal a stunning rebuttal to traditional interpretations, namely that robusticity increased in urbanites, when compared to their agricultural ancestors. Importantly, Magennis and Clementz caution that skeletal responses to lifestyle, nutrition, and social environments are both variable and contingent, making it crucial to utilize a multifactorial approach.

White and Longstaffe’s chapter (Chapter 12) continues to demonstrate the unparalleled intellectual insights that can be gained from in-depth, long-term, holistic, biocultural research in single regions and cultural periods: ancient Nubia and Egypt. Far from exhausting the topic, White and Longstaffe use the region and its people to demonstrate the value of bioculturally oriented anthropological isotopic studies. They intensively discuss the insights into adaptive domains, and population-level patterns of health and disease, that can be gained from isotopic reconstructions of diet and residential mobility. Importantly for students, they also identify key areas for future research, highlighting what anthropological isotopic studies may yield in the future on human–pathogen interactions, environmental change, and human–environment interactions, with the understanding that lessons from the past have great implications for current and future human communities.

The case study presented by Widmer and Storey (Chapter 13) deals less with health directly. Instead, it is an in-depth interrogation of what we know about ancient Mexican, or Prehispanic, cuisine as reconstructed through diverse data sets. Their analysis of floral and faunal remains found at archeological sites, combined with ethnohistoric and contemporary accounts of food use, provides a riveting and irresistible listing of what ancient people utilized for food. From insects and eggs from dozens of bird species, to algae and every imaginable reptile and mammal on land and in the waters, Prehispanic cuisine was anything but tortillas and beans. While those foods were foundational, literally dozens of other plants and animals were used to flavor and enhance what people ate. The take-home message in a broader context is that while humans did settle on monocrops, such as corn, in many parts of the world, they supplemented that part of the diet with a long list of nutritious indigenous and common plants and animals that provided texture, flavor, palatability, and spice to these cultigens. Modern agricultural societies could take a hint from these practices.
Part IV: Biocultural approaches to infectious disease
This section focuses on biocultural approaches to infectious disease, a major force in shaping human health and variation since our earliest evolution. In clear and engaging prose, Barrett (Chapter 15) takes on many of the misunderstandings and stereotypes surrounding recent (2014) events involving the Ebola virus and various epidemics of the disease from the 1970s to the present. Barrett draws on his long-time collaborative work with Armelagos, in which they traced the ways that culture affects human behavior and how these shape both the physical and social environments in which humans live. Understanding of these inherently biocultural contexts is the key to explaining the “why,” both proximate and ultimate, and the “how” of epidemics in the past as well as the present. Without this “deep time perspective” on diseases in general, we are doomed to interpret epidemics without understanding the long-term mutually interactive relationship that exists between humans and their pathogens. This contribution powerfully demonstrates our absolute need – in anthropology and related disciplines, namely public health and clinical medicine – to take a broadly biocultural approach to epidemic infectious disease.

In their contribution (Chapter 15), Smith-Guzmán and colleagues present an inherently biocultural model for differentially diagnosing the diseases responsible for ancient epidemics, with a case study focused on the infamous late fourteenth-century BC Hittite plague. Their model, demonstrated in the case study, seamlessly considers and integrates multiple epidemiological, ecological, social, political, economic, and even entomological variables that influenced and produced the “plague” in order to identify what disease may have caused it. Importantly, despite all of this complexity, the model is designed to be generalizable, therefore providing a framework for other researchers who need to empirically divine the causes of past epidemics, from the Plague of Athens to the Black Death. While one of the challenges to implementing the biocultural approach, as noted earlier, is operationalizing all of the highly contingent variables involved in biocultural interactions, Smith-Guzmán and colleagues masterfully demonstrate exactly how this can be performed.

Lastly, following a similar trend, Zuckerman and Harper (Chapter 16) demonstrate how paleoepidemiology and the biocultural approach can be combined to gain empirical insights into the origin, evolution, and distribution of diseases in the past, specifically the origin and antiquity of syphilis. Scholars have debated the origin of syphilis for upwards of 500 years, polarized between whether it originated in the New World and was brought to the Old by Columbus, or whether it was “always present” in the Old World. The authors employ rigorous epidemiologically informed criteria to evaluate the certainty of the diagnosis and date of putative cases of syphilis, and related treponemal variants, reported from the pre-Columbian Old World. Further, they use the biocultural approach to explain how and why syphilis has evolved over time in response to various sexual and environmental pressures, and evaluate arguments as to why pre-Columbian evidence for the disease is so scarce in the Old World.
Together, paleoepidemiology and the biocultural approach are moving scholars progressively closer to understanding whether, when “Columbus sailed the ocean blue,” he did more than “discover” the Americas, instead unleashing a terrifying disease upon the world.

**Part V: Biocultural approaches to understanding population dynamics**

Contributors to this section apply biocultural approaches to epidemiology, paleoepidemiology, demography, and paleodemography to gain a better understanding of disease patterns and the drivers of population dynamics. Mielke (Chapter 17) integrates the biocultural approach into epidemiologic transition theory (which models relationships between economic growth, population growth, mortality, and fertility) with the emphasis on demonstrating how understanding long-term patterns of disease mortality and their connections to demographic, environmental, and cultural factors is significant for comprehending modern epidemiological landscapes. Documenting, understanding, and modeling the dynamics of past epidemics also enables preparedness for future epidemics. As is particularly demonstrated by Mielke’s sophisticated dissection of epidemiologic transitions in the Åland Islands of Finland, these diverse factors, both biological and cultural, must be conceptualized holistically and integratively in order to effectively understand what drove morbidity (sickness) and mortality in the past and what may produce it in the future.

Zuckerman and colleagues (Chapter 18) also grapple with epidemiologic transition theory, here with the explicit aim of demonstrating how human host–pathogen interactions can be directly applied to improve human health in the present, through clinical treatments and public health interventions. The chapter pivots around the question: why are chronic inflammatory diseases (CID), like asthma, allergy, and autoimmune diseases, at high and increasing incidence in high-income, developed nations? This may strike home with many students, themselves increasingly afflicted with conditions like eczema, hay fever, and asthma. The hygiene hypothesis, which implicates contact with environmental microorganisms, parasites, and our gut flora in healthy immune function, is evoked to explain why CID incidence is high and increasing. Embedded in this framework of epidemiologic transition theory and the hygiene hypothesis, Zuckerman et al. provide a case study explaining why intestinal parasites, such as the pig whip worm, may soon be available from your local pharmacy to treat one particular CID, inflammatory bowel disease.

In their contribution, Schurr and colleagues (Chapter 19) synthesize archaeological, ethnographic, genetic, and historical evidence for several modern indigenous Caribbean populations to reconstruct the original peopling of the region, and address the complex biological and cultural impacts of assimilation, disease, and genocide brought about by European colonization and the trans-Atlantic slave trade on indigenous Caribbean communities. Historical discourses about
the Caribbean and circum-Caribbean have typically emphasized West African and European influence, generally neglecting indigenous people’s contributions to the biology and culture of the contemporary region. But Schurr and colleagues counter this with direct evidence that the islands were inhabited by a complex cultural mélange of people prior to European contact, with these conventional labels primarily a product of socioeconomic differences among indigenous populations, hegemonic colonial policies, and misinterpretations of ethnohistorical records. Importantly, this work also has direct, applied implications: indigenous groups, working directly with Schurr and colleagues, are using the synthesized evidence to reconstruct their lost heritage, empower their communities, argue for legal recognition as sovereign tribes, and exert more control over their cultural patrimony.

Swedlund and colleagues (Chapter 20) take a highly novel and interdisciplinary approach to thinking about the important factors that shape human health and population vitality. They work with demographic information, environmental constraints, and sophisticated models to project how well communities of humans living in the sparse and barren portions of the American Southwest could have survived during times of drought and other ecological impositions over the course of hundreds of years of occupation. The biocultural approach lies at the heart of this work, because it offers a way to systematically model biological features which make groups vulnerable – infants dying, frail elderly, males lost to war – and cultural factors that buffer groups or produce and exacerbate poor health – degrading the landscape with intensive farming, decisions to migrate or stay, and establishment and maintenance of trade networks. While these data help us to understand past populations and their responses to climate change and other factors, they can be extended to better prepare for future events as well.

**Part VI: Biocultural approaches to inequality and violence**

The final section of this volume includes three chapters that focus on the longer history and trajectory of inequality and violence in human groups. The biocultural approach is useful when trying to decipher particular kinds of suffering from the archeological record and from human skeletal remains. The biological data (derived from skeletal remains), the cultural context (reconstructed from artifacts and settlement data), and the environment (pieced together from ethnobotanical remains and ecological signals in the soils and trees) are combined in these analyses to paint a picture of what life was like in the past. Turner and Klaus (Chapter 21) heed the advice of Armelagos, who emphasized that the only way to make sense of the pathologies seen on ancient skeletons is to dig deeply into the cultural context. This can reveal the structures that may have been in place that caused some individuals to be linked to disease and trauma while others
were buffered or protected. This chapter provides a broad overview of all of the major areas wherein bioarchaeology, the study of human remains in their cultural context, has made inroads into understanding the human experience in cultures that are only known now by what has been preserved archeologically. Anchoring their discussion in state-of-the-art methods with applications to several regions of the world where they have worked, the authors highlight how the study of ancient burials and human skeletal remains has been enriched and enhanced through the biocultural approach.

Following this are two chapters that specifically highlight how human skeletal remains afford a glimpse into violence, pain, and suffering. Both of these case studies emphasize the biocultural approach, locating the origin and causes of violence that are embedded in political economic structures within the respective cultural systems. Pérez (Chapter 22) draws on the same theoretical approach to direct and structural violence as discussed in Turner and Klaus. He expands their discussion to provide a detailed overview of how deeply embedded violence is within societies. Violence that is patterned and directed at certain groups of people is often used to keep those groups subordinated and in a lower rank within the society. Violence keeps inequality in place by giving some – elites, those in power – access to things such as food and wealth, while limiting access for others. In a stunning example from the early twentieth century, Pérez highlights a massacre of over 100 men, women, and children in Sonora, Mexico, who were brutally attacked by the Mexican army for supposedly carrying out an uprising against the current governmental regime. Pérez’s multifaceted analysis incorporates data from the remains of the victims along with historic documents, permitting a detailed reconstruction of this massacre and its reverberating effects.

Martin and Osterholtz (Chapter 23) continue to look at forms of violence through a biocultural lens by investigating two contexts wherein trauma was identified on the remains of ancient indigenous communities from the American Southwest. In one context, a subgroup of adult females had been thrown into and buried in abandoned structures; their bones revealed a life of beatings and hard work. Applying the biocultural approach to investigate why these women had been so abused yielded an interpretation of structural violence whereby some groups practiced raiding for women. These captives were beaten into submission and then forced to do agricultural labor, ultimately dying with a long list of pathologies and trauma. A second case study focuses on the remains of 33 individuals – men, women, and children – who were not only massacred but also tortured; perimortem pathologies on bones of the feet revealed that they had had their feet cut and beaten in such a way that they were hobbled and could not run away. Without utilizing the biocultural approach, it would have been difficult to fathom the cause and purpose of these distinct pathologies, and reconstruct the psychosocial impacts that these traumatic experiences may have had upon the victims, the perpetrators, and the witnesses.
Conclusion

This volume, inspired by a great teacher and researcher within the biocultural approach, is designed to give students of anthropology a sense of the diverse pathways that research and careers in anthropology can take. The future for biocultural anthropology is exciting because there has been a rapid development of new frameworks for understanding and interpreting a wide range of problems that can be seen today at both the local and global levels. Food shortages, nutritional problems, disease and epidemics, increasing violence, and climate change are all in the daily headlines, and all of these topics are covered in the case studies in this volume. But the biocultural approach affords something that few other studies approaching these problems do: the case studies are broad, interdisciplinary, and holistic and they access information that comes from understanding the interplay of environment, biology, and culture.

Beyond the empirical data that anthropologists draw upon, biocultural approaches also use the rich and nuanced information that results from tracing the longer evolutionary arc – the “deep time” perspective – of where the behaviors that lead to these problems originated in the first place. The biocultural model, in its simplicity and elegance, provides a way to integrate these diverse sources of data and to make sense of them in an empirical and replicable manner. In almost every case study, data were obtained that provided information on the forces within cultures that systematically affect individuals, families, communities, and regional populations.

Yet challenges and new frontiers remain for the next generation of biocultural anthropologists to tackle, and we hope that this volume inspires students to do so. May a new generation of biocultural anthropologists interested in bettering the human condition take up the challenges posed by the research in this volume and continue to move it into new areas. Instead of inscribing and staying within intellectual borders, biocultural studies necessarily go beyond traditional lines into new terrain and this is where solutions to complex human problems lie.

References

Chapter 1: The development of biocultural perspectives in anthropology


Notes

1 Also known as the “biosocial” approach or perspective in some works.
PART I
Critical and synthetic approaches to biocultural anthropology
CHAPTER 2
Exploring biocultural concepts: anthropology for the next generation

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Introduction

Anthropology, one of the only academic disciplines to have largely avoided fragmentation and dissection into specialty areas, is in an exceptional position to bring together the disparate aspects of an interconnected and increasingly tangled world – one where human biology, social relations, language, ideology, and environment are bound together, yet in multiple states of renegotiation by different peoples. In offices up and down the corridors of anthropology departments, and especially for students graduating from these institutions, it would seem that we have much of the combined theory and expertise to start addressing the complex issues of rapid change that characterize our modern world system. Furthermore, a discipline that entertains pluralistic approaches, considers a range of biological and cultural diversity, and accepts as valid non-Western systems of knowledge is desperately needed. Expressed more modestly, we, as anthropologists, are probably better prepared than most to lead inquiry into the modern era of massive social and environmental transformations.

Through a case study focused on a predominantly Quechua population in the high Andes of southern Peru, I demonstrate how biocultural anthropology has evolved over the past several decades in its investigations of social and environmental transformation.

Background

Understanding massive social and environmental change
The future is likely to be a world where security, order, and sense of “control over” things will be substantially uprooted, even for affluent communities and especially for high-income developed nations. Because of the inevitable
interconnectivity of people and places, things long kept separate have come
together – sometimes gently with unanticipated consequences, sometimes with
great force and chaos. New peoples and cultures will encounter one another and
have to negotiate their combined needs, sometimes in peace and sometimes in
rebellion and war. And global economic integration will be resisted by attempts
to maintain local control and cultural identity that provide meaning in a world
becoming hypnotized by consumerism.

The humanities will need to work with the social and natural sciences towards
ends that truly serve humanity. Transdisciplinary sciences, such as political
ecology – the synthesis of political economy, environmental anthropology and
critical perspectives, the latter of which uncover power relations in our discourse
and analytical models (Hvalkof and Escobar 1998; Leatherman and Thomas
2001) – will have to address complex issues in which ecology, economics, health,
and personal satisfaction intersect in a manner not well comprehended by reduc-
tionist approaches to well-being. The redefinition of nature by biotechnological
innovations, global communications, growing consumption aspirations, expand-
ing inequities, pandemics, and environmental management will sow its own
contradictions. Global economic progress and local environmental and social
justice may well be placed in dire ideological contest comparable to capitalism
versus communism of an era past. Established religions and new forms of spir-
itualism will need to incorporate, or resist, these new realities. Growing public
recognition that the well-being of mind, body, and soul is dependent upon the
health of and access to food systems, the environment, and just social relations
will challenge dominant systems of knowledge and ways of knowing and acting.

**Scholarly engagement**

Science and academia, therefore, will be particularly tested to reevaluate their
construction of truth and whom it serves. And we will need to link theory and
knowledge with practice and engagement, listening to and working closely
with peoples negotiating these changes. Anthropology’s hope in engaging with
these issues lies particularly in a younger generation of anthropologists moving
through and just emerging from undergraduate and graduate programs in
four-field anthropology departments. There, they have an opportunity to be
exposed to considerable theoretical breadth that includes evolutionary theory,
environmental anthropology, political ecology, political economy, critical theory,
feminist approaches, racial and queer theory, poststructural and postcolonial
perspectives, power linguistics, phenomenology, semiotics, and hermeneutics.

These perspectives constitute different lenses with which to view and critique
the multiple realities of our times. While the discipline and our academic advisors
in recent times have encouraged us to remain within the confines of one of these
subfield orientations (and argue tenaciously for its legitimacy above all others),
to continue this mode would seem to deny the integrative promise that comple-
mentary perspectives provide in addressing the future (see Nader 2001). In short,
an integrated, holistic anthropology that can contribute beyond its disciplinary boundaries is desperately needed today.\(^1\)

**Exploring biocultural concepts**

While a biocultural or cultural biological orientation has long been at the core of the four-field approach, recognizing the ubiquity of these relations in all sorts of human phenomena opens up countless subject matters and allows new and sometimes complementary theoretical interpretations and perspectives. Simply put, bioculturalism explores how critical human biological characteristics (e.g., aspects of well-being such as lactase deficiency) are either adversely affected or enhanced in function or perception by sociocultural features. And, in turn, how biological features can influence social behavior and cultural traditions. Anthropologists exploring these issues are Armelagos *et al.* (1992), Blakey (1994), Brown and Yoffee (1992), Calcagano (2003), Downey (2012), Dressler *et al.* (2015), Dufour (2006), Farmer (2004), Goodman and Leatherman (1998), Gravlee (2013), Hadley and Crooks (2012), Himmelgreen and Romero-Daza (2009), Hruschka *et al.* (2005), Huss-Ashmore (2002), Leatherman (2005), Lende (2012), Martin *et al.* (2012), McDade *et al.* (2013), Panter-Brick *et al.* (2009), Schell *et al.* (2007), Singer (2011), Swedlund (2010), and Wiley (2004).

Because of the scope of examples available to anthropologists as we study different groups worldwide, this offers a particularly fertile field of investigation and one in which anthropologists can take a leadership role.

**Case study: the Quechua of southern Peru, 1964 to the present**

Presented is a case study that has gone on for half a century. Its relevance lies in how a biocultural approach gradually evolved and broadened in the study of a Quechua population in the high Andes of southern Peru. Research was mainly carried out by a series of multidisciplinary, international teams whose work built upon the findings of one another. Because the contributors are so numerous, I will only mention a few whose work led to the expansion of our biocultural anthropological perspective.

A brief review of these five decades illustrates how my version of the biocultural approach shifted in order to explain the realities encountered. The initial phase of our work in the 1960s and early 1970s was largely a biobehavioral orientation as to how native people adapted to the multiple stressors of high altitude: hypoxia and cold. Another stress condition was undernutrition and this led us to a study of farming practices from which an “Andean adaptive pattern” of coping responses was derived. By the 1980s, we expanded our biocultural orientation to incorporate a political economic perspective. This addressed household responses to illness and the underlying sociocultural systems of inequality and
exploitation that challenged adaptive capacity and limited agency. By the late 1980s and early 1990s, the study area became engulfed in the Shining Path (Sendero Luminoso) Revolution and psychosocial stress was added to the existing challenges confronting the population. Here, our attention shifted to how this affected the lives of local people and how cultural perceptions of themselves and their landscape were altered. This research experience has shaped my perception of what a biocultural approach should and could be.

**Early research**

As a young graduate student in 1964, I was invited to join a research team headed by Paul Baker, a biological anthropologist at Pennsylvania State University. At that time the International Biological Program’s Human Adaptability Section was set up to study how humans adapted to harsh environments around the world: the Arctic, deserts, tropical forests, etc. The Penn State contribution was to investigate high altitude and specifically how Andean resident populations adjusted to hypoxia, cold, and undernutrition. Hypoxia, from low oxygen pressure, was of particular significance since it is present continuously when at high altitude. As such, it compromises oxygen availability and in doing so affects all body tissues, including reproduction. This, then, constitutes one of the most severe stressors encountered by humans.

Since excellent work had been done on this topic by Peruvian physiologists, our primary question was whether the biological responses – increased pulmonary and circulatory function – were the result of genetic adaptation, that is, through long-term generational exposure and hence selection to high altitude. Or did they result more from developmental acclimatization by simply being born and growing up there? Critical here is the distinction between the terms “adaptation,” which implies a gene-based alteration, and “adaptability,” which refers to non-genetic acclimatization. The latter, called “plasticity,” can show how malleable humans can be in adjusting to adverse conditions and thus has special relevance to understanding how capable we are of adjusting to contemporary challenges in the course of our lifetime.

In order to test this, our research design called for finding one of the highest permanent communities in the Peruvian Andes where native residents carried out traditional activities of herding and agriculture. The District of Nuñoa, Department of Puno, in southern Peru, with a predominantly Quechua population living at 14,000’+ elevation, where oxygen pressure is reduced by 40%, was selected as the study site. From a biological standpoint, studying the effects of hypoxia was ideal because there are no behavioral or technological adjustments that might buffer the stressor and could confound our interpretations. On the other hand, cold stress could be buffered by clothing and shelter and thus the impact of cold depended on the adequacy of these technological items. Undernutrition, of course, was culturally embedded in agricultural practices having pre-Columbian and historical antecedents as well as current sociopolitical causes and consequences.
Chapter 2: Exploring biocultural concepts: anthropology for the next generation

Biobehavioral studies
Our biobehavioral approach began with cold studies since these gave us a chance to assess clothing type, shelter design, sleeping arrangements, and how eating patterns affected the maintenance of body temperature. This was hardly “real” cultural anthropology but provided a first step of interacting closely with families and getting to know their lifestyle. Our findings showed that the most vulnerable were young infants whose small size and poorer thermoregulatory capacity contributed to losing body heat more rapidly. We then inquired into how mothers protected their babies through heavy swaddling, transport under blanket wraps, and sleeping patterns that created a thermal neutral microclimate. Ed Tronick, a child psychologist who headed the study, referred to this as the “marsupial approach” to raising infants at high altitude (Tronick et al. 1994). Studies by Thelma Baker (1976) on child-rearing techniques complemented this work.

One general conclusion drawn was that behavioral and technological responses to cold were of the utmost importance and the biological responses affording better circulation to the extremities and higher metabolic rate served as back-up adjustments when “cultural” solutions were inadequate or failed. Although our research agenda at the time precluded studying how socioeconomic status (SES) affected adequate material protection against cold, this had an obvious dimension.

Growth studies
Another aspect to our early research was to measure the growth and development of children. Here, we found growth to be slow and prolonged, resulting in Nuñoa children being among the most growth retarded of Andean populations. This we attributed to altitude since, after all, that was the organizing theme of our research. Follow-up nutritional surveys showed that diet diversity was more or less adequate but energy intake was low. While the socioeconomic dimensions of this were also apparent, we were intent on working within an adaptive paradigm: a biological mode of inquiry. Thus, questions of politics, social status, and exploitation – however rampant in the Peruvian Andes – were not deemed an acceptable professional undertaking. These factors were considered outside of our area of expertise as biological anthropologists, too messy and polemical to get involved with, and would have been an unwelcome interpretation by our biological colleagues at the time. Unfortunately, such a bias still persists among many of our colleagues, to the peril of the subdiscipline’s ability to fully explain life conditions.

As a case in point, in my enthusiasm for discovering adaptive biological responses – again, the danger of working within a single paradigm and using too narrow a definition of adaptation – I wrote that slow growth and small adult body size saved expended energy, which it did. Here, I showed how smaller adults could perform rigorous agricultural activities at lower cost than larger individuals, and this seemed adaptive within the construct of my research
problem (i.e., saving energy). Had I looked harder into this relationship and used a broader adaptive scope, I may have considered that small body size might also have multiple dysfunctional effects as well. This oversight became clear in the subsequent “Small but Healthy” debates as reviewed by Pelto and Pelto (1989) who decried such interpretations as legitimizing a do-nothing approach to food assistance programs. For me, it was a wake-up call to the social and political consequences of the data we produce and the pitfalls of too narrow an interpretation of adaptiveness.

Energy flow studies
By the late 1960s, there was a florescence of ecological concepts, many with human applications, and I surmised that given the limited energy intake in the Nuñoa diet, an energy flow analysis might reveal how Nuñoa residents efficiently produced their food, consumed it, and expended energy (Thomas 1976). By and large, results confirmed this hypothesis. One of the more surprising conclusions was that in spite of energy-saving practices such as combining Andean crop production with herding as well as thrifty labor allocation, the households still could not produce enough food energy to meet their needs. The difference was made up through exchange between ecological zones where high-protein goods were traded down slope to the lowlands and, in turn, high-calorie foods were traded up. Hence, preconquest farming/herding on top of the Andes probably had to be linked to more productive agricultural communities in the lowlands, a seemingly important finding of cultural significance (see Murra 1985).

In addition to tracking energy flow, Bruce Winterhalder looked into access to essential resources: those items that people needed on a regular basis but could become scarce and had no other alternative. Here, he chose animal dung, which was seemingly ubiquitous in the countryside. The sparse forests could not provide enough wood for fuel and most forest patches were too far away. He calculated how much dung a family needed for cooking and fertilizing crops and then determined how many herd animals it took to produce these essential needs for the entire population. This led him to conclude that if the district herd size dropped below a certain level, cooking and crop production would be compromised, and urban residents without herd animals would not have enough fuel (Winterhalder et al. 1974).

Collecting data for the energy flow analysis took 14 months of fieldwork since seasonal variation in the annual cycle had to be accounted for. During that time, I got to know the Quechua people and their daily lives quite well, living among them and joining in production activities. Somewhat naively, I and other biological anthropologists and ecologists considered the project a good example of biocultural research. However, in presenting the results at anthropological conferences, it became clear that some cultural anthropologists did not agree. It was labeled mechanistic, empirical, functionalist, and too systematic, which it was. One referred to it as “benign neglect,” which in a sense it also was. However, it
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did provide some important insights into the workings of the sociocultural system that, in part, depended on these adaptive attributes.

Clearly, working out of a biological model that posited environmental stressors as challenging human biology and behavior and that had a goal of finding adaptive responses provided an insufficient depiction of the richness of Andean cultural formations. Also, by considering the Nuñoa region as a “traditional” high-altitude isolate—a closed system—we ignored its devastating colonial past, the control of lands by absentee lowland owners, and the international market for alpaca fiber that very much structured behaviors and constraints. For example, when I was doing my energy flow study in 1968 to 1969, Nuñoa was largely divided up into large ranches (haciendas) owned mostly by lowlanders whose ancestors had grabbed the most productive areas in the early twentieth century. Quechua families who worked the land, more or less as indentured servants, owed 40 days a year to the farm in exchange for having limited herds and agricultural plots. Since I was interested in household productive capacity under existing constraints, I regarded these 40 days as an externality to my model even though it put pressure on a family’s production. The point here is that we usually design our research within the confines of a certain theoretical perspective that then structures what becomes important to look at and, more seriously, how we interpret the results. I continue to stand by the importance of most of my results but now realize that adaptation to high altitude was but a part of a broader interpretation of the Nuñoa reality.

An Andean adaptive pattern

The culmination of our adaptive biocultural work was an attempt to generalize from what we had learned in Nuñoa to other Andean communities. Using a form of analysis employed in evolutionary ecology, whereby broad environmental attributes are described, I proposed a set of generic constituents of the Andean human adaptive pattern that would allow highland groups to get by and even flourish (Thomas 1979). We relied on our Nuñoa knowledge base (Thomas and Winterhalder 1976) plus a wide reading of high Andean ethnographies. From this, we proposed that the high Andean environment has four important characteristics: heterogeneity in time and space; unpredictability both seasonally and annually; low productive potential combined with soil erosion; and slow soil recovery rate when disrupted. In response to these environmental features, the proposed adaptive pattern showed high flexibility in shifting from one agricultural/economic pursuit to another, a reliance on multiple resources in cropping and herding as well as other productive activities such as textile making, and extensive information exchange about the environment and factors affecting production. These three constituents, in turn, have five subcomponents. First, multiple forms of cooperation or reciprocity; second, a rotation of crops and herds to prevent soil depletion; third, group regulations on use of the environment, especially for fragile areas or resources; fourth, high mobility that
included interzonal exchange; and fifth, extensive storage to counter environmental unpredictability.

The value of such a heuristic was that as changes were introduced to Andean communities, one had a basis for determining if aspects of the adaptive pattern were being eroded. In two instances, we used simulation modeling based on the energy flow data from Nuñoa to assess the adverse consequences if reciprocity were to significantly decline. Also, what would happen should a prolonged drought occur simultaneously with a significant reduction in the international price of alpaca fiber? In both cases, the predicted consequences were severe, especially for the poorer segment of the population (Thomas et al. 1982). Here again, while cultural anthropologists took interest in these conclusions, for them this work was not really cultural. In my mind, what was needed to address these issues was to show how cultural features such as the compadre system, which allowed families to choose fictive kin and therefore expand their cooperative network, served to reinforce their adaptive pattern. Had we been working more closely with a cultural anthropologist at the time, this would have been possible. We did, however, look closely at the social support system and through network analysis determined webs of dependency and support in different contexts (Carey 1990; Lyle and Smith 2014).

A political economic perspective

The need to incorporate the adaptive perspective, however important, into other theoretical viewpoints became clear as we moved into the 1970s. Agrarian reform dismantled hacienda ownership of vast tracts of land and turned them into state-run cooperatives. However badly run, these provided new opportunities for local governance and working conditions. More broadly, the world was changing and modernization was altering remote communities everywhere. This demanded new paradigms to understand such processes of change.

At the University of Massachusetts at Amherst, our graduate students were drawn to political economy courses and started to challenge our false assumptions of a “traditional” Andean community or a closed system for analysis, as well as some of the limitations of the adaptability paradigm. The adaptability paradigm is a functionalist perspective that shows how non-genetic biological change or plasticity responds to adverse environmental and social conditions. It is of critical importance in the assessment of challenges to human health and nutrition, but it fails to address agency, such as people’s active pursuit of reconstructing their environment, and complex sociopolitical transformation (Goodman and Leatherman 1998; Thomas 1998). After all, the Andes are portrayed by two dominant themes: adjusting to the harsh conditions and the chronic exploitation of native communities. Clearly, an accurate analysis needed to consider both of these.

Working with the students, we created a research proposal to return to Nuñoa to study the effects of illness on household production. We surmised that if the
stressors of cold, hypoxia, and undernutrition were to have an adverse biological effect, these would be recorded in ill heath and this was bound to compromise a family’s ability to get by. In an elaborate methodology (Thomas et al. 1988) that tracked seasonal change in illness episodes and their effect on productive behavior, we saw how profoundly illness not only reduced agricultural activities, and hence food production, but when sustained, led to household disintegration wherein families broke up and many members migrated out to larger towns and cities (Leatherman 1998). In turn, these consequences were embedded in long-standing and insidious patterns of racism, classism, and sexism directed at native populations.

By studying ill heath up close, these relationships became apparent. In what approached a phenomenological approach, a perspective which explores individual consciousness and direct experience, we interviewed and closely timed the activities of individuals who became ill, noting the consequences of different levels of illness both empirically and from personal testament (Leatherman 1998; Leatherman et al. 1986). Catherine Tucker (1987) extended this to the productive activities of children and the value of their work to the family, and Eva Iacono (1985) focused on infant care. Here, social models, and specifically political economy, helped us interpret how systematic exploitation worked through a process of surplus extraction, that is, the extraction through restricted access to land, low wages, unfair labor obligations, and distorted market prices for items bought and sold (Deere 1979). Such ubiquitous conditions also took a toll on self-esteem, challenged cultural identity, and degraded Quechua traditions.

Seen from this perspective, SES was clearly related to nutritional status, limited social support, frequency of illness, and the growth of children. It also became a better predictor of retarded growth than altitude (Leonard 1989; Leonard et al. 1990). Furthermore, we realized that hypoxia, which was assumed not to be buffered by behavior or technology, also had a SES component. Poorer families that were engaged in menial labor were more prone to hypoxic stress because they worked a lot harder and longer. The same applied to cold stress, which increased when clothing and shelter were inadequate. Households headed by single mothers were particularly vulnerable since many men migrated out in search of work and they were left with double duty, caring for the household and agricultural pursuits. When women could get employment, they received half the salary of men for the same job (Luerssen 1994). The educational system openly discriminated against Quechua values as well as their systems of knowledge and ways of knowing. And to access care in the regional biomedical system, patients frequently had to travel great distances to reach the clinic and then purchase their own medicines from a pharmacy, sometimes in a distant town and which served poorer people poorly. The clinic became the option of last resort and was referred to as the “morgue” (Stumo 2015). Is this not a form of bioculturalism?

Therefore, in taking a political economic perspective, our previously imagined traditional Quechua population, isolated on top of the Andes and adapting to
a harsh environment, morphed into a situation of blatant inequalities, wherein national and local laws were unjustly administrated, national institutions designed to serve the indigenous poor were poorly managed, and market prices for their products were manipulated by buyers. Although Quechua labor and knowledge formed the backbone of cropping and herding, surplus production was systematically extracted from them, and educators, physicians, and lowland agronomists degraded their knowledge system.

**Complementary perspectives**

I realized that this opened up a whole new set of questions and corrected previous perceptions of how things worked. Rather than replacing the adaptive perspective, our analysis built upon its findings, albeit in a somewhat altered manner. Of course, the Quechua of Nuñoa had to adjust to the environmental stressors that intruded on their lives on a daily basis, but they also had to negotiate social stressors that were just as severe. In striving for a synthesis of this information, we concluded that both perspectives offered valuable insights. People were adjusting as best they could to multiple sets of environmental and social stressors, but their adaptive fabric was wearing thin and the elaborate sociocultural options that had made the Andean world such a rich integrated land had long since been dismantled. Put crudely, the Quechua people were being used as beasts of burden in that they could better endure the conditions under which they had to work than the lowlanders, and from their heritage they knew how to make things grow and their herds reproduce in a land that lowland agronomists regarded as marginal. Given the oncoming trends of modernity and a growing awareness of social injustice, this long-standing tension inevitably was becoming apparent to everyone, poor and rich alike. The question that emerged was when and how would the agency of the Quechua, which was being profoundly suppressed, be activated (McClintock 1984; Starn 1991)?

**War and violence**

By the early 1980s, when we returned to study illness, these tensions were growing. The state-managed cooperatives were failing, inflation was rampant, and teachers – many with a social justice agenda – were now running the town government. They replaced members of the large land-owning class that had run the town since its inception as a municipality. Open disrespect was increasing, shown to the priests and other authority figures. Most significantly, the Maoist-inspired Shining Path (*Sendero Luminoso*) Revolution had become active in the central Peruvian Andes and was spreading southward onto the altiplano. By 1986, we were advised by local friends that it was best to leave, for both our own and their sakes. Shortly thereafter, occasional gunfire broke out in the streets and the systematic burning of ranch houses and killing or rustling of herds intensified. Our last student, Susan Luerssen, who did an excellent economic study of the area (Luerssen 1994), was the last to leave in 1987.
Law and order rapidly disintegrated from that point on as the town authorities and police fled, the town hall and police station were blown up, and cells of the Shining Path from outside the district took control. Nuñoa became a “red zone.” By and large, residents of Nuñoa were not directly involved in the terrorism but undoubtedly a number were sympathizers. A silence of fear spread across the landscape. People were afraid to converse with anyone except their most trusted relatives and friends for fear of being seen as government sympathizers. Gruesome public executions with command attendances took place in the plaza and authorities of all sorts, even the head of the women’s club, were considered suspect and were hunted down. Many were pulled off buses to be shot when trying to escape town. Access to outside markets was virtually severed and agricultural production suffered. These conditions persisted for five years until the army regained control of the town and turned it into a military zone.

During this period, all foreigners in the Peruvian Andes, anthropologists included, were considered to be suspect and left. It was not until 1996 that my wife and I returned to attend the marriage of a compadre who assured us all had returned to normal. Clearly it had not, and only a few of our closest friends would speak of those years. A sense of mistrust, especially among townspeople, pervaded interpersonal interactions and this was reflected in diminished reciprocity, a key component of Andean social relations and critical in agricultural production (Mayer 1974). In 2004 and 2005, Tom Leatherman, my wife, and I returned to assess the impact that the period of terror had had on the people of Nuñoa. Since many had fled, migrating to highland and coastal cities in southern Peru, we traveled from place to place looking for informants to interview, and then followed up with interviews in Nuñoa (Leatherman and Thomas 2008). What we learned through the words of our informants brought out yet another face of bioculturalism, that of war and rebellion, killings, personal tragedy, and persistent fear. Here, political ideology directly intruded on people’s lives throughout the country regardless of class or race, and the biological consequences of this were dramatic and multifaceted.

While we have not systematically studied these postrevolution consequences, it is clear that dramatic changes have occurred. In a perverse way the revolution, however horrible and mismanaged, drew people’s attention to social injustice and helped change national policy and assistance to the Peruvian Andean region. This had been a long time in coming. In the past, indigenous rebellions based on persistent injustices in Nuñoa were savagely put down in the 1920s and 1930s. Thereafter, for decades all was “silenced” and the Quechua absorbed the conditions imposed upon them as best they could. However, this resentment persisted, went underground and festered as parents saw their children growing up to assume their exploited roles in a system of disrespect, one that had dismantled their knowledge base and self-esteem and was compromising their very well-being. And then the opportunity to confront the system came: this is agency. Is this embodiment also not a form of bioculturalism?
A modernity of sorts

In the aftermath of the revolution, the national government realized that it had long left the altiplano “on ice” by providing minimal services. In response, a considerable increase in aid was given to highland municipalities, and national agencies and NGOs instituted improved public health and nutritional supplementation programs. Likewise, laws were passed and enforced whereby local mining companies were obligated to provide a portion of profits to nearby towns.

Today, a new town hall (the old one was blown up during the revolution) looks out over a plaza garden filled with flowers where officials were once hung from the trees. More importantly, Quechua family names dominate the government offices. Campesinos still ride to town on horses, but increasingly use motorcycles and some drive in pick-up trucks to their second homes. A new police station lies near the entrance of town, across the paved street from a new soccer stadium with real turf. A new covered market on Sundays is full of foods and commercial items (e.g., TVs, DVDs, polyester clothing, and kitchen utensils from China). New fundamentalist churches provide an alternative to the Catholic Church, and a slaughterhouse sends butchered carcasses out to nearby cities. Quality cheeses are also exported to Cuzco to make pizzas. The medical clinic has become a hospital with satellite clinics spread across the countryside. More and more people use trucks instead of llamas as cargo carriers. Finally, after passing under a large concrete arch upon entering town, one is greeted by a 20-foot statue of an alpaca flanked by two 10-foot ones.

Given such a description, all would seem to be well and, indeed, substantial improvements in people's lives have been made. Nevertheless, with a focus on building new structures, which can be seen as facades of modernity, it has been difficult to address the chronic poverty that still exists around the margins of town and into the countryside. Modernization brings with it a host of changes that inevitably dislocate ways of doing things, sometimes for the better but for some making the poor even more vulnerable. And so it is in this process of change that a new set of biocultural problems has arisen.

The reality is that such change has been occurring over the past three decades. Growing consumption norms compete with access to basic needs and reduced dietary diversity for the poor (Leonard 1989). This also contributes to opportunistic behavior that defies group regulations and cooperative activities. Vulnerable people once protected by the group are left out. In the countryside, agro-pastoralism remains important but young people would prefer to work in the cities or the mines. They talk of becoming teachers, nurses, engineers or lawyers but not campesinos, not pastores. This means that finding agricultural labor is increasingly more difficult and elderly herders either have to endure this hard work or give up farming and move to town. There, many are left without adequate support since their children and relatives have migrated elsewhere. The young men who seek work in the mines have heard of the real respiratory risks and injury from accidents – seven years of labor in the mines is considered to represent the longest possible tenure – but rationalize this because the work will
enable them to afford a motorcycle and thus improve their prospects of finding a wife.

Furthermore, reciprocity has largely been replaced by wage labor, food storage in rural households is minimal, and increased dependency on capital intensive technology favors the relatively wealthy families. The inevitable inequalities created lead to new forms of structural violence that need to be comprehended in a new biocultural context. The information generated can be directly applied and used to inform town authorities and agency officials of both the seriousness of the problems and how they might be addressed. Since such problems exist in communities across the altiplano, and more broadly the Andes, such work is essential in contributing to the aforementioned need of better understanding how human groups adjust to rapidly changing conditions.

In short, this ongoing case study has demonstrated how a biocultural approach can be broadened by integrating adaptive and political economic perspectives in a complementary manner. Furthermore, the incorporation of humanistic perspectives and ethnographic techniques made our depiction of Nuñoa considerably richer. Also, this case study provides a caution about working within only one theoretical framework if the goal is to realistically portray a group’s life conditions.

Discussion

Biocultural research areas

Unfortunately, many anthropologists still seem stuck in a period of specialization, segmentation, and separation – a Balkanization, so to speak – of the subdisciplines, that is challenged by broader trends taking place in the humanities and sciences. These trends increasingly emphasize interdisciplinary and transdisciplinary inquiry. Therefore, I would like to imagine bioculturalism’s potential in addressing a wide range of contemporary problems in a manner that draws on the complementary strengths of our holistic perspective. Below are some examples of high relevance and practical utility that need to be addressed.

While it is tempting to envision and construct problems around biology and culture as discrete variables – a reinforced dichotomy – in fact, they are inextricably part of one interacting matrix. And while at times their separation is warranted to achieve analytical clarity, recognition of this ongoing linkage opens up a host of important problems. Take, for instance, something as mundane as stance, the holding erect of the entire biological system: bones, muscles, and organs. How one stands can reflect a physical history of growth, diet, and injury, as well as ethnic identification, self-esteem, socioeconomic status, working conditions, and types of chronic exploitation. We might only want to know if poor nutrition leads to “stunting” and/or “wasting” from measures of stature/weight and the consequences of this, but the problem is so much richer than this if one really wants to understand the human condition of a particular individual or
group. And such holistic inquiry can lead to an area of study such as the anthro-
pology of the body as a truly biocultural endeavor. It seems that this is what
anthropology should be doing more of – going beyond the standard analyses by
adding a contextual richness to the issues being studied.

Below are a few examples of other “anthropologies” of the human condition
worthy of examination from this perspective.

- **Exploitation** and **inequality**: the biology of poverty, slavery, sex trade, sur-
plus extraction, household abuse, child labor, and the biology of hope and
despair.

- **War and violence**: refugee camps, child soldiers, narcotics trafficking, inter-
tribal violence, and the geography of pain.

- **Adverse environmental conditions**: climate change, pollution, ultraviolet
radiation, gold mining in the Amazon, drought, crop failure, and environmental
refugees.

- **Adverse social conditions**: social and psychosocial stress, structural vio-
lence, household disintegration, sexism, classism, and racism.

- **Health risks**: pandemics, syndemics, epidemics, chronic diseases, infant mor-
tality, under- and overnutrition, prostitution, bioethics.

- **Body modification**: tattoos and body piercing, cosmetic surgery, organ trans-
plants, sex changes, tight lacing, and binding.

- **Working and recreational conditions**: long-term computer use, marathon
running, gymnastics, brick making, sugarcane cutting, coal mining, and toxic
waste exposure.

- **Demographic shifts**: household/group consequences of mortality and mor-
bidity, fertility, changing reproduction rates, forced migration, crowding, and
depopulation.

### Conclusion

George Armelagos, to whom this volume is dedicated, made many contribu-
tions to the biocultural study of health and nutrition. He championed a bio-
cultural approach in medical and nutritional anthropology, often focusing on
historical and evolutionary changes in diets and nutrition as well as epidemi-
logic transitions (Armelagos et al. 1992, 2005). He joined the collective efforts of
UMass students and faculty to advance biocultural theory by merging perspec-
tives from anthropological political economy and human ecology and adaptabil-
ity. He was – and remains – exemplary as a colleague and friend.

The reality of our times of rapid change is that people adapt, adjust, accom-
modate, acclimatize, cope and resist – or not – in largely non-genetic ways.
Furthermore, the study of plasticity is undergoing a renaissance in both biol-
ogy and psychology as exposure in one’s life time – especially during the growth
and development period – is increasingly recognized as having a great influence on epigenetics, or genetic expression (Hicks and Leonard 2014; Non and Thayer 2015). The intent here is not to trivialize inquiry into genetic adaptation and evolution in humans, or deny that plasticity has a genetic component, but to emphasize that non-genetic routes of adjustment that have garnered considerably less attention in biological anthropology are the most relevant to interpreting and solving current conditions. Even in the high Andes, at the upper limits of human habitation where we expected to find ample examples of genetic adaptation, developmental acclimatization or human plasticity seems to explain much of the variation in adjusting to this harsh environment (Frisancho et al. 1995; Frisancho, in press).

Towards a biocultural theory
At times, anthropological theory leaps ahead by uncovering something so obvious to the general public – and its practitioners – that its existence has become normalized and hence relatively invisible. Mostly, however, our discipline unabashedly adopts theory from other disciplines. Whatever the source, feminist theory, queer theory, and critical linguistic theories are examples of addressing a set of power relations that existed all around us for generations, which most took for granted or begrudgingly accepted. In uncovering how and why these trends operated, their inquiry opened a set of new perspectives on how gender relations and words structured how we behave and treat each other and invaded our biology.

It has been argued that an expansion of problem areas addressed by a biocultural approach can better address these concerns, and that the incorporation of an array of theoretical perspectives that complement one another will amplify our views of reality. It is unavoidable that culture and biology dance together, sometimes in a graceful and seamless tango and at other times a clutchy foxtrot, stepping on each other’s toes. It would seem that this generation of advanced undergraduate and graduate students are the ones to grasp and take forward the realization of how biology, culture, and the environment are embedded within one another, and that new approaches and theories of non-genetic biological change await their discovery. Better understanding of the interactive limits of biological plasticity and sociocultural formations might be one place to start. More pragmatically, students capable of working with other professionals in academics or beyond, because of their breadth of scope, flexibility in utilizing a variety of methods, and ability to articulate a holistic vision of the problem, should be in a sought-after position.

Transformations are encompassing us. You can – and probably should – be part of anticipating their consequences. Choose a robust problem area, select a critical but manageable research area within it, and build out from there. Best wishes.
References


**Notes**

1 Sections above have been modified from earlier pieces (Thomas 1998, 2006) and are similar to views expressed by Laura Nader (2001) in her “Distinguished Lecture” to the American Anthropological Association in 2000.

**Endnotes**

CHAPTER 3
Local nutrition in global contexts: critical biocultural perspectives on the nutrition transition in Mexico

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Introduction

A Wenner-Gren conference held in 1992, and later published in an edited volume Building a New Biocultural Synthesis: Political-Economic Perspectives on Human Biology (Goodman and Leatherman 1998a), was a key, integrative moment in developing a critical biocultural anthropology. Biocultural anthropology is a holistic and necessarily broad approach to the study of human biology within social and cultural contexts. A critical biocultural approach furthers these considerations by paying particular attention to how historical and political economic forces help shape biological variation as well as recognizing the social contexts that shape the research process itself. In this chapter, we first discuss the emergence of a critical biocultural medical anthropology and some of the different research questions and projects that have employed this approach to explore topics ranging from nutrition and growth to stress and epigenetic changes. We then provide a case study in food and nutrition (Farb and Armelagos 1980) and explore the political economic forces linked to epidemiologic and nutrition transitions (Armelagos et al. 2005).

Background

Emergence of a critical biocultural approach

As medical anthropology was growing as a subdiscipline in the 1970s, an ecological model emerged that framed infectious disease as resulting from the interaction of host, pathogen, and environment (Armelagos et al. 1992). This model was used to examine specific human–environment interactions involving
disease or other biological indicators of stress and served as a framework for examining the evolution of disease and disease processes in epidemiologic transitions (Armelagos et al. 2005). Epidemiologic transitions refer to changing patterns of disease in response to changing population size and dynamics, social relations and technologies (e.g., medical advances and public health interventions), such as the relative reduction in infectious disease load and increase in chronic non-infectious diseases in many populations of the global north. The promise of such an integrative model led many to conclude that medical anthropology had achieved a theoretically coherent integration of biological, ecological, and cultural domains. Yet, because they framed human environments as closed, homeostatic systems, and hence were limited in analyses of cultural processes, these models were increasingly seen as constraining to studies of nutrition and disease.

At the same time that ecological models and the concept of adaptation were being reevaluated from within cultural anthropology, critiques and reformulations of these issues were emerging from within evolutionary biology (Levins and Lewontin 1985) and biological anthropology (Armelagos et al. 1992; Goodman et al. 1988; Leatherman 1996; Thomas 1998). In particular, there were significant critiques of the dominant school of evolutionary thought based on the notion of natural selection as an optimizing agent, known as the “adaptationist program” (Levins and Lewontin 1985; also Leatherman 1996; Singer 1989). Specifically, scholars questioned its tendency to see all or most phenotypic features as adaptations, its circular reasoning (e.g., identify a trait, search for its function and then conclude it arose to meet that function through selection and adaptation), and a failure to specify appropriate units and contexts of adaptive response (e.g., to distinguish the current utility of a trait from the reason for its origin). An overriding critique of the adaptationist program was that it viewed people as passively responding to autonomous, external environmental forces rather than recognizing their role in constructing those environments, which resulted in a conceptual alienation of the human organism from its environment (Leatherman and Goodman 2005a; Lewontin 1995; Smith and Thomas 1998). As a result, it also failed to evaluate how the costs of adaptive responses might generate new problems and constraints for human biology.

In the 1960s and early 1970s, human biologists were largely concerned with understanding adaptations to physical and biotic extremes. The initial assumption was that under stable, extreme conditions, human genetic adaptations would emerge and could be identified by investigators. However, two decades of research showed that human populations exhibited many more ontogenetic or developmental responses than genetic responses to environmental stressors (Frisancho 1993; Smith 1993). Thus, biological plasticity was recognized as the key to understanding the human adaptive process. It also became clear that groups living in challenging physical environments were often also living in social environments with limited access to means of production, economic opportunities, political power, health care, and education. The resulting stressors
with origins in relations of power, such as food insecurity and malnutrition, invariably had a greater impact on biology and health than did physical stressors such as high altitude and cold temperatures (e.g., Greksa 1986; Leonard 1989; Thomas 1998).

Biocultural research in the 1980s and 1990s increasingly became oriented toward documenting biological compromise or dysfunction in impoverished environments (as opposed to adaptations) and the biological impacts of social and economic change (Thomas 1998). Social environments took precedence over physical environments and measures of stressors expanded to include psychosocial stressors and their impact on health conditions such as hypertension and immune suppression (e.g., Blakey 1994; Dressler and Bindon 2000; Goodman et al. 1988; McDade 2002). Yet, while it became relatively common to associate biological variation with some aspect of socioeconomic variation, it was rare that the context or roots of the socioeconomic variation were addressed. Similarly, research on “modernizing” populations documented how devastating such changes can be on human biology and health, but provided little or no information about processes of modernization. The socioeconomic conditions, workloads, and environmental exposures that contribute to diminished health thus became seen as natural and even inevitable aspects of changing environments, rather than contingent on historical processes and social and economic relations (Leatherman and Thomas 2001). Similarly, biological responses that might allow for survival and the appearance of adequate functioning in a given environment were seen as successful adaptations without exploring the full range of costs and implications on other adaptive domains, described by Pelto and Pelto as “quitting early” (Pelto and Pelto 1989:13). These shortcomings were clearly demonstrated in the “small but healthy” debate (Pelto and Pelto 1989).

Emerging interests in the biological dimensions of poverty and inequality, and the need to frame these analyses in rich social and economic contexts, demanded new models and approaches with biological and biocultural anthropology. Specifically, these interests drew biocultural researchers to integrate perspectives from anthropological political economy with those from ecology and adaptability. Goodman and Leatherman (1998b) suggested a number of thematic shifts to biocultural approaches that came to characterize a more “critical biocultural” orientation, including an expanded view of environmental and historical contexts and contingencies, attention to the social relations that structure (and are structured by) human–environment interactions, and a notion of constrained human agency, what Levins and Lewontin (1985:246) called “conditional rationality,” in coping with social and environmental problems (see Goodman and Leatherman 1998b; Leatherman and Goodman 2011).

Critical biocultural approaches share much with the structural violence perspective (Farmer 2004) commonly used in anthropology and studies of global health to consider the systemic ways in which societal structures harm or disadvantage some individuals (Rylko-Bauer et al. 2009). There is also shared ground with the eco-social approach in public health, which “seeks to embrace a social
production of disease perspective while aiming to bring in comparably rich biological and ecological analysis” to answer “who and what drives current and changing patterns of social inequalities in health” (Krieger 2001:672). All three attempt to integrate history, political economy, and biology in social and environmental contexts that are “geographically broad” and “historically deep” (Farmer 2004:274). These perspectives also focus on the health inequities and limitations to human agency that result from social and structural inequalities. They specifically focus on how the many forms of social inequalities literally become embodied in biology and health; how lived realities “get under the skin” along multiple pathways of embodiment. In short, the goal of a critical biocultural approach is to link structures of inequality, constrained agency, and pathways to embodiment within historically and ethnographically grounded contexts, lived experience, and local biologies.

Trends in biocultural analyses
In recent decades, biocultural anthropologists have increasingly focused on the health and nutritional consequences of social and ecological vulnerabilities. Research projects and approaches have taken many forms and foci, including social inequalities and health, populations in transition, biopsychological stress and response, and the biological consequences of race and racism (Leatherman and Goodman 2011). These are illustrative of studies that go beyond standard measures of socioeconomic status (SES) to study vulnerabilities along multiple axes including race, gender, income, and occupation. It is now well accepted that social inequalities underlie health disparities across different contexts. Biocultural anthropologists have contributed to these observations through grounded research on the interactions among social inequalities, livelihoods, food security, nutrition, and illness (Leatherman and Jernigan 2015). Such work includes the reproduction of poverty and poor health in Peru (Leatherman 2005) and the interactions among economic vulnerability, food security, diets and nutrition in the United States, Costa Rica, and southern Africa (e.g., Crooks 1998; Himmelgreen and Romero-Daza 2009; Panter-Brick et al. 2008a). These examinations move beyond simple correlations of SES and nutrition and health outcomes in their efforts to track pathways through which inequalities and health are mutually constitutive and reinforcing.

A deeper appreciation of history makes clear that humans are invariably and constantly in transition – from prehistoric shifts in foraging to larger scale food production, to conquest and colonization, and integration into capitalist economies. Armelagos and colleagues (2005) frame this history in terms of epidemiologic transitions in disease patterns resulting from evolutionary, historical, and political economic processes associated with social change, and apply these transitions across time and space. Goodman and Armelagos (1985), for example, argued that political hierarchies and resource extraction from the peripheries to the center of precapitalist social formations in prehistory played
a key role in declining health in rural areas. Using historic records and modern epidemiological health surveys, Santos (1998) has researched the health effects of colonization on indigenous populations in Brazil through a series of historical events from initial contacts, to various economic booms and busts (e.g., rubber and timber), to more recent migrations of settlers into the Amazon.

Transitions to market-based economies can have negative, positive, and uneven effects on nutrition and health (Dewey 1989; Kennedy 1994; Leatherman 1994; Pelto and Pelto 1983). This unevenness in the effects of markets on economic success, health, and well-being provides the rationale of a recent and extensive multidisciplinary biocultural investigation in medical anthropology: the Tsimane Amazonian Panel Study (TAPS) (Leonard and Godoy 2008). TAPS began operating in 2002, and continues to collect longitudinal cultural and biological data on the Tsimane population living in 13 villages along the Maniquí River in Bolivia. The project was active during a time when road construction and shifts in economic activities led to increased market participation, changing lifestyles, and altered health status among the population (Godoy et al. 2009; Reyes-García et al. 2008, 2009). When shifts to markets occur in contexts of tourism, as in the Yucatán case study presented below, complex transformations in social relations, values, and status as well as economy, diet, and nutrition ensue.

Since the early 1980s, biocultural anthropologists have focused on psychosocial stress as a pathway to link lived experiences to biology (Goodman et al. 1988). Novel methods and techniques for measuring stress responses in the field, such as blood pressure, salivary cortisol, and markers of inflammation and immune function like C-reactive protein (Ike and James 2007), provide new ways to demonstrate the embodiment of lived experience of inequalities in social and cultural contexts. Research includes a focus on stressful life events (McDade et al. 2013; Mulligan et al. 2012), discrimination (Thayer and Kuzawa 2015), social support (Hicks 2008), cultural consonance (Dressler 2005; Sweet 2008), status inconsistency (McDade 2002), lifestyle change (Tallman 2015), war-related trauma (Panter-Brick et al. 2008b; Rodney and Mulligan 2014), and food insecurity (Gowda et al. 2012; Hadley et al. 2008). The goal is to not only apply these methods in the field but to connect specific mechanisms to larger ideological and political systems.

Biological anthropologists have been at the forefront of questioning the naturalization of the idea of race (Blakey 1998). It is now widely accepted that race is not in our genes but rather, race becomes biological through discourses and practices (Gravlee 2009). Racism is both a powerful psychosocial stress and a structural inequality. In general, epidemiologists attempt to develop methods that work across a wide variety of contexts, but context is important to understand how actions are interpreted and embodied. Also, most measures of racism focus on interpersonal issues and miss connections to the historic and structural features of the political economy of racism (Harrison 1995). Recently, medical anthropologists working with critical biocultural perspectives have begun to
address some of the inadequacies in these approaches by exploring how the lived experience of race and racism might lead to health differences. For example, Dressler and Bindon (2000) have examined the lives of African Americans in the southern United States in terms of cultural consonance or the ability of individuals to approximate in their own behavior the shared cultural models of their society. Similarly, Gravlee and co-workers (2005) begin with an ethnographic understanding of the meaning of skin color in Puerto Rico, and demonstrate how those local meanings of color and identity shape experiences of racism and blood pressure, mediated by SES incongruities (see Chapters 4 and 5).

To summarize, the importance of the examples cited above and many others is the way they make the social, cultural, and political economic relations of inequality central to the analyses of biology and well-being. These analyses strive to elucidate pathways and processes through which inequalities become embodied. In the following section, we present a case study that is part of the recent nutrition transition. The nutrition transition to which we refer is a trend observed in countries experiencing recent and ongoing development leading to significant changes in food availability, access, and cost (Popkin 2001; Popkin and Gordon-Larson 2004). The most common pattern is a shift away from more locally grown foods in favor of imported and processed foods which can often be purchased in higher quantities at less cost than local produce. In many cases, this transition has led initially to improved food security and nutritional status and is then followed by emerging overnutrition and increasing rates of overweight, obesity, and related metabolic illnesses. In this case study, we consider how international political economic processes led to patterns of change in food production, diet, and nutrition of indigenous groups in the contexts of the Yucatán of Mexico.

Case study: the “coca-colonization” of diet in the Yucatán

Our case study centers on changing patterns of agriculture, diet, and nutrition among Mayan children and adults of the Yucatán Peninsula in southern Mexico (see Figure 3.1). These rapid changes are an example of a nutritional transition, in this case linked to international tourism and increasing dietary delocalization. Individuals, households, and communities differentially experience and respond to tourism-led development, and differently reflect changing food systems and values in their diets and nutrition.

Along with many other Native American groups, the Maya have experienced a recent rise in chronic diseases such as diabetes and obesity. Nearly a quarter century ago, Federico Dickinson (1993) reported that in the commercialized center of Merida, the capital of Yucatán, 86% of women were overweight and about 50% were obese. This evidence of “overnutrition” or surplus of calorie consumption leading to overweight and obesity in the Yucatec Maya
is an apparent contradiction as the Maya have frequently been depicted as economically marginal, impoverished, and undernourished. Indeed, studies of Maya child growth, a key indicator of community-level nutrition, illustrated severe stunting and little change in growth between the 1930s and the early 1980s (Daltabuit 1988; Leatherman et al. 2010). However, by the mid to late 1990s, increases in both heights and weights were evident (Gurri et al. 2001; Leatherman et al. 2010). Despite these increases in growth, we found persistent indications of poor diet quality (Leatherman and Goodman 2005b). Now the
Maya are subject to what Dickinson has termed the “double-edged sword of malnutrition”: childhood undernutrition and adult obesity, also known as the “dual burden” (Doak et al. 2005). How did the dual burden of undernutrition coupled with overnutrition emerge in the Yucatán?

One of the more notable aspects of tourism development in the Yucatán is the commoditization of food systems, that is, the increased distribution and consumption of commercialized foods, and especially “junk foods,” which are calorie rich but deficient in micronutrients. Thus, a proximate answer to the above question is a trend toward the high fat and sugar consumption typical of western diets, i.e., a “westernization” of local diets. On the other hand, glossing processes of dietary change as westernization misses the changing local and regional dynamics of food systems and diets that are the result of global processes, including tourism-based social and economic change.

A “westernization” of Yucatecan diet is one form of a broader process of “dietary delocalization,” a process wherein local peoples consume foods produced out of the region (Pelto and Pelto 1983). Since ancient times, trade, internal colonization, and migration have promoted the exchange of foods across regions. After 1492, such exchanges became global, and more recently dietary delocalization has been increasingly linked to the commoditization and commercialization of food systems and diets (Dewey 1989; Pelto and Pelto 1983). Shifts from locally produced to market and commercialized foods have been associated with greater dietary diversity and improved levels of nutrition in industrialized nations (Pelto and Pelto 1983). However, the increased commoditization of foodstuffs typically coincides with increasing market prices that stress the budgets of the poor majority and frequently lead to reduced dietary diversity.

An assessment of changing food systems, nutrition, and health in the context of tourism-based economic and social transformations among the Yucatec Maya begins with the identification of several points of contradiction. Child growth has improved somewhat, but nutritional deficiencies persist, and at the same time, rates of adult obesity and diabetes are skyrocketing. Commoditization of food systems can lead to an overall increase in food availability, diversity, and consumption, but also heighten inequalities in access and detrimentally affect nutrition and health. From our perspective, these contradictions reflect the manner in which social, cultural, and health impacts of tourism-led development are distributed unevenly and experienced unequally among Mayan communities, families, and individuals. Much of this variation is influenced by the manner and degree to which communities, households, and individuals articulate with local production systems and with the tourism-based economy.

**Global contexts and local transformations of dietary change**

Throughout Latin America and much of the developing world, nations are turning to tourism as an efficient means of generating economic development and foreign capital. Mexico, and especially its Caribbean coast, is a major
destination for North American and European tourists. In the last four decades, the Yucatán Peninsula has been transformed from one of the Mexico’s most marginal regions, with few areas with paved roads and electrification, to a hotspot of global tourism. From the 1970s to the 1990s, Cancun on the Yucatán Peninsula (see Figure 3.1), the center of this development, grew from a fishing village of just over 400 inhabitants to the state of Quintana Roo most important city with a population of over 400,000 people (Daltabuit and Leatherman 1998). This development has been a significant economic success for the Mexican government, a few Mexican capitalists, and many foreign investors. However, such rapid and totalizing development does not come without cultural and economic costs (Daltabuit and Leatherman 1998; Pi-Sunyer and Thomas 1997). As environmental resources, labor, and food become increasingly commoditized and symbols of prestige become increasingly Western, Mayan culture, environments, and lives are inevitably changed.

Our concern here is with one form of change in particular – the commoditization of food systems and its link to dietary change, nutrition, and health. Here, we contrast food systems, diet, and nutrition in Mayan communities that differ in subsistence base and articulation with the tourist industry. The communities of Akumal and the recently built Ciudad Chemuyil are service villages to a popular resort on the Caribbean coast; that is to say that the villages were established largely as residences for those employed by the resort and other businesses associated with tourism. The local economy is based on wage work or commerce. Because these communities lack agricultural plots and have little land for home gardens, inhabitants are totally dependent on food from local markets.

Coba, in contrast, has had direct local involvement in the tourist economy through archaeotourism, focused on nearby archaeological sites, but maintains agricultural production and home gardens. Finally, Yalcoba is an inland farming community with little direct exposure to tourists, but substantial outmigration of men to Cancun on a weekly basis to work primarily in construction.

**Dietary delocalization and food commoditization**

While communities in the Yucatán are increasingly consuming foods from further and further away, the nature of changing food systems is markedly different for the coastal (Akumal and Ciudad Chemuyil) versus inland (Coba and Yalcoba) communities. In the coastal communities, a fully commercialized system is now in place. Foods are purchased from local stores and traveling vendors, often specializing in food stuffs from specific growing regions. In the two inland communities, products such as corn, beans, and squash from the milpa (agricultural fields) are harvested and available for consumption when in season. These are regularly supplemented by market foods and diets reflect these shifts. By the mid-1980s in Yalcoba, Daltabuit (1988) had already noted a shift from locally produced foods such as honey, tubers, posoles (stews), and wild meat toward commercial foodstuffs such as rice and pasta, sodas, and snacks.
This trend was further advanced in the 1990s as even maize and beans, two key staples, were increasingly purchased from government-subsidized stores or local tiendas (stores). Local tiendas also sell small quantities of produce (e.g., tomatoes, potatoes, cabbage, carrots, onions, garlic, and peppers) purchased from larger towns’ markets to be resold locally. While a greater variety of foods is available, prices are high. As one resident of Coba noted, “there are more foods available now, but no money to buy them” (Leatherman and Goodman 2005b:838). Some viewed this period as a time of steadily decreasing food availability, while others saw it as a time of growth in opportunity and consumption.

The most dramatic aspect of the commercialization of food systems in the region is the pervasive presence of Coca-Cola, Pepsi, other sugar-loaded drinks, and a variety of chips, cookies, candies, and other junk foods – locally called comidas chatarras. In the midst of the development of Cancun, Mexico had risen to become one of the world’s largest consumers of soft drinks, accounting for over 20% of Pepsi’s and 15% of Coke’s international sales (Jabbonsky 1993). Indeed, the Mexican market is so important that it has been the site of an ongoing “Cola War” between Coke and Pepsi – a fight over the “stomach share” of the Mexican people. Coke’s international company slogan is “an arms length from desire” – to make Coke available at every corner in every town or village in every part of Mexico (Pendergrast 2000). As Coke and Pepsi’s fight for greater stomach share intensifies, we can expect to see an even greater penetration of soda and snack foods in the diets of Mexicans and the Yucatec Maya.

**Diet and nutrition**

As shifts in foods systems are at the intersection of global and local economies, local diets and nutrition reflect actions and experience within these intersecting realities. We gathered information on household demography, economic activities, diet, and nutrition in a sample of 80 households from coastal and inland communities. A dietary survey (including food frequency and 24-hour recall instruments) provided information on the range of foods eaten, the source of foods, and their contribution to nutrient intakes (see Leatherman and Goodman 2005b for details on methods). We also estimated nutrient profiles in households from Yalcoba with steady employment in the tourist economy in or near Cancun, compared to those relying on their own subsistence production and irregular wage work to meet basic needs. This latter comparison is an effort to understand the dietary and nutritional consequences of differential involvement in local versus tourist economies.

Results are reported in greater detail elsewhere (Leatherman and Goodman 2005b), but overall findings are discussed here. The leading food categories in the diets of the communities we studied were tortillas, fats (oil and lard), sodas, snacks and sugar, beans, meat, and rice or pasta. Together, these foods comprised 68% and 78% of calories consumed in the coastal (Akumal and Ciudad Chemuyil) and inland (Coba and Yalcoba) farming communities, respectively.
Compared to inland communities, people in the coastal communities consume half the tortillas, but twice the fruits, between 1.5 and 4 times the meat, and three times the quantity of dairy and junk foods. The residents in Yalcoba who have steady employment in Cancun follow the coastal pattern. They consume just over half the tortillas, twice the meat, eggs, fruit, and dairy, and five times the bread eaten by their counterparts relying on farming and irregular wage work to meet their food needs. It appears that when it comes to diet in these research sites, you are where you work.

Together, sugar and junk food account on average for 16% of calories in the coastal communities, compared to 10.5% in Coba and 8% in Yalcoba. Because our dietary surveys recorded primarily foods eaten in the household, and most sodas and snacks are consumed away from home, these are likely to be underestimates. Local distributors of soft drinks in Coba and Yalcoba in 1996 and 1998 reported weekly sales reflecting an average per capita consumption of one cola per day and consumption is at least 50% greater in the coastal communities. For instance, in 1996, 75 school-aged children in Yalcoba reported average weekly intakes of 7.4 soft drinks (mostly Coke or Pepsi), 10.2 snack foods (e.g., chips or cookies), and 11.8 candies (e.g., lollipops). In an older work, Daltabuit (1988) found that during a morning school break in Yalcoba, it was typical for children to buy a soft drink and a snack, accounting for about 350 calories, or one-quarter of an elementary school child’s daily caloric intake. Chips and sweets are marketed in 1-peso packages – a price most people, and perhaps especially children, can afford.

We found that the diets in all of the communities showed potential deficiencies in a number of micronutrients, including vitamins A, B2, B12, and E, and especially the mineral zinc. The coastal communities exhibited a better micronutrient profile; only zinc was deficient in coastal diets. Coastal and inland households with steady employment also consumed more high-quality animal protein. Our analyses detected several potential deficiencies in Coba and Yalcoba: vitamin B2 or riboflavin, B12 (cobalamin) and vitamin E in Yalcoba, and vitamins A, B2, and B12 in Coba. In addition, Yalcoba households without steady incomes that were reliant on irregular wage work and marginal milpa (agricultural field) production experienced at least seasonal shortages in vitamins A and C, as well as deficiencies in many of the B vitamins and zinc. These vitamins are essential to immune health as well as growth and development and insufficient intake can lead to irregular and reduced growth. The potential micronutrient deficiencies described here can become more problematic in high maize diets and with increased consumption of soft drinks. Plant-based diets, high in fiber and phytates, are associated with increased requirements and low bioavailability of a number of micronutrients such as zinc, iron, calcium, and vitamin B12, all of which are necessary for hemoglobin production, bone health, growth, and brain development (Allen et al. 1992; Calloway et al. 1993). Thus, when the remaining “non-maize” calories come from sugar, soft drinks, and snack foods, micronutrient status inexorably worsens.
The dual burden of malnutrition

As noted earlier, Dickinson et al. (1993:315) have described a “double-edged sword” of malnutrition in the Yucatán, whereby undernourished and stunted children grow up to be obese adults. Subsequent research on the dual burden of malnutrition has identified a number of different scenarios in which the dual burden can exist within a single individual, a single household or community (Delisle 2008). Many scholars have argued that the dual burden may emerge as a result of a mismatch between environments and developmental programming (Hales and Barker 1992). Infants whose mothers experience marginal nutritional environments during their pregnancy or even before are born with a more “thrifty” metabolism, allowing them to quickly store fat. When populations undergo economic and nutritional transitions, like that which we are describing in the Yucatán, conditions are created for a significant mismatch that can increase the risk of obesity, diabetes, and cardiovascular disease for the population.

While we have not tested for the action of the thrifty phenotype as an underlying biosocial mechanism in the Yucatec Maya discussed here, our research does suggest that this dual burden is present in the Yucatán. Children in Yalcoba are growing taller but are still stunted compared to local and international growth standards (Leatherman and Goodman 2005b). This may reflect persistent micronutrient deficiencies since caloric intakes appear to be adequate. While obesity and diabetes have reached epidemic proportion in Mexican urban zones (Arroyo et al. 1999; Dickinson et al. 1993), conditions are not so extreme among rural communities. However, an analysis of adult weights from Yalcoba collected from clinic records (83 males and 214 females, most from the 1990s) found that about 40% of the men were overweight and 10% obese, and 64% of the women were overweight and 20% obese (Leatherman and Goodman 2005b). These levels fell short of those from urban centers in the Yucatán, but began to approach Mexico City estimates.

In summary, there is little doubt that Mayan diets and nutritional status are increasingly shaped by the intersection of tourism and allied global and local processes underlying a nutrition transition. It is not clear to what extent junk food consumption is associated with weight increases in this and other communities in the Yucatán. It certainly is an important part of the overall shift in food commoditization and toward diets adequate or excessive in calories but deficient in micronutrients like zinc. As more caloric intake is met through sodas and snack foods, this certainly does not improve nutrition and may prove to be particularly detrimental. The “Cola Wars” and consumption of comidas chatarras show no sign of slowing – and the emerging pattern of childhood undernutrition and adult overnutrition is a serious threat to well-being. Mexico is the leading per capita consumer of coke products (Case 2014) and has overtaken the United States as a global leader in obesity (at 32.8%; FAO 2013). Government actions and policies demonstrate that they do believe that increasing rates of obesity are linked to the consumption of soft drinks and other junk foods. In response to the
epidemic of obesity and diabetes, Mexico imposed a 1 peso (8 cent) tax on each liter of soft drinks and other sugary beverages in January 2014, and by March of the same year potential declines in sales of 7% were noted (Case 2014). The hope is that rates of obesity will fall in time.

Conclusion

The example outlined above demonstrates the process through which local diets are shaped by global political economic forces. The towns of the Yucatán have undergone a transition involving greater integration of local, regional, and global markets and food systems. While Coca-Cola has been consumed in the Yucatán since shortly after World War II, tourism-based economic development strategies and expanded transportation and electrification infrastructures have helped to make it a staple in Yucatecan diets. Interestingly, this case study speaks to the impacts of global tourism.

The changing food systems and diets are part of a larger pattern of dietary delocalization which has been a constant force in the Americas over the past 500 years. They are also a feature of a global nutrition transition measured more in decades but with rapid and dramatic effects on diet and health. Coke and Pepsi in the Yucatán serve as iconic symbols of global exchanges of goods and tastes. These food items less directly affect the diets of local residents and instead represent larger processes of economic development and nutrition transitions. In the Yucatán, coke is not replacing other foods so much as it reflects the commoditization of food systems and diets and stands for the increased consumption of high-calorie, low-nutrient foods that become part of a new set of tastes and practices. What was once a symbol of the West, of wealth, of whiteness, and of moments of respite amidst a long day of work in a hot and humid milpa, has become just part of everyday life.

Finally, this case study presents a more nuanced examination of local-level changes and impacts that make up broader epidemiologic and nutrition transitions. Individuals within human societies and cultures do not experience change equally but because of past experience and access to power and resources are more and less able to take advantage of opportunities and cope with potentially negative impacts. As Armelagos would have predicted, those with greater access to power and resources and with more economic and cultural capital have better diets and nutritional status. An increase in the diversity of foods is generally associated with better dietary diversity and better nutritional status. But one must be able to afford diversity, and for those who cannot, diets based on market access can reduce dietary diversity and impair nutritional status. Complicating matters, acquired tastes and habits for processed sweet, salty, and fatty foods, clearly evident in the Yucatán, turn dietary choices from micronutrient-dense to calorie-dense foods. The contingencies of past experience and present realities will continue to shape the nutrition and health transitions in these and other
groups. The goals of a critical biocultural approach – linking structures of inequality, constrained agency, and pathways to embodiment within ethnographically grounded local contexts, lived experience, and local biologies – are well suited to mapping these transitions into the future.

References


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**Notes**

1 For a longer analysis see Leatherman and Goodman (2011) and Goodman and Leatherman (1998a).
PART II
Biocultural approaches to identity
CHAPTER 4

Disease and dying while black: how racism, not race, gets under the skin

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Introduction

In the middle of the twentieth century and going back at least to the early 1600s, race was unquestionably thought to be real: it was deep, primordial, and biological (Smedley 1999). Racial differences and hierarchies of ability were conceptualized as natural facts, created by God or, later on, as molded by evolution. Once scientists became involved, in both academic and popular discussions, the preevolutionary idea of race became synonymous with human biological variation. Race, then and now, was used to explain deep differences in many key aspects of life, from educational attainment and intelligence, violence and crime, to wealth and health. This racial worldview took hold in the United States and Europe and spread to other countries throughout the world and was comforting to whites and those in power. Differences in wealth and health were not seen as due to the histories and current realities of racism, prejudice or unequal treatment but instead attributable to deep-seated biological differences.

The Civil Rights movement of the 1960s made particularly clear that something else might also be at work: whites and individuals of color inhabited different worlds and lived different and unequal lives. From segregation laws to subordinate schools and hospitals, individuals of color occupied inferior positions. While slavery had been abolished for well over a century, and Jim Crow laws had slowly been deemed unconstitutional, racial thinking and worldviews and institutional racism persisted and persist today (Smedley 1999). Laws change slowly; entrenched ideologies change even more slowly (Mills 1997).

Coming of age in the 1960s, I knew from even my limited experience that an ideology of deep and inherent differences amongst the races was everywhere. Races were separately educated and lived different and unequal lives. Some scientists and politicians spoke openly about the need for racial segregation and protection of the purity of the white race. Miscegenation laws were still on the books in some states – the last was overturned in 1967 – and marital laws,
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relating to interracial marriage, and voter rights legislation were being actively debated. Fed by a century of race-based science, everyday conversations among whites in the United States often took for granted the dominant worldview, which firmly embraced the relative inferiority of non-white races. These discussions may have struck a personal chord with me because they echoed what I had come to understand about the legacy of Nazi “science” and racial propaganda against the Jews, which intensified in the 1930s and drove the genocide of the Holocaust in the 1940s. These ideologies held Jewish inferiority at their core, and maintained the goal of rationalizing and generating scientific proof of this inferiority (Steinweis 2006). Moreover, I knew from witnessing them firsthand that living conditions and economic and educational opportunities in the United States varied greatly, and that much of the variation followed racial lines. I understood that this patterned variability must contribute to and widen differences in life outcomes between the races, such as in socioeconomic status, educational attainment, and health.

In a sense, the argument about the cause of racial differences in health, the topic of this chapter, is a version of the “nature versus nurture” argument or, in human terms, culture versus genetics. The nature side of the argument viewed racial differences as being attributable to genetic variation, while the nurture side viewed these differences as primarily due to the effects of environmental conditions, such as poor schools, unsafe neighborhoods, and the like. But these viewpoints are also different in a very significant way: the nature side, purporting that race is natural and synonymous with human genetic variation, is a foundational scientific error. Race is not the same as human genetic variation. Part of this chapter explores and exposes that error.

Importantly, it is not that the answers to what makes us different are due to either genetics or culture (and nurture). Rather, the study of race and health provides an example of the importance of thinking carefully about the ways in which human biology is genetic as well as cultural.

My personal epiphany about race came in 1973. It was in an undergraduate class taught by George Armelagos, to whom this volume is dedicated. Professor Armelagos explained that the idea of race as an explanation and synonym for human biological variation was once universally accepted in anthropology and that it had spread to other sciences and practices such as medicine and public health in the nineteenth and early twentieth centuries. But it proved to be a false theory. It was not so much that nurture was more important than nature; rather, as noted above, people had misunderstood the very nature of human genetic variation. Specifically, he explained that human biological variation is continuous, complex, and ever changing. As a static and typological concept, race is inherently unable to explain the complex and changing structure of human biological variation. By extension, race – as a genetic construct – could neither describe nor explain variation in health. To begin to comprehend human biological variation required evolutionary theory and, most especially, the incorporation of a process: a mechanism of evolutionary change. Armelagos went on to say that race is still
real. But that race, rather than being genetically based, is a cultural ideal – with biological consequences. The ideology of race is necessary for racism.

Students’ responses ranged from disbelief to transformation. Many in the room could not accept Armelagos’ claim that races-as-genetics was an outmoded idea. Others misunderstood his message, thinking that he was denying the reality of biological variation itself. I was one of the transformed students. I grew up in a working-class family in a town composed mostly of second-generation immigrants from Italy and Ireland. I was aware that I was perceived as Jewish and therefore as different from my Irish and Italian friends in some fundamental way. Yet when I attended a more diverse university, something striking happened: I became “white.” I was no longer perceived as being very distinct from other students of European descent. It was then that I learned about the fluidity of race: the color line demarcating races changes to fit the circumstances.

I was aware of the power of race as a worldview in 1973. I felt like progress was being made in the legislation for racial equality and in science for understanding the myth of race as a biogenetic concept. For instance, Lewontin (1972), in a groundbreaking article on the apportionment of human variation, had shown that most genetic variation was greatest within small groups and that race or continental origins explained only a small percentage of human genetic variation. But what I totally failed to understand was the racial worldview’s ability to persist after it had been proven to be unscientific. If asked then if race would survive as a way to think about human biological variation nearly a half century later, I would have answered a definite “No!” I was naive to the durability of a culturally, politically, and economically powerful idea. In particular, I was unaware of the deep, foundational nature of what Charles Mills (1997) calls our racial contract, explaining that racism, rather than being unintentional, is a foundational belief and core “social contract” among whites.

In this chapter, I explore connections between race, racism, and health. The two causal pathways that are used to explain health inequalities by race are contrasted. The first is that of genetic differences in disease susceptibility among races. The second is variation in lived experiences of discrimination, including subtle and more overt forms of racism among socially ascribed races. I argue that a genetic explanation is both epistemologically and epidemiologically flawed: human genetic variation maps poorly onto racial groups and genetic differences rarely work in isolation. Conversely, the preponderance of evidence suggests that racial differences in health are rooted in conditions that expose persons and communities of color to a life of increased stress, pollution, and poor health care. These everyday discriminations and institutionalized racisms have profound consequences for health that are worthy of greater scientific study and amelioration.

A just society has an opportunity as well as an obligation to improve the health of individuals in poor communities and communities of color. But we will do so only after we understand the root causes of health inequalities. Put more directly, we need to know how lived experiences of stress, pollution exposure,
poor nutrition, and other proximate conditions cause health problems. But also how they are caused by racial thinking and institutions that promote and support this worldview and, by extension, differential opportunities relative to race.

**Background**

**“Race” and health inequalities: two causal pathways**

Today, still, there are deep disparities in nearly every indicator of health by race in the United States (Kochanek et al. 2013; Olshansky et al. 2012; Smedley et al. 2003). In particular, whites do best and African Americans do worst on nearly every indicator of health from infant mortality to the prevalence of chronic diseases to life expectancy (Kochanek et al. 2013; Sacher et al. 2005). These fundamental differences represent different levels of suffering and of loss of life. More potently, they represent fundamental inequalities at a variety of levels among racial groups.

Why is it that such differences in health and disease persist among races? For well over a century, occasional debates – or more accurately, arguments made in parallel – have continued in the scientific literature and among various publics. Two arguments predominate. In one argument, racial differences in health are traced back to the God-given or evolutionary development of racial differences in genetics. This “raciogenetics” perspective accepts that race is a viable substitute or shorthand for genetic variation between populations. These genetic differences are assumed to be causes of disease as well as other racial differences (Goodman 2000). In the more recent counterargument, race-based health inequalities are causally traced to variation in the “lived experience” of those assigned to different racial categories. Here, lived experience refers to the totality of everyday conditions that are embedded into the fabric of social, personal, and institutional relationships. Some of these experiences are subtle personal interactions that communicate values based on phenotypic appearances, and others are more deeply and profoundly personal experiences of racism (Krieger et al. 2011). It appears, according to Krieger and other social epidemiologists, that daily exposure to living in a racist society gets into the body (Krieger et al. 2011). In this way, too, racism is biocultural.

In the following, I first outline the raciogenetic argument and then the lived experience/racism argument. I provide examples and a critique of the compromise position, which argues that both racial biology and lived experiences are important. Lastly, I conclude with a call for greater clarity as to what we mean by race when it is used in public health research and practice.

**The raciogenetic perspective**

The worldview that racial differences in health are due to natural or inborn factors is an old one that extends back to at least the early nineteenth century.
Frederick Hoffman (1896), for example, published a wealth of data on racial
differences in health in the United States. His influential treatise suggested that
the increased morbidity and mortality of African Americans in northern US cities
resulted from the collective, inborn inabilities of African Americans to survive the
rigors of the contemporary world. Cynically, Hoffman predicted their eventual
demise.

At the time Hoffman was writing, the dominant scientific and biomedical view
made clear that races were differentially susceptible to disease because they were
different in mental and physical traits. In effect, each race was more likely to
suffer from particular diseases. African Americans, for example, were viewed as
less “fit” for civilization and thus more prone to so-called diseases of civilization
than were whites.

Also, once sickle cell anemia, an inherited form of anemia, was identified as
being prevalent in African Americans in the late nineteenth and early twenti-
eth centuries, it was assumed to be a race-specific disease (Tapper 1999; Wailoo
1997). When Europeans began to present with symptoms of sickle cell anemia
in the 1920s and 1930s, physicians thought that they must be part “nègro,” with
African ancestry. The possibility that sickle cell anemia had nothing to do with
race, but much to do with evolution and genetics, specifically that it represented
a genetic adaptation that confers increased resistance to malaria, was not consid-
ered until the middle of the twentieth century (Livingstone 1958).

In the twenty-first century, the idea that germs obey the color line, or
that diseases are specific to one race or the other, has largely been dismissed.
But the remnants of the idea persist in ideologies maintaining that races are
quasi-scientific units with separate disease susceptibilities. Indeed, raciogenetics
persists as a dominant explanation for variation not just in conditions such
as sickle cell anemia, which are caused by single allele variants, but also for
variation in complex metabolic conditions, such as diabetes and cardiovascular
disease (Goodman 2000; Kaufman et al. 2015; Sankar et al. 2004).

In 2005, the US Food and Drug Administration (FDA) approved a medication,
BiDil, for use in African Americans. This was presumably because it was effective
in combating congestive heart failure in this group for reasons that were thought
to be intrinsic to the group’s biological characteristics (Temple and Stockbridge
2007). However, such a move only makes sense economically, through targeting
of a drug to a particular consumer group. It does not make sense based on the fact
that the genetic diversity of Africans and African Americans is great and largely
includes all the diversity found within European and Asian populations (Jones
and Goodman 2005; Yu et al. 2002).

Lastly, part of the explanation for the dominance of raciogenetics is that we
live in an “age of genetics” (Goodman 2013), a time in which genetics has taken
hold as the dominant explanation for most behaviors and conditions. Certainly,
genetic medicine is big business. And so it follows that genetics might explain
variation in health among races (Goodman 2000).
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The lived experience of racialization and racism

In part due to the emergence in the late twentieth century of social epidemiology, a field devoted to looking at how cultural and social conditions lead to disease and death, the consequences of everyday dietary habits, stress, pollutants, work conditions, and other aspects of daily life on health are coming to light. Part of the work in this field has pointed toward how life-long differences in living conditions, such as exposure to the stress of racism and pollutants, might explain the bulk of the variation in health among races (see, for example, Geronimus 1992; Williams et al. 1997). Social class, socioeconomic status, and experiences of racism are closely intertwined, and interact to affect life courses. Intersecting, they determine exposure to, among other things, healthy foods, pollutants, and experiences of discrimination, and rendering people differentially vulnerable to risk factors (Krieger 2003; Navarro 1990).

In some sense, the lived experience hypothesis, which proposes that life-long conditions are a major determinant of health and longevity, is profoundly strong and obvious. It fits the epidemiological data on racial differences in health mentioned earlier so well that even those who strongly back genetic explanations acknowledge the importance of lived experience in determining health outcomes (Satel 2002). Yet, for reasons noted later, the tendency in public health is not to eliminate the raciogenetic explanation entirely, but to acknowledge a role for both lived experience and genetics in producing health (Satel 2002). The problem with this compromise position is that it says little about underlying etiology. Ultimately, if one wishes to address and ameliorate health inequities, the relative importance of these distinct etiological pathways must be determined in order to inform public health actions and patient care.

The debate continues. It is both scientific and political in the sense that each of the two hypotheses points toward a series of actions that have scientific and political implications. In the following section, I present reasons why race should not be used as shorthand for human genetic variation. If race maps poorly onto genetic variation, as it does, then the raciogenetic explanation is fatally flawed.

Why “race” ≠ human genetic variation

Race is a powerful idea and a worldview that was invented and reified to explain variation in human biology, culture, and behavior (Smedley 1999). The underpinnings of this idea can be traced to classical Greek philosophical notions of ideal types and Christian ideas about a great chain of being. However, in the view of most historians of race and enslavement, the idea of biologically based human races was itself a more recent invention, with the first clear evidence for this categorical way of thinking emerging during the Renaissance and European expansion into the Americas and Africa in the fifteenth and sixteenth centuries (Smedley 1999). With the development of transoceanic travel and international migration, human differences were magnified. For the first time, individuals from vastly different parts of the world such as northern and southern Europe,
West Africa, eastern North America, and the Caribbean came into contact with each other. More importantly, politics, science, and ideology went hand in hand. Colonialism, imperialism, slavery, and the desire to exploit lands and people clearly contributed to the tendency toward value-laden, racialized thinking. Starting in the eighteenth century, natural historians such as Linnaeus began to classify humans into subspecies or races, facilitating the progressive dehumanization and disenfranchisement of those from places other than Europe.

However, we know now that raciogenetics is antithetical to the idea of evolution, that it does not fit the measurable reality of the structure of human variation, that it does not translate into a concept that is epidemiologically repeatable, and that it leads to a series of conflations that inhibit understanding of the cause, treatment, and prevention of disease.

The idea of race versus evolution
Race, as noted above, is a socially constructed idea about how human genetic variation is structured. Similar to the dismissal of the views that the sun revolved around the earth or that the earth was flat, the idea of separate and unequal races should have been cast aside with the development of evolutionary thinking (Goodman 1997). However, for the sociopolitical and socioeconomic reasons discussed earlier, it was too powerful to fail.

What is perhaps most scientifically problematic about the idea of race is that it includes no process for change; rather, it is cast as a discrete outcome or an end-result of a process. It lacks dynamism. To say that racial differences exist because of race is a tautology; tautologies are self-reinforcing pretenses, arguments constructed so that the proposition stated is logically irrefutable, while the lack of evidence or valid reasoning for the conclusion is obscured. There are in these explanations no explicitly theorized arguments relating to the processes by which racial differences came into being. Yet we know now that genetic variation arose as a result of human evolution and history. The idea of race, of stable and unchanging types, inhibits rather than advances studies of the evolution of human differences.

The structure of human variation
If the idea of race – dividing humans into some three or more racial groups – approximated in a useful way the geographic structure of human variation, then one could conceivably support the notion for the sake of expedience that race is an imperfect but acceptable stand-in for human genetic variation. So framed, the association of place and genetic variation does not explain everything, but it is a sort of “quick and dirty” approximation (Satel 2002). This position may have been defensible in the early to mid twentieth century prior to the application of modern genetics to human evolutionary studies. However, it is not defensible now given what we know about the following rules of human variation.
Human variation is continuous
Genetic and phenotypic variations tend to vary gradually across human populations. Definitions of race as a discontinuous category, reflecting clear “breaks,” are thus conceptually flawed: it is impossible to identify where one race begins and another ends. Skin color, for example, varies widely by latitude and degree of exposure to ultraviolet radiation. Take a walk from Norway to Nigeria and you will see slowly changing skin colors rather than clear breaks from light to medium and dark. Also, because Africa covers such a wide span of latitude, African groups exhibit a wide range of skin colors that overlap tremendously with individuals from other continents (Jablonski 2012). Like most other traits, such as the frequency of a genetic polymorphism or a phenotypic trait like nose shape, skin color varies slowly from one place to another. This gradual variation is referred to as continuous or clinal variation (Goodman et al. 2012).

Human traits vary independently from each other
Traits tend to vary independently of other traits. Race categories and classifications will therefore vary by the traits, whether genetic or phenotypic, used to classify them. A classification based on the allele for sickle cell anemia might include equatorial Africans, Greeks, and Turks – these populations exhibit high frequencies of the allele – while another classification based on lactase enzyme deficiency or lactose intolerance might include eastern and southern Africans with southern Europeans, Japanese, and Native Americans, populations which have high frequencies of lactose intolerance. There is no possibility for consistency in these groupings. As skin color is only linked with a few other phenotypic traits such as hair and eye color, it is true to say that “race is only skin deep” (Diamond 1994).

Within-race group genetic variation is much greater than variation among “races”
Starting with Lewontin(1972), studies have statistically apportioned variation in different genetic systems to different levels: among “races” and within “races” and within smaller populations such as the Hopi, the Ainu or the Irish. Lewontin (1972) collected data on blood group polymorphisms in different ethnic groups and races. He found that blood group variation among races statistically explains only about 6% of the total variation. These results show that if one is to adopt a racial paradigm, one must acknowledge that race will statistically explain only a very small proportion of genetic variation. Moreover, this small variation is better explained by geographic distance (Templeton 1998). As is shown in Figure 4.1, the geographic distance between any two groups is highly correlated with the genetic difference between them.

Yu et al. (2002) more recently compared a large sequence of DNA, 25,000 letters or base pairs for 10 individuals identified as members of each of the three main “races” typically used in medical studies: Asian, European, and African. They counted out the number of differences in the base pairs, or single
nucleotide polymorphisms (SNPs), between any two of the individuals. As shown in Figure 4.2, they found on average only about 0.6 differences per 1000 SNPs between two Europeans, two Asians and a European and an Asian. They went on to find more differences, about 1.1 per 1000 SNPs, between a European or Asian and an African. Their most surprising finding is that the average number of SNP differences between two individuals from Africa, about 1.3 per 1000, is greater than the average number of differences between an African and a European or Asian (see Figure 4.2). These results support the understanding that there is greater genetic variation in Africa because of the increased evolutionary time modern humans have spent in Africa, since their emergence there several hundred thousand years ago. Most startling perhaps is that Europeans and Asians, rather than being genetically separable, appear more accurately to be subsets of Africans. We truly are, it seems, all genetically Africans or, said more colloquially, we are all Africans under the skin.

**Race: a scientifically unrepeatable variable**

Race is impossible to define in a stable and universal way because race, as a genetic or evolutionary categorization of individuals, is not stable. Race varies with place and time because it is socially defined differently over time and place; the socially determined color line is dynamic. Some phenotypic variables, such as head and foot size, are classified into hat sizes and shoe sizes, and these systems work in that this sizing provides a guide to users looking for a good fit in their hats and shoes. However, a problem with race in practice is that there is no agreed-upon “race scale.” Ideas about race are fluid and based on different phenotypic cues. The salient cues change over time, place, and circumstance and
are always subject to social and cultural processes. If there is no way to consistently classify individuals, one cannot replicate past studies, which is a universal scientific necessity.

Indeed, this fluidity of race might help explain the paradoxical nature of forensic classification of races based on phenotypic criteria such as skull morphology (Goodman 1997). It is a trope in forensic anthropology that skull morphology can be used to identify race of the deceased with great accuracy. For instance, in their classic forensics text The Human Skeleton in Forensic Anthropology, Krogman and Iscan (1986) submit that race may be correctly determined from dry bone cranial morphology in 85–90% of cases. But this creates a paradox. If race is a biological myth, how is it that it can be so easily identified? This apparent paradox is reflected in an article by Sauer (1992), a prominent forensic anthropologist, subtitled “If races don’t exist, why are forensic anthropologists so good at identifying them?” But are forensic anthropologists that good at identifying race? Perhaps the proof is in the application.

Much of this trope is based on a seminal publication in forensic anthropology, Giles and Elliot (1962), entitled “Race identification from cranial measurements.” Giles and Elliot discuss their finding that a newly developed statistical technique, multivariate linear discriminant function, was more accurate for sorting skulls into races than a single measurement or index. This technique generates the
equation that best discriminates two samples into their appropriate populations. In developing the equation, an optimal break point is ascertained; values above the break point are assigned to one group and values below to a second. The break point represents the point at which the highest percentage of “cases” is correctly placed. To generate data for the equation, cranial metrics were collected from large samples of “white” and “negro” crania from collections in St Louis, MO, and Cleveland, OH, and for the Native American sample, from prehistoric skeletal remains recovered from Indian Knoll, KY (Figure 4.3).

They found that eight readily obtained measurements provided a fine set of discriminate equations. For example, the equation for separating white from negro males is as follows:

\[
3.06 \times (\text{Basion} - \text{prothion}) + 1.60 \times (\text{glabella} - \text{occipital length}) - 1.90 \\
\text{maximum width} - 1.79 \times (\text{basion} - \text{bregma height}) - 4.41 \times (\text{basion} - \text{nasion}) - 0.10 \\
\text{maximum diameter bizygomatic} + 2.59 \times (\text{prothion} - \text{nasion height}) + 10.56 \\
\text{nasal breadth}
\]

If the value obtained from this equation is above 89.27, then the cranium is assumed to be negro. If it is below 89.27, it is assumed to be white.

Giles and Elliot’s (1962) original test found that 94% of their Native American crania were correctly identified as Native American in their original study. However, in their original retest of a smaller, separate sample of Native American crania, the accuracy dropped to just over 80%. The accuracy declined when

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**Figure 4.3** Percentage correct classification of Native American crania to race. Original test and original retest of the data from Giles and Elliot (1962) and four retests by other authors. Note the sharp decrease in percentage correct on the retested samples.
New directions in biocultural anthropology

the method was applied to a different sample drawn from the same data set, yet remained high. However, the method has not retained this accuracy when applied to different sets of crania, as revealed in four studies that have tested the method. Each retested the method in forensic samples for which sex and race in life were known. While four is a small number, that the method has been independently evaluated at all is a tribute to its importance. Birkby’s (1966) retest employed 45 crania from a diverse set of archeological sites. Snow et al. (1979) evaluated the method’s accuracy for 52 white, black and Native American crania apparently representing forensic remains from in and around Oklahoma. Fisher and Gill (1990) applied the method to 43 Native Americans from the Northwest. Lastly, Ayers et al. (1990) employed crania from forensic cases previously identified as belonging to one of the three tested races. Totaled, these works represent a retesting of the method on 107 Native American crania.

Relatively speaking, the best results came from Birkby (1976) with 58.7% of Native Americans crania correctly classified using the method. However, the probability that race was incorrectly classified was 41.3%, almost as great as the probability of correct classification. Fisher and Gill (1990) found a probability of correct classification of 30.2%, which is less than that which would be correctly classified at random. Finally, Snow et al. (1979) and Ayers et al. (1990) generated probabilities of 14.3% and 18.2%, respectively. Fisher and Gill, Snow et al., and Ayers et al. generated probabilities of incorrect classification of 69.8%, 85.7%, and 81.8%, respectively. Importantly, three of the four retests generate probabilities of correct classification that are lower than through random assignment.

The question arises: is forensic identification of race absolutely unreliable? Native American skulls seem particularly hard to correctly classify, perhaps because the formulas are based on skulls from a prehistoric sample, and are not generalizable to modern individuals. However, the method does optimize some conditions that might not be true in actual practice. Of all the bones, crania are the most diagnostic of race. Sex needs to be identified before race can be for a given cranium, given the influence of sexual dimorphism, and this is often impossible in practice. A complete and undeformed crania is required. The results say nothing of harder to classify groups such as East Asians, as well as infants, children, and adolescents or individuals of so-called “mixed” races. Overall, given that this method for assigning race to crania is the most frequently cited and applied for this endeavor in forensics, what Brues (1990) called “the standard method” for the purpose, these results completely undermine attempts to generate universal, stable definitions for biological race.

Race: conflating lived experience and genetics

Other key methods of dividing individuals into groupings, such as social class, may also differ widely across time and space. Social class might also be hard to define in a repeatable way. However, although imperfect, measures of social class still provide a glimpse at the underlying processes through which social
and economic positions affect lived experience and health. Race, on the other hand, as discussed earlier, differs in the breadth of potential interpretations of the underlying processes. As previously noted, some individuals view racial differences in disease and health as due to genetics, while others view them as the consequence of the lived experience of race and racism. Obviously, this confusion has serious implications for theory and practice. One cannot perform predictive science based on a changing and indefinable cause.

**Conflating human genetic variation and race**

Human genetic variation does exist: it is real and measurable. But it is also more dynamic than one might assume. And the road from genetic factors to complex diseases and behaviors is exceedingly interactive and less than fully determined. Where we end up – whether a behavior or disease becomes manifest – is undoubtedly related, though partly and incompletely, to genetics. But none of this has anything to do with race.

A reasonable compromise position would be to accept the fact that racial inequalities in health are likely a result of both causal pathways: genetic and lived experience. This is known, as mentioned earlier, as the compromise position. It is commonly advocated by professionals in public health and clinical medicine, such as Francis Collins (2004), the powerfully placed head of the US National Institutes of Health (NIH). But Sankar *et al.* (2004) argue that such a position has the real consequence of overstating the importance of genetics, as well as continuing to conflate race with human genetic variation. It also has real-life consequences; Sankar *et al.* (2004) note that this position potentially diverts research funds away from studies of the socioeconomic determinants of health disparities.

**Case study: race versus racism**

A growing body of research has begun to show that race-as-genetics does not explain variations in morbidity and mortality between races. However, it does show that differences experienced by members of different races in daily life are powerful determinants of that variation. To demonstrate this, the following section takes an in-depth look at three aspects of health, homicides, low birth weight, and cardiovascular disease, that demonstrate the potent effects of the lived experiences of race and racism on health, disease, and well-being across the life course.

**Homicides**

In the 1980s, researchers and policy makers took note of the increased rate of murders in black communities and black perpetrators of these murders. This research, in fact, led to an initiative set out by the National Institute of Mental
Health (NIMH) to study inner-city youths and violence. This initiative and field of study reflected contemporary cultural ideologies in the United States that linked black culture and alleles found more commonly in black populations with a greater propensity for violence.

Within epidemiological studies of the topic, Centerwall (1984, 1995) sought to find more ultimate, fundamental causes of higher rates of homicide and violence in black communities. In two simple, brilliant studies, Centerwall examined contemporary patterns of domestic homicide, the murder by one individual of another in the same household, in two cities with large black populations, Atlanta and New Orleans. He found that domestic homicides in black families were about six times more common than in white families. At face value, this could support any theory as to causality, but in an intellectual milieu that promoted raciogenetic explanations, the favored explanation is just that: race and genetics. However, Centerwall (1984, 1995) found that something else correlated with homicide: residential crowding. Specifically, when the number of individuals per room in different areas of each city was controlled for, the differences in domestic homicide between races were almost totally eliminated. Crowding, a reflection of quality of life, was probably causally connected to violence because of its relationship to poverty, stress, and access to opportunity.

Infant birth weights

Infant birth weights are of great importance because they are the number one risk factor for infant mortality and for future developmental problems. Study after study has shown that the birth weights of infants born to black women are lower than those of white women in the United States (David and Collins 1997). The extent to which these lower birth weights among blacks are related to social or genetic factors has been unclear. However, given the consistency of the difference over time, different regions of the United States and over different social strata and economic classes, the medical assumption has been that the consistent difference must be genetic.

David and Collins (1997), in a paper in the prestigious *New England Journal of Medicine*, tested hypotheses as to the cause of the nearly 1 pound, on average, difference in black versus white birth weights. They used birth weight records from 1980 to 1995 from Illinois of over 90,000 infants. Most of these were born to white women (n = 44,046) and black women who were born in the United States (n = 43,222). They affirmed previous findings of a clear difference in birth weights: infants born to the white women had an average birth weight of 7.58 pounds compared to 6.80 pounds for those born to black women who were born in the United States.

The geographical birthplace of the mother was critical for this study; the authors sought to determine whether growing up in the United States, a racist country, where black residents are subject to the stresses of racism throughout
their lives, might lead to biological “weathering” (Geronimus 1992), and that this might be a cause of the lower birth weights. Weathering is the idea that blacks experience early health deterioration as a consequence of the cumulative impact of repeated experience with social or economic adversity and political marginalization. To assess the effects of weathering, David and Collins (1997) added the birth weight records of several thousand ($n = 3135$) black infants whose mothers were born in Africa, and spent a portion of their lives in Africa, despite having given birth in Chicago. Mainly because of the history of largely involuntary admixture between enslaved black women and white men during enslavement in the American South, most blacks in the United States have some European ancestry, but this is not true of African women. This allowed the authors to test whether genetic differences are the primary determinant of low birth weights, following the raciogenetic assumption that the infants born to African women were genetically “purer,” with less European admixture, and would have the lowest birth weights.

However, David and Collins (1997) found that the opposite was true: infants born to the black women who were born in Africa had an average birth weight of 7.33 pounds, just a quarter pound less than the infants born to white women. The distribution of birth weights in the three groups is shown in Figure 4.4. The close tracking of the distributions of infants born to black women and infants born to black women who grew up in Africa is strikingly clear, as is the lag in birth weights of infants born to black women who were born in the United States.

![Figure 4.4](image-url) Distribution of birth weights among infants of US-born white and black women and African-born black women in Illinois, 1980–1995. The calculation of frequencies was based on all singleton births in Illinois. The study population included the infants of 3135 black women born in sub-Saharan Africa, 43 322 black women born in the United States (a sample that included 7.5% of the total number of black women giving birth in Illinois), and 44 046 US-born white women (2.5% of the total number of white women giving birth in Illinois). Source: David and Collins 1997.
David and Collins (1997:1209) conclude “the birth-weight patterns of infants of African-born black women and U.S.-born white women are more closely related to one another than to the birth weights of infants of U.S.-born black women.” Moreover, the results strongly, and dramatically, smash the raciogenetics based-hypothesis and support the weathering-based hypothesis, that growing up under conditions of racism exerts a life-long, cumulative deleterious effect on health.

**Cardiovascular disease**

As Gravlee (2009) has noted, the default mechanism purporting to explain how darker skin color leads to high blood pressure and cardiovascular disease (CVD), which are dramatically more prevalent in blacks in the United States than in whites, assumes that diasporic Africans are genetically predisposed to high blood pressure (Boyle 1970). Because blood pressures are generally low in black populations in Africa, it has been proposed that this geographic and population-level difference could be attributable to processes related to enslavement in the United States. Specifically, in what is known as the slavery hypertension hypothesis, the harsh conditions (extreme crowding, dehydration, and heat) that enslaved Africans experienced during the transatlantic Middle Passage may have intensified selective pressures for electrolyte conservation in those who survived the journey. This would lead to elevated electrolyte conservation in many blacks in the United States who are descended from enslaved populations. Current patterns of excessive salt intake in US populations, including among blacks, would then exacerbate this electrolyte conservation, leading to high blood pressure and CVD. Following the assumption that dark skin is a good proxy for a higher degree of African ancestry, this combines to create a raciogenetic explanation for the high prevalence of CVD and high blood pressure in darker skinned black populations in the United States (Gravlee 2009) (see Chapter 5).

Is this a scientifically valid explanation? Recently, Kaufman and co-workers (2015) published the results of a metaanalysis on the ability and consistency of results from whole-genome studies to explain racial differences in cardiovascular disease. Their findings are directly relevant for unpacking the raciogenetic explanation for CVD and high blood pressure. First, they found that few studies documented any candidate genes that might account for even a small difference in CVD rates among races. And for those that do, the results are highly inconsistent among studies with different samples. A raciogenetic myth busted.

What then explains the differences in blood pressure and CVD by race? An intriguing start at answering this question comes from Gravlee and co-workers (2005), who proposed that darker skin color is correlated with lower social status and greater experiences of racism (see also Dressler 1991; Tyroler and James 1978). This would mean that the linkage between high blood pressure, CVD, and skin color might be due to the social signification of skin color, not genetics.
Gravlee and co-workers note that in raciogenetic explanations, pigmentation (skin color measured by spectrophotometry) can be associated with “color,” the social category, but that they are not equivalent: one is biological, the other is socially loaded. Thus, associating pigmentation with high blood pressure may reveal an incorrect mechanism for the linkage.

Gravlee and co-workers (2005) derived a test to separately evaluate possible causal mechanisms (see Chapter 5). Working with populations in Guayama, Puerto Rico, they measured skin pigmentation by standard reflectance spectrophotometry but also completed an ethnography-based classification of informants in their study into color–race categories. These included three socioeconomic status (SES) levels – low, medium, and high – and two color categories: negros (blacks) and those defined as lighter, either blanco (white) or trigueño (an intermediate category). In their results, they found that self-ascribed color, not skin pigmentation, was associated with blood pressure. This held true even when all of the usual co-variates for high blood pressure, such as age and use of hypertensive drugs, were controlled for. The interaction they found between SES and ascribed color is particularly fascinating: as SES increases, those who are classified as negros have higher mean blood pressures, whereas blood pressure decreases as SES increases for the lighter color group of blancos and trigueños. They explained that these findings are consistent with ethnographic studies of class–race dynamics in Puerto Rico, which have shown that color–race is relatively insignificant in low-SES contexts, but that racism is most pernicious in the middle and upper classes. Informants classified as negros who were of high SES lived in a predominantly light-skinned world. Because of this dissonance with their surroundings, high SES negros may have experienced much higher levels of institutional and interpersonal racism than their lower lighter-skinned, and even lower negros SES peers, leading to systemic, chronic stress and increased blood pressure.

**Discussion and conclusion**

In summary, race is not biological in the sense that it is the same as human genetic variation. However, race is a powerful cultural category that has biological consequences (Goodman et al. 2012; Gravlee 2009). Race is biological because it is a culturally meaningful phenotype. No single reason noted earlier may be sufficient to throw race as genetics, or raciogenetics, onto the scrap heap of surpassed scientific ideas. But considered in combination, the critical discussion above clearly suggests that it is time to move beyond raciogenetic thinking in public health. Such a move not only finally jettisons an outdated paradigm; it also provides the space in which to explore more fully the complex and critical connections between the experience of racism and health, and ultimately, the full range of causes of health inequities. For students of biocultural anthropology, the task is ahead of you.
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CHAPTER 5

Beyond genetic race: biocultural insights into the causes of racial health disparities

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Introduction

In the United States, it is well documented that blacks have higher mortality and lower life expectancy than other demographic groups (Wong et al. 2002). Differences in the burden of cardiovascular diseases, including heart attack, diabetes, and stroke, are among the most important contributors to these differences (Wong et al. 2002). The pervasiveness of these biological health disparities has led to debates about the underlying causes, with researchers generally falling into one of several camps. Among many within the medical establishment, there remains a persistent assumption that differences in health predicted by race categorization partially reflect the effects of genetic differences between racial groups (Kistka et al. 2007; Kramer et al. 2013). These researchers point to the fact that race membership often continues to predict disease risk after adjusting statistically for socioeconomic factors, combined with an assumption that populations carry different genes that influence the risk of developing these diseases (Burchard et al. 2003; Risch et al. 2002).

From a contrasting perspective, of which George Armelagos was among the leaders, most anthropologists have come to accept that races are best viewed as socially defined categories that do not have an underlying genetic basis (Armelagos and Goodman 1998; Livingstone 1962; Montagu 1942). Support for this position comes from the fact that genetic differences between groups tend to be small, while most genetic variation is found within groups (Brown and Armelagos 2001). At the same time, the race you are assigned to by society is known to shape the opportunities that are open to you, and the types and patterns of stressors that you experience. These in turn can have profound impacts on biology, and it is these differences in environments and experiences, rather
than genes, that most anthropologists view as driving the differing patterns of health and disease seen between individuals with different racial identities.

In this chapter, we build on the anthropological challenge to genetic race and critically evaluate the limitations of this concept as an explanation for contemporary race-related health disparities in racially segregated societies like the United States. We first discuss four factors that limit the utility of the genetic race concept and its applicability to racial health disparities. The first is that, whether we focus on physical features or genes, human variation does not come packaged in types or races, but is instead continuously varying, or clinal, and reflects complex histories of migration and gene flow between continents. Second, race membership – who is ascribed to what race – is socially and culturally defined, and not based upon genetic criteria. Third, unlike simple traits like eye color, most common chronic diseases that contribute to health disparities are “complex” traits that do not relate back to genes in a straightforward fashion. Lastly, in contrast to this, there are two powerful ways by which environments and experiences shape health disparities within and between societies, reflecting how the human body responds to and comes to create a record of these experiences. These include the cumulative negative impact of stressors, or “wear and tear,” and alterations in how bodies develop, or plasticity. To illustrate these pathways, we conclude with two case studies which show how the social, cultural, political, and economic realities of race within contemporary US society can lead to biological disparities in health, without needing to invoke genes or racial types.

Background

The illusion of genetic races

Most of us have likely learned that humankind can be divided into three races, reflecting ancestral roots in Europe, Asia or Africa. Although it is still common for many to think in these terms, anthropologists have realized for more than half a century that modern human diversity does not come in such a tidy package (Brown and Armelagos 2001; Livingstone 1962; Montagu 1942). Our drive to divvy up human variation and place it into a few categories speaks to the way that the human mind works and, in particular, how it simplifies phenomena in order to make a complex world more manageable and understandable. Although it may feel natural to think about human variation in terms of categories like black and white, or European, African, and Asian, human diversity is more akin to the continuous color gradations of the visual spectrum than the discrete bands of color – red, orange, yellow, green, blue, indigo, and violet – that our minds impose upon it.

Starting in the mid-twentieth century, Frank Livingstone (Livingstone 1962) noted that as one pans across the globe and views variation in human traits such as skin color, body size, and facial features, they do not come in distinct types but form continuously varying gradients, or clines. Flying from Copenhagen to
Dakar, you would be struck by obvious differences in features of appearance like skin or hair color. However, walking between those two populations, you would experience a continuous but imperceptible pace of change in these traits. Skin color would darken gradually as you moved from northern to southern Europe. It would continue to darken across the Mediterranean, and into Egypt and onward across Africa to the south, until reaching its darkest expression in the equatorial belt. There would be no obvious moment during your journey when you had crossed a threshold differentiating white from black, and the same would hold for other traits as well. This divide would be even murkier if exploring gradients in biology or appearance between Europe and Asia, which form a single supercontinent with greater opportunities for population movement and gene flow between them.

The recent advent of high-throughput genome sequencing technologies has provided a powerful tool to investigate the nature of human biological diversity. Since the initial sequencing of the human genome (Lander et al. 2001), technological advances have allowed the sequencing of genomes in thousands of individuals from across the globe. These studies consistently confirm what had previously been shown in earlier studies of blood groups or proteins: only a small part of the variability in human genes is explained by knowing what continent someone is from, or in what group they reside within a continent. Instead, the vast majority of genetic variation is found within human groups (Brown and Armelagos 2001).

While human genetic diversity does not cluster into tidy continental packages, as the traditional concept of race implies, it also turns out that we are an unusually homogenous species from a genetic perspective. There are only an estimated 150 000 chimpanzees living in the wild, compared to more than 7 billion humans. And yet, if you were to select two chimps at random, they would show substantially more genetic differences than would two humans (Prado-Martinez et al. 2013). There are many more humans but we all share a more recent common ancestor, and thus are more genetically similar to each other as a result.

Modern humans diverged from ancestral hominids around 200 000 years ago on the African continent. More recently, around 50 000 years ago, humans migrated out of Africa through the Nile corridor to colonize the rest of the globe (Pagani et al. 2015). Recent analyses suggest that the split between the original inhabitants of East Asia and Europe occurred between 40 000 and 20 000 years ago, and the split between East Asians and the lineage that peopled the Americas 20 000 years ago (Schiffels and Durbin 2014). Because humans have inhabited Africa for so much longer, the African continent harbors much greater genetic diversity than populations outside of Africa, and nearly all human genetic variants are found there (Long 2013). Populations outside of Africa can largely be viewed as subsets of this ancestral pool of African genetic variation, reflecting the narrower gene pools within the small “founder” populations of migrants that migrated out of Africa (Long 2013).

Local genetic adaptations have since arisen in both non-African and African populations, leading to biological features unique to local populations. One
example is skin color, which, as already discussed, follows a gradient across all continents that mirrors the intensity of ultraviolet radiation from sunlight. There is substantial variation in genes that contribute to differences in skin tone within Africa, and that evolved independently as populations moved to different latitudes, with different sun intensities, outside of Africa. This illustrates how natural selection shapes genetic variation *locally, within* continents, and thus contributes to the sizeable genetic differences between inhabitants of the same continent, or what would traditionally have been viewed as members of the same race.

Even if human genetic data do not support a simple race-based model of human diversity, they *do* reveal genetic differences between populations, some of which influence biology and thus could impact health. Might this global diversity in local population gene pools now contribute to race-related health disparities in a place like the United States? After all, in the United States, Europeans largely displaced the original Native American inhabitants of the continent, and initiated a slave trade that introduced Africans from a fairly narrow region of equatorial west and central Africa. Given that two geographically distant populations were brought side by side by these historical events – not unlike the experience of our jet-setting traveler between Copenhagen and Dakar – might genetic differences in their ancestral populations in Europe and Africa now contribute to contemporary health differences in the United States?

**Race is socially and culturally, not genetically, defined**

Black man, black woman, black baby  
White man, white woman, white baby  
White man, black woman, black baby  
Black man, white woman, black baby

*Dick Gregory (from Public Enemy, Fear of a  
Black Planet)*

For many people who grew up in the United States, the notion that human races do not have a firm genetic footing may be difficult to accept. We are conditioned to think of racial categories like *black* and *white* as corresponding to deep-seated differences between distinct types of humans. This impulse is part of what Smedley (Smedley and Smedley 2012:18) defines as the racial worldview: “a culturally structured, systematic way of looking at, perceiving, and interpreting” reality. But a fundamental lesson of anthropology is that each society develops its *own* culturally structured way of perceiving and interpreting reality. The racial worldview is but one way: a culture-bound product of unique demographic, political, and economic forces in US history. In other times and places, the same reality of human biological variation has been interpreted through other frames.
We don’t have to look far to find examples of alternative worldviews. In the United States, the rule of hypodescent, or “one-drop rule,” automatically assigns anyone with a perceptible trace of African ancestry to the category black (Harris 1964). This rule is what makes the civil rights activist and comedian Dick Gregory’s quote above ring true — and what explains how President Obama can be regarded as the first African American US president, despite having a mother who is defined as white. No such descent rule is evident in Latin American societies such as Brazil or Puerto Rico, where color terms are based on an individual’s physical appearance and even siblings can be assigned to different categories (Duany 2002).

A related distinction between the US racial worldview and other ways of seeing human difference concerns the extent of ambiguity in racial classification. The rule of hypodescent in the United States historically sustains a simple classification scheme grounded in the relatively well-defined black-white binary. In Latin America, by contrast, the primacy of appearance over descent leads to the proliferation of color terms that capture subtle variations along a continuum from dark to light. Sanjek (1971), for example, identified 116 terms in the Brazilian “racial lexicon,” and Duany (2002) listed 19 “major folk racial terms” in Puerto Rico. Usage of these terms is also more fluid than the US racial worldview allows.

These systems contrast with the United States in yet another important way: in some Latin American societies, including Brazil and Puerto Rico, “money whitens” (Degler 1971). In Brazil, interviewers were more likely to assign respondents to lighter categories if the respondents had more education, especially if they lived in mostly non-white places (Telles 2002), and non-white Brazilian parents with high levels of education are more likely to classify their children as white (Schwartzman 2007). Both examples illustrate how local conceptions of race emerge from cultural norms rather than underlying genetic realities.

Our emphasis on race as a worldview, rather than a genetically grounded set of categories, should not be taken to mean that it is merely a bad idea, or that it does not have real and serious biological impacts. The US racial worldview that emerged from the historical and economic realities in English North America (Harris 1964) today remains embedded in systemic racism that is experienced daily (Feagin 2006). Although race as most people understand it may be an illusion, that illusion and the system of oppression in which it is embedded have toxic — and even lethal — consequences for biology and health.

**Why most health disparities are not like eye color: moving beyond genetic determinism**

The culturally grounded criteria for race membership in any given society thus mean that self-identified race is often a poor proxy for genetic ancestry. In addition, a more fundamental challenge to the role of genes in health disparities comes from the fact that genes rarely have strong, direct effects on the biological...
and behavioral traits that underlie these diseases. Nearly everyone reading this likely first learned about genetics through examples like eye color, which has an unusually straightforward genetic underpinning. Blue eye color is a homozygous recessive trait, meaning that you must inherit blue eye alleles from both of your parents to have blue eyes. If you inherit only one blue eye allele, you will likely have brown or black eyes, depending on the other inherited allele.

Although this example has traditionally served as a staple of textbook discussions of genetics, it is ultimately misleading when considering the role of genes in most biological and behavioral characteristics. Let us take the example of a leading cause of ethnicity or “race”-based health disparities in contemporary societies: cardiovascular disease. Genome-wide association studies (GWAS) search for statistical relationships between a trait, such as high cholesterol or hypertension, and information on hundreds of thousands or millions of genetic variants measured at single nucleotide positions (single nucleotide polymorphisms, or SNPs) across the genome, often in samples of tens to hundreds of thousands of individuals. For some traits, GWAS has been quite successful in identifying genes that explain variation in a health outcome. For instance, one recent study pooled genetic data from several hundred thousand individuals, from multiple global populations, to disentangle the genetic predictors of cholesterol levels. The authors identified 95 genes that together explained a respectable 10–12% of the variability in each lipid risk factor (Teslovich et al. 2010).

Such successes have been the exception rather than the rule, and most attempts to link health disparity-related traits to genes have proven far less successful. Take, for instance, body weight, which, owing to the rising public health burden of obesity, has been subjected to intensive investigation by GWAS. One large GWAS analysis of 250 000 individuals identified 32 genes that together explained only 1.45% of the variation in the body mass index (BMI) across the pooled populations (Speliotes et al. 2010). In other words, in this sample nearly 99% of the variance in BMI could not be explained by knowing which of the measured gene variants individuals carried in their genomes.

What accounts for the marked differences in the success of identifying genetic influences on cholesterol levels and obesity? Although there are many factors involved, a fundamental one is a difference in complexity. Cholesterol is a simple molecule, and its production in the liver, its circulation in the bloodstream, and clearance from the body are governed by relatively few factors. It is precisely this simplicity that accounts for the clinical success of statin drugs in lowering LDL cholesterol levels (“bad cholesterol”), with reductions typically varying from 15% to 50% depending on dosage. This drug blocks the protein product of a single gene (HMGCR) that codes for an enzyme required for cholesterol synthesis (HMG-CoA reductase). It should come as no surprise that the HMGCR gene was also among the strongest genetic predictors of cholesterol levels identified by the GWAS study mentioned above (Teslovich et al. 2010). In contrast, there is no drug for obesity, because there are no comparably simple pathways governing the gain and maintenance of excess body fat in most individuals. Instead, body weight is
related to a dizzying array of factors, including our appetites and cravings, our emotions, the amount of heat that our bodies produce after we eat a meal, our gut microbiome, personality type, and other traits that influence our activity level. As we will discuss below, one’s risk for obesity is also powerfully shaped by our earliest experiences, beginning in the womb, when fetal development commits to different long-term metabolic settings depending on the nutritional conditions that we experience in utero. All of this biological complexity interacts with a similarly complex set of historical, environmental, cultural, political, and economic factors that vary across individuals and populations (Ulijaszek and Lofink 2006).

Thus, knowing someone’s genotype will tell you a lot about relatively simple traits like their eye color, skin color, and, to a certain extent, even their cholesterol levels. However, most traits of importance to health disparities, including common and important conditions like obesity, hypertension, depression, and diabetes, are far more complex, meaning that knowing which genes someone carries is less helpful in explaining who becomes sick and who stays healthy.

**Why environments matter more than genes for many health disparities**

While genes are poor predictors of who suffers from most common chronic diseases, the environments that we inhabit – such as our experience of stress, our diet, and other factors – are comparably strong predictors of our health. There are several factors that help us make sense of why this is. Some of these explanations are widely understood, while others are only recently coming to light as a result of breakthroughs in our understanding of biology and the ways in which our experiences can influence it. As we discuss next, environments can shape patterns of health in two basic ways: first, through the cumulative lived experience of daily life, or what we might call “wear and tear,” and second, by altering how our bodies develop biologically. Because both are crucial to understanding the origins of health disparities, we discuss each in turn.

**Wear and tear: the cumulative negative impact of adverse environments**

Until recently, most research on racial inequalities in health viewed these health disparities as a product of differences in socioeconomic status (SES). The basis of this approach is the observation that, in racially stratified societies like the United States, race is strongly associated with differences in common indicators of SES like income, education, and occupation. These indicators, in turn, are associated with inequalities in health outcomes. It stands to reason, then, that racial inequalities in health may be due at least in part to the unequal distribution of socioeconomic resources along racial lines.

This analytic strategy has produced mixed results. Some studies show that black–white differences in blood pressure, for example, disappear after controlling for individual or neighborhood-level indicators of SES (Morenoff *et al*. 2007;
Syme et al. 1974), but others show that African Americans have higher blood pressure than whites even within levels of education, occupation or income (Hypertension Detection and Follow-up Program Cooperative 1977). In every case, however, accounting for differences in SES substantially weakens the magnitude of blood pressure differences between racially defined groups. This pattern holds for other health outcomes, too (Williams and Collins 1995).

The incomplete success of the SES model prompted two lines of criticism that led to other approaches. The first is that “controlling” for standard indicators like income and education does not address underlying causes (Kaufman and Cooper 1999), since these variables don’t play a direct role in health. Consider, for example, that lower SES is associated with lower blood pressure in some societies (e.g., Ogunlesi et al. 1991). The next step, then, is to specify the intervening behaviors and exposures that shape the social patterning of health in a particular cultural setting.

One approach to this problem has been to focus on health behaviors such as smoking, diet, and physical activity, and related outcomes like obesity. These factors are known predictors of individual and population health, but they actually explain little of the racial disparities in health in the United States. For example, obesity explains 43% of the difference in hypertension prevalence between African American women in the United States and women in rural west Africa (Cooper et al. 1997). But within the United States, African American women are still almost twice as likely to have high blood pressure, compared to whites, even after controlling for obesity and SES (Bell et al. 2004).

A related line of criticism is that focusing too much on SES neglects the social significance of race itself. In racialized societies like the United States, categorizing people as black or white profoundly affects their life chances, such that racial classification is causally prior to standard measures of SES. As Richard Cooper (1984:721) puts it, “explaining racial differentials by education could in a causal sense be considered ‘overcontrol’: race is not confounded by the other variables; it is antecedent to them. It is race that influences class standing.” And of course, the implications of racial classification are not limited to inequalities in social class. It may also affect health through non-economic forms of discrimination, including access to quality health care (Smedley et al. 2002), residential segregation (Massey et al. 2001), and exposure to racism in everyday social interaction (Essed 1991).

The most common approach to this problem today regards perceived discrimination as a chronic psychosocial stressor that impacts health and health behaviors. So far, researchers have linked self-reported experiences of discrimination to a range of outcomes, including elevated blood pressure, breast cancer, coronary artery calcification, body mass index, abdominal adiposity, preterm birth, low birth weight, depression, poor sleep, substance use, and poor preventive health behaviors (Gravlee 2009; Lewis et al. 2015). The associations between discrimination and health are often complex and sometimes manifest in unexpected directions, but this pattern may reflect the early state of the science.
Ongoing work to improve the measurement of experiences of discrimination holds promise to further illuminate how the wear and tear of systemic racism impacts biological systems and health (Williams and Mohammed 2013).

**Developmental programming of later disease risk: biological memories of our early experience**

In addition to wear and tear, *developmental plasticity* refers to the ways in which our experiences modify our biology and health by altering how our bodies develop (Kuzawa and Thayer 2011). The human body has capacities for plasticity that influence features of our biology that are straightforward and visible, such as relationships between height, age at puberty, and access to nutrition during childhood (Tanner 1962), but also those which are hidden from view but are crucial determinants of long-term risk for developing many common chronic diseases. Indeed, research in recent decades has shown that prenatal nutrition, stress, and other early life factors can modify fetal development in a way that elevates risk for developing conditions like hypertension, diabetes, heart attack, and stroke decades later, in adulthood (Barker 1994). These relationships reflect plasticity in traits like metabolism, blood pressure regulation, and stress biology, which are altered developmentally in response to conditions experienced during gestation and infancy. In addition, early experiences often lead to chemical modifications to chromosomes, called *epigenetic* changes, that determine which genes are turned on and which are silenced, which can also impact later health (Jenuwein and Allis 2001; Waterland and Michels 2007). In addition to the impact of the prenatal environment, research has also shown the lasting health impacts of early postnatal factors, such as whether we are breastfed or how quickly we gain weight as children (Norris et al. 2012).

This research suggests that an individual’s risk of developing the most common adult chronic diseases, which are major contributors to health disparities, may be established, in part, by experiences much earlier in the lifecycle, often beginning prior to birth (Armelagos et al. 2009). By extension, some of the burden of disease in the current generation of adults may be traced to the social and environmental experiences of their mothers and other recent ancestors. For our present discussion, this means that the types of stressors that tend to be experienced differently according to one’s self-identified race, such as differences in discrimination, nutrition or other factors, may impact not only the person who experiences them but also health in the next generation (Kuzawa and Sweet 2009).

Some of the earliest evidence for these relationships came from findings in humans who were born as lower birth weight babies, suggesting that they experienced prenatal nutritional stress (Barker et al. 1989). Among the better documented changes observed in adults who were born small is a tendency to have muscle that is resistant to the effects of insulin, meaning that they are less efficient at lowering their blood sugar after a meal. Individuals who experienced prenatal nutritional stress also tend to put on less fat in the lower
body or limbs, and to preferentially deposit it instead in the belly (leading to a so-called “apple-shaped” or “android” pattern of unhealthy fat deposition). Fat in this abdominal depot is distinct, because it is perfused with nerve fibers from the brain that release hormones like adrenaline, which allows the brain to rapidly mobilize stored fats for use as energy when the body is confronted with a stressor or challenge. Not only do individuals who were born small deposit more fat in this depot, but when they experience stress their fat cells also mobilize these stored fats for energy use more rapidly, which exacerbates the insulin resistance in muscle and other tissues (Girard and Lafontan 2008).

While the negative health impacts of fetal undernutrition, as reflected in being born small, have received much attention, there are also powerful effects of being overnourished in utero, which has growing relevance as rates of overweight and obesity rise across the globe. When a pregnant mother is overweight or obese, she is more likely to have high blood sugar during pregnancy, which at its most extreme manifests in gestational diabetes. This high blood sugar, in turn, can overfeed babies and increase their own risk of developing diabetes and obesity as adults. This has led to the notion that obesity is a condition with a transmissible component (Benyshek 2013). That the tendency of obese mothers to give birth to babies with a higher risk of becoming obese is at least partially non-genetic is demonstrated by the finding that offspring born after formerly obese mothers have lost weight as a result of gastric bypass surgery are much less likely to become obese compared to their siblings born prior to their mother’s surgery, when the mothers were heavier and had elevated glucose and insulin during pregnancy (Smith et al. 2009).

In a similar fashion, when a woman experiences stress during pregnancy this can change how the offspring later responds biologically to stress (O’Connor et al. 2013; Tollenaar et al. 2011). In one recent study of an ethnically diverse sample in New Zealand, Zaneta Thayer found that women who reported deprivation or self-reported discrimination during pregnancy had higher cortisol levels during their pregnancy (Thayer and Kuzawa 2014, 2015). She followed up with the babies of these women, and found that those born to more stressed mothers produced more cortisol (measured in saliva) in response to the vaccinations that they received during their six-week pediatrician visits. This study shows that there are biological differences in how bodies respond to stress that are easily detectable soon after birth, and that are predicted by the stressful experiences of the mother during her pregnancy. Because cortisol is involved in a range of diseases, children born to mothers who experienced psychosocial stress during pregnancy may, as a result, be more prone to poor health in later life (Kuzawa and Sweet 2009; Thayer and Kuzawa 2011).

Can the biological “memories” of stress reach grandoffspring?
This work on developmental plasticity is showing how early life stressors, starting in the womb, can shape adult health by durably modifying development and long-term health. While these pathways of “biological memory” show how the
mother’s nutrition or stress might influence the health of her adult offspring, the story unfortunately does not stop here, because among the offspring are females who go on to become pregnant and have offspring of their own. This leads to an important question: might the original stress experienced by the mother also affect the health of her grandoffspring?

Although few studies in humans have investigated this, there are good reasons to suspect that the effects of the original stressor could be passed on, albeit more weakly, across several generations. This is because some of the long-term effects of an adverse gestational environment on the offspring’s adult health, such as insulin resistance, high blood pressure or inflammation, can negatively impact the gestational environments experienced by the next generation (Drake and Walker 2004). For instance, when a female fetus is exposed to a diabetic gestational environment, her heightened adult risk of diabetes increases the likelihood that her offspring – the grandoffspring of the originally diabetic mother – will also be exposed to a high-glucose, high-insulin gestational environment, thus perpetuating the pattern (Aerts and van Assche 2006; Castro and Avina 2002). Similarly, the heightened cortisol production in babies born to mothers who report having experienced discrimination during pregnancy, discussed in the New Zealand study (Thayer and Kuzawa 2015), might one day lead their bodies to expose the next generation to higher levels of cortisol during their own pregnancies.

Although evidence in humans still remains sparse, recent studies in other species, such as mice, even show that male experience can modify epigenetic factors that are transferred via sperm to offspring, and which go on to influence health across multiple generations (Kuzawa and Eisenberg 2014). Through epigenetic pathways of this sort, it is believed that early life stressors not only impact one’s own adult health but can be transformed into intergenerational pathways for the perpetuation of health disparities across several generations (Drake and Walker 2004; Kuzawa and Sweet 2009).

These examples illustrate how differences in our lived experiences can lead to biological differences, operating both through wear and tear and through changes in how the body develops. Given these biological sensitivities to environmental stress, we should not be surprised that members of the most socially disadvantaged groups within a society tend to also suffer from a greater burden of common chronic and psychological diseases.

We now conclude this chapter with two case studies that illustrate the power of these two pathways – wear and tear and developmental plasticity – to shape health along lines of socially defined race.

**Case study #1: hypertension in the African Diaspora**

A key test case for understanding the genetic and environmental influences on racial inequalities in health is the puzzle of hypertension, or chronic high blood
pressure, in the African Diaspora. This puzzle is significant not only because of its staggering toll on black lives but also because it is a focus of debate about the meaning of race and racism in contemporary science and medicine (see also Chapter 4).

Throughout the Americas, populations of African ancestry have higher rates of hypertension than do other groups in the same societies, as exemplified in the United States by the 45% higher hypertension rates among African Americans than among whites (Gillespie et al. 2013). Many clinicians and health researchers assume that people of African descent are genetically predisposed to develop high blood pressure (Pickering 2001). Wilson and Grim (1991) proposed that this predisposition may have resulted from the African slave trade itself: high mortality from salt-depleting conditions during the Middle Passage may have selected for salt-retaining genotypes among enslaved Africans, which would increase susceptibility to hypertension in today’s salt-rich environment. This so-called slavery hypothesis earned a place in clinical textbooks even before it was published in the peer-reviewed literature (Kaufman and Hall 2003), but it has been heavily critiqued on historical, evolutionary, and biological grounds (Armelagos 2005; Poston et al. 2001). By contrast, there is ample evidence that social factors contribute to hypertension within and between populations (Dressler 1999), but there remains no consensus about the causes of excess hypertension in the African Diaspora.

Debate about the relative importance of genetic versus environmental factors converges on the relationship between darker skin color and hypertension within populations of African descent in the Americas. This pattern has been interpreted as evidence of either genetic or sociocultural mechanisms (Boyle 1970; Tyroler and James 1978), but most early studies were unable to test these alternatives because they conflated two dimensions of skin color: the trait of skin pigmentation versus the cultural significance of skin color as a criterion of social status in color-conscious societies.

To address this problem, Gravlee and colleagues (Gravlee 2005; Gravlee and Dressler 2005; Gravlee et al. 2005) integrated ethnographic, epidemiological, and genetic techniques to disentangle the importance of biological and cultural factors as an influence on blood pressure in Puerto Rico. What they found was that, for Puerto Ricans defined as blanco (white) or trigueño (an intermediate term), higher SES was associated with lower blood pressure. For Puerto Ricans defined as negro (black), however, higher SES meant higher blood pressure, on average. This interaction makes sense in light of the ethnographic observation that racism becomes a more salient aspect of people’s experience in Puerto Rico as they climb the social ladder. In a follow-up study, Gravlee et al. (2009) extended this analysis to include DNA-based estimates of African genetic ancestry. Their results confirmed the basic anthropological critique of race by showing that culturally constructed categories like race or color are poor predictors of genetic ancestry. They also reported that the interaction between SES and color predicted blood pressure better than did genetic ancestry.
Although cultural categories are poor predictors of genetic variation, it is precisely because we take those categories for granted that they impact people’s lives in ways that our bodies register. The everyday wear and tear of being defined as black in a racially stratified society takes its toll in measurable biological outcomes that deleteriously impact health.

**Case study #2: does the experience of racial discrimination in the United States have intergenerational health consequences?**

In addition to wear and tear, another challenge to the presumed genetic contribution to the black–white disparity in cardiovascular health is the fact that US blacks also have lower birth weights than their white counterparts (Alexander et al. 1999) which, as reviewed earlier, elevates risk for hypertension, diabetes, and other cardiovascular diseases (Barker 1994). Although one may question whether the black–white difference in birth weight could be traced to genetic differences between these groups, there is strong evidence that this is not the case. For instance, recent US immigrants from the Caribbean and Africa were found to have birth weights nearly identical to those of US whites upon arrival (David and Collins 1997). However, among offspring born in the United States, birth weights began to shift towards the lower average African American birth weight (Collins et al. 2002).

The finding that the birth weights of immigrants and their descendants converge with those of their US ethnic counterparts provides compelling evidence that the black–white difference in birth weight is not likely due to genes (David and Collins 1997). Although the causes of the lower birth weights of African Americans and the offspring of African immigrants are not fully understood, factors associated with minority status, such as discrimination and racism, have been shown to predict prematurity and fetal growth restriction (Collins et al. 1998; Dole et al. 2004). Because a stressful fetal environment and fetal growth restriction, in turn, increase adult risk for conditions like hypertension, stroke, diabetes, and heart attacks, these findings suggest that the experience of race and racial discrimination could have impacts that transcend the exposed generation and potentially impact health in offspring and even grandoffspring (Kuzawa and Sweet 2009).

**Discussion and conclusion**

In this chapter, we have explored why the disparities in health that we see in relation to racial identity often have little to do with genes. Whether one studies bodily traits or genes, there is little evidence that race is a useful way to categorize this variation. Instead, most human traits vary as continuous gradients in
which the large majority of variation is found within, rather than between, the populations that inhabit different continents. We also see that, within a racially segregated society like the United States, one’s racial identity is not based upon genes but upon cultural and social criteria that reflect political, economic, and historical factors that lead to markedly different patterns of opportunity and stress among members of these groups. Our case studies illustrate important ways by which these differences in lived experience can lead to biological differences operating through wear and tear or by modifying early developmental biology. These are examples of pathways that connect the social and cultural realities of race as a lived experience to patterns of biology and disease, and thus illustrate how “race becomes biology” (Gravlee 2009).

References


CHAPTER 6

Political economy of African forced migration and enslavement in colonial New York: an historical biology perspective

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Introduction

Speaking historically, biocultural anthropology might be viewed as an extension of the Boasian idea that human biological plasticity is subject to the cultural environment in which it is embedded. Thus, biocultural anthropology, unlike biosocial anthropology and evolutionary ecology, conjoins biology and learned behavior in opposition to biological determinism (Blakey 1987). Our work, while also in the Boasian vein first inspired by the potential for immigrant acculturation (Boas 1911), is more specifically in the vein of Frederick Douglass (1854), who pointed to the biological effects of the economic and power relations of slavery and class. Racial discrimination and other political and economic inequities are important anthropological subjects at the core of most African Diasporic scholars’ work (Drake 1980; Harrison and Harrison 1999; Willis 1969). Douglass, unlike Boas, also questioned the possibility or desirability of “neutral” science and asked that scholars take the point of view of the enslaved and work on their behalf (Douglass 1854). This “activist” scholarship continues to define African American anthropology and cognate sciences (Harrison and Harrison 1999).

Douglass’s critical political economy of biology precedes the more extensive theoretical and methodical political economy of Marx (1867), yet demonstrates a common recognition of the influences of power, ideology, and economic inequity in the sculpting of human biology. Our branch of biocultural anthropology, in which political economy figures prominently, also reflects the explicit use of Marxist concepts and African Diasporic ideas (see Blakey 1988, 1996, 1998a; Blakey et al. 1994; Rankin-Hill 1997). We refer to the bioarchaeological implementation of a biocultural perspective as historical biology. Here, we use ‘political
economy’ to mean a historical analysis of the societal, and therefore biological, effects of power and the economy. In the development of American societies, capitalists’ means of securing profit for those who own property are associated with particular social structures, policies, and behaviors that differentially affect the biology of economic classes, culturally constructed biological races, and genders as well as the production of ideologies that mask these relations. Here, we show this through an examination of the historic effects of the enslavement of Africans in New York City.

Background

The African Burial Ground Project

Everything has a social history, and this includes the scholarship carried out by social scientists and other researchers. In the political economy of the biology of enslaved New Yorkers to be interpreted here, there is a material background of people, events, and institutions. The New York African Burial Ground Project began in 1992 when Blakey obtained an initial personal contract from the United States General Services Administration as its Scientific Director. The African Burial Ground sample, excavated between 1991 and 1992, represents more than 400 individuals recovered from a cemetery for both free and enslaved Africans, located just outside the wall of the colonial city of New York, in present-day Lower Manhattan, which was in use between the 1690s and 1794. The sample and its analysis represented an invaluable opportunity, as these skeletons comprised the largest and earliest historic skeletal sample of non-native people available for study in the Americas. The nineteenth-century First African Baptist Church (FABC) sample, the analysis of which was under the leadership of J. Lawrence Angel at the National Museum of Natural History, had been the largest such assemblage studied prior to the recovery of the New York skeletal sample. Rankin-Hill and Blakey had coordinated the completion of the varied research projects on the FABC after Angel’s death in 1986, when we, the archeological contractors (John Milner Associates), and the surviving Church reburied the remains at Philadelphia’s Eden cemetery. Rankin-Hill (1997) wrote the comprehensive monograph on FABC biohistory and organized a conference symposium on the project (see Chapter 7). However, a comprehensive volume including specialized studies of the individual biological anthropologists who worked on that sample was never developed. Indeed, it remained regrettable to us that Dickson Mounds paleopathological research by students of George Armelagos, despite its wide collaboration at our alma mater UMass, had never been brought together synthetically either. The African Burial Ground was an opportunity to achieve such synthesis if researchers of like mind could be organized and funding made available to allow them the time and resources for their work.

Researchers with long-standing experience in African American and African colonial archeology, history, and biological anthropology were enlisted. In particular, researchers from the African Diaspora with interest and expertise in these
areas were valued, and researchers who had shown a willingness to work with and for descendant and culturally affiliated communities were valued as well, especially in the context of an era filled with ethical debates surrounding NAGPRA\(^1\) and the repatriation of human remains to descent communities. Many of the most well-trained paleopathologists, specifically those who could work synthetically, creatively, and under newly emerging principles of public engagement (see Blakey 1998b, 2010; La Roche and Blakey 1997) (preponderantly students of Armelagos and of his students) were also enlisted, providing unique contributions and perspectives. For instance, Pamela Bumsted introduced the possibility of empirically tracing residential history over the life course of individuals in the Burial Ground through trace element and radiogenic isotope analysis of dental material, which was an emerging technique in dental biochemistry (see Dolphin and Goodman 2009; Kang et al. 2004 for further discussion). All told, the project brought together the expertise of biological anthropologists, including the University of Massachusetts, Amherst, Howard University, and the University of Oklahoma, and scholars from a number of disciplines at numerous research institutions from throughout the United States, Europe, and Africa. Many of these scholars were united by their embrace of a biocultural approach.

The political economy of the human biology of the New York African Burial Ground that follows was produced from the integration of skeletal information with that of archeologists, historians, geneticists, and others with expertise in regions of Africa, the Caribbean, and the Eastern United States from which the Burial Ground’s culture and biology emerged. This Diasporic and interdisciplinary project is clearly markedly in contrast with either the Darwinian evolutionary emphasis or journeyman forensic and racial emphasis of most (exclusively white) biological anthropology programs and projects in New York and elsewhere.\(^2\) One need not imagine the difference of analysis a diverse and descendant-led project would bring to the study of the human biological toll of slavery. That is entailed in the three volumes of this project upon which the following analysis is based (Blakey and Rankin-Hill 2009; Medford 2009; Perry et al. 2009).\(^3\)

**Case study**

**Background**

**The New York African Burial Ground**

The African Burial Ground sample consists of 419 skeletons, 301 of which are well preserved, buried just outside the wall of the colonial city of New York between the late seventeenth century and 1794. The sample represents about 3% of the cemetery, known as the “Negroes Burial Ground” in the 1700s, which likely contains about 15,000 burials (Perry et al. 2009). The vast majority of these individuals were enslaved at the time of their deaths, though some were free (Davis 1985; Medford 2009). The cemetery represents the largest colonial-era
cemetery in the country, and the earliest African cemetery in New York. The site was excavated by Historic Conservation and Interpretation and John Milner Associates in 1991 and 1992, and is now marked by the African Burial Ground National Monument in Lower Manhattan.

The theoretical uniqueness of the approach that we used rests largely on a clientage model in which the descendant African American community that took responsibility in New York became the “ethical client,” controlling the disposition of remains and contributing substantially to the research design that they and scholars on the project had to agree upon. We worked for them (see LaRoche and Blakey 1997). The sanctity of the site would be retained by its descendant community (a term we introduced to archeology) with the ultimate reburial of its human remains, at the present-day monument.

It is estimated that between 6800 and 7400 Africans were imported into the colony of New York between 1700 and the eve of the Revolutionary War in 1775. The higher estimates are based on undercounting of captives smuggled from New Jersey, and possibly other states to avoid tariff (Medford 2009). According to Lydon (1978:382–383), the minimum estimate, based on extant records for the eighteenth century, includes approximately 2800 or 41% brought directly from Africa and 4000 from the Caribbean (and, less significantly, the Southern colonies). Perhaps one-fifth to one-quarter of those disembarked in New York’s port remained within the city (Lydon 1978), with many living there for the rest of their lives and eventually being buried in the African Burial Ground. Some gained legal freedom, gradually building a free African population, but most died enslaved.

In collaboration with our ethical client, a major research focus of the project has been the relationship between the political economy of slavery in the urban north and the demography and health of the captive populations (see Blakey and Rankin-Hill 2009). This included analyzing the effect of the routing of captives to New York and the specific character of the market for forced labor in the colonial city on the observed demographic patterns (Rankin-Hill et al. 2009). Therefore the research objectives of the work presented here were to identify the nature of the political economic regime (the historically emergent terms or structure of the society’s power relations, labor, and resource distribution) in place during the period the African Burial Ground was in use; how the priorities and demands of the system were regulated and perpetuated; the factors that may have affected the implementation of the political economic program; and how the program impacted the lives of enslaved Africans in ways that can be observed demographically. The basic premise is that while demographic assessment is fundamentally biological in nature, providing a window into the adaptation, health status, and survivability of a population and its members, demography is equally reflective of the social conditions in which these organisms are embedded and upon which they are physiologically dependent.

Pervasive in many historical studies of African Americans is the concept that somehow slavery in the New World stands as an isolated historical deviation of
which the Western world should be ashamed, apologize for, rationalize, and/or study as a separate phenomenon. Others have studied American slavery from a more universal context, as Williams (1961:4) contends:

Slavery was an economic institution of the first importance. It had been the basis of Greek economy and had built the Roman Empire. In modern times it provided the sugar for the tea and the coffee cups of the Western World. … It produced the cotton to serve as a base for modern capitalism. … Seen in historical perspective, it forms a part of that general picture of the harsh treatment of the underprivileged classes, the unsympathetic poor laws and severe feudal laws, and the indifference … [of] the rising capitalist class.

Thus, enslaved Africans in New York were placed into a system that was already formulated, yet upon which harsh particulars of chattel slavery will be shown to develop. In the English colonies, Africans were legally and in practice treated as indentured servants until the legislation of the 1660s. Williams (1961:14) maintains in his controversial work *Capitalism and Slavery* that the origin of negro slavery:

… was economic not racial; it had to do not with the color of the laborer, but the cheapness of labor. … The features of the man, his hair, color, and dentition, his “subhuman” characteristics so widely pleaded, were only the later rationalizations to justify a simple economic fact: that the colonies needed labor and resorted to Negro labor because it was cheapest and best.

Southern plantation slavery was and continues to be the central focus of the majority of historical studies of slavery. Despite the voluminous anthropological, historical, and sociological literature, several areas of research remain underdeveloped. These include such topics as the cultural diversity and genetic heterogeneity of Western hemispheric African American populations that resulted from diverse African origins and admixture with diverse Europeans and/or Native Americans; the experience of urban and northern enslaved African Americans and freedmen during the colonial and antebellum periods; and the diverse and changing living conditions, health status, and lifestyles of African Americans both enslaved and free. Diverse modes of resistance to enslavement, recommended as important by the descendant community, were also found to have pervasive impact. Multidisciplinary, integrative research approaches to African Diasporic populations in the Americas have also rarely been undertaken. The project contributes to the development of these areas of underdeveloped potential with a focus on the location of points of embarkation for enslaved Africans and the characteristics of persons obtained there, the political and economic motives of Europeans in choosing those locations and characteristics, and the biological consequences for Africans of these regions and other related circumstances. Selection criteria included the number, sex, and age of the enslaved that would best fulfill the changing needs of the Dutch, English, and Euro-American populations of New York, weighted against costs of importation, maintenance, replacement, and the security of those engaged in the buying and selling of “human cargoes.”
Results

The trade in African captives

Data on the trade in captives for colonial New York are available from shipping records, which provide information on the place and timing of the trade, from newspaper advertisements, and from private/official correspondence, which indicate some of the parameters of local demand. While a number of cargoes direct from Africa came into New York in the seventeenth century, imports from the West Indies were much more important in the eighteenth century, up to the 1740s. After 1741, the trade shifted to an emphasis on direct imports from the African continent rather than from the West Indies (see Foote 1991; Kruger 1985; Lydon 1978).

We suggest that the age/sex structure and ultimately the sex ratio of colonial Africans among New York City’s colonial and early national (after 1780) African population were linked to changes in the port’s trade in captives, specifically due to changing selection criteria and the differences between African and West Indian cargoes. It is important to recognize that most captives from the West Indies were African born and had spent as little as a few weeks to several years of “seasoning,” a system of commercial and state-sanctioned torture meant to force human beings to behave as chattels, in the Caribbean (see Mullin 1995:86–88, 129–130). Intermittent periods of direct African trading and importation also occurred in 1705, 1710–1712, 1715–1717 and 1721 (Docs. Rel. Col. Hist. NY 5:814; Lydon 1978:377); the late 1720s and 1730s brought the largest cargoes of enslaved Africans from the West Indies. Later, in 1763, large shipments of enslaved Africans were brought in directly from the continent. Several factors drove the structure of the trade. In particular, the especially sharp (and permanent) decline in imports from the West Indies was most likely a reaction to the New York African “slave uprisings” of 1712 and 1741 followed by the subsequent conspiracy trials of 1742 (Medford et al. 2009).

These factors were a catalyst for the redirection towards importation from Africa. This redirection was based on a general impression that West Indian consignments often contained individuals who were potentially threatening to the stability of the slave-holding colony. Indeed, Akan (today Ghana and Ivory Coast)-led Maroons (runaway communities) defeated the British to establish treaty-protected territories in Jamaica in 1739 after years of warfare (Agorsah 1994). A shift toward the importation of captives directly from Africa reduced the portion of sale price associated with the seasoning of men while elevating the proportion of more physically vulnerable women and children captives who arrived with little martial experience.

Most slave holdings in colonial New York County were quite small (i.e., one to three persons), as was typical of urban areas, and households that included enslaved Africans usually had at least one female domestic. Despite its early agrarian nature of small farmsteads, enslaved Africans were also utilized as dock laborers, construction workers, and skilled craftsmen as well as field hands and domestics in the county. Historians have suggested that the New York
market shifted from one largely concerned with agricultural and dock labor in the seventeenth and early eighteenth centuries to one driven by the need for domestic servants in the mid-eighteenth century. Best obtained while quite young, girls were considered to be “ready” for productive domestic work in urban households at younger ages than boys, who were more likely to be needed for physical labor (e.g., Coll. NYHS, Colden Papers, Vol I p. 51). Thus, this early growth and development of the colonial port town of New York established the need for selecting particular ages and genders in the slave trade for the local marketplace. New York merchants, who were well aware of the local market, then initiated a preferential system for African cargoes more likely to include youths, especially girls, than West Indian shipments that held the largest proportions of men.

Age selection
The youth of new imports appears to have been a selling point in the slave market of New York City. Jacobus van Cortlandt wrote in 1698 that the New York market was for negroes aged 15 to 20 (cited in Foote 1991:82). It appears from historical accounts and documents that shipments from the continent contained young girls in particular, who then remained in the city because they were in demand as domestics in a characteristic urban market. Men and adolescent boys, though in demand as laborers in the port town, were more in demand in the nearby agricultural areas. It is important to note that through laws and tariff selection criteria, preferences and regulation were reinforced and institutionalized.

Africans from the continent who were more than four years of age were subject to an import tax as of 1732 (Col. Laws.); presumably, any younger were not taxed because of their high risk of dying and low potential for immediate productivity, while older ones were considered valuable commodities. Overall, it appears that enslaved Africans were put to work by their preteen years. This was certainly the case for domestic workers; males in their late teens would have been put to work at the most demanding types of physical labor on the docks, in construction, hauling, etc. Indeed, enslaved African men were in high demand in the West Indies where work in the sugar cane fields was very demanding (Mahoney et al. 2005; Wilkinson 1988) although women enslaved there have been shown to have often worked as hard as or harder than men (Moitt 2004).

In addition, there was a selection bias against older enslaved men and women in New York. Those over 50 years of age were valued at lower rates for tax purposes, with age 50 generally used as a cut-off for taxation. Colonial laws also reflect anticipated problems with holders of elderly Africans. In 1773 (Col. Laws 5:533), An Act to prevent aged and decrepit slaves from becoming burthensome within this Colony was passed by the provincial Assembly. Fines were levied for selling or freeing aged and/or helpless enslaved individuals. In 1785, a law was enacted requiring a certificate from the overseer of the poor for the enslaved who were over 50 years of age.
Sex selection and the sex ratio

Sex ratios are the comparison of the number of males to females. If equal, the ratio is expressed as 1:1, 1.0 or 100. If males outnumber females, the ratio will be over 1.0 or 100; if females outnumber males the ratio will be under 1.0 or 100. The local tendency for young women or early teens to be the primary choice for urban domestic/household enslavement in New York is corroborated in the New York census data (Table 6.1). For instance, the 1746 census indicates a sharp increase in girls over boys (in the under age 16 category). This corresponds to an inflated adult sex ratio for the year because there were fewer women than men because so many of the females were too young to be counted as adults (Table 6.2). Three years later, the sex ratio declined abruptly as girls aged and became women at 16–18 years of age. These fluctuating values for the 1740s most probably represent an influx of new captives rather than a natural population increase through increased fertility, the realized number of offspring.

Throughout the eighteenth century, sex ratios tended to indicate an excess of females or equal numbers to males. A substantially greater number of males are reported only for 1737. The proportion of males (but not their absolute

Table 6.1 New York African population by age and sex, eighteenth century censuses

<table>
<thead>
<tr>
<th>Year</th>
<th>Adults</th>
<th>Children</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Male</td>
<td>Female</td>
</tr>
<tr>
<td>1703</td>
<td>298</td>
<td>276</td>
</tr>
<tr>
<td>1712</td>
<td>321</td>
<td>320</td>
</tr>
<tr>
<td>1723</td>
<td>408</td>
<td>476</td>
</tr>
<tr>
<td>1731</td>
<td>599</td>
<td>607</td>
</tr>
<tr>
<td>1737</td>
<td>674</td>
<td>609</td>
</tr>
<tr>
<td>1746</td>
<td>721</td>
<td>569</td>
</tr>
<tr>
<td>1749</td>
<td>651</td>
<td>701</td>
</tr>
<tr>
<td>1756</td>
<td>672</td>
<td>695</td>
</tr>
<tr>
<td>1771</td>
<td>932</td>
<td>1085</td>
</tr>
<tr>
<td>1786</td>
<td>Males</td>
<td>Females</td>
</tr>
<tr>
<td></td>
<td>896</td>
<td>1207</td>
</tr>
</tbody>
</table>

Source: *Century of Population Growth*, checked against *Docs. Rel. Col. Hist. NY*. Some discrepancies in the Kruger and Foote numbers have been corrected.
Table 6.2 African adult sex ratio New York County 1703–1800

<table>
<thead>
<tr>
<th>Year</th>
<th>Sex ratio</th>
</tr>
</thead>
<tbody>
<tr>
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<td>107.9</td>
</tr>
<tr>
<td>1712</td>
<td>100.3</td>
</tr>
<tr>
<td>1723</td>
<td>85.7</td>
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<tr>
<td>1731*</td>
<td>98.7*</td>
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<tr>
<td>1737*</td>
<td>110.7*</td>
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<tr>
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<td>1749</td>
<td>92.9</td>
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<tr>
<td>1756</td>
<td>96.7</td>
</tr>
<tr>
<td>1771</td>
<td>85.9</td>
</tr>
</tbody>
</table>

*Note that in 1731 and 1737, the censuses counted persons over or under 10 years of age; thus “adults” were not all of childbearing years. The overall sex ratio for these years was 99.1 for 1731 and 110.6 for 1737.

The 1786 state census and the 1790, 1800, and 1810 federal censuses do not count blacks by sex. According to Kruger, local censuses for the early nineteenth century indicate ratios declining from 72.3 in 1805 to 65.8 in 1819 (Kruger 1985:370).

Source: Century of Population Growth. Discrepancies were found in Foote’s and Kruger’s numbers, and have been corrected. The numbers in Century of Population Growth were checked in Docs Rel. Col Hist. NY.

numbers) decreased most markedly following the 1712 African uprising, the alleged 1741 African “conspiracy” (Africans were accused of burning much of the town; see Davis 1985), and the American Revolutionary War. In the latter case, many Africans collaborated with the British in New York City and negotiated to depart with them, securing their own independence from slavery. Hundreds first embarked for Nova Scotia where an African Burial Ground also exists. Dissatisfied, they later negotiated their repatriation to Sierra Leone, West Africa.

Following the first two historic events, a relative excess of adult females is evident in the records, reflecting either an increased importation of females or increased sale and exportation of men to areas beyond the city. The substantially larger number of girls during the 1740s indicates the effects of high importation of enslaved African girls into New York City and/or sale of boys to areas outside the city. Lydon (1973), Kruger (1985), and Foote (1991) suggest that the English reaction to the 1741 African uprising in New York was the cause of this reduction in the relative (but increase in the absolute) number of African males who were imported during this period. On the one hand, it does seem odd that the absolute number of boys nearly doubled between 1737 and 1746 if indeed fear of rebellious males had actually brought about the skewed sex ratio. On the other hand, boys could be “indoctrinated” into not becoming dangerous men. Women and
older children were preferred for importation during this period, as were direct African imports, as a means of limiting the militant resistance of enslaved people (Foote 1991; Kruger, 1985; Lydon 1973).

Demands elsewhere in the international trade might also have had a negative impact on the availability of men for sale in New York. The sex ratio shifted steadily downward (a proportional increase in females) between 1703 and 1723, with a noticeable drop in the proportion of men to women appearing in the 1723 census. It is also the case that between the census years 1756 and 1771, the sex ratio went from 96.7 to 85.9. Conversely, the sex ratio began to climb (a proportional increase in males) during the years (the late 1720s and 1730s) that saw the heaviest importation from the West Indies (Figure 6.1).

Most historians have pointed to the low overall sex ratio for Africans in New York as a typical pattern for urban slavery (see earlier). Yet the significant fluctuation observed in the sex ratio appears to be highly associated with political upheaval and subsequent attempts at social and legal controls that preserved the institution of slavery and its profits. Biological risk factors that included workload, health status, nutritional status, and the mortality associated with environmental conditions of the population also need to be considered.

We followed these observations with a hypothesis that women were burdened by greater work demands as compensation for the reduction in the adult male workforce. A recent study dividing the Burial Ground sample into four temporal periods of the eighteenth century (Perry et al. 2009) indicates a steady increase in the arduousness of women’s work over time (Blakey 2014). William Daisley, at the Institute for Historical Biology, studied hypertrophy of the linea aspera (a muscle attachment in the back of the femur) indicative of strenuous lifting and walking with loads in the 187 observable adult femora. Of these, 68.4% had a hypertrophic linea aspera, and frequencies increased moderately for the total population from the Early Group in the late seventeenth century to 1735 (57%
hypertrophic), through the Middle Group (1735–1760) (69% hypertrophic), the Late Middle Group (1760–1776) (69% hypertrophic) until the Late Group at the close of the cemetery (1776–1795) (73% hypertrophic). Within the sample, sex-based patterns were more striking. While African Burial Ground males maintained a relative frequency of 71–72% manifesting hypertrophy throughout the century, 28% of females were hypertrophic at the beginning of the eighteenth century, jumping to 59% in the Middle Group and steadily rising to 73% (slightly higher than males) in the Late Group, which represents the early National period. An increased reliance upon African women for arduous labor may be evident in these patterns.

While hypertrophy of the linea aspera is but one musculoskeletal stress marker, it is an important general indicator of work stress on the lower body. Our mapping of bodies as a whole demonstrates a similar distribution of degenerative joint disease (osteoarthritis) for males and females, which is itself notable, and an approximately 26% greater frequency in the knees and nearly 20% higher frequency in the ankles and lumbar spine of females than in males (Wilczak et al. 2009). Therefore the biocultural evidence suggests that the labor required of enslaved New York women was increasingly burdensome over the course of the century in which men are periodically underrepresented.

**Mortality in New York**

Mortality for the seventeenth and eighteenth centuries in America was high, especially in urban areas. New York experienced very similar patterns of health and disease to other colonial American urban centers, in particular port cities such as Philadelphia. Within these, however, the impact of periodic epidemics had a differential effect on populations based on their health status and risk factors (Nash 1988).

Contemporary observers believed that black mortality throughout the northern colonies, especially among infants, was so high that only importations could prevent the black population from gradually dying off (Anthony Benezet (1773), Benjamin Franklin (1751), unnamed Bostonian chronicler (1775), cited in Nash 1988:33). Bills of Mortality for Philadelphia in the period 1767–1775 indicate an average of 75 burials of Africans per year; this represented about seven burials for every 100 blacks per year, a rate about 50% higher than among whites (Nash 1988:34). If a similar death rate were applied to New York, about 219 individuals would have been buried per year in the same period (based on the 1771 census count of 3137 blacks). In each of these circumstances, Africans were likely to have been undercounted, so mortality rates may have been higher. The Philadelphia rates, however, are more reliable than New York because of the Abolition Society’s active role in documenting the accomplishments and conditions of “people of color” in that city (Rankin-Hill 1997).

Environmental and living conditions during the colonial period tended to be unhealthy because of poor sanitation, indoor pollution (e.g., coal fires), non-potable water, and crowded dwellings. For the enslaved, conditions were even
more insalubrious, leading to high rates of morbidity and mortality (Curry 1981; Rankin-Hill 1997). In addition, American cities throughout the seventeenth to nineteenth centuries were “hot zones” for epidemics, providing perfect conditions for acute infectious diseases. Epidemics of smallpox, yellow fever, measles, diphtheria, influenza, and other unspecified fevers have been documented in colonial New York. Smallpox was the greatest source of epidemic “crisis” mortality in New York during the eighteenth century (Duffy 1968:34–35), with smallpox epidemics occurring in 1702, 1731, 1745–1747, and 1752. It is likely that smallpox accounted for a significant portion of the death toll, as it was endemic, acting as a fatal childhood disease, between 1756 and 1767 (Duffy 1968:53–58).

An examination of deaths reported in the 1731 smallpox epidemic indicates that both Europeans and Africans in New York suffered considerable losses. The 1731 Bills of Mortality represent individuals buried at the city’s church cemeteries, tallied by denomination. The number of “blacks” buried is then given, with no church denomination. This indicates that burials at the African Burial Ground were being counted in some form. It is not known how or by whom. During the period of smallpox reporting shown above, 477 Europeans (6.77% of their population) and 71 Africans (4.50% of their population) died in New York. The overall death toll for August–December 1731 was 7% of the Europeans and 5% of the African population. This difference in frequency may indicate an underreporting of black burials, not surprising since it is believed that the Burial Ground was most often utilized without direct observation by European Americans.

Although African deaths may have been underreported, another possible basis for a lower African death rate was the existence of smallpox inoculation. African societies, most notably the Akan people, practiced smallpox inoculation extensively. For instance, it was a “Guaramantese” or Akan-speaking man, renamed Onesimus, who taught the procedure to a Boston clergyman who shared it with physicians in Boston and London. One of these physicians, Zabdiel Boylston, used the technique in time to greatly reduce the impact of a Boston epidemic in 1721–1722 (Cobb 1981:1199–1200). While smallpox inoculation was commonly practiced in the West Indies (Medford et al. 2009), it was controversial among the English, who feared it could spread the disease and prolong its presence in Boston (Koo 2007). After all, inoculation was contrary to European medical intuition and many English colonials could not conceive of or admit to superior African medical knowledge (Koo 2007). The fact that many African New Yorkers had survived smallpox in their youth (whether in Africa, in the West Indies, or in the city) is attested to by the frequent citing of smallpox scarring in runaway descriptions from the city and as a selling point in sale advertisements.

**Paleodemography**

The New York African Burial Ground cemetery sample consists of 419 recovered burials, with 301 of these sufficiently preserved to allow accurate and detailed age
and sex estimation. Estimations of age and sex were based on multiple standard methods (Buikstra and Ubelaker 1994), with age and sex estimated for adults and age alone for subadults that are insufficiently morphologically distinct for reliable estimates of sex (Blakey et al. 2009). Skeletal remains included in the demographic study of the sample included adults ($n = 171$; 56.8% of the sample), representing both males ($n = 102$) and females ($n = 69$), and subadults ($n = 130$; 43.2% of the sample).

**Mortality**

The synthesis of the paleodemographic profile (see Rankin-Hill et al. 2009) and the political economic and historical epidemiological scenarios discussed above contextualizes the experience of enslaved Africans in New York. The impact of the political economic regimes’ selective processes, the intense physical labor, and disease environments of colonial New York are evident in the mortality patterns observed in the African Burial Ground skeletal sample (Figures 6.2, 6.3, Tables 6.3, 6.4). First, the low mean age at death for the sample of 22.4 years of age is even lower than that of a skeletal sample of seventeenth to nineteenth century enslaved Africans from the Newton Plantation in Barbados, who were engaged in the regime of gang labor for plantation sugar cane production, which was notoriously dangerous and exhausting (Handler and Corrucini 1986). In New York, which did not have a gang labor enslavement program, the low mean age at death points to the synergistic effect of political economy, environment, and biological susceptibility. Second, another trend revealed in the skeletal sample is that 45% of all the subadults died by age two. This suggests that infants and young children were at very high risk of dying, and that the potential for population replacement was being severely compromised despite low sex ratios that enhanced fertility. Third, adult mortality peaked in the fourth (30–40 years)

![Figure 6.2](image-url) **Figure 6.2** New York African Burial Ground mortality.
decade of life, by which time 30.1% of adults had died. This loss of adults created a reduction in potential reproductive members early on in the lifecycle. This finding also corroborates the severity of the impact of enslavement on the men and women interred in the African Burial Ground.

Importantly, mortality also varied between the sexes. Among females, 80.5% had died by age 40, compared to 54.1% of the males. Corroborating the historical evidence, this suggests that although women and girls were selected preferentially as domestic laborers, their lot was arduous, increasing their risk of dying...
Table 6.4 New York African Burial Ground subadult mortality

<table>
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<tr>
<th>Age category</th>
<th>n</th>
<th>% Subadults</th>
<th>% Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>0–6 months</td>
<td>29</td>
<td>22.31</td>
<td>9.6</td>
</tr>
<tr>
<td>7–12 months</td>
<td>22</td>
<td>16.92</td>
<td>7.3</td>
</tr>
<tr>
<td>12–24 months</td>
<td>21</td>
<td>16.1</td>
<td>7.0</td>
</tr>
<tr>
<td>2–3</td>
<td>6</td>
<td>4.6</td>
<td>2.0</td>
</tr>
<tr>
<td>3–4</td>
<td>7</td>
<td>5.3</td>
<td>2.3</td>
</tr>
<tr>
<td>4–5</td>
<td>13</td>
<td>10.0</td>
<td>4.3</td>
</tr>
<tr>
<td>5–6</td>
<td>3</td>
<td>2.3</td>
<td>1.0</td>
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<td>1.0</td>
</tr>
<tr>
<td>11–12</td>
<td>0</td>
<td>0</td>
<td>0</td>
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<tr>
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<td>3.1</td>
<td>1.3</td>
</tr>
<tr>
<td>13–14</td>
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<td>1.0</td>
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<td>2</td>
<td>1.5</td>
<td>0.7</td>
</tr>
<tr>
<td></td>
<td>130</td>
<td>100</td>
<td>43.0</td>
</tr>
</tbody>
</table>

young. Second, the third highest mortality is found in adolescents, aged 15–19. This has implications for population reproductive and replacement rates. High rates of mortality are also found among both males and females in the 15–24-year age group, which is indicative of the high rates of forced migration to New York for Africans of those ages. This age-specific peak in mortality is likely produced by some combination of the large number of new arrivals in this category, the vulnerability among those who experienced the horrid conditions of the Middle Passage, and perhaps the stresses of recent entry to adult work regimes by the American born. Third, some evidence of differential mortality is observed in the 15–19-year age group, in which 15.4% of females died compared to 10.8% of males, although this difference is not statistically significant. This result in particular, as well as the overall high mortality by age 40, indicates that women were being removed from the population during the portion of their life course when they were capable of reproducing. Indeed, this pattern continues to be shown in death records for interments at the subsequent nineteenth-century African American cemeteries in New York at Christie Street and Seneca Village, which show much higher numbers of dead girls than boys (Blakey et al. 2009:263), indicating that this pattern of differential mortality between the sexes continued after the colonial period.

Lastly, these paleodemographic trends corroborate and complement findings from analyses of historical/archival and medical historical sources, each with its own limitations (see Rankin-Hill 1997), about the conditions of enslavement. These include evidence of patterns of differential mortality, especially for males and females at ages associated with adult work regimes, poor living conditions,
and forced migration. The political economic organization of a pattern of increased stresses on women is distinguishable in market changes toward domestic work, reductions in male Caribbean forced migration consistent with social control, and an increase in less costly direct shipments of women and children from Africa.

**Population growth and fertility**

New York City municipal census data for the eighteenth century indicate an exceedingly slow growth of the city’s African population. The trends for New York County for 1698 to 1800 indicate that the African (“black”) population remained fairly low throughout the entire period. While population increase among Europeans was also slow, it was greater than amongst the “black” population for the same period, with slow growth during the early part of the century, followed by significant growth from mid-century onward (Table 6.5).

Table 6.5 Population of New York County, 1698–1800

<table>
<thead>
<tr>
<th>Year</th>
<th>Total</th>
<th>“Black”</th>
<th>“White”</th>
<th>% Black</th>
</tr>
</thead>
<tbody>
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<td>1698</td>
<td>4937</td>
<td>700</td>
<td>4237</td>
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</tr>
<tr>
<td>1703*</td>
<td>4391</td>
<td>799</td>
<td>3592</td>
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</tr>
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<td>1712</td>
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<td>8622</td>
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</tr>
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</tr>
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<tr>
<td>1790</td>
<td>31225</td>
<td><strong>3092</strong></td>
<td>28133</td>
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</tr>
<tr>
<td>1800</td>
<td>57663</td>
<td>***5867</td>
<td>51796</td>
<td>10.2</td>
</tr>
</tbody>
</table>

*From census of households in New York City (see below). These figures differ from those given in the 1703 census of the colony of New York, which listed only 630 blacks.

**Includes 1036 free and 2056 enslaved blacks.

***Includes 3333 free and 2534 enslaved blacks.

Source: Foote (1991:78) and White (1991:26), except 1703. Both Foote and White have corrected the raw figures. See also Kruger (1985:131), though there are some discrepancies in the percentages for 1786, 1790, and 1800.
only the New York African Burial Ground and some of the Caribbean islands did not have subsequent population increases after the early slow population growth (Fraginals 1977; Handler and Corrucini 1986). For example, in the lower western shore of Maryland in 1658, there were 100 enslaved Africans, approximately 3% of the total population; by 1710 there were 3500, constituting 24% of the population, primarily based on importations (from Africa and the Caribbean), increased birth rate, and a slight decrease in mortality (Menard 1975:32).

Why, with the ongoing importation of Africans to the port of New York, was there so little growth in the enslaved African population of the colonial city of New York? The historical accounts, demographic, and paleopathological assessments provide significant explanatory evidence directly associated with the changing economic imperatives of that developing colony. We further unpack and summarize these issues below.

**Sex ratios and mortality**

As reported above, the eighteenth century in New York City was primarily characterized by a low sex ratio among enslaved and free Africans. Importation directly from Africa shifted the sex ratio among New York City’s enslaved population in favor of girls and women, while shipments of Africans from the West Indies shifted the ratio in favor of males. The former shift is associated with the aftermath of, and English responses to, African rebellions. Due to the larger economic shifts discussed above, girls were considered ready for domestic work in urban households at younger ages than boys were for manual labor, ultimately increasing the demand for females (see Figure 6.1). Therefore, the high numbers of females and adolescent girls with the potential to reproduce at minimum should have led to a natural increase in the African population. Juxtaposed with this is the effect of high mortality, with differential patterns selecting against infants and toddlers, women and adolescent girls and boys. This establishes a synergistic effect, unique to New York City’s communities, which eliminated the procreative segments of the population and the progeny of those who managed to reproduce.

**Fertility**

Kruger (1985:403–420) has made the most ambitious attempt to analyze the meager data available pertaining to childbearing and fertility in New York’s enslaved African population. Almost no data are available on African women’s ages when their children were born. What is known is that in 1796, an individual named “Africanus” proposed emancipation of all enslaved females born after 1796 at age 17, along with all of the children they already had. He estimated that three-fifths of them would already have borne children at that age (Daily Advertiser, January 26, cited in Kruger 1985:405). Therefore, African young women were reproducing prior to age 17. Kruger (1985:410–412) calculated median birth spacing at 28 months, and inferred that during the period
1799–1826, breastfeeding appeared to have continued for 16–18 months after birth.\(^5\) Therefore, women were potentially capable of producing 4–6 children between the ages of 15–30 years.

**Child-to-woman ratios**

Despite the potential for population growth, the low child-to-woman ratios (a proxy for direct fertility data) derived from census data further attest to the absence of increase in the New York African population. The 1746 peak in African children in New York City may be associated with importations of girls and boys under 16, not to natural increase through births. This is evidenced by the marked decline in children per woman of childbearing years as importations abated (Figure 6.4). These data show clearly that an African woman of reproductive age (and her male partner) bore one or fewer children on average. If the number of children in the census who were actually born in New York is small then fertility in New York City may have been much lower than one (surviving) child per African woman of reproductive age.

**Paleopathology**

Paleopathological evidence from the project paints a picture of overall very poor health for enslaved and free Africans of colonial New York City. Females appear to have been involved in strenuous labor from adolescence onwards, with high rates of degenerative joint disorders, musculoskeletal stress markers (enthesopathies) (Wilczak *et al.* 2009), nutritionally inadequate diets, and high rates of general infections (Null *et al.* 2009). Evidence of syphilis, which has

\[\text{Figure 6.4} \text{ African child-to-woman ratio New York City.}\]
been associated with low fertility in the Caribbean (Khubadux 1989, 1991), was rare in the New York African Burial Ground sample, perhaps because they were newly exposed to the environment of European colonialism in which sexual exploitation of enslaved women was common (Khubadux 1991; Null et al. 2009). However, each of these factors, especially when acting synergistically, can have a negative impact on fertility and fecundity. The large number of perinatal, newborn, and infant deaths demonstrates fertility – there were children available in the population to die – yet survival past infancy was insufficient to produce a natural increase in population size.

In addition, paleopathological data from subadults indicate that those under the age of two were at high risk of mortality due to nutritionally compromised mothers, nutritional insufficiency, infection, and possibly infanticide (see below). This is evidenced by high rates of childhood dental enamel defects in those under 14 years of age (86.5%) who are the most likely to have been born in New York, 15–24 years of age (80%) and 25–55+ years of age (66.7%), the latter of which are consistent with those whose childhood defects are the most likely to have occurred in Africa (Blakey et al. 2009). Skeletal evidence of infection, porotic hyperostosis (Null et al. 2009), which may be indicative of nutritional deficiencies and hemolytic and megaloblastic anemias, and retarded growth and development (Goode-Null et al. 2009) was also common.

**Discussion**

The political economic regime (Figure 6.5) of enslavement in eighteenth-century colonial New York City established a biological lifestyle of arduous work for enslaved Africans, and increasingly so for adolescent and adult females over the course of the century. This resulted in physiological disruption due to the potentially synergistic interaction of intensive and chronic physical exertion and energy expenditure, utilization of dietary nutrients, utilization of marginal nutritional stores, exposure to environmental hazards, and utilization of immunological and psychophysiological responses. The demographic, paleodemographic, and paleopathological data suggest that these factors would have produced low fertility and fecundity, proportionate to the arduousness of women’s work, especially in the eighteenth century. These stressors appear to have been sufficient to overwhelm the advantages for fecundity of a low sex ratio and low skeletal presence of syphilis. The early mortality of women and of children is also explicable in light of these stressors. Together with the effects of the market, the demands of their labor and social life, and African resistance to European management of slavery, produced a continuous natural decrease in the African population of the City of New York. Over the course of the eighteenth century, Europeans and, towards the century’s end, European Americans compensated for this by continuous forced importation of Africans, with disproportionately large numbers of
Trade in Africans
Responsive to local political, social and economic forces
Mainly from West Indies through 1740
More direct from Africa after 1741

Urban situation
Typical low sex ratio
Demand for dockworkers and other day labor, domestic labor

Local market
Agricultural and public needs shifting in 18th century to domestic and day labor needs
Youth emphasized in local sales
Increasing demand for young girls for domestic drudge labor

Holding size
Small urban households with limited in-house labor needs
Average holding of enslaved Africans: 2.4
Sales of young children beginning at age 5
Neglect and disposal of older Africans

Social control
Political and market response to active resistance
Decreased importation of men, decreased importation from West Indies

Ideology
Unlimited Goods

Figure 6.5 Summary of relevant political economic factors.

women and children, who would come to comprise 20% of the city’s population by the War of Independence.

Finally, we mentioned at the outset that African Diasporic writers have typically emphasized the impact of racial ideology on the condition of their people. The bones do not tell us what people thought in colonial New York, although they do provide evidence of the material consequences of ideas that mediate decisions. We explained that lives of the enslaved were made harsh. Some consideration given to ideology helps explain why this was so. How, we should ask, did Europeans tolerate treating these obvious humans (engaged in human labor) in ways that by law were not tolerated amongst other Europeans?
The rare written perspectives of enslaved Africans themselves reveal European attempts to resolve this contradiction, both brutally and ideologically, whose shadowy effects were shown in the bones.

The immorality of an attitude that accommodates human expendability was disguised by the idea that Africans, as presumed non-Christians, were less than human, a function that passes to the idea of race by the nineteenth century (Smedley and Smedley 2012). There were also rare efforts of conversion, meant to ideologically construct New England slaveholders as charitable, but these too were met by the objections of the enslaved to their near intolerable condition (see Koo 2007). Attempts to make Africans believe it was morally acceptable to be used as another’s property were untenable by all accounts of enslaved Africans in the north east (Gates and Andrews 1998).

John Jea was born in Calibar in 1773 and was enslaved with his family in New York at the age of two years. He wrote that his fellow enslaved Africans worked from 18 to 21 hours per day with little food and frequent floggings; beatings and starvation were both used to force compliance. Having confronted his “mean master” about the duplicity of Christian slaveholders, Jea was forced by wrenching indoctrination to convert as a way of controlling him. But Jea found a way out through the contradiction. An enslaved New Yorker could be freed if he converted to Christianity, but that person would have to read the Bible in order to fully prove his conversion, and the enslaved were prevented from learning to read by the slaveholders. Jea successfully petitioned the city magistrates to become free by claiming to be able to read only the Bible, miraculously. He became “The African (“not an American”, p. 434) Preacher” and converted over 1500 fellow Africans in New York, aware of what conversion afforded to “deliver them ... out of all their distress (p. 397)” and to seek manumission by an extant “Act of Congress” (p. 395). Yet his own siblings were afraid to go before the magistrates in pursuit of legal recourse for their enslavement. His interpretation of the Bible stressed equality against the European interpretations that condoned inhumane chattel slavery. His first wife’s mistress tried to “persuade her not to be so religious, for she would make herself melancholy (p. 399).” Psychologically torn, his native wife killed their infant and her pregnant mother who had protected it (pp. 400–401) (John Jea’s narrative in Gates and Andrews 1998). These were desperate times.

**Conclusion**

The economic desires and environmental constraints established by New York slaveholders produced the conditions (Douglass said, “circumstances”) for physiological disruption that substantially impacted population growth. The economic strategy was one of “unlimited goods” since the enslaved captives could be replaced continuously. The enslavers had no financial incentive for
encouraging fertility or giving intensive care to infants, who demanded high investment but could do little work. However, abusive practices of the British Caribbean colonies, where infants were taken from their mothers immediately to minimize loss of labor, were not documented for New York (Genovese 1967; Weinstein and Gatell 1968). The city’s slaveholders also showed no desire to possess very young children, those under the age of four, nor to “breed” their captives as later generations of slaveholders would do for the domestic trade once the transatlantic trade in human captives ended, cutting off the supply of new imports. Importation satisfied their need for the enslaved to build and maintain the city and keep its products and profits flowing.

In early critiques of biocultural approaches in medical anthropology (Singer 1989), the biocultural approach was not considered broad enough because it did not specifically incorporate the impact of political economy. While a few of us did incorporate it, it is true that many human biologists attempting to integrate culture did (do) not (Goodman and Leatherman 1998:3–42 give a full discussion). Therefore, the African Burial Ground research project was created as an attempt to design an integrative biocultural approach to an historical skeletal population using a political economic lens. The particular characteristics of this sacred site of a population enslaved by a global trade in human cargo, within a nascent capitalist and industrial regime, with a rare archeological population of adequate size and a descendant community raising critical questions about their ancestors’ condition and struggle, pointed to the approach we ultimately took.

What we present here is a portion of the research methodologies, assessments, and results from a diverse group of specialists who worked together to cross-reference and integrate their diverse findings in order to reconstruct the lives of enslaved people in early New York. Each form of research method or resource provided information contributing to a mosaic African Burial Ground community. Documents, such as historical records, medical historical accounts, demographic records, slave owners’ wills, inventories or diaries, provide details, assessments, and the background to the time period and conditions. It is important to remember that measurements and assessments of skeletons only provide indicators; it is the analysis of these indicators within the framework of human biology, adaptation, ecology, and political economy that provides the broader nuanced picture of a population’s existence. Our choice of an appropriate “big picture” assigns meaning and gives direction to the story. None is more authoritatively objective than another, and plausible stories lie in the discussion among multiple lines of evidence.

The writings of John Jea, discussed earlier, are based on direct observation, unlike the chapter’s skeletal biology with which it may seem incompatible. But together they give us greater understanding. As “skeletons do tell tales,” Jea corroborates the evidence and “voices” his story. Let our science also elevate his voice.
Chapter 6: Political economy of African forced migration and enslavement

References


Douglass, F. (1854) *The Claims of the Negro, Ethnologically Considered: An Address, Before the Literary Societies of Western Reserve College, at Commencement*, Lee, Mann and Company, Rochester, NY.


Chapter 6: Political economy of African forced migration and enslavement


**Notes**


2 The definitive effect of such objectification is to “naturalize” the past by interpreting a population using naturalistic theories and methods that ostensibly distance the remains of people from the real historical decisions and cultural context that affected them. Indeed, this scientific procedure is itself read as though not in the real, subjective world in which scientists think and work. Thus, living descendants claims to a universal (since Neanderthal) human right to their memorialization are thus delegitimized.
(as is their humanity) by making their ancestors into objects under the authority of a postcolonial scientist community, a community comprised predominantly of persons who are socially positioned as the beneficiaries of the inequities of colonialism, slavery, and continuing white privilege. In the natural story, their ancestors bear no responsibility (and are not immoral) and their descendants imagine that they are uniquely neutral (“normal” or racially unmarked) representatives of humanity (Blakey 1990, 2001; Frankenberg 1994) whose advantages are merited, not taken from other people. The Phi Beta Kappa award winning *Ecological Imperialism* (Crosby 1986) says it all, referring to enslaved Africans as “portmanteau” organisms such as livestock, with God and nature as the creative hand of colonialism and slavery (Blakey 1989). Selective historic omissions, such as the effective denial of slavery in the North pervasive at the moment of the Burial Ground’s discovery, have accomplished a similar purpose. African Americans were rightly concerned that a European American forensic team would have sought the least critical interpretations of the physical evidence of slavery.

3 www.nps.gov/afbg/learn/historyculture/archaeology-reports.htm

4 Also see Cobb (1981) on the continuous denial of this fact by white medical historians.

5 These have been compiled for the period by the Office of Public Education and Interpretation of the NYABG Project. Historical biological evidence for nineteenth-century enslaved African Americans points strongly to weaning at ages 9-12 months with a modal two-year birth spacing associated with the breeding regime in which the fecundity of the enslaved was enhanced for the purposes of the domestic trade in captive people that followed the 1808 Anglophone laws prohibiting transatlantic trade (Blakey *et al.* 1994). The shortening of birth spacing by four months may evince a modest enhancement of fecundity and fertility, while changes in mortality with the likely emergence of an attitude of “limited good” probably deserves greater attention for explaining the rapid natural increase of African Americans in the nineteenth century.
CHAPTER 7
Identifying the First African Baptist Church: searching for historically invisible people

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Introduction

Since the 1950s, the experience of Afro-Americans in the Americas has been of interest to historians, anthropologists, sociologists, and, more recently, scholars of black and African American studies. In order to be clear in the use of terminology, Afro-American denotes African Diasporic Western Hemisphere populations; African American will be used only for North American (US) populations. Despite the diversity of disciplines involved, research on the experience of Afro-Americans in the New World (Western Hemisphere) can be characterized as yielding an overproliferation of works but an underdevelopment of approaches and scope.

Afro-American archaeological research has been extremely limited. Archaeological studies have primarily focused on reconstructing the lifestyles of African American communities in the north eastern United States (Baker 1982; Bridges and Salwen 1982; Paynter 1990; Schuyler 1982) and southern plantations (Otto 1975, 1982; Singleton 1985).1

Boas (1906, 1909) was the first anthropologist to seriously advocate a research focus on Afro-Americans during the early twentieth century. He proposed the creation of an “Africa Institute” of anthropological research focusing on the accomplishments of Africans, anatomical studies, and statistical analyses. This was to fulfill a twofold purpose: to eradicate racism by showing whites the positive attributes of African Americans’ African ancestors and disproving the biological, psychological, and moral inferiority myths concerning them; and to improve the African Americans’ self-images and conditions by making them less “despondent,” more hopeful, more proud of their heritage and ambitious to change their conditions. In addition, he suggested that anthropological research should focus on the American “negro” as an excellent example of a population undergoing culture change and environmental adaptation. Although
Boas’s innovative views have produced the modern configuration of American anthropology, his ideas concerning African Americans were heeded by few.

Despite the voluminous anthropological, historical, and sociological literature, several areas of research have been ignored. These include such topics as the heterogeneous nature of Afro-American populations because of diverse African provenance and admixture with diverse Europeans and/or Native Americans; the experience of urban African American enslaved and freedmen during the antebellum period; the living conditions, health status, and lifestyles of non-enslaved Afro-Americans; changing American sociocultural conditions (e.g., industrialization) and their impact on African American conditions; and the health status and biological adaptability of Afro-Americans. In addition, multidisciplinary, integrative research approaches to New World Afro-American populations have rarely been undertaken.

For example, in many New World societies, such as in Cuba, Brazil, Peru, and New Orleans, Louisiana, freedmen (enslaved individuals who obtained their freedom) were accepted as another social class with rights, privileges, and resources distinct from the enslaved. In the United States except for Louisiana, it was difficult to be manumitted (the purchase of freedom by an enslaved person or their relative). Freedmen were considered divisive, feared, and treated not much better than slaves, with no “place” in the society. Despite the obviously significant impact of this tenuous social status on the individual and the African American community, research on the subject is virtually non-existent. How did African American ex-slaves and freeborns survive in an urban environment that was hostile, where they were marginalized and had to live in a wage economy in a non-agricultural setting where food supplementation, through hunting, gathering, and small-scale farming, was limited or not possible? What were the conditions that manumitted slaves found upon receiving or buying their freedom? Were they different from those of freeborn Afro-Americans? This chapter begins to provide some answers to these questions.

The urban environment of colonial America was not a very healthy one. In particular, the residentially segregated European immigrant poor and African Americans both endured unsanitary conditions, exposure to infectious diseases, and dark, dank, congested neighborhoods. These environmental conditions, coupled with the generally low socioeconomic status of African Americans, enslaved and free, must have placed severe psychosocial and biological stress on individuals and their community.

Case study: Afro-American biohistory

During the last 30 years, Afro-American biohistory has evolved into the study of both the biological and sociocultural factors that have affected the health, fertility, morbidity, and mortality of New World Afro-Americans, the enslaved and their descendants, within an historical context, making it the meeting ground
for many disciplines. This expansive and complex area of research is not easily delineated because of its broad geographic, temporal, and topical range. The geographic range of Afro-American biohistory includes the entire New World. The majority of these studies focus on plantation societies of the southern United States (Cardell and Hopkins 1978; Gibbs et al. 1980; Kiple and Kiple 1977a), British West Indies (Craton 1976; Higman 1979; Kiple 1984; Sheridan 1975), Cuba (Eblen 1974; Fraginals 1977), and Brazil (Cooper 1986; Goodyear 1978), the major slaveholding territory in South America, and overall patterns (Genovese 1992; Tadman 2000). Temporally, Afro-American biohistory spans the fifteenth through nineteenth centuries, beginning with the first Africans arriving with the conquistadors and ending at the close of the nineteenth century when slavery was abolished from the hemisphere (1886 in Cuba).

Afro-American biohistory is not only the study of those who were enslaved, but of those “Afro-American societies” that were forged throughout the African Diaspora in the New World. Biohistorical studies must consequently take into account the diversity of these populations created by time, history, culture, geography, and ecology. Therefore, Afro-American biohistory should be considered as a field that studies the adaptations of humans of African origins to biological, environmental, and sociocultural stresses of involuntary migration and resettlement in the New World. The topical scope of the field encompasses issues of interest to economists, demographers, historians, physicians, political scientists, and anthropologists (see Rankin-Hill 1990 for further discussion).

Biohistorical studies should have a broader approach that would include a biocultural approach, focusing on the interactions of culture and biology; the investigation of adaptive strategies; the consideration of an ecological context for health and disease; a focus on localized Afro-American groups or populations, which would provide a means of assessing biological, cultural, and environmental conditions cross-culturally; and the consideration of intrapopulation variation. These approaches are fundamental to modern biological anthropological research and can contribute new information, perspectives, and reevaluations to Afro-American biohistorical research. The case study that follows on the First African Baptist Church cemetery site presents an example of a biocultural biohistorical research project.

**Background**

**Afro-American biohistory and biological anthropology**

During the late nineteenth and early twentieth centuries, physical anthropology contributed significantly to our understanding of African American anthropometry and growth and development. Modern biological anthropology, the field’s modern incarnation, on the other hand, offers a unique contribution to Afro-American biohistory in both scope and method. Biological anthropology’s most significant contributions are models for studying human populations from a biocultural perspective and skeletal biological analyses. It provides more direct
methods for health assessment since there have been very few skeletal populations of African descent available for study; those that were examined were treated from a “racial,” ahistorical, atheoretical approach. Therefore, biological anthropology provides a broader theoretical scope for Afro-American biohistory.

**Biocultural model**

The basic biocultural framework can be modeled to address a particular area of research or problem. An example is the paleoepidemiological research model (Figure 7.1) proposed by Goodman et al. (1984) for investigating the skeletal biology of archaeological skeletal samples, which provides a means for asking questions about the causes and results of stressors and physiological disruptions experienced in the past. In skeletal biology, the bones and teeth of prehistoric and historic skeletons are examined for evidence of pathologies, growth disturbances, and stress indicators. When placed in the context of a past population’s lifeways and history, analyses of these create ways to assess the overall health status of a skeletal sample and the once living population they represent, as well as the conditions that affected health in the past.

**The First African Baptist Church cemetery, Philadelphia, PA**

Here the focus is on the application of a biocultural approach to a biohistory of a nineteenth-century African American population. A critical goal was establishing who the people interred in the cemetery were, and what kind of community they lived in, as they had been rendered invisible in history and had been long forgotten under the pavements of Philadelphia. The overall results from the project, which established the context and substance of African American life during the time period, are summarized here, followed by a discussion of the material lives of African Americans and the women of the First African Baptist Church (FABC).²

**First African Baptist Church congregation**

The First African Baptist Church of Philadelphia was founded in 1809 by 13 persons, including the Reverend Henry Simmons. The first 30-member meeting house was established at 11th and Vine Streets with the aid of the Euro-American First Baptist Church and an “attitude of benevolent paternalism” (Parrington

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**Figure 7.1** Generalized model for the biocultural analysis of skeletal remains. Source: Goodman et al. (1984).
The Baptist Association of Philadelphia seated delegates from the FABC from its inception, unlike the Methodist, Presbyterian, and Episcopalian entities that first opposed the establishment of African American churches.

Brooks (1922), in his official history of the First African Baptist Church, states that in 1816 “a rift occurred in the congregation” due to the membership and aid to incoming ex-slaves, creating a schism. The splinter group, consisting of many of the original founding members, including Reverend Simmons, established a new meeting house two blocks away at 13th and Vine Streets. However, the dissident church ran into financial difficulties in 1822, and its property was sold at a sheriff’s sale. The congregation relocated the church and established a burial ground on Reverend Simmons’s land, at 8th and Vine Streets (Milner 1981). This location of the FABC site, where the meeting house and cemetery were situated, is illustrated in Figure 7.2.

The cemetery, discovered in 1980, is the burial ground of this dissident FABC congregation. The cemetery was used from circa 1822 until 1843. The Philadelphia Board of Health condemned the cemetery in 1841 due to overcrowding, but the congregation recorded interments in 1842 and a second Board of Health condemnation was decreed in 1843. Historical documents do not offer any information on the FABC from 1841 until the death of Reverend Simmons in 1851, when all his properties were sold. Therefore, the fate of this dissident FABC congregation appears to be lost. The original mother church, after years of declining membership (Brooks 1922), exists today at another location. Reverend Simmons’s properties were razed in the 1850s and replaced by a factory and a row of houses. The cemetery became the backyards, walls, and privies of these homes, which stood on the site until the 1960s when they were demolished and replaced.

Figure 7.2 First African Baptist Church location and African-American households residential segregation patterns (line density represents population density).
by a parking lot. Therefore, the FABC burials were preserved until their discovery and excavation in the 1980s (Parrington and Roberts 1984).

**Archaeology**

Excavation of the Philadelphia Commuter Rail tunnel led to the discovery of the FABC cemetery, which is located in the “Center City” area of Philadelphia. Following the discovery in November 1980, the cemetery was resealed for its protection and a document search was conducted to identify, date, and locate the cemetery in historical context. A four-year legal process ensued to determine legal responsibility and the proper course of action. Public hearings were held, and the present-day FABC congregation was consulted. The culmination was the placement of the site on the National Register of Historic Places.

Michael Parrington, of Milner Associates, excavated the cemetery in 1984 and 1985, uncovering approximately 140 burials that represent members of the FABC interred circa 1822 to 1843. Burials were sent to Dr J. Lawrence Angel of the Smithsonian Institution in Washington, DC, for analysis. The author, through a Smithsonian fellowship, was able to undertake the study presented in this chapter.

The archaeological investigation mapped the cemetery as consisting of two main rows running north and south (Figure 7.3). Many graves were closely aligned, with as little as 6 inches between them; multiple interments of as many as six burials in each plot were common. This pattern is probably an indicator of the congregation’s relative poverty and the general overcrowding in this part of Philadelphia during the nineteenth century (Parrington and Roberts 1984). Several pieces of pottery, single shoes on top of six coffins, and single coins placed near the head in eight burials, all considered customs of African origin, were the only artifacts found with the burials (Parrington 1985; Parrington and Roberts 1984; Parrington and Wideman 1986). Other artifacts or grave markings were lost to surface destruction when the housing, factory, and parking lot were constructed, thus obscuring information concerning individual identity or other cultural mortuary practices of the congregation.

**Materials and methods**

**FABC skeletal remains**

The FABC cemetery consisted of 144 burials (Parrington and Roberts 1984); of these, 135 skeletons were recovered, including 75 adult (56%) and 60 subadult (44%) skeletons. The adults consisted of 36 males and 39 females. The majority of subadults (55%) were under 12 months of age; 23.3% were 1–5 years old, and 21% were aged 6–16 years old. The adult age and sex distribution is summarized in Table 7.1; Table 7.2 summarizes subadult age distribution. Table 7.3 provides contemporary religious affiliations in Philadelphia, which includes the FABC congregation based on the 1838 census.
An investigation of the material lives of free African Americans in nineteenth-century Philadelphia faced a serious problem, that of their invisibility in the historical record. This is a common problem in studies of non-elite people in the historical past, especially members of the underclasses, who to a great extent were the essential elements of a growing society but remain obscure in the literature of the period. Elites leave significant documentation of their lives in a variety of forms such as tax records, church records, social registers, newspaper accounts, personal diaries, etc. These materials have a high probability
Table 7.2  FABC subadult mortality by age group

<table>
<thead>
<tr>
<th>Age in years</th>
<th>n</th>
<th>% Child deaths</th>
<th>% All deaths</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;1</td>
<td>34</td>
<td>56.7</td>
<td>24.3</td>
</tr>
<tr>
<td>&lt;2</td>
<td>11</td>
<td>18.3</td>
<td>7.9</td>
</tr>
<tr>
<td>3–5</td>
<td>4</td>
<td>6.7</td>
<td>2.9</td>
</tr>
<tr>
<td>6–15</td>
<td>11</td>
<td>18.3</td>
<td>7.9</td>
</tr>
<tr>
<td></td>
<td>60</td>
<td>100.00</td>
<td>43.0</td>
</tr>
</tbody>
</table>

Table 7.3  Denomination of church and color of households

<table>
<thead>
<tr>
<th>Denomination</th>
<th>Black</th>
<th>%</th>
<th>White</th>
<th>%</th>
<th>Totals</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Methodist</td>
<td>1973</td>
<td>59.9</td>
<td>31</td>
<td>0.9</td>
<td>2004</td>
<td>60.8</td>
</tr>
<tr>
<td>Baptist</td>
<td>204</td>
<td>6.2</td>
<td>48</td>
<td>1.5</td>
<td>252</td>
<td>7.6</td>
</tr>
<tr>
<td>Episcopalian</td>
<td>178</td>
<td>5.4</td>
<td>1</td>
<td>0.0</td>
<td>179</td>
<td>5.4</td>
</tr>
<tr>
<td>Presbyterian</td>
<td>194</td>
<td>5.9</td>
<td>0</td>
<td>0.0</td>
<td>194</td>
<td>5.9</td>
</tr>
<tr>
<td>Catholic</td>
<td>48</td>
<td>1.5</td>
<td>44</td>
<td>1.3</td>
<td>92</td>
<td>2.8</td>
</tr>
<tr>
<td>Lutheran</td>
<td>7</td>
<td>0.2</td>
<td>0</td>
<td>0.0</td>
<td>7</td>
<td>0.2</td>
</tr>
<tr>
<td>Dutch</td>
<td>0</td>
<td>0.0</td>
<td>1</td>
<td>0.0</td>
<td>1</td>
<td>0.0</td>
</tr>
<tr>
<td>Quaker</td>
<td>0</td>
<td>0.0</td>
<td>5</td>
<td>0.2</td>
<td>5</td>
<td>0.2</td>
</tr>
<tr>
<td>Unspecified</td>
<td>22</td>
<td>0.7</td>
<td>20</td>
<td>0.6</td>
<td>42</td>
<td>1.3</td>
</tr>
<tr>
<td>Non-church</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>519</td>
<td>15.8</td>
</tr>
<tr>
<td>Totals</td>
<td>2626</td>
<td>79.8</td>
<td>150</td>
<td>4.5</td>
<td>n = 3295</td>
<td>100.0</td>
</tr>
</tbody>
</table>

of being stored, inherited, collected, and eventually reprosed in archives. The few sources of documentation for the underclasses, such as church, almshouse (poor houses), and beneficial society’s records, are likely to be lost.

Yet Philadelphia, because of its particular social, religious, and economic characteristics, provided a relatively good source of information concerning African Americans. As a center for abolitionists and Quakers, Philadelphia became a hub of activity which generated invaluable records and information (albeit limited) concerning Philadelphia African Americans and their material lives. In addition, because of the city’s national historical role, there are diverse sources of national and city history that can potentially offer up documentation. Capitalizing upon this, the project’s research design included utilizing multiple methods: a document and literature search; demographic analyses employing paleodemographic and historical demographic methods; and skeletal biological analyses based on paleopathological methods. Data from these assessments were analyzed statistically and considered within a biocultural framework.

Document and literature review
The objectives of this review were to identify historical materials and relevant literature pertaining to nineteenth-century Philadelphia that would provide
a means of reconstructing the environmental and sociohistoric contexts of its inhabitants, with primary emphasis on African Americans; describing the African American population’s demographic, socioeconomic, religious, and sociocultural factors as well as their environmental and living conditions; clarifying what segment(s) of the African American population the FABC congregants represented; and describing morbidity and mortality patterns that would facilitate the interpretation of skeletal biological evidence (Figure 7.4). The review focused on uncovering the social and legal status of free African Americans in antebellum Philadelphia, the history of slavery and emancipation in the state and city, and the history and role of African American churches, particularly the First African Baptist Church.3

Paleodemography and historical demography
Paleodemography and historical demography provide invaluable population information when used concomitantly within skeletal biological studies. Paleodemography is the study of vital rates, population distribution, and density in extinct as well as extant human groups, especially those for which there are no written records (Buikstra and Konigsberg 1985:316); accurately aging and sexing each skeleton is fundamental to this enterprise (Angel 1969). Despite criticisms of paleodemography (Bocquet-Appel and Masset 1982; Wood et al. 1992) and reassessments (Armelagos and Van Gerven 1983; Buikstra and Konigsberg 1985; Greene et al. 1986; Johansson and Horowitz 1986), paleodemography continues to provide an essential means of understanding
the vital rates, population structure, and change of archaeological populations (Meindl and Russell 1998).

Historical demography studies vital rates, population structure, and change based on available documents. Birth, death, marriage, and/or tax records are examined to determine morbidity, mortality, and fertility in a population. In both prehistoric and historic populations, scrutinizing the age and sex structure and density of a population can provide information on health status, but the emphasis is on patterns of mortality (see Figure 7.4). Combined with archaeological data and skeletal evidence of physiological stress, the impact of nutritional inadequacy and disease on differential mortality can be assessed.

Paleodemographic analysis based on the age and sex of the FABC burials (Angel et al. 1987) generated insights into the vital rates, population structure, and, in turn, health status of the FABC sample. Historical demographic data from the US census, vital rate reports (Emerson 1827, 1837, 1848), and the FABC partial interment records were compared with these paleodemographic patterns, focusing on age/sex ratios, mortality patterns, and seasonality of deaths. In addition, historical demographic studies (Condran 1984; Condran and Cheney 1982) for Philadelphia during the latter half of the nineteenth century were used to place the paleodemographic and historical demographic assessments into context.

Skeletal biological analyses: methods of health assessments

Human bone provides an excellent source of information on health status because it is metabolically initiated, nutritionally tempered, physiologically controlled, and biomechanically shaped (Vaughn 1975). Bone provides a measure of biological and behavioral (cultural) factors that have affected the health of an individual and, in turn, their population, including nutrient intake, metabolism, genetics, aging, hormonal interactions, and biomechanical stress, diet, type and levels of activity, lifestyle, and reproductive history.

The skeleton is a dynamic system that undergoes growth and development throughout the individual's life span. The average human engages in bone growth between conception and age 20, achieving peak bone mass development between 12 and 40, but predominantly experiences bone resorption between age 30 and death (Martin et al. 1985). The above biological and behavioral factors can interfere with these processes, causing disease episodes and/or periods of arrested growth. These experiences can be indelibly recorded on the skeleton and dentition, leaving behind a means of assessing the individual's general health and disease history. Through observing these "historical remnants," both macroscopically and microscopically, aggregating them across the skeletal sample and placing them within a biocultural interpretative framework, the biological anthropologist has a means of measuring the health of the past population they represent. Analyses at the macroscopic level can include paleopathological analysis of the skeleton and dentition, anthropometric measurements, and assessment of growth and development. Anthropometric measurements and
the respective indices serve as a way to determine stature, growth patterns, and degree of sexual dimorphism in a skeletal sample and the population they represent. Anthropometric measurements and growth assessment provide data that can then be correlated with paleopathological analyses to clarify and elaborate the health status of a population. Microscopic analyses can include bone histology and biochemical and biomolecular analyses. In addition, reconstructing the skeletal sample’s demographic patterns provides another data source to assess their general health status in terms of morbidity and mortality.

**Paleopathology**

One of the foci of paleopathological analysis is reconstructing population health status through identification of specific and non-specific stress indicators on individuals in a skeletal sample. Stressors are considered to be extrinsic variables that affect the organism’s ability to function; the body responds through experiencing stress, to varying degrees, which can manifest on the skeleton in a variety of ways. Some individuals may be biologically or culturally buffered from the stressor, meaning that they might experience minimal or short-term stress, and not manifest an osseous record. However, disease states lasting as few as four days can interrupt growth, producing growth arrest markers such as enamel hypoplastic defects on teeth. Chronic stresses can permanently affect growth and development and alter adult skeletal dimensions, reducing adult stature (Buikstra and Cook 1985:444).

Even with extensive environmental reconstruction and substantial archaeological data, it is difficult to ascertain the exact source of stressors experienced by past populations. In addition, the skeletal system, which has numerous biological functions and interfaces with several other systems, tends to react in limited generalized ways to stressors as an adaptive mechanism. And, it is usually the last biological system to react to malnutrition and disease stress (Ortner 2003).

Many disturbances may produce similar results, and the identification of a single causative agent may not be possible. This is particularly true in the case of nutritional deficiencies, in which the synergistic effect of multiple deficiencies, or of interactions with infectious disease, is frequently a complicating factor (Huss-Ashmore *et al.* 1982:399).

Demographic and burial information was recorded for each individual, adult and subadult, including sex, age, stature, age group, and burial group. Each adult skeleton was examined for evidence of pathology, trauma, and/or joint degeneration, with the description of the pathologies including their location, severity, and status at time of death, as well as whether a specific diagnosis, such as tuberculosis, could be attributed or whether the lesion was non-specific, such as periostitis, the subperiosteal deposition of bone (following Mensforth *et al.* 1978). Skeletal evidence of trauma was recorded as well indicators of undernutrition and metabolic diseases, such as porotic hyperostosis, porous lesions on the cranial vault. Additionally, congenital, biomechanical, and non-specific anomalies were also recorded, as well as indicators of growth arrest, such as linear
enamel hypoplasias and hypocalcifications, areas of reduced enamel and areas of reduced calcification in teeth associated with growth arrest at physiological disruption (from Blakey 1986).

**Results and discussion**

**The material lives of Philadelphia African Americans**

Names will never be linked to all of the individual skeletons. Nevertheless, when synthesized and interpreted through a biocultural model, data on the cemetery have revealed the identities of many of the once invisible congregants and uncovered many aspects of their lives. In fact, many of the characteristics of the Philadelphia African American community as a whole, and aspects of their material lives, have been ascertained. The biocultural model for the FABC (Figure 7.5) synthesizes the most significant factors and their interactions involved in understanding the conditions and experiences of free nineteenth-century African Americans in Philadelphia.

**Environmental constraints**

The sociohistoric and historical demographic data for the African American community (e.g., literature, census records) establish that urban living was a stressful, unstable experience, which increased African Americans’ susceptibility to disease, trauma, and mortality. Densely populated neighborhoods, small dwellings, and large households (mean 6.6 persons) using common privies situated in dark alleyways were prime reservoirs for the proliferation and spread of pathogens in this residentially segregated city.

Philadelphians, as a whole, were exposed to environmental pollutants, such as contaminated drinking water from the nearby rivers and contaminated milk due to the lack of temperature control and sanitary codes for urban dairies (Cheney 1984). Also, occupational exposure of laundresses and domestic servants to contaminated water via river washing and low water temperatures, soiled clothing, and linens increased African American women’s risk of contracting infectious diseases. This is particularly relevant to FABC women, since 79% of African Baptist women were laundresses or domestics/day workers.

The cultural buffering system for FABC congregants was composed of internal and external mechanisms. The African American community and FABC congregation had established religious, economic, social, and familial internal buffering mechanisms. Philadelphia African Baptists had their church congregations and beneficial societies as sources of emotional, social, and economic support. They lived in large, multiadult households, which may have functioned as domestic networks (Stack 1974) by linking households of relatives or church/society members. European American associations like the Quakers, which supported and, at times, aided African American families, churches, and/or communities, also served as external buffering mechanisms.
Figure 7.5 Synthesized FABC biocultural model.
FABC congregants lived during a volatile period in Philadelphia, characterized by rising discrimination, violence, including race riots by European Americans against African Americans, kidnapping and reenslavement, declining socioeconomic conditions, and disenfranchisement. African Americans, already in the lowest socioeconomic strata, found themselves in a cycle of economic depression throughout the nineteenth century.

Contemporary rapid population growth in Philadelphia, due to European American immigrants and African Americans migrants (e.g., runaway slaves and freedmen), also had the long-term effect of decreasing African Americans’ access, economic, ecological, and political, to employment, quality nutrition, and housing. These limitations further increased African Americans’ susceptibility to disease, trauma, and mortality due to increased exposure to occupational and environmental stressors and limiting resources.

Host resistance encompasses the biochemical, genetic, immunological, and physiological constitution of individuals. Resistance or susceptibility to stressors is thus contingent upon the biological life cycle stage and general health status (Goodman et al. 1984). The historical demographic and the FABC skeletal evidence indicate at-risk groups (predicted by life cycle stage) were in fact differentially affected, especially fetuses, young children, and reproductive age females. Parasitism, infections, and a variety of anemias, all aggravating factors compromising resistance, have been documented through the available literature and archival documents or observed in the FABC skeletal analyses. Other aggravating factors such as marginal nutrition can be inferred from the historical literature and potentially exacerbating biological processes (e.g., menstruation, lactation) can be assumed to be operational in the FABC population.

Based on the environmental and sociocultural reconstructions and the aggravating factors affecting host resistance, Philadelphian African Americans experienced, at minimum, episodes of physiological disruption. Many experienced repeated infections and/or undernutrition, which would have decreased their resistance to further insults. The FABC skeletons indicate that despite recovering from insults and consequent physiological disruptions, many individuals may have been rendered less adaptive and resilient throughout their lifetimes and manifested growth, behavioral, reproductive or cognitive problems and/or earlier mortality. Growth disruption, pathology, and differential patterns of mortality as observed in the FABC remains are indicators of these physiological stressors.

FABC congregants experienced in utero, childhood, and adult episodes of undernutrition and stress from disease, and suffered subsequent disruptions of growth. FABC subadults constituted 44% of the skeletal sample; of these, 21 had deciduous dentition for assessment. Dental enamel defects were observed on 92.5% of their teeth. The majority of enamel defects had developed during the prenatal period, indicating that maternal health, as well as fetal health, had been compromised during the gestational period. A total of 50 adults had dentition; all adults with teeth exhibited an enamel defect, and 84.3% had multiple stress episodes during their childhood (ages 1–6).
Nutritional deficiencies and metabolic disease (e.g., porotic hyperostosis) were observed in 53% of the FABC adults. In addition, 25% of the FABC adults ($n = 19$) had skeletal evidence of infectious disease. Of these, 78% ($n = 15$) exhibited evidence of both generalized infection and nutritional deficiency, which appeared to act synergistically, exacerbating poor health (Rankin-Hill 1997).

In contrast, the incidence of less severe nutritional disorders, such as rickets (childhood vitamin D deficiency) and osteomalacia (adult vitamin D deficiency), suggests a dietary regime that provided marginal to adequate calories, although nutrient content and bioavailability apparently fluctuated based on sociohistoric accounts and the skeletal evidence (e.g., remodeled lesions). Despite disease stress and environmental risks, FABC free African Americans had a reduced risk of dying when compared to other Diasporic Afro-Americans, enslaved or free. Therefore, FABC congregants were more likely to live longer and die later than other Afro-American populations. Thus, FABC congregants and free Philadelphia African Americans, as represented by the FABC sample, were generally healthier than their enslaved or emancipated counterparts.

**The material lives of African American and FABC women**

African American women were in high demand as domestics and were recruited from outlying areas; manumitted, emancipated, freeborn, and runaway slaves came to Philadelphia for employment. The African American population structure reflects this, since younger females were present in greater numbers throughout the first half of the century (Figure 7.6) (Nash 1988).

![Bar chart](chart.png)

**Figure 7.6** Philadelphia free African American population 1830–1840.
Social status in general was derived from male spouses, as it was for European American women. There were a few educated and entrepreneurial women in the African American community (e.g., teachers, shopkeepers, musicians, midwives). In the African American community, women primarily worked outside the home, and child labor was also essential to the survival of the family (Tables 7.4, 7.5). In 1838, a pattern of female-headed households was already becoming apparent in the African American community. Overall, 28% of all African American and African Baptist (including FABC) households were female headed, and widows headed 32% of these households. The remaining households were headed by single (42%) and married (26%) women, apparently without spouses present (Table 7.6).

Female socioeconomic status was tenuous, as demonstrated by almshouse records and the existence and proliferation of beneficial societies, especially those for unmarried women. The Philadelphia Almshouse 1838 record book for colored women provides insight into their socioeconomic vulnerability. The almshouse apparently separated women by general medical categories (e.g., lying in for pregnant women, medical for the ill, lunatic asylum for the intemperate and insane). These records indicate that major life events, such as widowhood and childbirth, were some of the documented causes of poverty and consequent institutionalization for African American women. “Increased family” was a significant cause of entry for many women, some of whose infants were born in the almshouse. Old age, illness, and “debility,” which may be associated with

<table>
<thead>
<tr>
<th>Table 7.4 Afro-American and African Baptist heads of households</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sex</strong></td>
</tr>
<tr>
<td>Male</td>
</tr>
<tr>
<td>Female</td>
</tr>
<tr>
<td>Widows</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Table 7.5 Male heads of household occupations</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Occupation</strong></td>
</tr>
<tr>
<td>Laborers</td>
</tr>
<tr>
<td>Waiters</td>
</tr>
<tr>
<td>Porters</td>
</tr>
<tr>
<td>Seamen</td>
</tr>
<tr>
<td>Coachman</td>
</tr>
<tr>
<td>Carters</td>
</tr>
<tr>
<td>Shoemakers</td>
</tr>
<tr>
<td>Miscellaneous</td>
</tr>
<tr>
<td>NR/female head</td>
</tr>
</tbody>
</table>

NR, no response.
Chapter 7: Identifying the First African Baptist Church

<table>
<thead>
<tr>
<th>Occupations</th>
<th>% Afro-American</th>
<th>% African Baptist</th>
</tr>
</thead>
<tbody>
<tr>
<td>Washerwoman</td>
<td>34</td>
<td>43</td>
</tr>
<tr>
<td>Domestic</td>
<td>29</td>
<td>36</td>
</tr>
<tr>
<td>Cotton mill worker</td>
<td>6</td>
<td>–</td>
</tr>
<tr>
<td>Cook</td>
<td>3</td>
<td>–</td>
</tr>
<tr>
<td>Dealer</td>
<td>3</td>
<td>–</td>
</tr>
<tr>
<td>Dressmaker</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>Whitewasher</td>
<td>2</td>
<td>–</td>
</tr>
<tr>
<td>No response/female</td>
<td>14</td>
<td>6</td>
</tr>
<tr>
<td>Miscellaneous</td>
<td>5</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>100</td>
</tr>
</tbody>
</table>

n = 3295
n = 204

Aging, were also causes of poverty. Other recorded causes, such as “blind, lame, deaf and dumb, idiocy, intemperance, vicious, and insanity” (almshouse record book 1838), speak to a society ill prepared to care for people with special needs.

Homelessness appears to have been a problem, based on the proportion of women who entered the almshouse who were actively working (38%); two-thirds of these women were “incurable” yet working. This bears witness to the resilience and tenacity of these women, who were ill or in perilous social circumstances yet continued to work and live in the almshouse, which foreshadows the contemporary urban phenomenon of homeless shelters.

Socioeconomic, social, and spiritual support was integral to the survival of the African American community. African American women were active in their churches and beneficial societies. Most beneficial societies were self-help organizations and prototypes for the black insurance companies of later years (DuBois 1899; Spencer 1985). Female members of the FABC established such a society, the First African Baptist Female Union Society of Philadelphia, for unmarried women aged 21–45 in 1829. Members paid $1.25 a week. Duties and benefits included visiting the sick and distressed members of the society; weekly payments ($1.00) to those too ill or old to work; providing secured loans to members if the society was debt free and had funds above $50.00; a decent, plain burial (not to exceed $20.00); and members could bequeath resources to the society, such as real estate and chattels. In addition, members could not be intemperate, be involved in criminal behavior or conduct themselves in an immoral manner, clearly demonstrating the social control role that many of these societies exerted (Table 7.7).

One female FABC congregation member, Mrs Sylvia (“Sylvie”) Dean, could be found in document cross-referencing. Mrs Dean, a founding member of the society, was identified as a head of household in the 1838 census and as a consistent contributor in the 1834 FABC Penny Collection Book. Mrs Dean was a widow whose occupation was listed as “washer.” She lived in a six-person household...
with at least four other adults and perhaps a child. While several FABC men were identified in cross-referenced documents, Mrs Dean was the only woman; this reveals how in many ways, being a woman, poor, and African American intensified invisibility in the historical record.

The skeletal remains of the FABC congregants evidenced the impact of their material lives on health status and mortality. Their arduous occupations, such as being a washerwoman, began early in adolescence, leaving indelible marks on the skeleton of overworked muscles and joints. The combination of physical exertion, marginal and fluctuating nutrition, and the rigors of life in a segregated, environmentally stressful community demanded biological and psychosocial responses beyond the limits of tolerance; this led to chronic disease and early death for many. In addition, the material lives of women not only affected their own health and mortality patterns but also those of their unborn fetuses and living children.

Compared to other Afro-American skeletal series (Table 7.8), the FABC skeletal sample had better overall health status. However, the FABC did repeat the three major patterns observed in other Afro-American skeletal populations: high infant and childhood mortality; periodic undernutrition and infectious disease; and high frequencies of degenerative joint disease and muscle hypertrophy. These general patterns were present in the FABC, yet distinctly different patterns also emerged associated with variation in environmental, occupational, and political economic contexts.

A number of comparisons can be made. The ubiquitous occurrence of hypoplastic enamel defects in the dentition of FABC subadults and adults indicated periods of in utero and childhood stress, though many survived into adulthood. The very high frequency of enamel defects points to the difficulty of nineteenth-century African American life, whether born enslaved or free (Curtin 1969; Nash 1988; Rankin-Hill 1997). For instance, the difference in hypoplasia severity rates, low in the FABC and high in the Newton Barbados sugar plantation sample, illustrates the differential impact of political economic systems on growth disruption and overall health status. The rigors of intensive

### Table 7.7 Household beneficial society membership

<table>
<thead>
<tr>
<th># Members</th>
<th>African American</th>
<th>African Baptists</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>%</td>
</tr>
<tr>
<td>None</td>
<td>1551</td>
<td>47</td>
</tr>
<tr>
<td>1</td>
<td>761</td>
<td>23</td>
</tr>
<tr>
<td>2</td>
<td>656</td>
<td>20</td>
</tr>
<tr>
<td>3</td>
<td>205</td>
<td>6</td>
</tr>
<tr>
<td>4 or more</td>
<td>122</td>
<td>4</td>
</tr>
<tr>
<td>All households with members</td>
<td>1744</td>
<td>53</td>
</tr>
</tbody>
</table>
Table 7.8 Afro-American skeletal series (prior to 1996)

<table>
<thead>
<tr>
<th>Site/location</th>
<th>Time periods</th>
<th>Burial #</th>
<th>Lifestyle</th>
<th>Preservation</th>
<th>Analysis/status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Newton, Barbados</td>
<td>1660–1820</td>
<td>103</td>
<td>Plantation slaves</td>
<td>Fragmentary</td>
<td>Months**</td>
</tr>
<tr>
<td>Colonial sites</td>
<td>1690–1820</td>
<td>29</td>
<td>Plantation slaves</td>
<td>Poor–good</td>
<td>Indefinite*</td>
</tr>
<tr>
<td>St Peter’s Cemetery New Orleans</td>
<td>1720–1810</td>
<td>13</td>
<td>Urban slaves</td>
<td>Poor</td>
<td>3 years**</td>
</tr>
<tr>
<td>Colonial sites</td>
<td>1690–1820</td>
<td>29</td>
<td>Plantation slaves</td>
<td>Poor–good</td>
<td>Indefinite*</td>
</tr>
<tr>
<td>St Peter’s Cemetery New Orleans</td>
<td>1720–1810</td>
<td>13</td>
<td>Urban slaves</td>
<td>Poor</td>
<td>3 years**</td>
</tr>
<tr>
<td>Catoctin Furnace, Maryland</td>
<td>1790–1820</td>
<td>31</td>
<td>Industrial slaves</td>
<td>Poor/fragments</td>
<td>Indefinite*</td>
</tr>
<tr>
<td>Waterloo Plantation, Surinam</td>
<td>1793–1861</td>
<td>38</td>
<td>Plantation slaves</td>
<td>Poor–good</td>
<td>?</td>
</tr>
<tr>
<td>FABC 8th Street, Philadelphia</td>
<td>1821–1843</td>
<td>144</td>
<td>Ex-slaves/freeborn</td>
<td>Poor–good</td>
<td>3 years**</td>
</tr>
<tr>
<td>FABC 11th Street, Philadelphia</td>
<td>1810–1822</td>
<td>89</td>
<td>Ex-slaves/freeborn</td>
<td>Poor–good</td>
<td>5 years**</td>
</tr>
<tr>
<td>39CH778, South Carolina</td>
<td>1840–1870</td>
<td>36</td>
<td>Plantation slaves</td>
<td>Poor–good</td>
<td>1 year**</td>
</tr>
<tr>
<td>Oakland Cemetery, Atlanta, Ga</td>
<td>1866–1884</td>
<td>17</td>
<td>Poor and indigent</td>
<td>Fragments–excellent</td>
<td>?**</td>
</tr>
<tr>
<td>Cedar Grove Cemetery, Arkansas</td>
<td>1890–1927</td>
<td>78</td>
<td>Rural farmers</td>
<td>Poor–excellent</td>
<td>2 weeks**</td>
</tr>
</tbody>
</table>

Remains available Smithsonian Institution. Reinterred.

Sugar cane production slavery led to greater growth disruption and earlier death in Barbados compared to the urban-dwelling service and labor economy of enslaved and freeborn African American Philadelphians. In general, there were lower rates of nutritional defects and less severity (i.e., porotic hyperostosis, osteomalacia, enamel hypoplasias) in FABC congregants’ remains than in other Afro-American skeletal series. The evidence for the higher rates of nutritional deficiency (e.g., porotic hyperostosis) in FABC adults speaks to the more episodic nature and interaction of marginal nutrition, physical labor, and environmental stress characterizing urban dwelling versus more rural communities. In addition, the other populations represented here exhibited more prolonged chronic nutritional problems, such as rickets and growth disruption, as reflected in adult mean stature. Also, the FABC sample had lower generalized non-specific infection disease rates than other samples. This is probably associated with the more acute nature of epidemics and seasonally driven infectious disease in urban environments such as Philadelphia (Rankin-Hill 1997; Torchia 1977).
Lastly, in general, the FABC remains exhibited lower rates of osteoarthritis, with less severity, than other samples, yet with multiple joint involvement. They also had higher frequencies of osteophytosis (52% of FABC vertebrae: males 69.4%; females 35.9%). Osteophytes are bony growths that develop on bone extremities, particularly frequently in osteoarthritis, a degenerative disease of joint cartilage. This is likely attributable to the carrying and lifting of very heavy loads. Other samples, especially the samples representing rural farming populations, had higher rates of osteoarthritis, with more severity and fewer joints involved; their rates of osteophytosis were lower but higher in severity. These differences may be associated with the more diverse or generalized biomechanical requirements experienced by urban-dwelling populations counterpoised to the more specialized and intensive biomechanics of fieldwork.

**Conclusion**

The biocultural biohistory of the First African Baptist Church cemetery population represents an example of the contributions that historical skeletal populations can provide to our understanding of the past and the present. As a research approach, it substantiates that each skeletal sample should be examined and understood within the context of their reality and not just the sum total of frequencies and metrics. Using multiple avenues of research and diverse data sources with theoretical principles of biological anthropology and biocultural modeling provides an opportunity to delve into the biology, culture, environment, and sociohistory of the time period.

In terms of African Diasporic populations and communities, it is critically important to begin with the understanding that these are heterogeneous populations biologically and culturally, with a few rare exceptions. That they were heterogeneous from the moment their ancestors were captured 300 plus years ago because the continent of Africa was diverse in ecology, biology, genetics, and culture and the nature of the Atlantic slave trade created further heterogeneity, even with the genetic bottleneck effect of the Middle Passage (Cobb 1939). This is a basic point that is rarely considered because of the foundational premise of “race” in biological anthropology’s history, which continues to plague much of contemporary research (see Chapters 4 and 5).

In the case of the First African Baptist Church cemetery population, using the biocultural approach provided a means to examining nineteenth-century African American life from the individual level, to the FABC congregation, to the African American community to the city of Philadelphia and its role in the region during the nineteenth century. Therefore, individuals who were invisible under the ground, invisible in the city’s historical memory and the historical record were identified and placed into American history and the biohistory of the African Diaspora.
References


Milner, J.A. (1981) *Professional services proposal for provision of archeological and osteological investigations of an early 19th century cemetery adjacent to Construction Section Number of the Center City Commuter Connection Philadelphia, Pennsylvania.* Unpublished MS.


Notes

1 See Blakey (2001) for a review of bioarchaeological studies of the African Diaspora.

2 See Rankin-Hill (1997) for an expanded discussion.
Several institutions and library collections were visited and consulted, including the Historical Society of Pennsylvania, Philadelphia Baptist Association, Balch Institute, African-American Museum, Philadelphia Social History Project Archives at the University of Pennsylvania, Temple University Urban Archives and Collection, City of Philadelphia Archives, State of Pennsylvania Archives, Library of Congress, and the National Archives.
PART III
Biocultural approaches to health and diet
CHAPTER 8

“Canaries in the mineshaft”: the children of Kulubnarti

Paul A. Sandberg¹ & Dennis P. Van Gerven²

¹Sam Noble Oklahoma Museum of Natural History, University of Oklahoma
²Department of Anthropology, University of Colorado at Boulder

Introduction

At the end of the nineteenth century, miners began taking canaries into the mineshaft. When the canaries stopped singing, the miners knew that the carbon monoxide levels were too high and it was time to get out. As the members of society most sensitive to nutritional and economic deprivation, infants and children are like those canaries in the mineshaft. Measures of cultural florescence and decline in technological and economic development often belie this biological reality. When infants and children sicken and die in increasing numbers, the culture is failing quite apart from the trappings of material achievement. An understanding of childhood health and disease in the past is an illuminating window onto the biocultural landscape in which human societies confront the challenges of survival in a changing world.

In this chapter, we present some 35 years of research into the mortality and disease of infants and children from two contemporaneous communities in medieval Nubia. Their skeletons were exhumed from the medieval Christian site of Kulubnarti (AD 550–800) in a remote region of Upper Nubia known as the Batn el Hajjar (“belly of rock”). The two communities lived side by side but had different living conditions. We will show how the human costs and consequences of social status and economic advantage are revealed from the perspective of each community’s most vulnerable members – the infants and children – “the canaries in the mineshaft”.

Our approach is biocultural, a research framework pioneered by George Armelagos (Armelagos 2008; Armelagos et al. 1982, 1993). Armelagos envisioned the cultural environment as a system by which humans adapt to their natural environment. But culture is also an environment in and of itself to which humans must adapt, and as such, biology and culture interact with one another in complex ways.
We begin with a brief primer on Nubia and the archaeology of Kulubnarti to provide a cultural context before we turn to the biological analysis of the subadults of Kulubnarti. We present research on two kinds of pathologies that affect growing infants and children: cribra orbitalia and growth defects in tooth enamel, specifically enamel hypoplasia and enamel microdefects. We end with results from recent stable isotope analyses that have shed light on the connection between the weaning process and stress events.

**Case study: Nubia and Kulubnarti**

Nubia occupies a portion of the Nile valley extending from the First Cataract at Aswan in Egypt, southward to the Fourth Cataract near the Sudanese capital of Khartoum (Figure 8.1). It is divisible into lower and upper regions. Lower Nubia extends southward from the First Cataract at Aswan to the Second Cataract at Wadi Halfa on the modern Egyptian/Sudanese border. Upper Nubia begins at the Second Cataract and extends southward to a less constant border, often reaching the Fourth Cataract and occasionally as far south as Khartoum.

The Nile passing through Lower Nubia is broad, slow moving, and productive for the human population inhabiting its banks in terms of agriculture as well as travel. Upstream and to the south, the Nile in Upper Nubia passes through a rocky region called the Batn el Hajjar (“belly of rock”) where river navigation is difficult. In the Batn el Hajjar, ancient and modern populations have always

![Figure 8.1 Map of Nubia with cataracts labeled first through fifth.](image-url)
remained huddled along the river, extending only as far as irrigation would per-
mit, which is no more than 1–2 km and often much less (Adams 1977). This
region of Upper Nubia is described by Adams (1977:26) in this way:

The tortured landscape of bare granite ridges and gullies which characterizes this part of
Nubia begins at the bank of the river itself; alluvium exists not as a continuous floodplain,
but only in protected pockets and coves. Fields and tiny hamlets hug the banks wherever
such soil is available, but for long stretches neither natural nor cultivated vegetation is to
be seen.

For these reasons, the environment has never permitted large population centers
in this region.

Interest in Nubian archaeology has been driven by the construction of increas-
ingly higher dams at Aswan, the First Cataract of the Nile. The first dam was com-
pleted in 1902 and enlarged between 1929 and 1934. Each construction created
a larger reservoir, inundating more of Lower Nubia. Construction of the Aswan
High Dam began in 1960. When it was completed 10 years later, it was 12,570
feet long, 3,220 feet wide at the base and 364 feet high. Its reservoir was 340 miles
long. The entirety of Lower Nubia was inundated. In response to the imminent
flooding, UNESCO funded an international campaign, the Nubian Campaign, to
save the monuments of Egypt and Nubia (Smith 1962). The Nubian Campaign
began in 1959 and continued through 1973. During that time, some 18 foreign
expeditions from around the world identified over 1000 archaeological sites and
excavated over one-third of them (Adams 1977).

The site of Kulubnarti was not initially a priority for excavation because it
is located about 80 km south of Wadi Halfa (the current northern tip of Lake
Nasser) and was in no danger of flooding. It also dated to the early portion of
the Christian period of Nubian history, considered to be too recent to be of much
significance. Nubia adopted Christianity in about AD 55. The Christian period
extended to the early fourteenth century when the Christian King at Dongola
(Nubia’s capital at the time) was replaced by a Muslim prince and Christianity
was no longer the official religion of Nubia (Adams 1977).

Nevertheless, Kulubnarti had importance. It was located in a portion of the
Nile, the Batn el Hajjar, for which there was a sparse archaeological record, and
it had also been occupied continuously from Christian through modern times.
Indeed, one of its cemeteries continues in use today. This was significant because
there was little archaeological record of the transition from Christianity to Islam
in Nubia.

With completion of the UNESCO campaign in 1969, William Y. Adams, the
former director of the Nubian portion of the campaign, mounted an expedition
to Kulubnarti. Two cemeteries were discovered in the course of excavation; one
(21-S-46) on an island adjacent to the west bank and a second (21-R-2) on the
west bank near the modern village of Kulb.

Logistics would not permit excavation of the cemeteries in 1969, and there-
fore a second expedition was mounted in 1979, jointly led by the University of
Colorado at Boulder and the University of Kentucky. The Colorado-Kentucky
excavation (led by D.P. Van Gerven) disinterred 218 individuals from the island cemetery and 188 from the mainland cemetery. Both are early Christian in age (AD 550–800). Radiocarbon dating determined that the cemeteries represented two contemporaneous early Christian communities; the island cemetery had a mean date of 719 CE and the mainland mean was 756 CE. The island cemetery was excavated in its entirety but only the early Christian portion of the mainland cemetery was excavated. As already noted, the mainland cemetery has been in continuous use to this day.

While the cemeteries represent neighboring communities living within two miles of one another, the archaeological evidence indicates that they were economically and socially distinct (Adams and Adams 2006). The mainland cemetery represented a village of freehold farmers who were relatively prosperous by the standards of Upper Nubia. In comparison, the island residents were likely landless itinerants living in shanties and working for their landed neighbors.

There is archaeological evidence in support of that interpretation as well. The architectural ruins suggest that the island houses at Kulubnarti were shanties with walls made of little more than stacked rocks. Preserved doorways were often less than 1 m high. The mainland villagers lived in well-built houses and worshiped in a beautifully built church of mortared brick. The church was double vaulted and adorned with murals. In contrast, the island church was a more modest structure built among the large boulders dominating the island’s terrain (Adams and Adams 2006).

Remnants of woven shrouds found in many of the burials also reflected the economic difference between the communities. The large majority used by the islanders were made from locally produced wool. The mainland villagers’ shrouds were of far finer quality, often made of cotton or linen. Both materials would have been imported at considerable cost. According to Adams and Adams (2006:14), “Putting the evidence together from the two cemeteries, it appears that the two populations were chronologically and culturally similar, but the people of 21-S-46 [the island] represented an underclass that was socially distinct and economically deprived.” Kulubnarti has given us two communities living physically as neighbors but socially and economically distinct. Together, they provide an opportunity to explore the consequences of social advantage and economic well-being from the perspective of the infants and children.

**Methods**

**Analysis of infants and children**

The human remains at Kulubnarti have provided a wonderful opportunity to conduct biocultural investigations. The combination of desert heat and virtually no rainfall (less than 1 mm per year) made preservation of both soft and skeletal tissue extraordinary. Many individuals were mummified, including infants, and several newborns still had twine attached to their umbilical cords. Fetuses were buried in pots within graves. Small and fragile fetal and infant remains are largely underrepresented in the archaeological record due to preservation. Their
presence in the Kulubnarti sample presents a rare opportunity to include them in our paleodemographic and paleopathological analyses. The age distributions and sample sizes are presented in Table 8.1.

Cribra orbitalia (Figure 8.2a), enamel hypoplasia (Figure 8.2b), and enamel microdefects (Wilson’s bands) (Figure 8.2c) and are indicators of what is referred to as generalized stress; these are often termed “non-specific” stress indicators. Skeletal lesions can be categorized into two basic groups: those that result from a particular pathological condition, and those that may result from several different conditions. With regard to the former, a suite of skeletal lesions may point to a particular condition (such as those caused by treponemal infections like syphilis and yaws) (see Chapter 16). In paleoepidemiological terms, a test for a disease has high sensitivity if there is a high correspondence between the prevalence of a suite of indicators (in this case skeletal lesions) and the prevalence of individuals in a population that actually have the disease (true positives). A test for a disease has high specificity if those who do not actually have the disease also lack the suite of lesions (true negatives) (see Boldsen and Milner 2011).

<table>
<thead>
<tr>
<th>Age at Death</th>
<th>Island (N)</th>
<th>Mainland (N)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0–1</td>
<td>41</td>
<td>12</td>
</tr>
<tr>
<td>2–3</td>
<td>34</td>
<td>20</td>
</tr>
<tr>
<td>4–6</td>
<td>54</td>
<td>22</td>
</tr>
<tr>
<td>7–9</td>
<td>19</td>
<td>9</td>
</tr>
<tr>
<td>10–12</td>
<td>24</td>
<td>8</td>
</tr>
<tr>
<td>13–15</td>
<td>16</td>
<td>11</td>
</tr>
<tr>
<td>16–18</td>
<td>16</td>
<td>12</td>
</tr>
</tbody>
</table>

**Table 8.1** Age at death categories and sample sizes for the island and mainland cemeteries.

**Figure 8.2** (a) Cribra orbitalia. (b) Enamel hypoplasia. (c) Cross-sectional view of a tooth showing Wilson’s bands.
It would be very useful if every condition left tell-tale signs on the skeletons of afflicted individuals and those signs were absent in all individuals not suffering from the disease (high sensitivity and specificity). Unfortunately, many relatively common disease conditions have variable effects on skeletal tissue, and certain lesions can result from several potential conditions. This often leads to an underestimation of the prevalence of a particular condition in past human populations, depending on the balance between sensitivity and specificity for that condition. We can, however, gain valuable information about the general health and well-being of past populations by focusing on the frequency and severity of lesions that can be caused by a variety of disease conditions. These lesions are called generalized stress indicators.

Signs in bones and teeth of interrupted growth, for example (e.g., enamel hypoplasia), do not indicate a particular pathological condition, but rather some assault (or series of assaults) on the body capable of interrupting normal growth. The cause may have been an infection, nutritional deficiency or psychological stress, or some other condition that disrupts positive energy balance and thus growth and development. Generalized stress indicators have tremendous value to the paleopathologist because they measure the overall health status of individuals and populations more effectively than any specific disease event (Goodman et al. 1988). Cribra orbitalia, enamel hypoplasias, and enamel microdefects do not reflect specific diseases but rather aspects of the overall health of those afflicted.

However, these conditions alone give us little insight into the biocultural interactions that produced them. Nor do they reveal their consequences on the health and well-being of the communities of which they are a part. Understanding the consequences requires a demographic context. We turn now to a comparison of the communities from the perspective of life expectancy.

Figure 8.3 illustrates mean life expectancy by age in the two communities. Life expectancies are calculated from the age-at-death distribution of the population, specifically the rate of reduction in the number of individuals from one age category to the next. What we see is an almost nine year (8.6) difference in life expectancy at birth between the mainland and island communities (Van Gerven et al. 1981). In the sample, life expectancy increases with age through the young adult years. This is to be expected. Those infants who survive the stresses of their first years have a greater likelihood of surviving on to their adult years. The mortality data can further be used to test a hypothesis: if the differences in infant life expectancy are the result of differences in underlying health, then higher frequencies of generalized stress can be predicted in the island infants and children.

Results

Cribra orbitalia

Cribra orbitalia (CO) involves one of several lesions on the roof of one or both eye orbits (see Figure 8.2a). These range from a concentration of small
pinhole-like perforations on the orbital surface to an outgrowth of coral-like “spongy” bone. CO has long been argued to be related to a morphologically similar type of lesion of the cranial vault called porotic hyperostosis (PH) (e.g., Angel 1966; Stuart-MacAdam 1989). These lesions are the result of an expansion (hypertrophy) of red blood cell-producing bone marrow sandwiched between the inner and outer surfaces of the bone and have been etiologically linked to anemia since the 1960s (Angel 1966; Carlson et al. 1974; Moseley 1974; Stuart-MacAdam 1987).

Anemia is a pathological indication of an underlying deficiency in either red blood cells or hemoglobin, the protein within red blood cells that carries oxygen to human (and all vertebrate) tissues. Anemia can result from both genetic and acquired pathological conditions that either prematurely destroy red blood cells or produce too few functioning ones. Genetic anemias are relatively rare and include thalassemia and sickle cell anemia. Acquired anemias are the result of either blood loss or deficiencies in the elemental and molecular constituents necessary for red blood cell production (erythropoiesis). The most common acquired anemia is the insufficient intake or storage of iron, a crucial element for functioning red blood cells (see later). Deficiencies of the micronutrients vitamin B12 and folate can also lead to insufficient erythropoiesis by impairing DNA replication during red blood cell production (the megaloblastic anemias). Parasitic infection and insufficient nutrient absorption in the gut (as occurs with weanling diarrhea) can exacerbate the situation.

Anemia is thought to cause CO because the body compensates for a net loss in functioning red blood cells by increasing the marrow spaces responsible for erythropoiesis, which in subadults are located in the cranial diploe and long
bone medullary cavities. There has been recent debate in the literature regarding which types of anemia are the most likely culprits for CO (and more specifically, PH), particularly whether or not iron deficiency per se can cause marrow hypertrophy (Oxenham and Cavill 2010; Walker et al. 2009). Walker et al. (2009) argue that megaloblastic anemias caused by micronutrient deficiencies (e.g., vitamin B12, folate, vitamin C) are more likely proximate causes of CO, while Oxenham and Cavill (2010) maintain that iron deficiency anemia alone can result in the lesions. While there are potentially confounding interpretative implications of dismissing the iron deficiency hypothesis (see McIlvaine 2015), there are good reasons to believe that in Nubia, in ancient as well as modern times, the synergistic effects of an iron-poor diet and parasitism collude to produce CO, and as a result, the occurrence and distribution of CO is a useful non-specific indicator of stress at Kulubnarti (Mittler et al. 1994). A diagnosis of iron deficiency at Kulubnarti demands an understanding of the biological and cultural forces in play.

Acquiring sufficient iron to support red blood cell production is a losing battle for the majority of the world’s population. Iron deficiency, and specifically iron deficiency anemia, remains one of the most severe and important nutritional deficiencies in the modern world (Stoltzfus 2003; WHO 2001). Populations of Egypt and Nubia today and in the past are very much a part of that problem. The problem is not just the abundance of iron in the environment; it is also the availability of iron in the diet. Humans are more efficient at extracting iron from animal flesh – heme iron – than they are at extracting iron from plants (non-heme iron), even when the plants are abundant in iron (Lucca et al. 2002). This difference creates a particular problem for modern-day Nubians. Nubians have been subsisting on a high-carbohydrate, low-animal protein diet for thousands of years. Millet, wheat, and barley are dietary staples, and animal protein is far less plentiful. Villagers today run small herds of goats but seldom eat them. They are not even milked in the dry season when fodder is less abundant (Adams 1977). Problematically, cereals are not only low in iron, but they also contain phytate. Phytate is used by many plants, including cereals, to store phosphorus, but unfortunately for humans, iron bound to phytate is not biologically available or digestible (Brune et al. 1992; Rheinhold 1982). It should not come as a surprise, then, that iron deficiency anemia is the number one nutritional problem from Cairo to Khartoum (May and Jarcho 1961). In addition, diets low in animal foods can also lead to the micronutrient deficiencies that produce megaloblastic anemias, such as vitamin B12. With similar subsistence and dietary patterns in the past, and without any outside medical and/or nutritional intervention, these problems were no doubt experienced by people living in ancient Nubia.

Infants and children face two great challenges to their survival and both are exacerbated when the mother is iron deficient (Zimmerman and Hurrell 2007). The first is at birth and the second is at weaning. There is an important relationship between infants and their physical environment as they are weaned. High incidences of parasitic and bacterial infection are well documented in modern
Egypt and Nubia and this would certainly have been the case in ancient times. Hookworm infection and schistosomiasis in particular are common in both Egypt and Nubia (Campbell Hibbs et al. 2011). The effect of parasitic infection is devastating with regard to anemia due to internal blood loss and a general lowering of resistance to subsequent infections. For example, in modern developing countries, 25% of all cases of anemia, 35% of cases of iron deficiency anemia specifically, and 73% of cases of “severe” anemia were attributable to hookworm infection alone (Stoltzfus et al. 1997).

Ancient Nubians, like modern impoverished Nubians, struggled against infections throughout their lives, but they faced their greatest peril during their first years of life. This is reflected in data on life expectancy. The transition from breastfeeding to solid foods was a dietary but also immunological challenge, fought against bacteria and parasites. Worst of all, the challenges of infection had to be confronted at the very moment the infant’s first lines of defense were taken away—breast milk and the antibodies it provided. All of these factors combined to produce a syndrome known as “weanling diarrhea.” As the name implies, weanling diarrhea primarily affects infants who are just beginning to utilize sources of food other than breast milk (McDade and Worthman 1998). In its most severe form, it causes extreme dehydration and malnutrition, often leading to death; weaning is second only to birth as a cause of infant mortality (Katzenberg et al. 1996). In order to avoid weanling diarrhea and all of its attendant consequences, the infant must be physiologically and developmentally prepared, and have the bodily resources at the outset to recover quickly after each successive illness. Preparedness comes at the mother’s breast but unfortunately, 59% of pregnant women suffered from iron deficiency anemia in Sudan in 2009 and 2010 (WHO 2013), resulting in iron-poor milk.

If we put these factors together from the infant’s perspective, the consequences are dire. Nubian fetuses are nurtured in the womb by iron-deficient mothers; as neonates and infants, they consume iron-deficient breast milk. As they move past infancy, the situation gets worse. Breast milk loses much of its nutritional quality over time and may be providing very little nutrition by weaning (Victora et al. 1984). In addition, exclusive breastfeeding beyond six months (a practice for which we have preliminary evidence at Kulubnarti; see later) would have increased the chances of iron-deficient children (Marques et al. 2014). They are then weaned onto the iron-poor diet of their mothers and assaulted repeatedly by diarrheal episodes and infectious microbes and parasites in the food they eat, the water they drink, and the fields in which they play. In sum, the weaned children are more iron deficient than they were at birth, and other bodily resources necessary for proper growth and development are compromised as well, leaving them ill prepared for the conditions they are about to face as a freestanding individual.

Now let’s look at the analysis of cribra orbitalia at Kulubnarti in light of what we know. The iron deficiency hypothesis predicts a concentration of the lesion
among infants and children, differences between the communities, and a correspondence between the lesion and mortality. The data in Figure 8.4a meet those expectations. On the island, lesion frequencies reach 24% by age 1 compared to 0 (birth) on the mainland. In addition, the frequencies continue to rise until ages 10–12 on the island while they begin to decline by age 4–6 on the mainland.

Cribra orbitalia heals over time (Lallo et al. 1977), which is why older individuals also have the lesion. If we plot the frequency of active lesions by cemetery (Figure 8.4b), an even more striking pattern emerges. The samples were too small for a between-cemetery comparison beyond ages 4–6 but the pattern is clear. The frequencies of active lesions are 33% higher among the island children ages 2–3 and 31% higher among the 4–6 year olds.

Another question remains. Is there a relationship between the presence of cribra orbitalia and survival? That is to say, did the conditions underlying the lesion have an impact on life expectancy? Figure 8.4c provides an answer quite clearly. Mean life expectancy is dramatically lower for those with an active lesion at the time of their death (Mittler and Van Gerven 1994). Furthermore, the greatest disparity occurs through and beyond the weaning years, and then closes towards the end of childhood. This pattern is precisely what we would expect if there were connections between the lesion, weaning, and mortality.

Paleopathologists are in the business of making circumstantial cases. A jury can be led to a conviction beyond a reasonable doubt based on circumstantial evidence. The key for the prosecution is demonstrating that multiple lines of evidence lead to the same conclusion. Any one line by itself is not enough, but together they make the case. If we are to conclude that the island children are sicker than their mainland counterparts, we must have multiple lines of evidence. We now move onto our next research investigation: enamel hypoplasia.

**Enamel hypoplasia**

Enamel hypoplasias are surface defects in tooth enamel resulting from a disruption in enamel formation due to any number of physiological stresses and sometimes trauma (Goodman and Rose 1990; Goodman et al. 1980). They often appear as bands of depressed enamel (see Figure 8.2b), but they can also appear as a series of pits. When several occur together, they represent a chronologically ordered series of stress events. Because enamel is incapable of repair, hypoplasias provide a permanent record of childhood stress during the period of tooth crown formation. As such, the age of occurrence of a hypoplasia can be estimated by measuring its spatial position and comparing this to the developmental schedule of the tooth (e.g., Goodman and Rose 1990; Ritzman et al. 2008).

Although the underlying causes of enamel hypoplasias are variable, their peak occurrence generally coincides with the weaning and postweaning period in modern and archaeological populations. Therefore, they likely result from the suite of stresses associated with the weaning process, much like many cases of cribra orbitalia. The association between hypoplasia and weaning stress is also supported by data from modern, nutritionally stressed children (Goodman et al.
Chapter 8: “Canaries in the mineshaft”: the children of Kulubnarti

Figure 8.4 (a) Percentage frequency of cribra orbitalia by age at death category for the island and mainland cemeteries. (b) Percentage frequency of active cribra orbitalia by age at death category for the island and mainland cemeteries. (c) Average life expectancy by age at death category for individuals with and without the cribra orbitalia lesion. (d) Percentage frequency of enamel hypoplasia by age at death for the island and mainland cemeteries. (e) Intervals between hypoplasias in years. When multiple hypoplasias are present on single teeth, 80% of them occur within six-month intervals in the island cemetery. Most hypoplasia events in the mainland cemetery are separated by a year of recovery. (f) Correlation between percent frequency of hypoplasia and cribra orbitalia for the cemeteries combined. Each data point is a whole-year age at death category (1–5yrs). Data for (a)–(c) from Mittler and Van Gerven (1994), (d,e) from Van Gerven et al. (1990) and (f) from Van Gerven et al. (1995).
New directions in biocultural anthropology

1992; May et al. 1993). The analysis of enamel hypoplasia in bioarchaeology is as common as that of cribra orbitalia. Enamel hypoplasias represent stresses experienced during childhood but unlike bony lesions, which remodel over time, they are evident in adults. Therefore, we can use the skeletons of adults to peer into their childhoods to see how stressful they were.

The ability to estimate age of occurrence combined with age at death, sex, and cemetery has permitted multiple points of comparison. Figure 8.4d shows the frequencies of hypoplasias in the permanent canine tooth by age of occurrence. The two communities are virtually indistinguishable in the age distribution of hypoplasias for the first four years and then diverge sharply (Van Gerven et al. 1990). The frequency of hypoplasias drops by 42% (65% to 23%) on the mainland over the subsequent 1.5 years but remains high on the island for the next two years.

The island children also experience shorter recovery periods between episodes than their mainland neighbors. We see in Figure 8.4e that 80% of the hypoplasias among the island children occur from one six-month interval to the next without interruption. Only 30% occur across contiguous intervals among the mainland children. On the mainland, the majority (70%) are spaced by at least a year.

The higher frequency and duration of growth interruptions among the island children, compared to their mainland counterparts, correspond well to the higher frequency of cribra orbitalia observed among the island children. And both bear witness to the cost of economic privation on the most vulnerable members of the island community.

Although both cribra orbitalia and hypoplasia indicate episodes of childhood stress, it is important to assess the extent to which they occur together as part of an overall childhood stress syndrome and whether they had an impact on childhood mortality (Katzenberg et al. 1996). If we focus on the childhood years during which both cribra orbitalia and hypoplasias are actively forming, the correlation between the two is striking (Figure 8.4f). Figure 8.4f shows the relationship between the percentage of individuals in age categories one year through five years (whole-year categories) exhibiting hypoplasia and cribra orbitalia. The correlation is almost perfect.

We can combine our stress indicators together into a demographic context by comparing their frequencies to probability of dying (Van Gerven et al. 1995). All three increase, peak, and decline together (Figure 8.5). This provides our strongest evidence for a synergistic relationship between the stresses underlying both cribra orbitalia and hypoplasia and mortality in infants and children.

**Enamel microdefects**

We made our observations of both cribra orbitalia and enamel hypoplasia macroscopically, at the organ level. Conditions such as these and others must involve
changes at the tissue level as well. Changes at the tissue level reflect smaller scale or subtler levels of stress. Many studies of both bone and enamel tissue have demonstrated that to be the case (e.g., Goodman et al. 1980; Martin and Armelagos 1986; Mulhern 1996). One such tissue-level, non-specific stress indicator is the occurrence of microdefects in enamel. They are related to hypoplasia but occur at a microscopic level.

Enamel is produced by cells known as ameloblasts. Beginning at the cusp tip, they move in a perpendicular direction away from the dentine, a bone-like mineral which underlies enamel. As the cells move away from the dentine, each excretes an organic matrix that is then mineralized into an enamel rod. Each completed rod is approximately 0.001 mm in diameter. If a child is sufficiently physiologically stressed, the ameloblasts are interrupted. When they resume, their rods are left with a slight distortion – a defect – at the point where the disruption occurred. When a tooth is sectioned and examined under a microscope, these defects running across adjacent rods appear as dark bands, or microdefects (see Figure 8.2c). All humans have at least one, the neonatal line, which reflects the trauma of our birth.

The microdefects are known as accentuated striae of Retzius or Wilson’s bands (Rose 1977). Hypoplasias are the macroscopic manifestation of these smaller growth defects. For Nubian skeletal samples, specifically the Kulubnarti adults, the number of Wilson’s bands found in canine teeth were counted and the percentage of affected enamel was calculated by expressing the number of changes at the tissue level as well. Changes at the tissue level reflect smaller scale or subtler levels of stress. Many studies of both bone and enamel tissue have demonstrated that to be the case (e.g., Goodman et al. 1980; Martin and Armelagos 1986; Mulhern 1996). One such tissue-level, non-specific stress indicator is the occurrence of microdefects in enamel. They are related to hypoplasia but occur at a microscopic level.

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six-month intervals with at least one Wilson’s band as a percentage of the total number of intervals present on the tooth’s surface (Karhu 1991).

Figure 8.6 shows that the island children not only had more Wilson’s bands overall, but a larger percentage of their enamel was involved. This indicates that the island children were being stressed far more continuously than their mainland counterparts. This fits well with the observation of more continuous hypoplasias among the island children, and suggests that the island children were both sicker and sick more frequently.

**Stable isotope analysis**

Non-specific stress indicators in bones and teeth at Kulubnarti coincide in age of occurrence, are associated with a higher probability of dying when they occur in their highest frequencies, and are likely the result of the nutritional and immunological stresses associated with the weaning process. Enamel hypoplasia, cribra orbitalia, and the probability of dying all peak at age four (see Figure 8.5). But when was weaning really occurring? Did the Kulubnarti children suffer the most stressors during the weaning process, or after it was complete?

Stable isotope analysis of bones and teeth provides an independent estimate of the timing of the weaning process. Isotopes are versions of elements that are distinguished from one another by the number of neutrons in their atomic nuclei; those relevant to reconstructing weaning age, such as nitrogen, are stable as opposed to radiogenic isotopes, which undergo radioactive decay. The proportions of certain isotopes in bones and teeth reflect the isotopic composition of the body when the tissues formed, which in turn reflects aspects of diet and physiology (Fry 2006). The isotopic composition of bones and teeth is measured using a mass spectrometer and normally expressed as a ratio between the proportions of the two isotopes of interest and an agreed-upon standard (in “δ” notation).

![Figure 8.6](image)

**Figure 8.6** Number of Wilson’s bands and percentage of enamel affected by cemetery. Data from Karhu (1991).
Most nitrogen, in nature as well as in biological tissues, is nitrogen-14 (\(^{14}\text{N}\)), and a tiny amount (<1%) is nitrogen-15 (\(^{15}\text{N}\)). The proportions of these isotopes in biological tissues vary according to trophic level. \(^{15}\text{N}\) becomes more abundant relative to the more common \(^{14}\text{N}\) with increasing steps in the food chain (Schoeninger and DeNiro 1984). A zebra, for example, has more \(^{15}\text{N}\), and a higher nitrogen isotope value, than the grass it eats, and a lion has a higher value than the zebra it eats.

The relationship between nitrogen isotopes and trophic position is relevant for studying weaning behavior because a nursing infant is a trophic level higher than his or her mother. This is because a nursing infant only consumes breast milk, which is derived from human tissue. As a result, the nursing infant’s tissues have a higher nitrogen isotope value than the mother’s tissues. The infant’s values decline when milk is supplemented with local foods, and reach values typical of adults once the weaning process is complete. This pattern has been demonstrated with modern mother–infant pairs (Fogel et al. 1989; Fuller et al. 2006). In the archaeological record, the nitrogen isotope values of bone collagen (the primary protein in bone) can be measured for individuals of various ages at death, and examined for the ages when nitrogen isotope values drop to more typical adult values. This is an independent measure of the timing and duration of the weaning process.

Figure 8.7 shows the general pattern of change in nitrogen isotope values by age at death for the combined cemeteries (Turner et al. 2007). There is

![Figure 8.7](image_url)  
**Figure 8.7** Nitrogen isotope values of rib collagen by age at death. Each data point is the mean of a category. There is considerable variability at each age, but the mean line is a reasonable representation of the trend in the data. The declining values represent the weaning process. Here, the average three year old was not completely weaned, but weaning was complete for most five year olds. Data from Turner et al. (2007) and Sandberg et al. (2014).
considerable variability around this trend, but it conveys a reasonable average pattern. From these data, weaning appears to have been completed by age five. If we compare these ages to our hypoplasia and cribra orbitalia data, there is good correspondence, as one would expect.

However, cross-sectional analyses like these, while incredibly useful, may present a biased picture of the weaning process. Everyone in the skeletal sample is there for a reason: they died. Since weaning and its associated stresses are tightly linked to mortality (see Figure 8.5), it stands to reason, particularly from a biocultural perspective, that some weaning practices might contribute to mortality while some might be more successful. Akin to the use of hypoplasias to look at childhood stress events in individuals who survived to adulthood, the nitrogen isotope composition of single teeth can be measured in many places to create a profile similar to Figure 8.7, but for single individuals (Beaumont et al. 2012; Eerkens et al. 2011; Henderson et al. 2014). This is possible because, like enamel, dentine does not turn over once it is mineralized. Using this new high-resolution stable isotope method, we can now ask the questions: Is the weaning process for those that survived distinct from those that did not? Do hypoplasias occur during the weaning process or after it?

Figure 8.8a shows the nitrogen isotope profile for a single individual compared to the generalized pattern from Figure 8.7. Each data point in the individual profile represents the nitrogen isotope value of an approximately 1 mm subsection of dentine corresponding to the age when that portion of dentine formed. From these data, it appears that this individual weaned earlier than the average non-survivor (Sandberg et al. 2014).

This pattern is perhaps surprising given the immunological benefits of breast milk. But this pattern is not without precedent in the modern world. In famine events, East African women have been documented to extend the weaning process because adequate weaning foods are unavailable (Lindstrom and Berhanu 2000). With time, breast milk becomes nutritionally inadequate to sustain the growing infant on its own, and in this situation the infants are primarily suffering and dying from a nutritional shortfall.

The positions of enamel hypoplasias are overlaid on the nitrogen isotope profile for this individual in Figure 8.8b. This allows us to directly evaluate the relationship between weaning behavior and stress events that cause growth disruptions. The width of the bands represents the width, and therefore duration, of the hypoplasia. The growth disruptions occurred during, rather than after the weaning process. But this need not always be the case. In another individual, a wide band of successive hypoplasias occurred after nitrogen isotope values declined to typical adult values, suggesting postweaning stress (Sandberg et al. 2014).

The timing of weaning and the association between the weaning process and hypoplasia are also evident in four other individuals analyzed in this way (Sandberg et al. 2014). The completion of weaning varied between the second and fifth years. With the limitations of a small sample size in mind, it appears as
Figure 8.8 (a) High-resolution nitrogen isotope profile from the permanent first molar of individual “R26” overlaid on the mean line from the rib collagen data. The individual appears to have been weaned earlier than the average non-survivor. (b) A high-resolution nitrogen isotope profile from the permanent first molar of individual “R26.” The vertical bars represent the timing of enamel hypoplasias on this individual’s permanent first molar or permanent canine. The hypoplasias occurred during the weaning process, rather than after weaning was complete. Data from Sandberg et al. (2014).

though extended weaning may have been a last-ditch effort to keep infants alive when nutritious weanling foods were in short supply. In many cases, this effort was not successful. This suggests that we are observing a biocultural response to nutritional availability.
Conclusion

Infants and children are the most vulnerable members of any society and the most sensitive to the biological effects of social and cultural forces. Many different scientists, using different bones and teeth, have studied these residents of Kulubnarti for over three decades. Some aspects of the research have focused on struggles common to all of the children, and there is no doubt that weaning was a serious challenge to them all. That said, each study has led to a single interpretation: the children of the island suffered greater biological stresses than their more economically advantaged mainland counterparts. Greene and co-workers (Greene et al. 1986) estimated that just to maintain their numbers, fertility rates on the island would need to have reached the maximum observed among living populations. The descendants of the mainland community are still living at the site of Kulubnarti in the modern village of Kulb. The island community has long been abandoned. While we can never know what became of them, the children - the canaries in the mineshaft - were telling their communities to leave or die.

The biocultural approach adopted here is not limited to the study of past human populations. Indeed, it has become a dominant paradigm in modern human biology and medical anthropology (e.g., Goodman and Leatherman 1998; Wiley and Allen 2009). Furthermore, the biocultural approach provides a means to connect past human experience with disease to the health challenges humans face in the modern world (e.g., Armelagos and Barnes 1999; Armelagos et al. 2005), and George Armelagos has been an enduring influence in this endeavor for over 50 years.

Acknowledgments

To quote Isaac Newton: “If I have seen further it is by standing on the shoulders of giants.” Generations of anthropologists have seen further because they have stood on the shoulders of George Armelagos. His influence permeates the Kulubnarti research and has inspired our biocultural approach. References cited can never do that justice. The impact of his vision, passion, and intellect will always be felt. He was one of the great anthropologists of his generation.

References

Chapter 8: “Canaries in the mineshaft”: the children of Kulubnarti


CHAPTER 9

Biocultural investigations of ancient Nubia

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Introduction

Stretching along the Nile River from the Sixth Cataract north of Khartoum, Sudan, to the First Cataract at Aswan, Egypt, the region of Nubia (Figure 9.1) has a long history of study in archaeology and biological anthropology and has been foundational in the development of the biocultural paradigm. Beginning in 1813 with exploration by Burckhardt (1819) and the 1842–1845 archaeological survey led by Lepsius (1849–1859 [1970], 1852 [2010]), the region and its past inhabitants became better known through the First and Second Archaeological Surveys of Nubia conducted from 1907 to 1911 and 1929 to 1934 due to heightening of the original dam in Aswan (Firth 1912, 1915, 1927; Reisner 1910). The reports on the human remains (Batrawi 1935; Smith and Jones 1910) were largely descriptive and emphasized racial affinities. However, some of the medical professionals who documented human remains from these projects laid the groundwork for the biocultural approach through their use of clinical epidemiology and ethnographic analogy in order to understand disease among ancient Nubians (see Baker and Judd 2012 for a thorough review). For example, the intersection of biology, culture, and environment used to contextualize human remains and a population-based approach that included statistical analyses were already evident in early studies of Nubian paleopathology by Marc Armand Ruffer (e.g., Ruffer 1914, 1918, 1920; Ruffer and Rietti 1912) and Frederic Wood Jones (e.g., Jones 1908a,b, 1910a,b). It was not until the 1960s, however, that this foundation was built upon in the Nile Valley.

The importance of Nubian studies in the development of the biocultural paradigm is highlighted in this chapter. Archaeological salvage work due to dam construction has stimulated much of this research, which initially focused on Lower Nubia. This comprises the area between the First and Second Cataracts, roughly from Aswan, Egypt, to Wadi Halfa, Sudan. Subsequent research expanded to sites in the Batn el Hajar, a rugged area extending to
the Dal Cataract (see Figure 9.1). More recent work at sites such as Gabati, Kerma, Tombos, Amara West, and in my project area around el-Ginefab has shifted the focus to Upper Nubia, between the Dal and Sixth Cataracts. This work has revealed considerable variability in mortuary behavior, expression of social identity, and health status. In this chapter, the biocultural perspective of
these investigations is emphasized, as well as how the Bioarchaeology of Nubia Expedition (BONE) has implemented a biocultural approach.

**Background**

**Development of the biocultural paradigm in Nubian studies**

With the construction of the Aswan High Dam, an international appeal to rescue monuments and document archaeological sites extending to the Second Cataract was issued in March 1960 by the United Nations Educational, Scientific and Cultural Organization (UNESCO 1960). This call to save the cultural heritage of Nubia, with incentives provided to foreign projects by the governments of Egypt and Sudan, led to a massive influx of archaeologists (Adams 1977:83–86). Many teams included biological anthropologists for the first time in order to help excavate and document burials in a multitude of cemeteries. This collaboration between archaeologists and biological anthropologists coincided with the development of a new perspective. Dubbed “bio-cultural” by Don Brothwell in the landmark volume *Diseases in Antiquity*, this new approach related cultural development with the “ever changing environment” throughout human evolution to illuminate “patterns of human disease through time” (Brothwell 1967:56).

The explicit attempt to consider the ways in which environment and culture affected the health of past peoples reflected a shift from descriptive case studies to population-level research in paleopathology (Brothwell 1967:68). Comparative data on trauma from Jones (1910a) and other Nubian examples were also highlighted (Brothwell 1967). The Lower Nubian skeletal series excavated during the 1960s, particularly those generated by the team from the University of Colorado and the Scandinavian Joint Expedition (Vagn Nielson 1970), as well as the later 1979 Kentucky-Colorado Expedition (see Chapter 8), motivated biological anthropologists to contextualize human biology within a cultural and environmental framework, going well beyond typical descriptive reports on age, sex, skeletal and dental metrics, and pathology.

Most influential was a paper published in *Science* by George Armelagos (1969) that summarized the main findings of his doctoral dissertation (Armelagos 1968), in which pathology and mortality were compared in skeletal series from the Wadi Halfa area that dated to the Meroitic (c. 350 BC–AD 350), Ballana (or X-Group, c. AD 350–550), and Christian (c. AD 550–1400) periods. The article’s subtitle, “Changes in disease patterns from 350 B.C. to A.D. 1400 demonstrate the interaction of biology and culture,” underscores the paradigm shift. Armelagos (1969:255) conducted problem-oriented research on ancient Nubians that investigated “differences in disease processes which result from cultural differences” through the use of a paleoepidemiological model that “entails study of the host, the disease, and the environment.” His outline of political-economic changes that occurred from the Meroitic through Christian periods informed his understanding of lesion frequencies and their changes through time. While acknowledging
a reliance on archaeology for understanding the culture and lifeways of past people, including reconstructing “cultural stresses” that may have “affected biological processes,” Armelagos (1969:255) also recognized that the “examination of pathological conditions may provide insights into cultural practices.”

The investigation of anthropological questions in a biocultural, population-based perspective marked a major change in the way human skeletal remains from archaeological contexts were studied. The explicit acknowledgment of the interaction between biological and cultural variables within a particular environment stimulated a more holistic perspective and spurred the development of bioarchaeology as a bridging field within anthropology. Such problem-oriented research emphasized processes rather than description and typology.

Within a decade after the rescue work, a flood of publications on ancient Egyptians and Nubians advanced the population approach (e.g., Brothwell and Chiarelli 1973). Studies of large skeletal samples excavated during the UNESCO campaign suggested biological continuity and adaptation to changing cultural and environmental circumstances rather than population displacement or replacement (Baker 1997:107–108). For example, changes in craniofacial and dental morphology, particularly a reduction in robusticity from the Mesolithic through Christian periods (roughly about 12 000 BC to AD 1400), were related to functional demands associated with changes in diets and subsistence strategies over time (e.g., Armelagos et al. 1981:35–37, 1984:133–139; Carlson 1976; Carlson and Van Gerven 1979; Greene 1967; Van Gerven 1982; Van Gerven et al. 1973).

The impact of changing subsistence patterns on biocultural adaptations became a focus of research. Morbidity, or disease, was assessed through methods of paleopathology and paleoepidemiology. Mortality, or death, and other vital statistics (e.g., age and sex composition) and population parameters (e.g., life expectancy and mean age at death) were analyzed through techniques of paleodemography, principally through construction of life tables from which graphs were generated to show mortality and survivorship (e.g., Armelagos 1968:410–479, 1969:259; Green et al. 1974; Swedlund and Armelagos 1969). These statistics and curves could be compared within and between samples. Infant mortality was found to be high across the Meroitic through Christian periods, characteristic of intensive agriculturalists, but early childhood and adult life expectancies and survivorship improved after the disintegration of the Meroitic empire, suggesting that local autonomy led to better living conditions (Armelagos 1968:474, 1969:259; Armelagos et al. 1981:49–52).

Frequencies of pathological lesions in these skeletal samples were related to environmental and cultural factors, particularly the intensification of agriculture and irrigation practices, to understand their origin and cause, or etiology. A new focus on skeletal indicators of stress that are not specific to a single condition, but may develop in a variety of circumstances, also emerged at this time. These markers included dental enamel defects, such as enamel hypoplasias, which indicate a disturbance in tooth formation from overall arrested growth during infancy
and childhood caused by experiences of great stress. They also include porosity on the skull vault, known as porotic hyperostosis, or on the roof of the eye orbits, cribra orbitalia, which are associated with various metabolic conditions, including anemia. Juveniles were affected by cribra orbitalia in high frequencies, yet microdefects of the teeth decreased in frequency from the Meroitic through Christian periods, leading investigators (e.g., Carlson et al. 1974; Rudney 1983:464–465; Rudney and Greene 1982) to suggest parasitic disease, particularly malaria, schistosomiasis, and hookworm infection, as the probable cause. These lesions were related not only to subsistence and environmental factors, but to the political and economic changes occurring over this time span (Armelagos et al. 1984; Martin et al. 1984).

The data collected and bone samples imported to the United States from the Wadi Halfa sites by Armelagos (Figure 9.2) and colleagues George Ewing and David and Kathleen Greene led to a number of doctoral dissertations (including my own) and research on patterns of bone growth and maintenance throughout the life course (e.g., Armelagos et al. 1972, 1984:139–143; Dewey 1969; Huss-Ashmore 1982; Huss-Ashmore et al. 1982:424–432; Martin and Armelagos 1979, 1985; Mielke et al. 1972), as well as reconstruction of diet and its nutritional adequacy (e.g., White 1993; White and Armelagos 1997; White and Schwarz 1994; see also Chapter 12).

Research on bone structure at its cellular level (histology) led to the discovery that some ancient Nubians had incorporated tetracycline, a naturally occurring antibiotic, into their bone cells during life (Bassett et al. 1980). It was hypothesized that Streptomyces, the mold-like bacteria that produce tetracycline, contaminated grain stores used in making bread and beer (Armelagos and Mills 1993:9–10; Bassett et al. 1980). This inadvertent byproduct suggests the accumulation of a grain surplus and illustrates the effect that cultural practices can have on human biology: the consumption of grain contaminated with tetracycline, or products made from it, may have mitigated rates of systemic infection among the Ballana period populace of the Wadi Halfa area (Armelagos et al. 1981:47–49; Martin et al. 1984:208). This contention was supported by investigation of remains from the Christian period site of Kulubnarti near the Dal Catarct (see Figure 9.1). At Kulubnarti, the lower frequency of tetracycline-labeled bone cells suggests limited ingestion, perhaps due to small-scale food production with little surplus storage (Hummert and Van Gerven 1982:362). The effects of tetracycline ingestion were suggested through rates of periosteal reaction, another non-specific indicator of stress caused by inflammation of the periosteum, the outer covering of bones. At Kulubnarti more than 40% show periosteal reactions (Hummert and Van Gerven 1982: 360), but only 2.8% of the Ballana period sample from Wadi Halfa was affected (Armelagos 1968:table 25; Armelagos et al. 1981:47–49; Martin et al. 1984:208). The presence of malaria (Miller et al. 1992) and schistosomiasis (Miller et al. 1994) in remains from the Ballana period North Argin (NAX) cemetery, however, suggests that tetracycline levels were insufficient to protect people from effects of parasitic infections.
The discovery of tetracycline in these human remains demonstrates the ways in which the investigation of bone biology and pathology may inform our understanding of cultural practices in the past. The hypothesis that tetracycline formed in grain stores that people subsequently consumed, however, needs to be tested broadly by examining tetracycline presence or absence in Nubian skeletal remains from different regions, time periods, and subsistence regimes.

Despite these breakthroughs, many archaeologists in the decades following the UNESCO campaign viewed biological anthropologists (and bioarchaeologists) as specialists rather than integral members of field and research teams. When
included in subsequent fieldwork, bioarchaeologists’ research on human remains was often limited to descriptive chapters or appendices of site monographs (e.g., Judd 2001) without linkage to the cultural context of the burials (i.e., grave facilities and their spatial relationships, body positioning, grave inclusions, etc.) that archaeologists often deem to be in their purview or neglect altogether, thereby constraining a biocultural perspective. Additionally, those working on accumulated skeletal collections in the United States and elsewhere became increasingly removed from the contexts in which these remains were recovered, as many of these investigators had never visited Nubia.

**Nubian bioarchaeology in the twenty-first century**

A resurgence in biocultural investigations has occurred in the early twenty-first century, partly due to developments in the field of bioarchaeology that have placed increased emphasis on social roles and identity in our understanding of past peoples (e.g., Agarwal and Glencross 2011; Gowland and Knüsel 2006; Knudson and Stojanowski 2009). Incorporation of social theory and careful contextualization have promoted biocultural investigations of extant and newly formed Nubian skeletal collections. Additionally, dam construction and development continue to necessitate rescue work in Sudan. Fieldwork associated with the Merowe Dam Archaeological Salvage Project (MDASP) from 1996 through 2009 (Ahmed 2003), for example, led to the formation of additional large collections of human remains and in-depth archaeological documentation. Bioarchaeologists have become essential members of many teams, some overseeing cemetery excavations and others directing their own projects. Long-term research at sites such as Tombos and Amara West, recently excavated sites including R12 and Gabati, as well as continuing work on previously excavated collections from Kerma, Kulubnarti, Semna South, and the Wadi Halfa area are producing new insights into regional and temporal variation of past lifeways, social identity and organization, and mortuary practices.

While descriptive reports on human remains continue to appear as separate chapters and appendices in site monographs, bioarchaeologists have contributed substantially to interpretation of the site and its inhabitants’ lifeways in many recent publications; for example, the brief Summary and Conclusion of the R12 monograph (Salvatori and Usai 2008) is authored by all contributors to the volume, including three bioarchaeologists. The incorporation of multiple perspectives in such monographs enriches our understanding of the past. Descriptive reports are essential, however, as they present raw data for comparisons among contemporaneous sites and across time. In some cases, whole volumes are devoted to human remains, much as they have been since the First Archaeological Survey of Nubia (Smith and Jones 1910).

At Gabati, a Meroitic through Christian period cemetery, Margaret Judd (2012) contextualizes the skeletal remains and provides extensive interpretation of the findings in her discussion chapter (Judd 2012:63–73) and the final chapter
relating the individuals to their mortuary context (Edwards and Judd 2012). The vast quantities of data presented are situated within the community structure, subsistence practices are related to diet and dental hygiene practices, and disease indicators discussed in respect to nutritional adequacy of the diet and sanitation. Trauma is considered in the way it was sustained – through violence, accidents, or repetitive stress. Comparisons of Gabati to contemporaneous sites to the north illuminate similarities and differences in both biology and behavior across Nubia from the Meroitic through Christian interval (c. 350 BC–AD 1400). Of note is the identification of “major shifts in the balance between agricultural and pastoral lifeways during the period of use of this cemetery,” which may have influenced the documented changes in burial practices (Edwards and Judd 2012:83; see also Edwards 1998). Because the rates of childhood mortality, dental disease, and other skeletal indicators at Gabati do not conform to expectations for intensive agriculture, differences in subsistence practices between southern and northern Nubia from the Meroitic through Medieval periods are indicated (Judd 2014:1121). This conclusion echoes Trigger’s (1994:336) characterization of Sudan’s “narrow and discontinuous floodplains… which were able to support fewer sedentary farmers than were found north of Aswan,” while its savannas “maintained larger numbers of pastoralists.” Drawing on multiple interrelating biological, cultural, and environmental factors, studies like Judd’s (2012) contribute to additional research questions and avenues of investigation.

Research on schistosomiasis further illustrates the biocultural approach, linking biological factors with cultural practices and their impact on the environment. Schistosomiasis is a parasitic disease carried by freshwater snails infected with *Schistosoma*. For instance, Alvrus (2006) used enzyme-linked immunosorbent assay (ELISA) to detect the presence of two antigens specific to schistosome infection in preserved soft tissue from Meroitic individuals at Semna South. Porotic hyperostosis and cribra orbitalia were scored to test for associations between schistosome infection and presence of these lesions; schistosomiasis can contribute to anemia. While the lesions were most common in juveniles, including infants, the highest frequencies of schistosome infection occurred in young and middle adult males, reaching 100% (Alvrus 2006). The age and sex patterning of schistosomiasis at Semna South was compared to clinical and ethnographic information on modern Egyptian and Sudanese populations, notably the infection’s relationship to intensification of agriculture and irrigation systems; this shift in technology increased human exposure to the snail host and schistosome worms. A subsequent study by Campbell Hibbs *et al.* (2011) used ELISA to detect antigens specific to *Schistosoma mansoni* in soft tissue from burials at the Wadi Halfa Ballana period cemeteries and Christian period Kulubnarti. The infection rate was significantly higher in the Wadi Halfa group than at Kulubnarti. This difference was attributed to irrigation agriculture at Wadi Halfa, which provided additional habitat for the snail host. In contrast, the flood agriculture practiced at Kulubnarti decreased exposure to the parasite (Campbell Hibbs *et al.* 2011:295). Human
alteration of the environment, therefore, had adverse biological consequences for the Wadi Halfa population.

Much of the biocultural research on ancient Nubia has emphasized the more recent Meroitic to Christian period populations. Biocultural studies of other eras in Nubian history, especially the Kerma period, c. 2500–1500 BC, and succeeding period of ancient Egyptian colonization during the New Kingdom (c. 1500–1000 BC), have been conducted more recently. Centered on the urban site of Kerma, just south of the Third Cataract, the first empire of ancient Nubia, or Kush as the Egyptians called it, dominated the region throughout the Kerma period. Large royal tumuli at the Kerma cemetery and subsidiary burials surrounding these massive tombs were excavated by George Reisner from 1913 to 1916 (Dunham 1982; Reisner 1923a,b).

The royal tombs at Kerma contained as many as 300 individuals, as well as animals, most in corridors leading to the burial chamber or in ancillary chambers within the tumulus. Reisner (1923a) proposed that those in these corridors were sacrificed, yet no osteologist was involved in the fieldwork or examined the remains for trauma. Collett (1933:268) later noted healed trauma in three of 114 females and 16 of 141 male skulls in her craniometric study, and Filer (1992) compared cranial trauma at Kerma with an ancient Egyptian sample from Giza. With Judd’s (2000) analysis of both cranial and infracranial skeletal remains from Kerma and other contemporaneous rural sites, a more complete understanding of trauma frequency and patterning was obtained. High rates of trauma (42% of Kerma adults and 80% of those from rural sites) were found, with injury recidivism, or repeated trauma, more common in those with incidents of non-lethal violent trauma, particularly in the rural sample (Judd 2002, 2006). Although the rate of multiple injuries is similar to those in modern cross-cultural clinical studies (Judd 2002), the most common injuries at Kerma were to the cranium and ulna – a pattern quite different from clinical studies of trauma in India and Nigeria (Judd 2004). The comparison of rural and urban communities highlights the environmental and occupational hazards of rural life and increased risk of accidental injury compared to Kerma, where those interred in royal and elite tomb contexts likely had a more sedentary lifestyle (Judd 2002:99, 2006:329–330).

Judd (2006:325) also challenged Reisner’s (1923a) notion that individuals found in the corridors of royal tombs were sacrificed, as she found no evidence of perimortem trauma. Judd and Irish (2009) subsequently tested Reisner’s (1923a) contention that these people were mostly female members of the king’s retinue who committed suicide to accompany him in death. Adults interred in subsidiary graves cut into the royal tumuli or around their perimeter also showed no perimortem trauma (Judd and Irish 2009:714). Those in corridors did not display a significantly greater frequency of healed trauma or more severe injuries than those in subsidiary graves and exhibited no evidence of abuse or torture prior to death, as would be expected if they were prisoners of war. Instead, males in subsidiary graves had higher frequencies of trauma (Judd and Irish 2009:715–716). Cranial measurements confirmed that those in subsidiary
and corridor contexts were from the same population; additionally, information on burial position, orientation, and accoutrements indicated conformation to local traditions (Judd and Irish 2009:716–719). If the people in the corridors were sacrificed or did not wish to die, the means used to kill them did not leave any traces on their skeletons, although they may have been dispatched in other ways or died willingly (Judd and Irish 2009). Buzon and Judd (2008) also evaluated several indicators of physiological stress between the allegedly sacrificed and non-sacrificed samples. No significant differences were found between groups and the frequencies of the non-specific stress indicators suggested that overall health was comparable to other contemporaneous Nubian samples (Buzon and Judd 2008). Based on these studies, the presumed sacrifices were no different from their contemporaries and do not seem to represent a specially selected group.

At Kerma, Judd (2006:330) found evidence of larger and more severe cranial injuries than in the rural sample. She interprets this difference as a reflection of increased local tensions and military conflicts with Egypt at the height of the Classic Kerma phase, when Egypt was in political disarray. With the conquest of Kerma by New Kingdom Egyptian pharaohs around 1500 BC, however, most of Nubia came under Egyptian control. The effect of Egyptian colonization on the inhabitants of Tombos, an Egyptian colonial town located a short distance north of Kerma at the Third Cataract (see Figure 9.1), has been intensively investigated. Buzon and Richman (2007) addressed the effects of Egypt’s changing political strategies in Nubia by assessing rates of trauma in the New Kingdom cemetery sample from Tombos and found a lower frequency and different pattern of injury than Judd (2004) reported at Kerma. Statistically significant differences in the rates of cranial trauma attributable to interpersonal violence and fractures of the ulna from parrying blows suggested that Nubians who adopted Egyptian cultural norms were rewarded, promoting a more peaceful co-existence over an extended period of culture contact (Buzon and Richman 2007:789). The low frequency and mild severity of osteoarthritis and musculoskeletal stress markers in the Tombos sample also indicate that they engaged in less strenuous activities than those in other Nile Valley samples (Schrader 2012), supporting Smith’s (1998, 2003) contention that Tombos was an Egyptian administrative center.

Rather than assuming that individuals buried in Egyptian style at Tombos were all immigrants, Buzon (2006a) compared biological affinities with the ethnic identities expressed in death. Cranial measurements were used to assess biological relationships among several Egyptian and Nubian skeletal samples, while grave architecture, body position and orientation, and accompanying artifacts were used to identify Egyptian-style versus traditional Nubian burial practices for each grave. Buzon (2006a, 2008) found variability in both biological and ethnic composition of the cemetery. Interestingly, while many Nubians adopted Egyptian burial practices and others maintained Nubian traditions, a few Egyptians adopted local Nubian practices. Subsequent stable isotope analyses that allow assessment of where a person spent their childhood support the mixed Egyptian
and Nubian origins of the New Kingdom populace at Tombos, but indicate that only local (versus non-local) people were buried there during the succeeding Napatan period, when Nubians subjugated Egypt (Buzon and Simonetti 2013; Buzon et al. 2007).

Non-specific skeletal indicators of stress at Tombos were also assessed in the New Kingdom populace to investigate whether or not they benefited from integration into the Egyptian system (Buzon 2006b, 2008). Although rates of most conditions were comparable to contemporaneous Nile Valley samples, childhood growth (evidenced by shorter adult stature) was compromised and active lesions of cribra orbitalia were pervasive among those who died in childhood. Buzon (2006b, 2008) concludes that these middle-class residents of Tombos were not protected entirely by integration into the Egyptian colonial system, and their children may have experienced increased rates of infection, especially parasitic and diarrheal diseases. Rates of dental disease were also similar to comparative samples, except for antemortem tooth loss and tooth wear that was especially high in adult males. This led Buzon and Bombak (2010:381, 384) to postulate that physiological and potential mental stress caused by sociopolitical changes may have increased rates of bruxism, the clenching and grinding of teeth, in this group. The people from the later Napatan cemetery at Tombos experienced similar rates of dental enamel hypoplasia and periosteal reactions as those from the New Kingdom sample, but show a statistically significant increase in cribra orbitalia (Buzon 2014). Healing of the orbital lesions among the Napatan adult sample, however, suggests that differing social and biological factors and improved conditions allowed them to survive this physiological disruption. Continuing fieldwork and research at Tombos are interweaving archaeological and biological information, contextualizing people and place as they negotiated differing social and political circumstances (e.g., Smith and Buzon 2014a,b).

Case study: operationalizing a biocultural investigation: the Bioarchaeology of Nubia Expedition

The Arizona State University Bioarchaeology of Nubia Expedition (BONE), with fieldwork initiated in 2014, aims to understand the dynamics of past populations at the top of the Great Bend of the Nile River (see Figure 9.1). Spanning more than 30 km along the right (north) bank and more than 3 km into the desert, the project area encompasses nearly 100 km². This project integrates bioarchaeology and landscape archaeology in a holistic manner that considers the density and placement of habitation, cemetery, and rock art sites within the landscape. Further, as subsistence practices and sociopolitical changes occurred throughout time, the biological and cultural consequences of differing circumstances on the region’s inhabitants are addressed.

Building on work conducted as part of the MDASP from 2003 to 2009 (Baker 2014; Smith and Herbst 2005), satellite remote sensing data combined
New directions in biocultural anthropology

with in-field survey, geophysical prospection, and excavation are integrated to characterize archaeological sites and land use in the region, and to explore the potential connections between them in new ways. At present, 228 sites have been recorded in the project area through limited survey, with some as old as the Early (>250,000 years ago) and Middle Stone Ages (250,000–60,000 years ago) and more frequent settlement and cemetery sites from the Mesolithic (c. 8600 BC) through Christian periods (up to AD 1400). Multidisciplinary expertise is essential, including geoarchaeological assessment, satellite and aerial imagery analysis, magnetometry survey, documentation of rock art, acoustical recording of rock gongs (tone-sustaining bedrock outcrops exhibiting cup marks from repetitive striking [Kleinitz et al. 2015]) as well as analyses of artifacts, human and animal remains, and spatial information. Aspects of mortality, health, diet and nutritional status, activity patterns, inter- and intrasite biological affinities, and social identity discerned from the skeletal remains of past peoples may then be situated within well-established archaeological and environmental contexts.

Drawing on archaeology, topography, and hydrology, this integrative research permits individual sites to be placed within a broader environmental context in which an intentionally constructed mortuary landscape is postulated for the Kerma period. The floodplain, now dominated by agricultural fields and groves of date palms, contains remnants of large Meroitic to Christian period cemeteries often built atop much older Neolithic to Kerma period sites (Baker 2014). Sites on the desert terrace include Paleolithic to Neolithic scatters of lithics and settlement structures and Kerma period cemeteries. Distinct clusters of graves are found on topographically prominent points along wadi systems, former watercourses, with sightlines from each that visually link a cluster with several more cemeteries. Thus, these intervisible grave clusters are not isolates, and must be understood as part of a larger, perhaps purposefully conceptualized mortuary landscape overlooking the settlements of the living. Cemeteries on which recent excavation has focused consist of round to oval rock superstructures. Within these, variability in grave architecture, body orientation, and grave inclusions suggests the possibility that different clusters may belong to different segments of a larger group or may comprise unrelated groups of people. Graves excavated in 2015 contained no pots, in contrast to graves at other nearby sites, indicating that they date to an earlier period or belong to a more mobile, pastoralist group. This question can be addressed through radiocarbon dating and future studies of biological distance (biodistance) to assess the degree of relatedness within or between groups and via stable isotope analyses to assess residential mobility and dietary differences.

Later Meroitic to Christian period sites and the earlier settlements on which they were often built have rapidly disappeared under agricultural fields, housing, and other development, leaving a patchwork of seemingly separate sites on the floodplain. However, historic satellite imagery of the project area permits analysis of land use since the 1960s. Coupled with on-the-ground survey and interviews
with local residents, modern land use and its impact on archaeological resources in the area are being evaluated, allowing us to characterize fragmented sites on a past landscape. This work suggests that a vast mortuary landscape was constructed on the floodplain beginning in the Meroitic period (c. 350 BC–350 AD), distinct from the earlier realm of the dead and closer to the living. At this time, a network of stone forts was erected in the region (Crawford 1953), including one found in the BONE project area in 2015, providing additional context for the shifts in mortuary practices and social identities expressed among the dead. Evidence of interpersonal violence, absent so far among the Kerma period sample, appears at this time in both men and women, including healed cranial depression fractures, sharp-force trauma, and one man whose sternum is pierced by an iron arrow (Baker 2008:Figure 7). Archery equipment was placed in the graves of some late Meroitic and Post-Meroitic males at the Ginefab School site. Those with archery equipment show no statistically significant differences in musculoskeletal stress markers compared with other males from this period, indicating that they were not specialized archers, although a sexual division of labor is apparent in the late Meroitic through Christian periods (Nagy and Baker 2013). Avulsion, or purposeful removal, of one or more of the four lower incisor teeth occurs in approximately 12% of Meroitic and Post-Meroitic male and female adults and 7% of the Christian period adults (Bolhofner and Baker 2012) but has not been found in the Kerma period sample thus far, suggesting it also appears as a marker of social identity at this time of increasing strife.

Major changes in burial practices and organizing principles of the cemetery are notable between the late Meroitic/Post-Meroitic and Christian components of the Ginefab School site. The earlier graves often have enormous rock-ring superstructures with subsurface burial shafts and chambers containing a single individual flexed on his or her side along a north–south axis and accompanied by numerous pots and jewelry, and often with cut animal bones indicating the inclusion of choice pieces of sheep or goat meat (Baker 2014; Harris and Baker 2013). In contrast, Christian period graves are marked by small rock cairns over narrow, rectangular grave shafts in which the deceased was laid on his or her back in an extended position with the head to the west and feet to the east without accompanying objects. Most Christian graves are clustered at the east end and south-east edge of the site.

Analyses of biological affinities within the cemetery indicate that related males were buried near each other in the pre-Christian component, but related adults of both sexes and many children were buried close together in the Christian period (Nado and Baker 2013; Seidel and Baker 2013). This alteration in kinship organization of the cemetery may reflect changing concepts of social organization and the family during the Christian period (Nado and Baker 2013). Additional research is under way to assess the effects of increasing aridity, differing subsistence practices, and changes in social and political circumstances on the past people of this area.

Chapter 9: Biocultural investigations of ancient Nubia
Conclusion

This chapter demonstrates the use of a biocultural approach in the investigation of ancient Nubia from the 1960s to the present and the ways in which these studies have enriched our understanding of ancient Nubian identity, society, lifeways, and adaptations. Further exploration of population dynamics and biocultural adaptations within Nubia must take a broad view through time, and address climatic changes as well as differing subsistence strategies. It is increasingly imperative that archaeological projects be multidisciplinary. Learning how people used and perceived their landscape in the past and how present alterations to that landscape affect our reconstructions is a critical component of recent biocultural research in Nubia. Through integration of biological, cultural, and environmental data, a perspective pioneered by Jones, championed by Armelagos, and continued today by others, our comprehension of ancient Nubians will continue to advance.

Acknowledgments

My research on ancient Nubia was inspired by George J. Armelagos, my graduate advisor at the University of Massachusetts, Amherst. Thanks are due to Molly Zuckerman and Debra Martin for organizing this volume. Christopher Sevara has contributed substantially to advancing the goals of the BONE project, particularly in landscape archaeology. The BONE research is funded by the Qatar-Sudan Archaeological Project and a private donor, and is conducted in cooperation with Sudan’s National Corporation for Antiquities and Museums.

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CHAPTER 10

Life and death in nineteenth-century Peoria, Illinois: taking a biocultural approach towards understanding the past

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Introduction

One of the greatest strengths of the biocultural approach within paleopathology, the study of ancient disease, is its ability to appreciate human complexity. Human disease, both past and present, is not simply due to the presence or absence of a pathogen; it is inextricably linked to factors such as host nutrition, growth and development, genetics, social and economic conditions, religious beliefs, environment, and immunological response. In short, in order to understand disease in the past, we need to know a great deal about the environment as well as the individuals affected. Often this is best tackled by adopting a population approach.

The population approach in paleopathology is straightforward. It seeks to explore the role and impact of disease within past populations, rather than within a given individual. The strength of this approach is that isolated incidences and unique experiences can contribute to a broader understanding of the impact of disease in a given context over time. Much has been written about the population approach. Angel (1981), Armelagos (1994, 1997, 2003, 2008), Armelagos et al. (1982), Armelagos and Van Gerven (2003), Buikstra (2010), Buikstra and Beck (2006), Buikstra and Cook (1980), Grauer (2012), Roberts and Buikstra (2012), Roberts (2006), and Zuckerman et al. (2012), to name a few, have clearly outlined the trajectory of paleopathology from a field that focused almost exclusively on individuals and case studies, to a multifaceted tactic that seeks to explore health and disease on a broader scale and through the incorporation of many disciplines. When patterns of morbidity, the presence of disease in an individual or population, and mortality, the death
of an individual or population, are constructed through the analysis of many skeletons, the unique life experiences of individuals are obscured in favor of broad snapshots of larger groups across time and space. Recent applications of this approach include Verano and Ubelaker (1992), who investigate health and disease in the Americas; Grauer and Stuart-MacAdam (1998) and Agarwal (2012), who examine the roles that sex and gender play in human disease; Goodman (1999), who highlights the biological consequences of inequality in antiquity; Steckel and Rose (2002), who amass, through the efforts of many researchers, data to assess changes in health and disease over millennia within the Western Hemisphere; Roberts and Cox (2003), who assemble skeletal data to explore health and disease in Britain; Cohen and Crane-Kramer (2007), who tackle aspects of ancient health during human agricultural intensification; and Zuckerman (2014), who gathers the work of researchers exploring the second epidemiologic transition, and the changes in patterns of mortality associated with industrialization (see Chapter 18).

But by no means does the population approach render the life of a given individual inconsequential. Saul and Saul (1989), Boutin (2011, 2012), Baadsgaard et al. (2012), and Stodder and Palkovich (2012), for instance, make it abundantly clear that analytical emphases on individuals offer rich insight into life and death in the past. These authors, building on theoretical works developed in social and biological anthropology, archaeology, and feminist, gender, and identity studies, underscore the malleable and changing nature of human social relations during and after death. Status and interpersonal relationships profoundly change throughout life. The presence and/or impact of disease can be interpreted and reinterpreted during life depending on one’s age, sex, access to resources, religious convictions, and ideology, and again are renegotiated and acted upon after death. One take-home message from adopting this approach is to be wary as a researcher (or reader!) of conclusions that imply that we irrefutably know what others thought in the past, or why actions were taken, or behaviors displayed. We do not. We can, nevertheless, develop robust, testable theories that seek to capture the complex interchange between human behavior, life and death, and health and disease (Buikstra and Beck 2006; Larsen 1997; Martin et al. 2014).

Focusing on groups, rather than individuals, has a number of benefits. First, it allows us to create and recognize patterns. Scientists love patterns, for they serve as a basis for prediction and thus, explanation. Finding skeletal remains of a single individual dying at a particular age might prove key to ascertaining developmental problems and/or the presence of a pathogen. However, determining that a large portion of a skeletal sample died at that age allows us to evaluate the environment within which these individuals lived (and died), as well as genetic relationships and/or aspects of the host–pathogen dynamic. Studies centered on the epidemiology, etiology, and evolution of specific conditions such as syphilis and other forms of treponemal disease (see Powell and Cook 2005), tuberculosis (see Roberts and Buikstra 2003), and nutritional deficiencies (see Brickley and Ives 2008) exemplify the benefits of this approach.
Chapter 10: Taking a biocultural approach towards understanding the past

However, broadening the aperture of the lens through which one views the world does not necessarily lead to greater clarity. As any photographer will tell you, add more light and you will lose depth of field. Focusing on populations, rather than an individual, poses similar problems for paleopathologists. For instance, we overlook detail – lives of individuals are ignored in favor of patterns created by many. We are pressed to make assumptions. We assume that the skeletal sample under investigation adequately reflects the presence of disease in once living populations. But as Wood et al. (1992), Waldron (1994), Hoppa and Vaupel (2002), and Pinhasi and Bourbou (2008) point out, this might not be the case. People move in and out of groups – or populations – all the time, and may or may not be buried in the area in which they were born, so the relationship between individuals during life is not necessarily reflected in the relationships between bodies buried upon death. Detecting the presence of disease poses similar problems. Some diseases impact the host so rapidly and forcibly that the person dies before their skeletal system has time to react macroscopically. In these instances, the individual may appear to be healthy, based on the gross appearance of the skeleton, since lesions are absent. Alternatively, noting multiple skeletal changes might lead the analyst to conclude that an individual was extremely sick when in fact, the presence of skeletal lesions could be interpreted as “healthy” since the individual was obviously able to wage an immunological response to the stressor(s) and live through the stressful period.

One way to address these issues is through careful integration of auxiliary data (Cohen 1994; Goodman 1993; Wright and Yoder 2003). Careful archaeological excavation and analysis (see Buikstra 1991, 2010; Buikstra and Beck 2006), and vigilant exploration into the historical records (see Herring and Swedlund 2003; Mitchell 2011, 2012; Saunders and Herring 1995), enhances our understanding of morbidity and mortality in the past. Hence, the goal of this chapter is to synthesize skeletal analyses with archaeological data and historical information as a means of understanding life in nineteenth-century Peoria, Illinois. Using census records, along with other historical documents, the skeletal manifestations of health and disease, especially the presence of high juvenile mortality, are evaluated. Taking a biocultural approach, which explores the relationship between biology and culture, towards understanding the past allows us to begin to understand how disease and human biology are intricately tied to human culture.

Case study: life and death in nineteenth-century Peoria

Background
Peoria, Illinois, is a city poised on the banks of the Illinois River, which is a major tributary of the great Mississippi River. Throughout the nineteenth century, Peoria was the second largest city in Illinois. Balance (1870) indicates that in 1855, a census was initiated, under the direction of the County Commissioner’s Court.
City residents included 1776 males and 1771 females under the age of 10 years old, and 4696 males and 3615 females over the age of 10 (11,858 total residents) (Balance 1870:202–203). A census was taken close to 10 years later, in 1864, which concluded that there were 17,227 residents, a number that the Board of Aldermen believed was a gross underrepresentation (Balance 1870:204). Irrespective of the possible inaccuracies, it appears that the city of Peoria grew rapidly between 1840 and 1860, and that the number of residents under the age of 20 was almost equal to the number over the age of 20 (from Balance 1870:204). The allure of thriving industries brought many immigrants to Peoria. Surrounded by fertile cornfields and possessing a readily available transportation system on a major river, the city became renowned for its whisky distilleries and manufacturing of farm equipment.

Along with growth and prosperity came the need to attend to the dead. The Peoria City Cemetery, encompassing a square city block, was platted in 1842. It was designed to serve as the resting place for all residents, wealthy and indigent alike. By as early as 1861, according to the *Peoria Daily Transcript* on December 4th, the City Council began discussing the impending need for more space: all plots had been sold, but not necessarily filled, and options for expansion were explored (Bird and Grauer 2012). However, similar to the predicament of other urban cemeteries, space was both limited and expensive. A new facility, the Springdale Cemetery and Mausoleum, located approximately five miles away and outside the city limits, was opened in 1877. As the City Cemetery continued to decline, measures were taken by families of the deceased, as well as by city officials, to disinter and move bodies to the new, much more aesthetically acceptable facility.

Determining the number of bodies originally interred in the cemetery, as well as calculating the number moved, is difficult due to poor record keeping and uncoordinated private and public actions. In 1857, according to Springdale Cemetery records, 53 bodies were moved to Springdale Cemetery, with fewer and fewer being moved until shortly after 1900 (Bird and Grauer 2012:8–9). On March 20, 1883, the Committee on Public Grounds and City Property reported that there were “some six hundred bodies still remaining in said Cemetery” (Proceedings of the City Council, Book H:347), and requested that funds be appropriated for their removal and that the property be formally vacated. Without much fanfare or consternation, the City Cemetery became Lincoln Park in 1886. In 1910, through the generosity of Andrew Carnegie, a library was built on the property and remains today as the Lincoln Branch of the Peoria Public Library.

In 2009, due to plans to expand the public library building, an excavation was undertaken to assess and preserve any impacted human remains. Preliminary shovel probing and backhoe removal of overburden coinciding with the 15,000 square foot footprint of the proposed new building revealed approximately 300 features, most appearing as grave shafts (see Figure 10.1). The unexpected – at least to city officials – scope and expense of excavation lead to an amendment
Chapter 10: Taking a biocultural approach towards understanding the past

Figure 10.1  Map of the Peoria Public Library excavation showing the existing library, the location of detected grave shafts, the original proposed footprint of the new building (the outermost line within which all grave shafts appear), and the final reduced footprint of the proposed building (the square within which a more limited number of grave shafts were recorded). The original plat of the cemetery has been overlaid, appearing as numbered squares and rectangles of varying size. Source: Bird and Grauer (2012).

of the footprint. The greatly reduced footprint would impact fewer features, and exposed features within the former footprint would be reburied without further disturbance. Hence, by the conclusion of the excavation, 86 individuals were fully excavated and brought to Loyola University, Chicago, for analysis.

Methods
Demography
The collection of demographic data was based on established protocols outlined by Buikstra and Ubelaker (1994). This included independently utilizing the maximum number of techniques possible for each skeleton to determine age at death and sex. Age at death for juveniles was assessed using multiple methods: Scheuer and Black (2000) to evaluate the developmental pattern of human bones and the timing of epiphyseal fusion, and Ubelaker (1987, 1999), Moorrees et al. (1963a,b), and Schour and Massler (1940a,b, 1941, 1944) to evaluate the development and eruption of juvenile and adult dentition. Adult aging was assessed using morphological changes to the pubic symphysis (Brooks and Suchey 1990; Hartnett 2010; Todd 1921a,b), the auricular surface of the ilium...
(Lovejoy et al. 1985), and cranial suture closure (Meindl and Lovejoy 1985). Determination of the sex of adult skeletons was based on sexual dimorphism of the cranium and os pubis (Phenice 1969; Volk and Ubelaker 2002; Walker 2005, 2008).

**Paleopathology**

The paleopathological data were assessed macroscopically and with the use of dissecting and digital microscopes. For this study, and the purpose of reconstructing population-level patterns of health and disease, particular attention was paid to the presence of several lesions. These included periosteal reactions, or “reactive” bone changes, which are areas of subperiosteal bone deposition associated with inflammation and/or infection (Weston 2012). Porotic hyperostosis was also recorded, and was recognized by pitting and diploic thickening on the superior margins of the eye orbits and/or the parietales of the cranial vault. This lesion has been arguably associated with the presence of iron deficiency anemia and metabolic disorders (Brickley 2008). Traumatic lesions, both from accidental and interpersonal trauma were recorded, along with indicators of joint changes associated with degenerative joint disease or injury (Jurmain et al. 2012; Wedel and Galloway 2014). Lastly, the presence of enamel hypoplasias, which are linear or pitted defects to the enamel of teeth, was recorded. These are associated with periods of growth arrest and disruption of enamel deposition due to the presence of stressors during childhood development, including sustained fever or chronic disease, severe nutritional deficiency, diarrheal diseases, and other factors (Armelagos et al. 2009; Hillson 2000).

**Historical data**

The 1850 and 1860 census records, containing mortality schedules, along with a published Death Report for 1872 (Peoria Daily Transcript, February 6, 1873), were also used in this analysis.

**Results**

**Skeletal analysis**

Based on the analysis of all skeletal material recovered from the excavation, it appears that juveniles under the age of one year old constitute the highest proportion of the skeletal sample (n = 30, 36.1%), while 1–4.9 year olds make up the next highest percentage (n = 16, 19.3%) (Table 10.1). Adults of all ages are equally distributed within the sample, but a disparity between females and males between the ages of 20 and 40 years old is evident.

A number of pathological lesions were recorded for the Peoria City Cemetery skeletal sample (Table 10.2). Periosteal reaction was noted in 29% (12/42) of individuals over the age of three years old. However, 11 individuals under the age of three (11/44, 25%) displayed reactive bone (Table 10.3). Porotic hyperostosis was found in 19% of the sample (12/64), while 42% (31/74) displayed
Table 10.1  Demographic profile of skeletal remains recovered from the Peoria City Cemetery (age at death could not be determined for two individuals).

<table>
<thead>
<tr>
<th>Age At death</th>
<th>n</th>
<th>Percent</th>
<th>Female</th>
<th>Male</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;1 year old</td>
<td>30</td>
<td>36.1%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1–4 years old</td>
<td>16</td>
<td>19.3%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5-10 years old</td>
<td>8</td>
<td>9.6%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10-15 years old</td>
<td>1</td>
<td>1.2%</td>
<td></td>
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</tr>
<tr>
<td>15-20 years old</td>
<td>1</td>
<td>1.2%</td>
<td></td>
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<tr>
<td>20-40 years old</td>
<td>8</td>
<td>9.6%</td>
<td>8</td>
<td>0</td>
</tr>
<tr>
<td>40-60 years old</td>
<td>10</td>
<td>12%</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>&gt;60 years old</td>
<td>9</td>
<td>10.8%</td>
<td>3</td>
<td>6</td>
</tr>
<tr>
<td>TOTAL</td>
<td>83</td>
<td></td>
<td>15</td>
<td>12</td>
</tr>
</tbody>
</table>

Table 10.2  Most frequent pathological conditions recorded in the Peoria Cemetery sample.

<table>
<thead>
<tr>
<th>Pathological conditions</th>
<th>n</th>
<th>N</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trauma (fractures)</td>
<td>7</td>
<td>74*</td>
<td>9%</td>
</tr>
<tr>
<td>Joint alterations</td>
<td>18</td>
<td>30**</td>
<td>60%</td>
</tr>
<tr>
<td>Periosteal reaction</td>
<td>12</td>
<td>42***</td>
<td>29%</td>
</tr>
<tr>
<td>Porotic hyperostosis</td>
<td>12</td>
<td>64*</td>
<td>19%</td>
</tr>
<tr>
<td>Enamel hypoplasia</td>
<td>31</td>
<td>74*</td>
<td>42%</td>
</tr>
</tbody>
</table>

* Age > fetal/newborn.
** Age >20 years old.
*** Age >3 years old.

enamel hypoplasias in their dentition. Healed fractures were found in seven individuals. Other signs of trauma included four individuals with Schmorl’s nodes, which are an indicator of considerable stress placed upon the vertebrae. Two individuals exhibited spondylolysis of the lumbar vertebrae. These fractures are often associated with vertebral stress. Lastly, two individuals displayed os acromiale, a condition noted by the failure of the acromion process of the scapula to fuse or fuse completely. This can serve as an indicator of strenuous use of the shoulder during childhood and adolescence, when bone epiphyses have not fully fused.

Historical records
An examination of the mortality schedules derived from the 1850 and 1860 census records and the published Death Report for 1872, that enumerate the number and causes of death in Peoria, highlight a variety of mortality patterns for residents. For instance, the mortality schedules reveal high child mortality, specifically for those under the age of five years old (Table 10.4, Figure 10.2).
Table 10.3 Juveniles in the Peoria Public Cemetery skeletal sample displaying reactive bone (adapted from Grauer et al. 2013 and Drissell et al. 2012).

<table>
<thead>
<tr>
<th>Burial number</th>
<th>Age at death</th>
<th>Orbits</th>
<th>Maxilla</th>
<th>Mandible</th>
<th>Sphenoid</th>
<th>Temporal</th>
<th>Scapula</th>
<th>Zygomatic</th>
<th>Alveoli</th>
<th>Parietals</th>
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<tr>
<td>126</td>
<td>195</td>
<td></td>
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<td>268</td>
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<tr>
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</table>

Dark shaded squares = lesions found bilaterally.
Light shaded squares = lesions found unilaterally or only one side was present for evaluation.
Chapter 10: Taking a biocultural approach towards understanding the past

Table 10.4 Comparison of demographic profiles derived from mortality schedules and skeletal analysis.

<table>
<thead>
<tr>
<th>Age at death</th>
<th>&lt; 1 yr</th>
<th>1–4 yrs</th>
<th>5–10 yrs</th>
<th>10–15 yrs</th>
<th>15–20 yrs</th>
<th>20–40 yrs</th>
<th>40–60 yrs</th>
<th>60+</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1850 census</td>
<td>56</td>
<td>47</td>
<td>11</td>
<td>7</td>
<td>56</td>
<td>35</td>
<td>15</td>
<td>237</td>
<td>83</td>
</tr>
<tr>
<td>1860 census</td>
<td>119</td>
<td>158</td>
<td>44</td>
<td>14</td>
<td>12</td>
<td>58</td>
<td>35</td>
<td>35</td>
<td>475</td>
</tr>
<tr>
<td>1872 report</td>
<td>106</td>
<td>116</td>
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</table>

They also reveal a many causes of death, which varied over time (Figure 10.3). Cholera and “consumption,” which is known as tuberculosis today, were the most common causes of death in 1850. By 1860, consumption and scarlet fever (a bacterial infection associated with strep throat), were most common. However, by 1872, “brain fever” (a febrile condition be caused by a wide range of

Figure 10.2 Mortality profiles derived from skeletal analyses and mortality schedules.
Figure 10.3 Common causes of death recorded in the mortality schedules.

pathogens or conditions), consumption, and “summer complaint” (acute diarrhea often caused by bacterial contamination of food), were the most common causes. Temporal changes are also evident in the deaths of the youngest residents of Peoria. Focusing on the death of those under the age of two years old (Figure 10.4), cholera, “lung fever” (pneumonia), measles, summer complaint, and whooping cough were the most common causes of death in 1850. By 1860, measles, scarlet fever, summer complaint, and whooping cough predominated.

Causes of mortality patterns are also recorded for adults. For instance, deaths recorded for women between the ages of 20 and 50 years old indicate that in 1850 28.1% (32/114) and in 1860 21.6% (37/171) were reported as related to complications of childbirth.

Discussion

It appears from the skeletal data and mortality schedules that juvenile mortality was high in Peoria during the mid-nineteenth century. However, it is critical to examine two questions: are the data biased and if so, how? Also, what do these apparent trends tell us about life for residents of nineteenth-century Peoria?
First, the data are not without bias. Historical records indicate that the cemetery was platted to provide burial for “poor persons and strangers” along the eastern and southern edges of the property. The area of excavation excluded these densely packed areas. Hence, the skeletal sample might reflect wealthier residents, who commonly manifest different patterns of morbidity and mortality from those of lower socioeconomic means. Also, clear evidence exists from archaeological and historical sources that hundreds of bodies were moved to the new Springdale Cemetery between 1856 and 1886, excluding these individuals from the skeletal sample analyzed here. As this endeavor took considerable resources and definitive decisions, the bodies of wealthy families and male patrons were perhaps more commonly moved than those of young women and children. Thus, the result is a skeletal sample that might be composed primarily of individuals of “comfortable” but not wealthy means, women, and those predominantly of young age. Mortality data from census records are equally biased, but in different ways. Reporting deaths, along with causes of death, and demographic information, such as age at death, varied in accuracy from census to census and place to place. Overall, underenumeration of deaths is a common error found in mortality records.

Overall, the paleopathological data supplement the historical record. The high percentage of individuals displaying periosteal reactions (over 35%), which are
often associated with inflammation and/or infection, and pathological conditions associated with physical labor, namely os acromiale and spondylolysis, suggest that a substantial segment of this sample lived arduous lives. Children, in particular, appear to be biologically and socially vulnerable. Both the historical documentation and the skeletal analysis suggest that high mortality rates were commonly found in this sector of the population.

Determining the cause of these high mortality rates is difficult. Mortality records list diverse causes of death for children. The skeletal record can only tell us that children suffered from some condition or pathogen – not specifically what condition or pathogen. However, it is interesting to note that the skeletal sample has a high proportion of individuals (children and adults) with enamel hypoplasia, suggesting the presence of stressors that temporarily interrupt growth and development. The sample also yields a high proportion of children with reactive periosteal lesions. This might suggest, with further research, that metabolic conditions, such as scurvy, actually exacerbated infectious and/or bacterial diseases. Causes of death listed in the mortality records, such as summer complaint, cholera infantum (a non-contagious bout of severe diarrhea, diarrhea), and “inflammation of the bowels” (inflamed intestines associated with diarrhea and abdominal pain), might be linked to the consumption of spoiled milk. This might be linked in to growing industrialization, occurring during the nineteenth century in Peoria, and to women’s increasing involvement in wage-labor outside the home. Wage-working women, needing to leave their infants and return to work relatively soon after giving birth, might have opted to wean their children onto cow’s milk and grain (Stevens et al. 2009; Wickes 1953). However, this “formula” spoiled quickly during the hot summer months. Scurvy and anemia are also common conditions in children with a high intake of cow’s milk (Brickley and Ives 2008), and would have served as compounding stressors during early childhood.

**Conclusion**

Peoria, Illinois, was a burgeoning nineteenth-century river city. Skeletal analyses of 86 individuals excavated from the Peoria City Cemetery (ca. 1839–1886) were compared to contemporary mortality records. Results indicate that juveniles under the age of five years old constitute the highest proportion of the cemetery sample and the mortality schedules. The high percentage of individuals displaying joint alterations, enamel hypoplasia, and pathological conditions associated with physical labor suggests that a substantial segment of the population lived arduous lives. Children of Peoria were biologically and socially vulnerable members of their community and took the brunt of economic circumstances. This is witnessed by a high percentage of juveniles displaying bone lesions associated with infection and inflammation. While the etiology of the lesions remains
unknown, further research is being conducted to explore whether weaning practices, along with early childhood diets, contributed to metabolic conditions that rendered children vulnerable to bacterial and viral infection. It is hoped that by combining skeletal analyses with historical documents, a more nuanced snapshot of life in the past, both biological and cultural components, will be created. Without doubt, taking a biocultural approach allows us to examine ways in which biology affects human culture, and human culture affects biology. The complex interaction serves as our foundation as we seek to understand how these people lived and how they died.

**Acknowledgments**

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Special thanks, as always, goes to George Armelagos, whose guidance, insight, curiosity, occasional patience, unflinching sense of humor, fabulous cooking, and unwavering commitment to students (past and present) set the foundation for so many of our life’s work and passion. He is deeply loved and sorely missed.

**References**


CHAPTER 11

Does industrialization always result in reduced skeletal robusticity?

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Introduction

Bioarchaeology concentrates on the contextual analysis of human skeletal remains. It is the context that can provide a rich history and broaden interpretations of past lifeways, including such things as diet and nutrition, accident history, disease, and work or occupation history, among other things. Prehistory is most often the focus of bioarchaeology research but analysis of historical samples can broaden our perspective of the recorded past. This chapter is focused on the historical past, in particular the nineteenth century in the United States. Some may ask, why study human remains from the nineteenth century if we already have a substantial written record of the period? This written history tends to highlight the social and political elite, largely ignoring the working class, at least in the United States.

In order to better understand that past, it is essential to consider both the biology of the people and their culture. Indeed, it can be most helpful to have some recorded history as it can fill in some parts of the culture picture not available in prehistory, but one often untapped resource is the human remains themselves. Careful analysis and measurement of those remains, combined with written literature and powerful statistical techniques, can aid in revealing changes that may have occurred in the skeleton over time or that might be a result of certain habitual activities. These generally are events or activities that are often overlooked and not recorded so one of the ways to provide a partial picture of that history is to study the human remains.

Recently, Ruff and colleagues (2015) conducted a study in which they examined nearly 2000 individual skeletons from across Europe extending from the Upper Paleolithic (11 000–33 000 years ago) through the twentieth century. The question they addressed concerns the decline in skeletal robusticity (bone strength relative to body size) with increased sedentism associated with the change in subsistence practices from foraging to agriculture. In that paper, the authors argue that mobility levels began to drop with the onset of food...
production but the transition was a gradual one. Especially noteworthy was the decline in femoral robusticity, and they further note that the lack of change in bone strength with mechanization and urbanization resulted in only small changes in skeletal robusticity (Ruff et al. 2015).

Studies of skeletal robusticity in the United States have focused primarily on subsistence transitions in prehistory. Very few studies have looked at skeletal robusticity in modern populations. This study challenges the assumption that industrialization and urbanization did not result in changes in skeletal robusticity, as advocated by Ruff et al. (2015). Changes in work activity and work intensity among people of different status, especially lower-class working people, are expected to be associated with changes in skeletal robusticity.

The purpose of this study is to examine postcranial skeletal robusticity in nineteenth-century working-class people from North America. Specifically, we will describe the skeletal robusticity of the Colorado Insane Asylum skeletal collection and compare it to three other nineteenth-century skeletal samples: the First African Baptist Church cemetery sample from Philadelphia, a portion of the Dunning Cemetery in Chicago, a cemetery used by a poor house, and the Eastern State Hospital sample, a cemetery associated with a nineteenth-century mental hospital in Lexington, Kentucky. These skeletal samples presumably represent largely working-class individuals, people who are lower status, and we would expect their activity intensity levels to be very high. The comparison will provide a means of understanding the variability of the skeletal response to nineteenth-century industrialization in North America. This will provide the foundation to compare these working-class samples to other skeletal samples derived from the middle and affluent classes and will take a step toward addressing skeletal changes associated with industrialization. It is precisely these working-class individuals whose voices we rarely hear in the historical literature and this biocultural analysis can help shed light on a sample of the lower class.

**Background**

Many studies in bioarchaeology have used skeletal robusticity as a means to make interpretations about mobility and workload in past human populations. This is because skeletal robusticity emphasizes the interactions between biology and culture and provides an interpretive framework for understanding many of the observed differences in skeletal size and shape. These observed differences can be used to reconstruct activity patterns of past populations (Larsen 2015).

There are many ways to define skeletal robusticity. The simplest defines skeletal robusticity as the thickness of a long bone diaphysis or shaft (Pearson 2000; Stock and Shaw 2007). Ruff and colleagues (1993:21–22) specifically define skeletal robusticity as “strengthening or structural buttressing of a skeletal element through the addition of bone tissue, and it is usually assumed to be a response to higher mechanical loadings.” Robusticity can also refer to joint
Chapter 11: Does industrialization always result in reduced skeletal robusticity?

Surface area or shaft cross-sectional geometry, as well as measures of other biomechanical properties. These measurements can be restricted to individual skeletal elements or explored as a distribution across the entire skeleton. Overall, these different measures all facilitate the same predictions of musculoskeletal massiveness which in turn are used to reconstruct activity level and types of activity engaged in by past populations (Larsen 2015; Pearson 2000; Pearson and Leiberman 2004; Ruff et al. 2006).

Skeletal robusticity is firmly grounded in the biomechanical concept of the functional adaptation of bone (Larsen 2015; Pearson 2000; Pearson and Leiberman 2004; Ruff et al. 2006). This concept is defined as the phenotypic plasticity of bone in that bone will respond to its mechanical environment with changes in size and shape (Larsen 2015; Pearson and Leiberman 2004; Ruff et al. 2006.) The mechanical environment includes both mechanical stress and strain. Stress is created by the application of force. An example is ground reaction forces exerting stress on the lower limb during locomotion. These stresses can vary in intensity and direction, creating strains on the bone of varying magnitude. As strain increases, bone will initiate osteoblastic activity, or bony growth, in an effort to return bone to a more mechanically stable system. It is important to note that bone remodeling is not functionally ideal. The skeletal system performs multiple functions beyond physical support such as mineral storage and immune response. The morphology of bone, then, is a compromise between these different physiological demands (Larsen 2015; Pearson 2000; Pearson and Leiberman 2004; Ruff et al. 2006).

In general, the concept of bone functional adaptation is a biomechanical model that emphasizes the interplay between genetics and the environment. As such, changes observed in skeletal robusticity between populations are, in fact, the outcome of functional adaptation of bone to its unique mechanical environments. It is for this reason that skeletal robusticity provides key information on the behavioral activity of past populations (Pearson and Leiberman 2004).

Temporal trends in skeletal robusticity have been used to examine the postcranial skeleton within the genus Homo. It is shown that there has been a generalized trend of femoral robusticity reduction or, in other words, a gracilization since the time of Homo erectus. Specifically, the amount of cortical bone in the femoral shaft has diminished, with contemporary humans exhibiting the least amount of cortical bone. As noted above, this general trend shows a marked change following the Neolithic (agricultural revolution) during periods of subsistence transition that resulted in a decline in mobility and an increase in sedentism (Ruff 2006; Ruff et al. 1993, 1994, 2015). Although the decline in skeletal robusticity is observed, there is a tremendous amount of variation in recent humans so that the percentage cortical area overlaps extensively with all other specimens examined (Ruff et al. 1993).

Of particular interest here are those studies that demonstrate the variation in skeletal responses to mechanical stress in recent human populations. Larsen (1995), Ruff and colleagues (1984), and Ruff and Larsen (1990) examined this
relationship in prehistoric Native American populations from Georgia in order to
dertail the changes in bone size and shape which accompanied the shift from a for-
aging and fishing subsistence strategy to one of maize agriculture, as well as the
later subsistence shift during the Spanish mission period. After the subsistence
transition, there was a reduction in femoral robusticity and sexual dimorphism.
The reduction in femoral robusticity suggests that the subsistence transition and
later agricultural intensification resulted in a decrease in mobility with a marked
increase in sedentism. The reduction in sexual dimorphism suggests that males
and females in the Georgia sample were engaged in similar mobility patterns,
whereas previously males were more mobile than females, even though both
males and females were more mobile than their agricultural counterparts (Larsen
1995).

Larsen (2015) also reported changes in humeral robusticity. Unlike the femur,
the humerus exhibits more variation in expressed robusticity between individ-
uals and even between left and right limbs. This variation is due to the fact that
the humerus is not engaged in locomotion but rather in various activities includ-
ing lifting, dragging, and pounding, among others. As such, the humerus has
more nuanced responses to changes in activity, work, and the division of labor
(Larsen 2015; Ruff et al. 2006). Male humeral bilateral asymmetry (the differ-
ce in robusticity of the left and right limbs) remained largely unchanged while
females experienced a marked reduction in humeral asymmetry. This suggests
that males may have continued practicing similar load-carrying activities while
females had more pronounced behavioral changes after the adoption of agricul-
ture (Ruff and Larsen 1990).

Following along similar lines, Bridges examined femoral and humeral size
and shape among prehistoric populations from Alabama (Bridges 1989) and Illi-
nos (Bridges et al. 2000). In both settings, changes in long bone size and shape
were documented but these changes differed from those reported by Larsen.
The differences between the two studies may be the result of theoretical differ-
ences. Larsen favors interpretations that define subsistence in discrete categories
while Bridges incorporates the use of mixed or transitional subsistence. In both
Alabama (Bridges 1989) and Illinois (Bridges et al. 2000), it was found that long
bone strength increased with the intensification of maize agriculture, but not
the adoption of maize. In the Illinois samples, males show virtually no change in
leg robusticity through time but show a decline in humeral asymmetry, thought
to reflect adoption of the bow and arrow in this region (Bridges et al. 2000).
Females show an increase in leg strength and humeral robusticity during the
Middle Woodland, a time when seed domestication was apparently intensified.
Bridges and colleagues’ study shows that the gross categorization of subsistence
does little to help predict changes in skeletal robusticity, and that local geography
and cultural contexts must also be considered.

Hogue and Dongarra (2002) also present data supporting the variability of
the skeletal response to subsistence transitions. Their investigation of prehistoric
populations in Alabama and Mississippi shows an increase in femoral robusticity
after the adoption of agriculture. Their interpretation is that agricultural activities, such as hoeing a field, exceed the mechanical strains experienced under the previous foraging lifeway in the region. A similar trend is also noted in a study conducted by Wescott (2006). Given the disparate findings of these studies, it would seem that habitual activity, mobility, terrain, work, and gendered division of labor all contribute to observed skeletal robusticity and that this observed skeletal robusticity may not, for a given population, fit the generalized gracilization trend of our genus.

The studies outlined above not only demonstrate the variability of skeletal robusticity but also the sorts of mechanical activities, such as broad subsistence changes, intensification, and even possibly use of the bow and arrow, that can be gauged from skeletal elements. The femur is predominantly used as a measure of gross motor activity and mobility while the humerus is linked to general activity levels and load-carrying activities (Larsen 2002; Ruff 2006). It is expected that femoral robusticity should be fairly uniform in the skeletal remains of nineteenth-century working-class samples while humeral robusticity should be more variable and dependent upon the specific mechanical environments associated with occupation (Larsen 2015; Ruff et al. 2006; Wescott 2006).

Another important aspect of skeletal robusticity is the changes that occur during growth and development. As age increases, bone becomes less responsive to mechanical stress (Pearson and Leiberman 2004; Ruff et al. 2006; Stock 2006). In part, this is due to the shifting balance between osteoblasts (bone-forming cells) and osteoclasts (bone-resorbing cells) as an individual ages (Pearson and Leiberman 2004). During development, there is a marked increase in osteoblastic activity which allows for more dramatic changes in external dimensions of bone in response to mechanical stress. The implication is that external dimensions of a skeletal element may be more indicative of childhood and younger adult mechanical environments than older adult environments (Pearson and Leiberman 2004; Ruff et al. 2006; Stock 2006). No longitudinal studies have been conducted that explicitly test differential responsiveness between adults and subadults to mechanical stress. However, Ruff and colleagues (2006) suggest that adult modifications are cumulative in nature and even though the sensitivity of bone cells to mechanical stress is reduced in adulthood, external remodeling persists. For example, in adults severe atrophy of bone occurs with disuse regardless of the mechanical environments experienced during childhood (Ruff et al. 2006).

Many contemporary studies of skeletal robusticity use cross-sectional geometric methods. Engineering principles of mechanics and beam theory are used to assess bone strength in relation to the mechanical strains applied to them. In order to control for bone size, the percentage cortical area of the long bone cross-section is calculated. This provides an estimate of the bone’s resistance to compression and tension forces. From this information, the second moment of area (the distribution of bone about an axis) and section modulus (flexural strength)
are calculated which provide a measure of a bone’s resistance to bending and torsional strains. Traditionally, these cross-sectional analyses take a cross-section of the long bone in question; however, non-destructive techniques such as computed tomography (CT) scan and radiography can also be used. See Pearson (2000), Ruff (2000), Ruff and Larsen (1990), Stock (2006), and Stock and Shaw (2007) for examples of cross-sectional geometric analyses, including those that use CT scanning.

Body size, or mass, must be controlled for in skeletal robusticity analyses. Many cross-sectional analyses standardize by estimating body size from skeletal stature and bi-iliac breadth of the pelvis whereas many external dimension analyses simply use the length of the skeletal element (Hogue and Dongarra 2002; Larsen 2015; Pearson 2000; Ruff 1991, 2000; Stock 2006; Stock and Shaw 2007; Wescott 2006). The use of length measurements for standardization is particularly helpful when analyzing humeral robusticity because there is a weaker correlation between humerus size variables and body mass (Ruff 2000; Stock and Shaw 2007).

There are some obvious drawbacks to using cross-sectional geometry. First and most importantly, it may not be possible to cut a long bone to obtain cross-sections. Further, the cost of CT scans may make it financially unfeasible. In addition, collections may be situated in remote locations or museums and it may not be possible to take the collections to a place where scans could be obtained or to take a CT scanner to the skeletons (Stock and Shaw 2007).

As a result of these drawbacks, external dimensions of long bones often have been used to assess skeletal robusticity. These analyses are based on the idea that larger external dimensions of a long bone correspond to larger cross-sectional geometry and can provide similar estimates of skeletal robusticity comparable to those produced by cross-sectional analyses (Pearson 2000; Stock and Shaw 2007; Wescott 2006). There are some limitations, however. For example, an individual suffering from bone loss due to osteoporosis may have large external bone dimensions but their percentage cortical area may be reduced because of medullary widening. Similarly, chronic under-nutrition can also result in a reduced amount of cortical bone (Stock and Shaw 2007).

External bone measurements are typically taken using a pair of sliding calipers, an osteometric board, and a tape measure. The advantage of these methods is that they are extremely cost-effective and can be done virtually anywhere. There are also comparative data from studies that utilize external dimensions for skeletal robusticity assessment (e.g., Larsen 2015; Pearson 2000; Stock and Shaw 2007; Wescott 2006). Stock and Shaw (2007) note that in order for these external measurements to be truly comparable, more controlled body standardization is required. Instead of standardizing robusticity indices by long bone length, they demonstrate that standardizing by the product of long bone length and femoral head diameter provides a better estimate of body size.
Case study: testing ideas about robusticity and industrialization

A series of studies of a late nineteenth-century Colorado Euro-American skeletal sample prompted the study that is reported here. In examining this skeletal series, we noted that the degree of visual skeletal “robusticity” or “rugosity” was quite marked. We wanted to compare the Colorado sample to other generally contemporaneous skeletal samples in order to provide an empirical means of explaining the observed robusticity. Further, the question of gracilization of the skeleton with industrialization was seriously called into question when looking at the skeletal remains. To suggest that industrialization led to a significant decline in physical activity and physical workload is a broad generalization that no doubt describes some but not all people. Furthermore, our contemporary image of industrialization is one of automation and even computer-controlled production, which no doubt colors our perceptions of “modern” gracilization. The gracilization trend deserves to be examined more closely and in a context-specific manner, especially looking closely at the working class who did not benefit from the same levels of mechanization.

Unfortunately, there is little in terms of empirical measurement in the literature pertaining to the actual workload experienced by people in the nineteenth century during industrialization. Largely, this is because the methods and technology to measure workload did not exist. However, time allocation studies do show that in London, through time, more hours per day are devoted to work in the later nineteenth century than earlier even though the change is not statistically significant (Voth 1998). During industrialization, many corporations sought to increase profits by accelerating both machine and worker; machines moved more quickly and workers had to hasten their production activities as well. The number of hours worked by unskilled laborers increased during the nineteenth century as companies attempted to squeeze out higher production numbers (Minge-Klevana et al. 1980; Shackel 2004; Shelton 1984; Voth 1998; Walton 1987). Coupled with the long hours, much of the work in many industries was physically intensive. For example, in the coal-mining industry miners would spend the majority of their work hours entombed in poorly ventilated mine shafts hammering down and shoveling up massive amounts of heavy coal. In an average day, a miner would fill between one and two carts full of coal each weighing between 2240 and 3360 pounds (da Costa Nunes 2002; Holt 2001). Other strenuous professions included dock workers, farmers, ranchers, laundresses, domestics, and undefined general “laborers.” These industrialized types of work replaced earlier agricultural work where farms were generally small, family-run businesses with some limits to surplus production. Even with the introduction of the steel plow pulled by a horse or ox, the workload for the farmer is quite great. Hoeing and weeding the field is still done by hand. It is not until we see industrial-level farming with a great deal of mechanization that
physical workload diminished. The physical workload for at least the working class in the nineteenth century was no doubt substantial.

Skeletal robusticity has not been consistently measured and evaluated for the nineteenth-century working class. At least a partial explanation is that few historical period skeletal collections have been available for analysis, both because there are not many cemeteries that have been excavated and often, even if a cemetery is excavated, the skeletons are reburied shortly after exhumation. The Dunning Cemetery in Chicago is a good example of that process (Grauer and McNamera 1995).

As stated earlier, the goal of this paper is to empirically determine the skeletal robusticity of the Colorado Asylum skeletal sample and compare it to other working-class skeletal samples from the nineteenth century. It is expected that skeletal robusticity should be relatively great. It is difficult to estimate the workloads of individuals in the Colorado Insane Asylum except that the very brief admission record shows the most common type of occupation listed, whether male or female, was “laborer” (Magennis and Lacy 2014). The history of people who died and were buried in the cemetery on the hospital grounds is unknown, but given that Colorado was a frontier with people flocking out to the state to start a new life, it is our assumption that many who ended up in the state institution were lower status and therefore laborers. Ultimately this comparison will provide the foundation from which future comparisons of the working-class sample from the Colorado asylum to other skeletal samples representing contemporary middle and affluent class communities can be made. It is expected that the working class of the Colorado asylum will counter the general assumption of gracilization during industrialization while the more affluent classes will follow the general pattern of gracilization due to differentiation in occupation between the classes.

**Materials**

The primary skeletal collection analyzed in this study is from the unmarked cemetery associated with the late nineteenth-century Colorado Insane Asylum located in Pueblo, Colorado. The cemetery was discovered on the grounds of the Colorado Mental Health Institute when the Department of Corrections began construction of a new building, the San Carlos Facility. In 1992 approximately 132 individuals were disinterred. Later, when activities were undertaken to expand the facility, about 25 additional individuals were disinterred. Historical data as well as coffin nail type indicate that the cemetery was used between 1879 and 1899. The 155 recovered individuals are housed at Colorado State University and of those, 100 individuals were included in this study.

The Colorado Asylum collection is almost exclusively adults. Previous analyses of the skeletal collection as well as admission records showed that males far outnumbered females in the institution and this is reflected in the cemetery, with adult males making up about 75% of the sample. Furthermore, admission records indicate that individuals institutionalized in the asylum were
predominantly derived from the working class (Magennis and Lacy 2014). Females in the institution had typically been employed as domestics while the majority of males were employed as a general "laborer," farmer or miner prior to institutionalization (Magennis and Lacy 2014).

The Colorado Insane Asylum ascribed to the philosophy of “moral treatment” which operated under the premise that mental illness was treatable. Mental illness was believed to be the result of living an immoral lifestyle and the preferred manner of treatment was to place patients in a completely controlled and balanced environment that was segregated from greater society. This reinforced the gendered relationships and roles dominant in society. Females predominantly worked as seamstresses, cooks, and domestics in the asylum while males worked outdoors as laborers in the gardens and nearby orchard (Painter et al. 2002).

As was the case with many nineteenth-century asylums, shortly after it opened in 1879 it quickly experienced financial difficulties. The biannual reports to the Colorado legislature from 1879 to 1899 indicated that the asylum was overcrowded and understaffed. Many patients, especially the chronically ill, were restrained in order to prevent disorder and facilitate long periods without monitoring. The large patient to attendant ratio effectively resulted in a shifted focus from treatment of mental illness to simply maintaining their physical health (Painter et al. 2002).

The collection was aged and sexed using traditional means (see Bass 2005; Buikstra and Ubelaker 1994; White and Folkens 2000). Pelvic morphology was relied on most heavily, paying special attention to features of the pubic bone, including the length of the superior ramus and the subpubic angle, greater sciatic notch size, and the flare of the ilia. Cranial features included nuchal muscle markings, size of the mastoid process, temporal lines, and size of the brow ridges, among other criteria. A number of metrics were also obtained, but of particular interest are the postcranial metrics of both right and left femora and humeri. From the femur, the measurements include bicondylar length, maximum head diameter, and anterior-posterior (A-P) and medio-lateral (M-L) diameters of the midshaft (see Buikstra and Ubelaker 1994:69–84). From the humerus, the measurements include maximum length, vertical head diameter, and the maximum and minimum midshaft diameters (Buikstra and Ubelaker 1994:69–84). Skeletal robusticity indices for both the femur and the humerus were calculated from the external measurements. For a list of calculations and indices, see Table 11.1. We were also able to obtain metric data from three other nineteenth-century skeletal samples, from which we calculated the skeletal robusticity indices. These were interments from the First African Baptist Church, Philadelphia, the Dunning Cemetery, Chicago, and the Eastern State Hospital, Lexington, KY. Each of these cemeteries is briefly described below.

The First African Baptist Church (FABC) in Philadelphia is associated with two cemeteries, one at 10th Street and Vine and the other at 8th Street and Vine (Crist et al. 1997). Beginning in 1983, large-scale development projects in Philadelphia resulted in the excavation of both cemeteries. The cemetery sample
Table 11.1  Descriptive statistics for the femur and humerus of the Colorado Insane Asylum sample.

<table>
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<th>Measure</th>
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<th>95% Confidence interval</th>
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<th>Standard deviation</th>
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<td>3.06</td>
<td>46.565–48.061</td>
</tr>
<tr>
<td>F 21*</td>
<td>43.70</td>
<td>3.66</td>
<td>42.038–45.372</td>
<td></td>
<td></td>
<td>F 22*</td>
<td>42.37</td>
<td>3.93</td>
<td>40.634–44.120</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Bicondylar length</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td><strong>Max length</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F 21*</td>
<td>429.02</td>
<td>21.36</td>
<td>419.299–438.748</td>
<td></td>
<td></td>
<td>F 21*</td>
<td>306.90</td>
<td>18.89</td>
<td>298.306–315.504</td>
<td></td>
<td></td>
</tr>
<tr>
<td>M L</td>
<td>70</td>
<td></td>
<td>452.31</td>
<td>27.70</td>
<td>445.702–458.912</td>
<td>M L</td>
<td>65</td>
<td></td>
<td>323.94</td>
<td>20.01</td>
<td>318.989–328.906</td>
</tr>
<tr>
<td>F 23*</td>
<td>427.59</td>
<td>21.27</td>
<td>418.390–436.784</td>
<td></td>
<td></td>
<td>F 22*</td>
<td>304.18</td>
<td>19.89</td>
<td>295.359–313.004</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>AP M Dia</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td><strong>Max M Dia</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M L</td>
<td>74</td>
<td></td>
<td>30.72</td>
<td>3.44</td>
<td>29.924–31.521</td>
<td>M L</td>
<td>70</td>
<td></td>
<td>23.57</td>
<td>1.57</td>
<td>23.201–23.950</td>
</tr>
<tr>
<td><strong>ML M Dia</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td><strong>Min M Dia</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M R</td>
<td>75</td>
<td></td>
<td>28.45</td>
<td>2.21</td>
<td>27.945–28.965</td>
<td>M R</td>
<td>70</td>
<td></td>
<td>19.49</td>
<td>1.52</td>
<td>19.133–19.859</td>
</tr>
<tr>
<td>F 22</td>
<td>26.01</td>
<td>2.64</td>
<td>24.839–27.187</td>
<td></td>
<td></td>
<td>F 23*</td>
<td>16.65</td>
<td>1.78</td>
<td>15.894–17.436</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Robusticity</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td><strong>Robusticity</strong></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

* t-test (accounting for unequal variances) differences between males and females at p<0.001.

AP M Dia, anteroposterior midshaft diameter; F, female; L, left; M, male; Max Head Dia, maximum head diameter; Max M Dia, maximum midshaft diameter; Min M Dia, minimum midshaft diameter; ML M Dia, mediolateral midshaft diameter; R, right; Vert head dia, vertical head diameter.
used for this analysis is the one at 8th and Vine which dates from approximately 1824 to 1842. In that sample of 135 individuals, 75 are adult: 39 female and 36 male (Rankin-Hill 1997). Rankin-Hill notes that, according to burial and church records, the occupation engaged in prior to death by the men was predominantly that of laborer, although there were a notable number of men who were employed as waiters. For the women, the predominant type of occupation was laundress or domestic. All individuals interred in the cemetery were African American, but only a minority of the household heads were ex-slaves; most were freeborn. Overall, associated documentary records indicate that like most African Americans in nineteenth-century Philadelphia, FABC congregants were lower class and led generally stressful lives filled with high, life-long levels of occupational physical activity. Of the adults in the sample, 57 were sufficiently well preserved to be included in this study (see Chapter 6 for further discussion of this assemblage).

Remnants of the Dunning Cemetery situated on the west side of Chicago were discovered and excavated in 1990. The part of the cemetery excavated is thought to be associated with the Cook County Poor Farm which had been established in 1851. Not unlike the Colorado Insane Asylum, the poor house was overcrowded and poorly managed. The inhabitants were from the lower class but were not classified as insane; the insane were incarcerated in the adjacent Cook County Insane Asylum. According to Grauer and McNamara (1995), historical sources suggest that the cemetery was used from 1851 to 1869. In 1869, a request was made to the city to remove the graves and rebury them in a location immediately to the west. Obviously not all individuals were successfully moved in 1869 because in 1990, 120 individuals were exhumed and reburied, and 52 adults are included in this analysis.

The Eastern State Hospital cemetery dates from 1824 to 2013, although no recent individuals from the institution are buried in the unmarked cemetery. Nealis (2014) suggests that the identifiable coffin nails and lack of screws recovered around the burials indicates that most individuals were interred between 1839 and 1861. It is hypothesized that many of the deaths were the result of a cholera epidemic. Nealis (2014) suggests that patients constituted a cross-section of socioeconomic classes. The cemetery yielded a minimum of 189 individuals, but many of them were in “mass graves” where multiple individuals were interred, some of which occurred due to prior digging disturbance and the disturbed burials were put into a single grave. Preservation of the remains is generally poor but 85 adults are included in this study, many of which are incomplete.

The comparative samples generally predate the Colorado Insane Asylum collection by at least a generation. However, we believe that these nineteenth-century skeletal series, in general, are very comparable to the asylum in that most if not all of the individuals are from the lower class and are poor, and most of the individuals examined shared in hard physical labor. For comparative purposes, we also use data presented by Wescott (2001, 2006) on known Early and Modern Industrialists from the Robert J. Terry Anatomical
Collection. The Terry Collection dates from 1917 to 1966 and consists of individuals who were used as cadavers for dissection in the medical school at Washington University in St Louis. The individuals in the collection were largely those who were not claimed by relatives from various St Louis morgues and the bodies became the property of the state. Rather than bury those individuals at taxpayers’ expense, they were donated to the medical school. Today the Terry Collection is housed in the Anthropology Department at the National Museum of Natural History, Smithsonian Institution (Hunt and Albanese 2005). We use the individuals from the Terry Collection as analyzed by Wescott (2001, 2006) for comparison in this study.

**Methods**

The femoral and humeral data are used to compare the four cemetery samples as well as to examine sexual dimorphism within each sample. The data are also used to compare skeletal asymmetry within the Colorado Asylum and the FABC collections as these two collections have data for both the left and right femur and humerus. All cemetery data are initially divided by sex and into four age categories. The age categories are 30 and younger, 30–40, 40–50, and 50 and older. Initially, \( t \)-tests were used to compare the means in each age category by sex. This allowed us to determine whether there are any particularly low or zero values in any of these categories that would have an impact on further data analysis. To compare all four sites, while accounting for both age and sex, a least squares regression was run using STATA (version 12.1 2014) on the robusticity indices. Because we are especially interested in any differences among the skeletal samples and Early and Modern Industrialists, we examined the difference in means between all the archaeological samples and means presented by Wescott (2001, 2006) for the two Industrialist groups.

**Results**

Results from the Colorado Asylum collection are presented first. In the Colorado Asylum skeletal sample, there is a statistically significant difference (\( p < 0.001 \)) in sexual dimorphism for most of the skeletal measurements, including femur and humerus head diameters, and their length and shaft diameters. After standardizing by bone size, however, skeletal robusticity of the humerus – but not the femur – is statistically significantly different between males and females. This is shown in Table 11.1.

Similar results are also observed in the other three-nineteenth century series. In all cases, male bone dimensions exceed female bone dimensions. After standardization for bone size, there are no statistically significant differences between males and females in femur robusticity, while there is still pronounced, statistically significant sexual dimorphism in humerus robusticity. Those data are not presented here but do indicate that there is marked sexual dimorphism in all the nineteenth-century working-class samples.
We also examined bilateral asymmetry of both the femur and the humerus in the Asylum and FABC collections. As mentioned above, right and left bone measurements were collected only for these two skeletal series. The Colorado Asylum collection exhibited some asymmetry in the anterior-posterior midshaft diameter of the femur, with the left femur being larger than the right. The FABC collection showed no femoral asymmetry. No notable humeral asymmetry is observed in either collection.

Least squares regression analysis was used to compare the nineteenth-century archaeological samples to determine the influence that sex, age group or site has on the robusticity indices. Table 11.2 shows the results of the regression analysis where the reference category is males over age 50 years in the Colorado Asylum sample. The regression shows the marked difference between males and

<table>
<thead>
<tr>
<th>Robusticity Index</th>
<th>Left FRI¹ b(SE)</th>
<th>Left HRI² b(SE)</th>
<th>FRI (Head)³ b(SE)</th>
<th>HRI (Mid)⁴ b(SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex²</td>
<td>−0.00605∗(0.00167)</td>
<td>−0.00110∗(0.00173)</td>
<td>0.264(1.41)</td>
<td>−0.556∗(0.0872)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Age category⁵</th>
<th>Left FRI¹ b(SE)</th>
<th>Left HRI² b(SE)</th>
<th>FRI (Head)³ b(SE)</th>
<th>HRI (Mid)⁴ b(SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Under 30</td>
<td>−0.00433</td>
<td>−0.00131</td>
<td>−0.783</td>
<td>−0.0688</td>
</tr>
<tr>
<td>(0.00210)</td>
<td>(0.00226)</td>
<td>(1.81)</td>
<td>(0.113)</td>
<td></td>
</tr>
<tr>
<td>30–40</td>
<td>−0.00302</td>
<td>−0.00049</td>
<td>−0.904</td>
<td>−0.0270</td>
</tr>
<tr>
<td>(0.00204)</td>
<td>(0.00211)</td>
<td>(1.70)</td>
<td>(0.106)</td>
<td></td>
</tr>
<tr>
<td>40–50</td>
<td>0.00251</td>
<td>0.00350</td>
<td>2.61</td>
<td>0.174</td>
</tr>
<tr>
<td>(0.00236)</td>
<td>(0.00249)</td>
<td>(1.95)</td>
<td>(0.125)</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Site</th>
<th>FRI (Head)³ b(SE)</th>
<th>HRI (Mid)⁴ b(SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>FABC</td>
<td>0.00575∗</td>
<td>0.287∗</td>
</tr>
<tr>
<td>(0.00206)</td>
<td>(0.103)</td>
<td></td>
</tr>
<tr>
<td>Dunning</td>
<td>0.00232</td>
<td>0.139</td>
</tr>
<tr>
<td>(0.00258)</td>
<td>(0.129)</td>
<td></td>
</tr>
<tr>
<td>Eastern State</td>
<td>−0.00923∗∗</td>
<td>−5.68∗</td>
</tr>
<tr>
<td>(0.0005143)</td>
<td>(0.0221)</td>
<td></td>
</tr>
<tr>
<td>Hospital</td>
<td>0.005226</td>
<td>0.115</td>
</tr>
<tr>
<td>(0.00230)</td>
<td>(0.115)</td>
<td></td>
</tr>
</tbody>
</table>

| Constant      | 0.132            | 123.70          |
| (0.00146)     | (0.077)           |

| n              | 176              | 167             | 177              | 167             |
| R²             | 0.232            | 0.272           | 0.147            | 0.271           |

¹FRI: Femoral Robusticity Index;  
²HRI: Humerus Robusticity Index;  
³FRI (Head): Femoral Robusticity standardized by head diameter;  
⁴HRI (Mid): Humerus midshaft robusticity after Wescott (2001);  
⁵Reference category: age 50+. See text for detailed descriptions.  
⁶Reference category is female. See text for detailed description.  
∗p<0.01.  
∗∗p<0.001.  
FABC, First African Baptist Church.
females exhibited in these collections. Sex has a statistically significant impact on femoral and humeral robusticity. It is also important to note that the FABC sample exhibits significantly larger humeral and femoral robusticity than the other samples. Also the Eastern State Hospital sample has a statistically significantly smaller femur robusticity than the Colorado Asylum sample.

In an effort to compare the archaeological samples with the Early and Modern Industrialists, the difference in means for the robusticity indices as reported by Wescott (2001, 2006) is compared to each skeletal sample. In order to make the comparisons, we needed to create two more robusticity indices to match those reported in Wescott (2001, 2006). The first is the femoral robusticity index standardized by femoral head diameter instead of physiological length. The second is the humerus midshaft robusticity index. The results of the comparison are presented in Table 11.3. See Table 11.4 for equations.

Observe that the difference of means generally shows that working-class males in the archaeological samples exhibit greater robusticity than either Early or Modern Industrialist males, although the statistical significance of those differences varies by sample and index. The exception is that Eastern State Hospital males had somewhat lower mean robusticity indices compared to both Industrialist samples. Females often show femoral robusticity that is lower than that exhibited by either of the Industrialist samples, especially in the Dunning Cemetery and Eastern State Hospital samples. In comparison to the Early Industrialists, nineteenth-century females express comparable humeral robusticity; however, when compared to Modern Industrialists, females from all four archaeological sites have significantly larger mean humeral robusticity. It is important to highlight that males and females of the First African Baptist Church sample in all comparisons had statistically significantly larger robusticity indices when compared to the two Industrial samples; the exception is the comparison of FABC females to the Early Industrialist’s humeral midshaft robusticity index.

Discussion

Ruff (1988) noted a general trend that with industrialization there was a decrease in the sexual dimorphism of the femur. In the Industrial era males and females shared similar mobility patterns as evidenced by similar femoral robusticity measures (Ruff 1988). The nineteenth-century samples examined here also support this trend. However, the difference is there is marked sexual dimorphism in the humerus; males are more robust than females. The implication is that although mobility patterns were not different between the sexes, there is still a pronounced gendered division of labor. Males were engaged in more physically demanding occupations than females. For example, in the Colorado Asylum sample, this could be the difference between female domestic labor and male silver mining.

Auerbach and Ruff (2006) also note that with industrialization, there is a reduction in the asymmetry of long bones. Overall, both the Colorado
Table 11.3  Difference of means between the nineteenth-century samples and the Industrial samples presented in Wescott (2001, 2006).

<table>
<thead>
<tr>
<th>Measure, by Sex</th>
<th>Colorado Insane Asylum</th>
<th>First African Baptist Church</th>
<th>Dunning Cemetery</th>
<th>Eastern State Hospital</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>Diff means(95% CI)</td>
<td>n</td>
<td>Diff means(95% CI)</td>
</tr>
<tr>
<td><strong>Early Industrialists</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FRI (Head) M</td>
<td>71</td>
<td>3.4 (0.77, 6.02)**</td>
<td>23</td>
<td>6.82 (3.91, 9.72)***</td>
</tr>
<tr>
<td>FRI (Head) F</td>
<td>22</td>
<td>0.79 (−3.62, 5.20)</td>
<td>25</td>
<td>5.85 (2.73, 8.96)***</td>
</tr>
<tr>
<td>HRI (Mid) M</td>
<td>64</td>
<td>0.17 (0.007, 0.33) *</td>
<td>19</td>
<td>0.53 (0.29, 0.76)***</td>
</tr>
<tr>
<td>HRI (Mid F)</td>
<td>22</td>
<td>0.02 (−0.24, 0.29)</td>
<td>17</td>
<td>0.28 (−0.07, 0.63)</td>
</tr>
<tr>
<td><strong>Modern Industrialists</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FRI (Head) M</td>
<td>71</td>
<td>1.3 (−1.03, 3.63)</td>
<td>23</td>
<td>4.72 (2.05, 7.38)***</td>
</tr>
<tr>
<td>FRI (Head) F</td>
<td>22</td>
<td>1.69 (−2.49, 5.87)</td>
<td>25</td>
<td>6.57 (4.00, 9.46)***</td>
</tr>
<tr>
<td>HRI (Mid) M</td>
<td>64</td>
<td>0.27 (−0.02, 0.56) *</td>
<td>19</td>
<td>0.63 (0.29, 0.96)***</td>
</tr>
<tr>
<td>HRI (Mid F)</td>
<td>22</td>
<td>0.31 (−0.04, −0.66) *</td>
<td>17</td>
<td>0.57 (0.15, 0.98)**</td>
</tr>
</tbody>
</table>

* t-test accounting for unequal variances.
Comparison to Early Industrialists: (*p<0.05),
**(*p<0.01),
***(*p<0.001).
Comparison to Modern Industrialists: (*p<0.05),
**(*p<0.01),
***(*p<0.001).
Asylum and the FABC samples support this trend in that there is only a single asymmetrical feature, femoral M-L midshaft diameter, in the Colorado Asylum sample. This is of uncertain significance.

The comparison of the four archaeological samples shows that there are few differences in femur robusticity. There are, however, some notable differences between the archaeological samples and the two Industrial samples. In particular, the males and females of the FABC sample both exhibit greater femoral robusticity when compared to the Colorado Asylum and the Industrial samples. Additionally, the Colorado Asylum males have a larger femur robusticity when compared to Early Industrialists but this comparison does not reach statistical significance against the Modern Industrialists. It is quite clear that the FABC males and females are very robust compared to almost any other sample. We assume that is because the people in the FABC sample had very heavy workloads. However, it cannot be ruled out that there may be some genetic difference in skeletal robusticity, something that needs to be examined more broadly.

The larger femoral robusticity in the Colorado Asylum males and FABC males and females suggests that working-class males participating in the nineteenth-century industrialization were engaged in particularly strenuous work. It is noted by others (Bridges et al. 2000; Wescott 2001), however, that there are many factors that affect variation in femoral robusticity, including environmental variation, growth and development, age at first engagement with activity, as well as other cultural differences. For example, one might assume that people who immigrated to Colorado in the nineteenth century, at least those who were interred in the asylum cemetery, were likely lower class and poorer individuals in their place of origin too. Those same physically demanding occupation conditions would have predated their move to Colorado. Also, as noted earlier, femoral robusticity is strongly linked to mobility. It is expected that with the rise of industrialization, there was a marked increase in sedentism. Even if members of the lower class were working in labor-intensive jobs, the evidence presented here suggests that their mobility, in terms of traversing the landscape, was reduced.

We should add, however, that using more sophisticated techniques available through cross-sectional geometric methods may provide more insight into the
robusticity indices we have calculated. Perhaps differences in cortical area could be used to distinguish between mobility patterns and weight-bearing patterns and as such allow a more nuanced exploration of working-class labor activities and their effects on the femur. When humeral robusticity is compared between the four archaeological sites, there are very few differences; however, there are important differences when compared to the Early and Modern Industrialists. The Early and Modern Industrialists were generally of a lower class or poor given that those individuals were unclaimed bodies obtained from morgues in St Louis in the earlier part of the twentieth century. It is not entirely certain what the individuals from the Terry Collection would have been doing as occupations, but it did not seem to be as rigorous as the workload experienced by the nineteenth-century individuals. On average, both males and females from the archaeological sites exhibit greater humeral robusticity than the Modern Industrialist. Further, the generalized gracilization trend that occurs with industrialization was not a uniform occurrence. Also, as humeral robusticity is linked to increased arm motor activity, it suggests that these nineteenth-century individuals were engaged in intensive physical labor.

These interpretations, however, are colored by nutritional and economic factors. Costa and Steckel (1997) and Komlos (1998) show that human stature in the United States was compromised during the Industrial Revolution. It has been shown over and over again that poor nutrition, especially coupled with infectious disease, results in reduced stature (Bogin 1999). It is argued that industrialization was associated with crowded factories, increased urbanization, tenement living, and demanding fast-paced work, which resulted in a deterioration of health coupled with a decline in stature (Costa and Steckel 1994). The question becomes, then, what is the interplay between stature, robusticity, and nutrition? When under nutritional stress and in a mechanically intensive environment, does the skeletal system sacrifice stature for robusticity or are both compromised? Based on the results of the robusticity analysis of the four archaeological samples, it would appear that robusticity is not unduly compromised. Ultimately cross-sectional geometric methods may be more helpful for understanding these confounding factors than the external dimensional analyses done here, as cross-sectional geometric methods are becoming more refined and precise.

**Conclusion**

Based on a biomechanical model, it has been argued that the industrialization was accompanied by both skeletal gracilization and a reduction in skeletal dimorphism. This trend is easily observed in the contemporary United States and the rest of the developed world. Our postindustrial society has marked workload reduction when compared to the developing world. This workload reduction has resulted in limited sexual dimorphism and increases in stature.
This study tested the hypothesis of decreased skeletal robusticity and diminished sexual dimorphism with industrialization by using external dimensions of the femur and humerus to assess skeletal robusticity of those who lived during the nineteenth-century industrialization process.

The finding that there was increased skeletal robusticity in the archaeological samples, particularly the First African Baptist Church and the Colorado Insane Asylum, when compared to the Industrialist samples has tremendous implications. First, it supports the need to reevaluate the generalized trend of gracilization with industrialization, for just as when evaluating the subsistence transition from foraging to agriculture, the skeletal response is variable and context dependent. The gracilization trend is too simple to be informative about the Industrial Revolution. Second, it also shows that the nineteenth-century working-class people represented by these skeletal samples were in fact engaged in physically demanding work brought about by transformation of labor during the Industrial Revolution. Indeed, it seems that a class-specific phenomenon is exhibited in the samples included in this study.

There are many questions that remain to be addressed. Importantly, at what age did individuals enter the workforce? The nutritional history of the nineteenth-century people represented here needs to be better known. Is it possible to tease out specific activities from skeletal robusticity? Perhaps as technology advances, we will be able to probe more fully the effects of nutrition and culture on the skeletal response to mechanical stress. An immediate next step would be to further contextualize the working class by a comparison to the middle and upper classes who did not engage in strenuous physical labor.

At the beginning, we pointed out that few historical skeletal collections have been studied intensively. There are a number of reasons why this is the case, but one important reason is that in the United States, cemeteries of Euro-Americans are either not disturbed or the skeletons are immediately reburied when encountered, with only cursory data collection and analysis. Our study provides a much needed window on the culturally created mechanical environments in which the working class of the nineteenth century labored. It will take a concerted interdisciplinary effort to create a clearer picture of the lifeways of the lower class. This would include explicitly delineating occupation, workload, nutrition, and mortality, to name a few, in conjunction with skeletal analysis. This will only serve to enhance our understanding of industrialization during the nineteenth century and therefore enhance our understanding of the origin of the modern world in which we live.

**Acknowledgments**

We would especially like to thank Anne Grauer for providing access to the Dunning Cemetery data and Kristen Fuhrman for putting them into a format that we could easily use. Stuart Nealis was most helpful in providing the femoral and
humeral data from the Eastern State Hospital in Lexington, Kentucky. I know he and colleagues are still working on those data and sharing with us is particularly appreciated. Lesley Rankin-Hill graciously made available to us the long bone data from the First African Baptist Church. Indeed, those individuals are robust! We would also like to thank Michael Lacy for statistical assistance. Any errors are ours alone, however. Finally we would like to thank Molly Zuckerman and Debra Martin for their efforts in putting together this volume to honor George Armelagos, a great anthropologist deserving very high accolades.

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Chapter 11: Does industrialization always result in reduced skeletal robusticity?


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CHAPTER 12

Stable isotopes and selective forces: examples in biocultural and environmental anthropology

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2Department of Earth Sciences, The University of Western Ontario

Introduction

Although the biocultural paradigm emerged about a decade prior to the first anthropological use of stable isotopic analysis in the late 1970s, the paradigm and the methodology have developed in parallel and have resulted in equally prominent approaches to anthropological research. The biocultural paradigm is the main interpretive lens for understanding relationships among culture, biology, and environment, and isotopic analysis is one of the few methodologies that can inform all three aspects of those relationships. Since the earliest use of stable isotopes for tracking the rise and spread of agriculture in North America in the 1970s (Vogel and van der Merwe 1977), the reconstruction of plant domestication, and dietary and subsistence behaviors still dominate isotopic research. This is not only because the most obvious applications of isotopic analysis are food related but also because food is a major selective force in human evolution. Diet, however, is only one of three main forces of selection, the others being disease and physical environment. Human behavior and culture interact with, and add synergy to, each of these forces, and they all produce biological stress to which humans must adapt via both individual-level and population-level survival and reproduction.

Assuming that stress is any physiological disruption resulting from any insult (Goodman and Leatherman, 1998: 177), the life histories of disease and physiological stress, geographic relocations and changes in food and water consumption recorded in the chemistry of our body’s tissues can simultaneously reflect the nature of, and biocultural response to, physical environments that are both abiotic (e.g., temperature, rainfall, aridity) and biotic (plant and animal communities). Our biochemical responses should also indirectly reflect landscape
change, possibly even the creation of built landscapes, e.g., concentrated urban
dwelling. Integrated records enable better understandings of our adaptive history
and capacity in relation to the synergy among changes in diet and environment,
and the evolution of pathogens and the spread of disease. Isotopic methodology
and the biocultural interpretive paradigm have been around long enough
now that available data are approaching the critical mass necessary for moving
inference of selective forces and evolutionary processes to a higher level.

The goal of this chapter is to encourage the development of a new phase in
the combined use of stable isotopic methodology and biocultural thinking, one
in which both existing and newly built data sets are used to provide evidence
for the operation of selective forces. Interest in these forces is found through-
out scholarship in bioarchaeology and paleopathology, particularly in studies of
diet, disease, and epidemiologic transitions pioneered by Armelagos (1969; Bar-
rett et al. 1998). Epidemiology is the study of patterns of disease, or morbidity,
and death or mortality, by age and sex related to fertility and life expectancy.
The fundamental epidemiological and demographic shifts that human societies
have experienced throughout time are as follows. The ‘first epidemiologic tran-
sition’ is associated with the ‘Agricultural and Neolithic Revolution’. The rise of
agricultural intensification resulted in increased morbidity due to more impover-
ished crop plant diets, increased population density and the consequent spread of
infectious disease. The close contact of humans with animals during their domes-
tication also resulted in the rise of zoonotic diseases, such as anthrax (Armelagos
& Cohen 1984; Larsen 2006).

The “second epidemiologic transition,” which encompasses both the “Age of
Receding Pandemics” and the “Age of Degenerative and Man-Made Diseases,”
is associated with industrialization. In this transition, nineteenth-century pub-
lic health initiatives combined with germ theory led to decreased mortality from
infectious disease, increased life expectancy (30–50 years at birth), and the resul-
tant rise of morbidity and mortality from chronic and degenerative diseases as
people began to live longer (Omran 1971, McKeown 2009) (see Chapters 16
and 17). Lastly, there is the “third epidemiologic transition,” which is ongoing
since the 1980s and associated with increased globalization. Against a backdrop of
further decreased mortality, increased life expectancy (over 50 years), and expon-
ential population increase, it features increased morbidity and mortality from
the reemergence of some bacterial infectious diseases and the rise of new infec-
tious diseases. This population profile has led to the following epidemiological
characteristics. Degenerative and metabolic diseases associated with overeating
or diets that are high in calories but micro- and macro-nutrient poor, which con-
tinue to rise in prevalence (see Chapter 3). These include obesity, cardiovascular
disease, and diabetes. Neoplastic diseases, or cancers, also continue to rise as a
result of long life spans and many of these are anthropogenic, i.e., created by
pollutants in food, air, water, and soil associated with human activity. The evo-
lution of antibiotic-resistant pathogens has also caused the re-emergence of some
bacterial infectious diseases, such as drug resistant tuberculosis. Since the 1980s
these factors, combined with increased globalization, have also produced the rise
and global spread of new, ‘emerging’ infectious diseases, especially viral diseases,
such as severe acute respiratory syndrome (SARS), Ebola, human immunodeficiency
virus (HIV), and H5N1 avian influenza (i.e., “bird flu”) (Barrett et al. 1998;
Esche et al. 2010; Omran 1971) (see Chapter 14).

Emphasis is placed here on the southern Egyptian/northern Sudanese region
of the Nile Valley, a region that has been fundamental to bioarchaeological
research since the 1960s (Armelagos 1968, 1969). However, a few examples
come from other, less intensively studied regions. Known as ancient Nubia, it
is still one of the most intensively researched regions in bioarchaeology (see
Chapters 8, 9, and 21). Armelagos (1968, 1969) followed their health through
three three major cultural changes. The first is the Meroitic period (AD 0–130),
during which the Wadi Halfa region was controlled and used by the Kingdom
of Meroe, also known as Kush, as an agricultural hinterland with the help
of the newly developed waterwheel technology. The second is the X-Group
period (AD 350–550), which represents the rise of politically autonomous
units following the fall of Meroe, and a drop in the level of the Nile. The third
is the Christian period (AD 550–1400), during which there were a series of
phases (Early, Classic, Late) that reflect varying levels of political, economic, and
environmental stability. Although Egypt was conquered by Arabia and brought
under Islamic rule during this time, Nubia retained the Christian faith, and
experienced a general increase in population growth and trade.

Armelagos and his students found that the Wadi Halfans suffered from
conditions emblematic of both the first and second transitions. They suffered
from conditions characteristic of the first transition, namely nutritional diseases,
such as iron deficiency and osteoporosis, dental disease, and infectious diseases,
mainly parasitic, but also from common modern non-infectious, degenerative
and human-made conditions, such as arthritis and neoplasms, that charac-
terize the second transition (Armelagos 1969; Campbell Hibbs et al. 2011). In
many ways, therefore, the ancient Wadi Halfans have much to teach us about
adaptation.

Food availability is determined by environment, such as whether it is coastal or
interior, tropical or temperate, and characteristics such as climate, altitude, sea-
sonality, soil quality, and landscape type. It is also determined by its technological
capability to overcome constraints, such as through agriculture, irrigation, stor-
age, processing, fertilization, and trade. Diet is further patterned by biology, such
as age and sex, social complexity, belief systems, and the ability of the culture to
buffer biological needs from environmental stressors. The physiological response
to diet is nutrition, which plays a major role in health status, ranging from specific
deficiencies of vitamins, minerals or macronutrients, to overconsumption, each
of which affects susceptibility to disease. Food choices and preparation, including
consumption of parasite-bearing foods, such as fish, or improper cooking, and
seasonality can also play a role, through factors like temporary food shortages
or seasonal influenza. These factors are related to the patterning of infectious
disease. Disease patterning is also a function of population density, sanitation, and geographic mobility. These factors play important roles in all of the epidemiologic transitions.

### Background

#### Isotopic analysis

**The tissue clock**

The human remains excavated and analyzed from Wadi Halfa, Sudan, still constitute one of the largest and best preserved skeletal samples in the world (see Chapter 8 and 9). Natural mummification of soft tissues due to the aridity of this region enabled diagnostic capability for pathological conditions evident in the mummies approaching that of modern clinical medicine. This moved mummy studies to a new analytical level, which included thinking in terms of populations (i.e., the population approach; see Chapter 10), rather than of individuals or small groups of individuals. The scale of this perspective is imperative for epidemiological research, and for integrating paleopathology into epidemiology, a field of scholarship known as paleoepidemiology (see Chapter 17). This endeavour can only be conducted with validity on large populations.

Preservation of multiple tissues also enabled use of the tissue clock in the Wadi Halfan skeletal sample. The tissue clock is the record of biological life history found in the tissues of human bodies. The isotopic compositions of body tissues reflect those of food and water consumed during tissue formation. Hence, they provide direct evidence of our environmental experiences. Isotopic compositions are measured using a mass spectrometer and expressed as δ-values in *per mil* (‰) units relative to internationally standard reference materials (e.g., for carbon, originally a fossil carbonate, and now Vienna Pee Dee Belemnite (VPDB); for nitrogen, atmospheric nitrogen (AIR), and for oxygen, Vienna Standard Mean Ocean Water (VSMOW)). Because each tissue takes a different length of time to form and/or replace itself, the body contains a record of environmental experiences at different times during life. The Wadi Halfa sample enabled the earliest bioarchaeological dietary life history approach to disease and diet (White 1991).

The life history approach now involves reconstruction of many other individual experiences across the life span, including geographic relocation, disease, and cultural activity. This approach is similar to what might be expected for a full forensic analysis but when taken to a population level, it can provide much greater paleoepidemiological detail.

The slowest tissue turnover rate occurs in adult bone, which represents a homogenized record of the last 15–25 years of life. Short-term environmental change is recorded in soft tissues, such as skin representing two weeks, and muscle representing one month, as well as in incrementally growing tissues, such as hair, nail, and dental tissues, specifically enamel, dentine, and cementum. These tissues can represent long and permanent unbroken sequences of different
formation periods (daily, weekly, annually), for up to two years or more before death. Except in cases of functional wear where part of the record is lost, and or worn or damaged dentine, which is capable of remodeling under stress. Isotopic compositions reflect a variety of environmental conditions, as discussed below, that can combine isotopic life histories of diet and residence with disease experience.

This record now allows us to not only reconstruct aspects of changing biocultural behavior, but also to identify possible epidemiological risk factors. For example, age and gender are common risk factors for many nutritional and infectious diseases, especially those in infants and females of childbearing age. Risk factors may also include short- or long-term changes in diet or climate, such as seasonal food availability and climate fluctuations or longer periods of extreme aridity or rainfall that can affect food production and/or produce physical stress. Both individual relocations and large-scale movement of people can not only spread infectious disease but also increase susceptibility to it. Furthermore, risk factors may be altered both positively and negatively by culturally determined behaviors such as food choice and cuisine, medical systems, climatic buffering technology and behavior, and landscape alteration. Therefore, a biocultural approach is the most comprehensive one for understanding paleoepidemiological risk factors and the patterning of disease.

**Carbon and nitrogen isotopes in paleodiet and paleoenvironmental research**

Dietary interpretations from carbon and nitrogen isotopic data are primarily based on differences among photosynthetic plant types and position in the food chain, also known as the trophic level. The two main photosynthetic pathways used by terrestrial plants are C₃ (Calvin–Benson) and C₄ (Hatch–Slack). These are distinguished by how much they exclude atmospheric ¹³C during photosynthesis. C₃ plants, which exclude the most – and therefore incorporate the least ¹³C – are by far the most common worldwide and include most grains, all trees, shrubs, fruits, and vegetables. Plants using the C₄ pathway, and showing less net discrimination against ¹³C, are heat adapted. The domesticates of these are mainly tropical grasses, such as maize, millet, sorghum, and sugarcane. Both pathways are used in a third plant type, characterized by Crassulacean Acid Metabolism (CAM). These plants consist of succulents and cacti, which are rarely of dietary significance.

While carbon isotopic compositions are most commonly used for reconstructing plant consumption, they can also indicate both long- and short-term environmental change. This is because plant photosynthetic types (C₃, C₄, CAM) are adapted to different kinds of environments, such as heat, photoperiod, altitude, and latitude and will therefore vary in abundance accordingly (Tieszen 1991). Global environmental change, specifically the wide-scale burning of fossil fuels, has added large amounts of ¹²C-rich carbon dioxide to the atmosphere.
since the Industrial Revolution and created a systematic change in the carbon isotopic compositions of plants. Consequently, postindustrial vegetation is depleted of $^{13}\text{C}$ by 1.5‰ relative to plants that grew for most of the time humans have occupied the earth. Modern C$_3$ plants have a mean carbon isotopic composition of $-26.5$‰, which is distinct from that of C$_4$ plants ($-11$‰). This difference has enabled reconstruction of the domestication and spread of C$_4$ agricultural plants, such as maize, millet, and sorghum (e.g., Schwarcz et al. 1985; van der Merwe and Vogel 1978).

With the shift away from hunting and gathering to agriculture, animal meat sources decreased. Dietary protein sources and trophic level are generally reconstructed using the nitrogen isotope composition ($\delta^{15}\text{N}$) of protein-bearing tissues. Nitrogen-fixing plants, such as legumes and blue-green algae, have $\delta^{15}\text{N}$ values close to 0‰ but other terrestrial and marine plants have $\delta^{15}\text{N}$ values ranging from 2‰ to 6‰. With each level in the food chain, $\delta^{15}\text{N}$ values increase by 3–5‰. For terrestrial food webs, carnivores have the highest nitrogen isotope compositions, but even higher $\delta^{15}\text{N}$ values occur in marine and aquatic webs because they not only have more trophic levels but they also have a higher $\delta^{15}\text{N}$ baseline (except for nitrogen-fixing, blue-green algae-based reef systems).

The global effects of the Neolithic transition/agricultural revolution on the main measures of human health – fertility, fecundity, morbidity and mortality – were first seriously considered by Armelagos and Cohen (1984) in the landmark work Paleopathology at the Origins of Agriculture. They challenged the popular idea that agriculture improved the quality of human life. Examining changes in population health all over the world, authors contributing to the volume found that the greater assurance of food supply created by agriculture resulted in greater fecundity and fertility, which resulted in population increase and density. However, the transition was also marked by a reduction in quality of health, as the shift from the more varied diet of the hunter-gatherer to a dependence on cereal monocrops, combined with ecological change resulting from landscape modification and greater population density resulted in greater morbidity and mortality, especially from acute infectious and parasitic conditions.

This volume set the stage for isotopists and paleopathologists to take the examination of the first epidemiologic transition to the next analytical level. They did so by testing the hypothesis that diet was associated with diseases that affect the skeleton, such as iron deficiency and osteopenia, which is lower than normal peak bone density. Both of these conditions can have several different causes such as parasites or multiple childbirths respectively (e.g., Turner & Armelagos 2012; White 1986; White and Armelagos 1997; White et al. 2004, 2006; Wright and White 1996). To date, however, little has been done to broaden the use of isotopic analyses to investigate the spread of infectious disease or reconstruct relationships between the physical environment, geographic mobility, and disease.
Case study: isotopes and epidemiological risk factors/synergies at Wadi Halfa and surrounding regions

Knowledge of epidemiological risk factors can be used to identify the potential of evolutionary forces to operate on populations or segments thereof, such as gender, age, and socio-economic status. Isotopic studies of change in diet and environment related to seasonality and/or mobility, and their synergies with pathology, can further enable the detection of evolutionary forces and help us to understand our biological and cultural capacities for adapting to stress under different conditions. Long-term studies can demonstrate the ability of culture to either buffer or exacerbate the stress of these forces on populations.

The Wadi Halfa Nubians offer examples of all of the above. A significant failure of cultural buffering in this region was human-induced environmental/landscape change. The powerful Meroitic Kingdom (AD 0–130), centered further south, introduced widespread irrigation agriculture to the Wadi Halfa area in order to turn it into an agricultural hinterland. The resulting ecological and landscape change produced the unintended consequence of endemic (regularly occurring and persistent versus epidemic) schistosomiasis (Miller et al. 1992). Schistosomiasis is a parasitic disease carried by freshwater snails infected with the blood fluke parasite, *Schistosoma*. Even today, schistosomiasis is one of the world’s most important water-based diseases from a global public health perspective (WHO 2002). With about two-thirds of the ancient Wadi Halfa adult population infected, schistosomiasis must have had a profound effect on working capacity and mortality (Campbell Hibbs et al. 2011). The epidemiological effects of water-borne parasitic and infectious diseases might be further examined using their relationship between water source, via oxygen isotope compositions (see later) and biosocial variables of status, gender, and age (e.g., Lightfoot et al. 2014).

After the fall of the Meroitic Kingdom, irrigation enabled the X-Group population to survive a period of increased aridity and a naturally occurring drop in the level of the Nile. Not surprisingly, isotopic data for this time period also indicate a not surprisingly significantly greater consumption of $C_4$ staples, millet and sorghum, which are much better adapted to arid conditions (White and Schwarz 1994). Other important cultural buffering attempts included seasonal $C_3$ and $C_4$ crop rotation and food storage, where the heat-adapted but least nutritious $C_4$ foods were consumed in summer. Although food storage was commonly practiced, isotopic analysis of sequential hair segments from root to tip from Wadi Halfa mummies showed that food storage was mainly a precautionary measure against crop failure because people ate their crops mostly in the season in which they were harvested (Schwarz and White 2004). Fruit and vegetable crops, however, would have been less available at the hottest time of the year, so the combination of nutritional and heat stress made the summer a period of high morbidity and mortality (White 1993), a situation that
New directions in biocultural anthropology

still exists today. Nonetheless, these populations were likely buffered from many infectious diseases by processing grain in the form of beer, which produced *Streptomyces*, an actinobacterium that fluoresces in bone and has antibiotic properties (Bassett et al. 1980; Nelson et al. 2010). The relative absence of infectious disease in these populations may indicate consumption of therapeutic doses (Armelagos 2000).

Isotopic data reveal that culture change, marked by the return to political and economic autonomy during the X-Group period, had both positive and negative effects on biological adaptation. Breastfeeding, which has culturally determined rules and parameters for duration and cessation of weaning, creates a trophic level isotopic effect. Because nursing infants consume only breastmilk, which is a human tissue, they are one feeding level higher than their mothers. The late beginning and long process of weaning, which occurred between two and six years of age at Wadi Halfa, as indicated by $\delta^{15}N$ and $\delta^{18}O$ values throughout the Wadi Halfa temporal sequence, would have exerted a protective effect against protein deficiency. However, since breastmilk is nutritionally inadequate for the dietary needs of children over approximately six months of age, such prolonged breastfeeding would have predisposed them to iron deficiency (White and Schwarcz 1994; White et al. 2004). Iron deficiency was endemic in childhood, as were high levels of early childhood growth disturbance, as indicated by dental pathology (Rudney 1983). Throughout life, isotopic data also indicate that anemic individuals consumed more C$_4$ foods and protein from lower trophic levels.

Nonetheless, childhood health improved during X-Group times, increasing life expectancy (Rudney 1983). Sexual dimorphism, however, which generally signals increased stress experienced by males, decreased during the X-Group period (Vagn Neilson 1970). Isotopic data indicate that although males consumed more C$_3$ foods and protein from higher trophic levels than females throughout the sequence, during X-Group times their C$_4$ food consumption equalled that of females and the trophic level of their protein dropped (White and Schwarcz 1994). Notably, the dietary pattern that characterizes both anemia and male stress is the same. A variation of this theme is found in the diets of individuals with osteopenia. These individuals were mostly female, but also males and juveniles (Martin and Armelagos 1985). Osteopenic individuals also consumed significantly more C$_4$ foods, but instead had higher $\delta^{15}N$ values (White and Armelagos 1997). High $\delta^{15}N$ values are not only associated with osteopenia and osteoporosis but can also be induced by starvation, pregnancy, and diseases that cause a negative nitrogen balance, such as infection from trauma or wounds, arthritis, and acquired immune deficiency syndrome (AIDS), or pregnancy (Fuller et al. 2004; Katzenberg & Lovell 1999; Olsen et al. 2014; White and Armelagos 1997; Williams 2008).

Although analysing unhealthy individuals might invalidate the use of nitrogen isotopic data for some paleodiet studies (but see Olsen et al. 2014), they could be used to identify epidemiological risk factors. For example, work by
Williams (2008) west of the Nile in the Dahkleh Oasis combines segmental nitrogen isotope data from hair with the solar alignment of burials. This integrated method significantly advanced detailed information on the timing of trauma and healing, conception, and pregnancy relative to timing of death. The majority of conceptions could be traced back to a cultural fertility event, the Feast of Maat. This work vastly improves our understanding of female risk of morbidity and mortality in particular, and emphasizes the role of culture in biological outcomes. The above studies are also a good reflection of how isotopic analyses can inform understandings of our chemical, morphological (e.g., body height), and physiological (e.g., length of breastfeeding, nutrient requirements) adaptive domains.

One of the most important factors in the geographic spread of infectious disease is travel, which can be identified through tracking change in the isotopic compositions of incrementally growing tissues, comparing earlier and later forming tissues, and/or comparing the tissues of individuals with known environmental baseline δ-values. The two elements whose isotopic compositions are most commonly used for reconstructing paleomobility are oxygen and strontium, although carbon and nitrogen can also be used when there are differences in ratios of C₃ to C₄ foods and/or protein source or trophic level among the regions of interest. For example, carbon and nitrogen isotopic data for humans have been used at the northern Sudanese site of Kerma to identify the presence of “outsiders” or non-locals for the region (Thompson et al. 2008). Environmental variables such as rainfall, humidity, temperature, altitude, and distance from the ocean are reflected in the oxygen isotope composition of meteoric water (Dansgaard 1964), which is in turn reflected in body water, and then in the phosphate (δ¹⁸Oₚ) and structural carbonate (δ¹⁸Oₛₐ) of mineralized tissues (Longinelli 1984). Variability in δ¹⁸O values of archaeological skeletal tissues can be caused by seasonality, the presence of water sources subject to different degrees of evaporation, the possible consumption of foreign foods with high water content, and some pathological conditions. For example, females from Wadi Halfa with evidence of osteopenia had the lowest δ¹⁸Oₚ values, which could indicate that osteopenia was more frequent or severe in women. Alternately, it may indicate that the sample included a large number of breastfeeding females who had high water flux rates (White et al. 2004).

Geographic mobility is only detectable when involved locations and/or water sources have significant climatic and/or physiographic differences. Nile river water has graduated δ¹⁸O values that reflect increasing evaporation from source to delta. It is also virtually the only water source for those living on its banks and the Nile was also the main corridor for north–south travel in the region. Because of its central location, it is not surprising that Wadi Halfa had among its dead isotopically identified non-local individuals who must have been travellers (White et al. 2004). If these individuals brought infectious bacterial diseases to Wadi Halfa, they did not take hold, possibly because the consumption of antibiotics through antibiotic-laced beer was widespread and conferred
immunity. Disease could have also travelled east to west via the caravan travel and trade routes between Nilotic settlements and the Western Desert oases. For instance, at the Dahkleh Oasis, which draws its water from a fossil aquifer with a distinctive δ18O value, the discovery of a male with skeletal evidence of leprosy (Hansen’s disease) and a Nile Valley isotopic composition has led to the suggestion that oases may have been used as places of exile for such diseased individuals (Dupras and Schwarcz 2001).

Radioactive decay, geological age, and compositional variability among rocks, minerals, and seawater lie at the root of strontium isotope variations, which are used as tracers in anthropological studies of geographic mobility. As one of the isotopes of rubidium (87Rb) decays, 87Sr is formed. Higher 87Sr/86Sr ratios occur in rocks and minerals that are richer in Rb, which follows K, and/or which are older, thus allowing more time for decay of 87Rb to 87Sr. Rocks and minerals that are poorer in K, and hence Rb, and/or geologically younger have lower 87Sr/86Sr ratios (Faure and Powell 1972). Strontium isotope ratios are, therefore, a function of the age and type of rock. Seawater also has a characteristic 87Sr/86Sr ratio at any given time. This ratio has, however, varied throughout geological time depending on the age and sources of strontium delivered to the oceans. Strontium isotope ratios are typically measured using thermal ionization mass spectrometry (TIMS) or laser ablation-multi collector-inductively coupled plasma-mass spectrometry (LA-MC-ICP-MS).

Over time, rock breaks down into soil water, and strontium moves into soil water and then through the food chain without significant alteration of its isotopic composition (e.g., Comar et al. 1957). Variation can be created by local factors, but the strontium isotope compositions of diets directly reflect local geology, and almost all strontium in the body is found in mineralized tissue. The strontium isotope composition of seawater is similarly transferred to calcium-bearing tissues in marine organisms. Both strontium and oxygen isotope analyses have pushed back the biological evidence for long-distance interaction between Egypt and Nubia to the New Kingdom period (∼1050–1400 BC) (Buzon & Bowen 2010; Buzon & Simonetti 2013; Buzon et al. 2007). The next step in paleomobility studies would be to correlate the presence and incidence of infectious disease with isotopically identified individual travelers and immigrants, and its spread in past populations.

Isotopes and paleoenvironments
Traditional approaches to isotopic reconstruction of paleoenvironments include the use of incrementally deposited materials. For long-term records, these include lake and marine cores, ice cores, speleothems, which are mineral deposits formed from groundwater within underground caverns, and tree rings. Incrementally formed animal tissues, such as otoliths, or inner ear bones, shell, horn, antler, teeth, and hair provide shorter records of change. These records can only be extended across long periods of time when samples that can be
correlated with each other are available. Unfortunately, many chronologies of climate and ecological change created in this way either often predate human occupations of the regions involved (e.g., Brook et al. 2010; Nicoll 2001; Osborne et al. 2008; Stanley et al. 2003) or are unavailable for many regions. In other cases, these chronologies have not been linked to human experiences except to identify associations between climate change and the fall of civilizations (e.g., Issar & Zohar 2004; Weiss 1997). Environmental and ecosystem change, when integrated with dietary and disease patterns could, nonetheless, demonstrate presence of selective pressures.

The use of human remains for the strict purpose of environmental reconstruction is largely unexplored, and would likely be frowned upon for ethical reasons in many places. We do not advocate the analytical destruction of human tissues for the sole purpose of environmental reconstruction. We would, however, like to alert researchers to the possibility that there may be inherent climate or environmental records in samples of human remains that have been previously analyzed for both diet and mobility ($\delta^{13}C$, $\delta^{15}N$, and $\delta^{18}O$). Where human remains are not available because of politics or preservation, the remains of both wild and domesticated animals often make good proxies for reconstructing not only food domestication and the rise of agriculture and pastoralism, but also cultural and economic change, social organization, and ideology (e.g., Szpak et al. 2014). Isotopic data for animals can provide additional evidence of landscape change as it is related to climate change and/or human subsistence behavior and population growth and decline (e.g., Morris 2015). As more and larger sets of human and animal data are produced to investigate anthropological and ecological issues and questions, there is increasing potential to mine the environmental and landscape information that they contain.

The nitrogen isotopic composition of plants reflects rainfall and aridity; as rainfall decreases, $\delta^{15}N$ values of plant and animal tissues tend to increase. It can also reflect altered soil quality caused by nutrient loss or fertilization. Nutrient loss related to environmental degradation and ecological change could be signaled by a gradual reduction of $\delta^{15}N$ values as environments reach their carrying capacity and populations are forced to consume protein from lower trophic levels. Fertilization in agriculture can be artificial or be the result of natural processes, such as the annual deposition of nitrogen-rich silt during annual flooding of large rivers like the Nile (e.g., Jenny 1962). The $\delta^{15}N$ values of bone collagen also indicate that such an occurrence happened over time at Wadi Halfa (White and Schwarcz 1994). In this case, the fertility of the Lower Nile came at the expense of the Upper Nile. Fertilizing soil is also a human behavior that, in ancient times, was most likely to be organic via dungs, slurries, fish, seaweeds, and guano, and produced plants with higher $\delta^{15}N$ values. Whether fertilization is a process of nature or a purposeful human act, it induces environmental change. Although first seen as a source of error in paleodietary research, fertilization systematics are now being used to reconstruct the rise of intensive agriculture
and its link to animal domestication, husbandry practices (e.g., complete captivity, controlled herds, and pasturing locales), and land use patterns (Balasse 2014; Hamilton & Thomas 2012; Makarewicz and Tuross 2012; Szpak 2014). The next steps could be to tease out the environmental change associated with human behavior, and reconstruct the relationship between animal husbandry and domestication practices and the rise of zoonoses, diseases with animal origins that infect humans (e.g., Barton et al., 2009; Donoghue 2011).

Paleotemperature can be reconstructed from the oxygen isotopic composition of non-mammalian animal proxies. For example, growth rings in the shells of mollusk species directly reflect the temperature of surrounding water bodies during shell formation. Because humans and all other mammalian species have a tightly regulated, consistent body temperature, the isotopic composition of the ambient air temperature will not be recorded directly in mineralized tissues. Rather, these tissues will reflect environmental effects on the oxygen and hydrogen isotopic composition of the water consumed. For example, seasonal shifting in $\delta^{18}O$ values related to fluctuating levels of the Nile has been reported in a preliminary study of variation within human osteons, the main structural unit of bone (Schwarcz et al. 2004). By long-term extension, when bulk bone $\delta^{18}O$ values from Wadi Halfa humans are combined with those from other studies, a record of the average Nile environment can be reconstructed from Predynastic (6950–4950 BC) to modern times (Geirnaert and Laeven 1992; Iacumin et al. 1996; White et al. 2004). This record indicates a long period of increased aridity that began around 1500 years BC (Geirnaert and Laeven 1992; Jackson 1957) as well as climatic variability in source regions (Bell 1970; Butzer & Hausen 1968; Pollard 1968) and more recently, the evaporative effects of the Aswan dam.

**Discussion and conclusion**

The explanatory power of stable isotope analysis combined with the biocultural paradigm holds much promise for future understanding of how the evolutionary forces of diet, disease, and physical environment have operated on humans throughout space and time. In addition to serving the goals of paleopathologists to reconstruct pathogenesis and epidemiology, understand histories of diseases, and inform medical knowledge, theory and practice, such integrated lines of evidence also inform paleoenvironmental research. This approach would improve our understanding of the impact of climate and environmental change on populations and their biological and cultural adaptive capacity. The aggregate information derived from all of these efforts should ultimately be funneled into a biocultural model that can benefit modern quality of life and biological well-being.

As the work of Armelagos with the Nubians at Wadi Halfa has taught us, the biocultural approach in bioarchaeology provides data that enable us to better
understand stressors and their effect on ancient populations. Stress can be caused by any evolutionary force, and inferred from isotopic data that directly indicate short- or long-term change in diet and climate, or indirectly indicate susceptibility to disease experiences. Our main buffer against these stresses is culture, but culture, particularly its technological aspects, can also create stress on an enormous scale. This is dynamic evident: in the changing dietary and health profile of Wadi Halfans during the Agricultural Revolution and the associated first epidemiologic transition, in the changing disease and demographic patterns of the other epidemiologic transitions, and in the modern concern for human-made climate change, pollution, and landscape alteration.

Ultimately, the goal of the biocultural isotopic anthropologist should be to integrate isotopic data on geographic mobility and diet with changes in the physical and cultural environments, and in patterns of disease and demography. Such integration would make epidemiological risk factors more clearly detectable. More specific knowledge of the dynamics of those risk factors and their biocultural outcomes in ancient populations should inform the way we handle similar modern situations. Currently developing methodological approaches in isotopic research will further the quality and specificity of our reconstructions. First, these include expanding ways of using the tissue clocks, which will involve new ways of micro-sampling and help to minimize sample destruction, and second, expanding knowledge and application of other isotopic systematics, such as sulfur, hydrogen, and iron and third, the combination of multielement isotopic data to hone our ability to identify food consumption and geographic relocations, and lastly, developing further the use of amino acid isotopic analysis to distinguish between influences of diet versus metabolic, physiological, and disease stresses on isotopic composition.

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New directions in biocultural anthropology


CHAPTER 13

The cuisine of prehispanic Central Mexico reconsidered: the “omnivore’s dilemma” revisited

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Introduction

In 2010 George Armelagos reviewed and commented on Michael Pollan’s popular book, The Omnivore’s Dilemma (Pollan 2006). In this text, Pollan characterizes the modern grocery store as a nutritional minefield, which has negatively impacted human health through the undesirable array of foods that it offers, all of which constitute an unhealthful diet. The omnivore’s dilemma in its original context represents a serious predicament for omnivores. According to Armelagos (2010:163):

It references the conflict in which organisms have a need to increase the variety of foods to meet their nutritional requirements (neophilia) in the context of fear that the novel substance they are about to eat may be deadly (neophobia).

In his critique, he provided a discussion of the origin of the omnivore’s dilemma, the role that it plays in the development of human food choices, and how it impacts food choice in an environment of abundance. To this end, he employed a biocultural approach that explicitly considers how the composition of the human diet reflects both biology and culture. That is, diets meet the biological requirements for human nutrition through cultural choices of what is edible.

One critical point in dealing with the food crisis contemporary societies face, with such things as soaring rates of obesity, particularly among children (Ogden et al. 2014), and related poor health outcomes such as diabetes and high cholesterol, is an understanding of how the abundance of food has become a component of the environment for many human populations (Pollan 2006). Armelagos (2010) notes that Pollan does not address the evolutionary roots of the omnivore’s dilemma, nor does Pollan consider it in the context of cultural evolutionary dietary change. Because of the evolutionary trend
towards encephalization (increasing brain size) exhibited over the last 2 million years in hominin evolution, additional energy was required to fuel these large brains. This meant that from an evolutionary perspective, hominins required high-quality food to fuel their ever-increasing brain size. This led to an evolutionary selection in hominins for taste preferences for sugars and fats, so that foods containing these substances would be chosen when they were found in the natural environment (Armelagos 2010).

To these, the umami (savory or pleasant) taste preferences can be added, which are a proxy for protein. Protein is also a high-quality food item, as is salt, an essential nutrient in a dry climate. These flavor preferences are encoded in taste sensors on the tongue that can sense sweet, salty, and umami, which are considered to be pleasant tastes, as well as sour and bitter sensations, which are considered to be undesirable tastes. Sour tastes lack sugar, and potential poisonous flavors are possible in the case of bitter-tasting foods (McGee 2004). In addition, added caloric energy is extracted from all food items when they are “predigested” through the use of cooking (Wrangham 2009). Cooking predates modern humans, but it is a crucial part of most human food preparation today. Wrangham (2009) postulates that cooking was present in *Homo erectus* populations around 2 million years ago, although good evidence for hearths is only found around 850,000 years ago, and that the brain expansion at that time constitutes indirect evidence of cooking.

What we see then from this picture is a genetic adaptation to certain food preferences and the behavioral ability to add calories to foods through cooking. These cravings for fat and sugar are hard-wired into our species (Armelagos 2010) and facilitated by cooking. Importantly, cooking converts simple sugars and amino acids into numerous complex molecules through a Maillard process, the browning that makes toast smell and taste good, for example (McGee 2004). These molecules were primarily recognized by hominins as a desirable aroma created by the use of roasting and dry cooking. This reinforced the behavioral desirability of cooking even though it is a more energetically costly method of food preparation in terms of time and fuel to create the fire for cooking. This allowed both hominins and modern humans to parse the potential food options found in the environment and select the most desirable over less desirable choices. This is highly adaptive in a foraging subsistence strategy, which was the characteristic strategy of hominins throughout their evolution, all modern humans until roughly 12,000 years ago, and which persists for some modern foraging societies. Armelagos (2010) made the observation that when cultures became sedentary and settled into permanent villages, they became more dependent on the domesticated foods of agriculture starting 12,000–10,000 years ago.

One of the advantages of permanent residency in villages is that it decreased the energetic cost of food capture, resulting in more potential net energy; mobile foragers expend significant calories in the daily search for food. However, Armelagos (2010) pointed out that sedentism and agricultural food production resulted in a dramatic decrease in the number of dietary items in any given
agricultural diet. Problematically, many of these were more limited nutritionally when compared to potential food items found naturally and consumed by foragers. Armelagos also noted that the overall health of settled agriculturalists declined in comparison to their foraging counterparts (see Armelagos and Cohen 1984).

Yet it is agreed that there are advantages to agricultural food production over foraging. These include the ability to store food, resulting in an annual food supply, thus minimizing subsistence risk; raising domesticated animals by feeding them agricultural byproducts, such as grain stalks that are inedible for humans, while creating steady access to meat, milk, and other animal products; and the ability to have a constant supply of soft foods, enabling early weaning of infants. The advantages of food production, food storage, and settled life increase the energy available from the diet, thereby eliminating part of the omnivore’s dilemma. Armelagos (2010:164) considers cuisine to be a defining event in human cultural evolution that emerged around 12 000–10 000 years ago along with sedentism and the development of agriculture.

Armelagos (2010:164) follows Rozin’s (1982) definition of cuisine, which considers cuisine to be a cultural system composed of four components. These are the items in nature that are considered to be edible; how these items can be captured, eaten or processed into food; the flavorings that are added to food to improve its taste; and lastly, the rules that govern its consumption. The first is the limited number of food items typically based on the local environment. These are known as the staples of the diet. Secondly, how the food is prepared? For example, potatoes are peeled, sliced into strips, and fried in oil in the United States, while in Mesoamerica corn is soaked in lime water, ground into a paste, rolled out into circular sheets, and cooked on a griddle. The third aspect involves ingredients added to these staples, such as spices, condiments, sauces, and the like to enhance the flavor. It is this category of food that largely distinguishes a culture’s cuisine. Examples would be the practice of putting ketchup (flavoring) on French fries (potato being the staple) in the United States, while in Mesoamerica it would be putting a chile sauce (flavoring) on a tortilla (corn being the staple). The fourth component in the diet has to do with the rules of consumption. In the United States, the main meal of the day is taken in the early evening, while the main meal of the day in Mexico is in the middle of the afternoon. Also, certain foods are only seen as being appropriate for particular meals, such as cereal for breakfast in the United States.

Armelagos (2010) further notes that when food scarcity is no longer an issue and dietary expansion is possible, brought about by industrial food production, a new environment of food availability and abundance is created. This permits greater food choice for humans, making it easier to optimize their evolutionary selective preferences for foods containing fats and sugars, as well as salt. Industrial food production can then be tailored to the biological cravings of humans, which is exactly what the modern food industry today is doing, as documented by Moss (2013) in his book *Salt, Sugar, Fat*. Moss notes that the global food industry
is modifying food by the addition of salt, sugar, and fat to appeal to our genetic predispositions for these food characteristics. This is actually a violation of the fourth component of cuisine: when food is eaten. Much of this is snack food, such as chips or candy, obtained outside the traditional culturally appropriate meal times and as nutritionally unnecessary additions to the daily food intake (see Chapter 3). These can also be more easily obtained at any time of the day through purchase in vending machines, convenience stores, and gas stations as well as grocery stores. The traditional location for obtaining food, the home, has seen shifts in the balance of the nutritional quality of food because of the abundance of high-fat and high-sugar foods in grocery stores, where staples and seasonings are obtained.

The remainder of this chapter characterizes prehispanic cuisine of Mexico in the context of Armelagos's notion of cuisine as described above and the changes that take place as dietary items shift in importance. The prehispanic period represents the era before Spanish contact in 1519 CE. What we discover is that the prehispanic cuisine of Central Mexico, especially that of the Basin of Mexico, where Mexico City is located, in the highland environmental zone known as the Tierra Fria, was extraordinary in its dietary diversity (Figure 13.1). More

![Figure 13.1 Map of the Prehispanic Basin of Mexico with Both Teotihuacan and Tenochtitlan and the Lakes. Adapted from Basin of Mexico-en.svg, Creative Commons International 4.0.](image-url)
importantly, the nutritional quality of these dietary items provided a healthy and balanced diet for the prehispanic people living in the Tierra Fria. This cuisine is largely “invisible” to Western notions of appropriate foods but in fact, it is these items that act as the flavorings to staples – the second component of Armelagos’s definition of cuisine – that make it so nutritious and healthy.

Case study: prehispanic cuisine of Central Mexico

Prehispanic Mesoamerica

Prehispanic Mesoamerica included most of Mexico, Guatemala, Belize, and parts of El Salvador and Honduras. It was the locus of complex pre-Columbian societies, such as the Aztec and the Maya, and united by general similarities in life ways and cultural traits. The focus here is on Central Mexico, and more specifically on the Basin of Mexico, a highland plateau over 2000 meters in elevation called the Tierra Fria, because it is semi-arid and can experience frosts. One of the more distinctive environmental characteristics of the Basin was the extensive system of freshwater lakes, but one, Lake Texcoco, was brackish. The Basin of Mexico, where the present capital Mexico City is located, had some of the most urban and politically centralized societies, influential across much of Mesoamerica, before the arrival of the Spanish in 1519 CE (Sanders et al. 1979). The Aztec capital of Tenochtitlan was located here, in addition to numerous other urban centers, totaling a population around 1 million (Sanders et al. 1979). Earlier, circa 0–600 CE, the urban center of Teotihuacan, with a possible population of 100 000, was present in the north-eastern Basin (Sugiyama 2012).

There is detailed information on various foods that Teotihuacan and the Aztecs consumed, as well as how foods were processed, available from sixteenth-century Spanish chronicles. But there has also been considerable retention of traditional foods and their social contexts into the modern era, allowing researchers to reconstruct prehispanic cuisine (Staller and Carrasco 2010), including in relation to the “omnivore’s dilemma.”

History of prehispanic cuisine in the Basin of Mexico

The prehispanic cuisine of the Basin of Mexico did not suddenly appear with the development of the Aztec culture but gradually evolved from the foraging and collecting subsistence strategy of the first inhabitants, who existed there prior to 3500 years ago in the Archaic period (6000–1500 BC). Freshwater lake resources were very important to this preagricultural adaptation in the Basin, even allowing permanent year-round settlement (Niederberger 1979). Faunal food items recovered by archaeologists and apparently consumed by the foragers included migratory waterfowl, deer, rabbits, voles, cotton rats, fish, turtles, snakes, and Ambystoma, a salamander. Plant foods included wild rice (Zyzaniopsis), amaranth (Amaranthus), goosefoot (Chenopodium), tomatillos (Physalis), Portulaca, a plant
with fleshy edible leaves, and teosinte (*Zea mexicana*), the progenitor to maize (Ilitis 1983). Teosinte was initially utilized for its sugary juice before becoming a staple of later sedentary populations (Smalley and Blake 2003). In the same trend, Archaic foraging populations of Mesoamerica utilized many plants for their sugary juices, including maguey (*Agave* spp.), sotol (*Dasylirion* sp.), mesquite (*Prosopsis* sp.), jocote (*Spondias purpurea*), the fruit of the nopal cactus (*Opuntia* sp., also known as tunas) (Bruman 2000), demonstrating the importance and desirability of sugar among Mesoamerican populations. For instance, Hernando Cortés wrote to the King of Spain in 1520 that syrup from cornstalks and maguey, as well as honey from bees, was sold in the great marketplace of Tenochtitlan (Bruman 2000:57). The sap from maguey was fermented into an important nutritious beverage that was a staple in the Highland Mesoamerican diet (Parsons 2010).

Discussion of cuisine with agriculture begins with the domesticated crop of maize (*Zea mays*), which was commonly interplanted with beans (*Phaseolus* spp.) and squash (*Curcurbita* spp.) in the fields called *milpas* (Coe 1994). In the sixteenth century, the Spaniards quickly identified maize as a dietary staple for the prehispanic cultures of the Basin of Mexico, similar to wheat and rice in other parts of the world. Although certainly one of the most important commercial crops in the world today, based largely on processing corn into syrup and oil – which was not possible until the nineteenth century (Coe 1994) – maize is often criticized because it is deficient in amino acids, specifically lysine and tryptophan, and has a low availability of the B vitamin niacin (Nuss and Tamunhardjo 2010). Overconsumption of maize can lead to pellagra, a serious vitamin deficiency caused by a chronic lack of niacin, or vitamin B3 (Coe 1994). However, in Mesoamerica, prehispanic communities had learned to soak and cook maize in alkali-water, made with ashes and lime (calcium oxide), since at least 1200–1500 BC, which makes the niacin biologically available. This alkali process is known by its Aztec-derived name, *nixtamalization*. In addition to increasing the availability of niacin, nixtamalization also softens the maize kernel’s hull, making maize more palatable and easier to grind, and increases the calcium and protein content of the grain as well as the availability of lysine and tryptophan (Staller 2010). The maize is soaked and cooked until soft, when it can be ground into dough and made into tortillas and tamales, although it was also consumed as a drink. Nixtamalization generally eliminates the chances of developing pellagra, which is unknown where the process is used in the New World, despite heavy consumption of maize in some areas (Coe 1994).

Spanish chroniclers reported that the traditional meal of Aztecs at 1519 CE consisted of “tortillas, a dish of beans, and a sauce made from tomatoes or peppers” (Staller 2010:54). Tomatoes and chile (peppers of the genus *Capsicum*) were important ingredients in prehispanic diets. Two types of tomatoes were consumed, the green husk tomato or tomatillo (*Physalis*) and the plump red tomato (*Solanum*) (Coe 1994), with the tomatillo more commonly eaten. It is interesting that the sauce mentioned above is either tomato or chile, as it is the combination
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of both that is common today, as well as the general use of chile to flavor many dishes (Staller 2010). While nixtamalization increased the availability of amino acids in maize, the addition of beans to the diet balanced out maize consumption and enabled prehispanic communities to acquire the complete range of amino acids needed for normal protein synthesis (Coe 1994). Beans could be dried, which was the more common form of processing, and stored, or eaten young and green.

**The adequacy of cuisine: paleopathological evidence**

One way to judge how well the cuisine and diet are able to overcome potential nutritional deficiencies is to look at the paleopathological indicators of morbidity on the skeleton. Skeletal evidence from multiple archaeological sites representing prehispanic Mesoamerica can be brought to bear on this issue.

One important archaeological site, the Tlajinga 33 compound in urban Teotihuacan, represented the residence of lower-status artisans, lapidaries in various media, and ceramic producers. Excavation of this site has yielded information on food consumption and a skeletal sample with which to study lifestyle and health in this early urban environment (Storey 1992; Widmer 1987). The Tlajinga 33 skeletal sample has a high prevalence of three non-specific indicators of paleopathology. These are generalized indicators of biological stress, rather than lesions particular to a specific disease state. They include periosteal reactions, enamel hypoplasias, and porotic hyperostosis. Periosteal reactions consist of subperiosteal bone deposition indicative of trauma, general infection, and inflammation, among other causes. Enamel hypoplasias are areas of reduced enamel deposition on teeth, representing a period of growth arrest caused by physiological disturbance during growth and development, often from malnutrition or severe diarrheal disease (Storey 1992). Lastly, porotic hyperostosis consists of circumscribed areas of pitting and porosity on the external surface of the cranial vault. In paleopathology, this has traditionally been attributed to either hereditary or acquired anemia, often iron deficiency anemia. Because there are no hereditary anemias present in prehispanic times in Mesoamerica, hereditary causes are unlikely in this context (Walker *et al.* 2009).

A recent reevaluation of the argument that the marrow expansion (hypertrophy) responsible for porotic hyperostosis could be caused by iron deficiency anemia has instead indicated that the cause may be actually megaloblastic anemia, which is often caused by vitamin B12 deficiency (Walker *et al.* 2009). The premature death of red blood cells in megaloblastic anemia triggers the kind of overproduction of cells that leads to marrow hypertrophy, whereas this expansion requires sufficient iron stores, which are not likely to be available in the case of iron deficiency (Walker *et al.* 2009:112). This indicates that the nutritional deficiencies indicated by porotic hyperostosis should be extended beyond iron in a given skeletal sample. Vitamin B12 is a water-soluble vitamin normally
involved in the metabolism of every cell of the human body, especially affecting DNA synthesis and regulation, fatty acid and amino acid metabolism. It is found in most animal-derived foods, which means that vitamin B12 deficiency, which can potentially cause severe and irreversible damage to the brain and nervous system, can be a health concern for vegetarian or vegan individuals, as well as those with limited animal-based contributions to their diets (Stabler and Allen 2004). Porotic hyperostosis primarily manifests in infancy and early childhood, which is particularly a problem for infants whose mothers have B12 deficiency. If megaloblastic anemia is survived, porotic hyperostosis heals. It can, however, still be recognized on the skeleton for years afterwards and scored by osteologists in adults; the remnant porosity and uneven surface indicate that the individuals suffered from anemia in infancy or childhood.

Skeletons from Tlajinga 33 had surprisingly little porotic hyperostosis, with just five cases (15%) in the crania that could be evaluated for the lesion. Four of the crania, including two subadults, manifested healed lesions, and only one subadult exhibited active, though severe, lesions. Based on this, the residents of Tlajinga 33 seem to have had adequate vitamin B12 in the diet. For all prehispanic periods to 1519 CE, foods were incorporated into the cuisine that provided additional nutrients, preventing B12 deficiency. While many of these are unfamiliar and unsavory to many of us, these foods provided essential nutrients, such as fat and protein, and were important components of prehispanic cuisine. We will discuss the terrestrial dietary resources and then the aquatic resources in the following section.

**Supplemental dietary resources**

**Terrestrial dietary resources**

**Plants**

Parsons (2010) has convincingly argued that the distinct maguey and cactus plants found in the Tierra Fria provided an essential complement to the more obvious seed crops, such as maize and beans, for agriculturalists. The maguey plant is still an important supplementary food in the Basin of Mexico, providing edible flesh from its leaves and fibers that can be used for cordage and fuel. It can be intercropped with any seed crop, thereby doubling the energetic and nutritional output of a unit of land and potentially yielding more calories than seed crops on a unit of land (Evans 1990; Parsons 2010:117). The fermented sap of the maguey was an important beverage called *pulque*. It possessed a number of desirable traits for its consumers. First, it provided a safe potable liquid, because of an alcohol content of 4.5% and a high acidity with pH of 3–4. Secondly, pulque contains concentrations of most macro/micronutrients, which, together with lactic acid bacteria, provide probiotic properties. These are the “good” bacteria that aid in proper digestive function (see Chapter 18). Thirdly, it contains the enzyme phytase, which increases the bioavailability of iron and zinc, the most deficient minerals in maize. Fourth, the high concentration of vitamin C
in pulque enhances the absorption of iron, and possibly zinc, into the digestive system (Correa-Acensio et al. 2014). Maguey sap is also high in niacin, thiamine, riboflavin, calcium, iron, phosphorus, potassium, and zinc, providing important required vitamins and minerals in the Basin of Mexico (Parsons 2010). The flesh can be baked into a cake-like food, with 347 calories and 4.5 grams of protein per 100 g. More importantly, cultivating maguey greatly increases food security, since it is a highly reliable crop, less susceptible to adverse climatic conditions than maize (Parsons 2010).

Parsons (2010) only briefly touches upon cacti as an important food resource. They grow in the same climates and location as maguey, and both the pads and the fruit of the nopal cactus are eaten. Nopal is the most important cactus in the Basin of Mexico for dietary purposes. Nopal pads are nutritionally similar to maguey and so provide another alternative to maguey leaves. The seeds of the nopal fruit, commonly called tunas in Mexico today, were very common in the paleobotanical sample at Tlajinga 33 in Teotihuacan (McClung de Tapia 1987), indicating that they were a component of the diet.

So while maize is clearly the symbolically central food item for prehispanic Mesoamericans and represents the main staple, maguey and nopal certainly complemented maize, and it is these seeds, sap, and flesh that together provide the distinctiveness, caloric adequacy, and security of the highland Mexican cuisine. These would also contribute to the high C4 signature in the diet seen at Teotihuacan (Morales et al. 2012).

Domesticated animals

Central Mexican cuisine contained a limited but important number of domesticated animals that were utilized for food. These are the dog (*Canis familiaris*), the turkey (*Megagallo*), and possibly quail and rabbit. With the exception of rabbits that can consume plant fibers indigestible by humans and so are less costly to produce, dogs, turkeys, and quails were fed maize, as has been determined by isotope analysis of their bones that show a high C4 protein isotope signature (Morales et al. 2012). While the flesh of these animals is high quality and particularly important as a source of vitamin B12, they are expensive to raise because they compete with humans for food. Nevertheless, they were clearly desirable since their remains have been found in the poor apartment compounds, like those in Tlajinga 33, albeit in very low frequencies. However, one byproduct of avian animal husbandry does appear to be important: egg production.

Fragments of turkey and quail eggshell were recovered from the Tlajinga 33 excavations (Widmer 1987). Not only are eggs high in protein and fat, they are also excellent sources of vitamin B12. Starbuck (1987:80) discounts the importance of turkey meat as a food source, since it only accounts for 10% of the meat consumed at Teotihuacan based on its quantity in the recovered faunal bone. At Tlajinga 33, 12% of the bone fragments were from turkey (Alvarez and Ocano 1989), thus supporting the frequency of consumption and the low importance
of turkey meat at Teotihuacan. Turkey and quail meat are important for protein and, more importantly, vitamin B12. Quail meat and skin, raw, contains \(0.43 \mu g/100\ g\) of vitamin B12 while turkey, drumstick, meat and skin, cooked, roasted, has a vitamin B12 composition of \(2.46 \mu g/100\ g\) (http://ndb.nal.usda.gov/ndb/nutrients/ is the source for these and subsequent measures for the vitamin). To put these values into perspective, chicken leg meat and skin, stewed, has only \(0.20 \mu g/100\ g\) of vitamin B12. While flesh was probably infrequently consumed, Starbuck fails to recognize the potential importance of turkey eggs in the diet. The same can be said for quail eggs. In other words, you not only get to eat the turkey and quail meat but also the eggs. These eggs represent an often archaeologically invisible additional animal protein source because of the very small size of the eggs and their shell fragments.

Faunal remains of two species of quail, the bobwhite (Colinus sp.) and the Montezuma quail (Cytronix montezuma), were recovered in the 6 mm screened samples from Tlajinga 33, accounting for 3.7% and 5.4% of the total faunal elements. There can be little doubt that quail were raised at Teotihuacan for their eggs and their meat, with the former probably being more important in the diet than the latter. Also important is the relatively high vitamin B12 content of these eggs. Quail eggs have \(1.58 \mu g/100\ g\) and turkey eggs have \(1.69 \mu g/100\ g\) of vitamin B12. Thus, from eggs alone, the Tlajinga residents could have largely avoided the vitamin deficiency and megaloblastic anemia. But there were still other foods that were part of the cuisine, considered edible and used to add flavorings to meals.

**Terrestrial small wild animal remains**

Remains of other terrestrial wild animal resources were also found at Tlajinga 33. Numerous remains of small lizards were recovered in the heavy fraction flotation (HFF) samples from the excavations. These are not intrusive into the cultural strata since they are burned, indicating that they were dietary items. For instance, a small burned rodent mandible with teeth was recovered in the HFF. This is important because of the 445 bone fragments of rodents recovered, 271 of these were burned, indicating that they were consumed rather than intrusive. While today, many humans would consider rodents to be vermin, these were an important nutritional component to the diet for the ancient Teotihuacanos as they were obviously were part of the Teotihuacan cuisine. Squirrels, the closest food animal we could find within the USDA nutritional database to the recovered rodents, have a very high vitamin B12 content. Wild game squirrel, cooked and stewed, has vitamin B12 values of \(6.51 \mu g/100\ g\). Rodents, including mice, are abundant in the ecosystem of Teotihuacan and present at Tlajinga 33 along with pocket gopher and ground squirrel, which were also found in the faunal remains (Alvarez and Ocana 1989). These would have provided important sources of vitamin B12, again indicating another food source important for preventing megaloblastic anemia.
Insects
Perhaps the most important dietary items in the Prehispanic diet to quantify, yet the most difficult, are insects. These high-protein food sources are still consumed today and can be found in the traditional markets of Mexico as well as in upscale Mexican restaurants in Mexico (Cohen et al. 2009). There are three main insects that were consumed: Chapulin, or grasshoppers, and two varieties of the maguey worm, the meocuiles (Aegiale hesperia) and the chinicuil (Hypopta agavi) (Ramos 1982). Besides these three, insects could also be consumed as larvae and eggs. While we have no ethnohistorical or archaeological evidence that the larvae of insects were consumed, their consumption in rural Mexico today suggests that they were consumed in prehispanic times (Ramos-Elorduy 1997). Ramos-Elorduy et al. (2011) have recently identified 67 species of Lepidoptera (butterflies) that are eaten principally in their larval stage in 17 states of Mexico, so this was another potential protein resource.

Eggs of the common ant, Liometopum apiculatum, called escamoles in Mexico, have recently been found to be extraordinarily nutritious (Melo et al. 2013) yielding high quantities of calories, protein, fat, and minerals. These ants make their nests at the bases of maguey and nopal plants and so the propagation of these plants increases the supply of these highly nutritious eggs. Together, these insects and their eggs can be added as flavorings and would have been important additions to the diet. However, while insects and their larvae provide large amounts of protein, they generally are not sources of B12 and so would not prevent megaloblastic anemia.

Aquatic food resources
Perhaps the most interesting and distinctive food component in the cuisine of highland Mexico, and one that seems unlikely in a largely arid environment, is the lacustrine foods associated with the five interconnected lakes in the Basin of Mexico. Cultural adaptation to the plants and animals goes back 8000 years from the present, as discussed earlier for the preagriculturalists of the Basin. This is evidenced by excavations at Zohapilco on the lacustrine shores of the Chalco-Xochimilco Lakes (Niederberger 1979).

Spirulina is an alga growing on the lake surface that produces rapidly and contains all eight essential amino acids. It is easily removed and consists of 65–70% protein by weight (Parsons 2010:129), so it would be a valuable resource for the diet. Furthermore, spirulina is known to contain large amounts of vitamin B12, but unfortunately this has now been shown not to be bioavailable to humans (Dagnelie et al. 1991). For vitamin B12 absorption, simultaneous consumption of animal protein is required.

As with terrestrial ones, aquatic insects, their larvae, and eggs were also important dietary items in the prehispanic period (Parsons 2008, 2010:129–130). Aztec period (sixteenth century AD) ethnography indicates that incredible numbers of insects and their larvae and eggs were collected and made into cakes with other
food items (Parsons 2010), although it is not possible to quantify the amounts from the documents. These insects contained important protein, fat, and other nutrients, but unfortunately, they do not represent sources of vitamin B12. So once again, an important protein source that was consumed in the Tierra Fria lacked B12, so the people of the prehispanic Basin must have had to turn to other animal sources for their dietary needs. Several of these sources, however, are typically small in size and so required the specialized 1 mm data recovery techniques mentioned earlier (HFF) earlier to document their use (Widmer 1987).

The crawfish *Cambarellus (Cs.) montezumae* is found in the Basin of Mexico. These crustaceans, although only 2 cm in length, are highly nutritious, providing 15.9 g of protein per 100 g. More importantly, they are also extremely good sources of folate, which is required for fetal infant growth, and vitamin B12, providing 37 μg/100 g of folate and 2 μg/100 g of vitamin B12 (Álvarez and Rangel 2007; Arredondo-Figueroa et al. 2011).

Fish were of major importance to the diet, but this contribution is not immediately clear from the available evidence. For instance, Starbuck (1987:84, Table 2) notes that only 15 fish bones were recovered in all of the Teotihuacan Mapping Project data collection. In the Tlajinga 33 faunal analysis, no fish bones were reported despite screening through 6 mm mesh (Alvarez and Ocana 1989). This low frequency of fish was recognized by Starbuck (1987:77), reinforcing the seeming lack of importance of fish to the Teotihuacan diet. However, this interpretation is purely a function of the small size of the fish and the recovery techniques used by the Teotihuacan Mapping Project, which would have failed to capture small fish remains. Demonstrating this, Niederberger (1979:134), who used recovery techniques that enabled capture of small faunal remains, recovered numerous tiny fish bones from the Zohapilco site. These belonged to three freshwater groups: the white fish and charales of the genus *Chirostoma*, the commonly called yellow fish of the genus *Girardinichthys*, and the cyprinids. Tiny fish are abundant in the lakes of highland Mexico today, and the Zohapilco results indicate that the fish would have been available for Teotihuacan and Tlajinga 33. The fish could have been even more important in prehispanic times, since the frequency of species and their size increase with the areal extent of individual lakes (Lyons et al. 2000:65, Figure 2).

The lakes that were present in the Basin of Mexico had a surface area of 1000 km$^2$ (Sanders et al. 1979). This would have made them some of the largest in the highlands and similar in size to the largest lake that is present today, Lake Chapala, which has a surface area of 1250 km$^2$. Today, 50 of the species of fish that inhabit these freshwater lakes of the Mexican highlands are under 300 mm in maximal length (Lyons et al. 2000). Only 21 species have maximal lengths greater than 100 mm, only four species have lengths greater than 300 mm, and, only a single species has a maximal length over 335 mm: a catfish that grows to a length of 1 m (Lyons et al. 2000). Tiny fish vertebrae and scales were common in the HHF samples of Tlajinga 33, and their presence is evidence that fish were important in the subsistence base. Typically, such
small fish would be eaten whole, so finding their remains archaeologically indicates the loss of these food items rather than discard of non-edible portions of the fish. So the frequency of remains from loss represents the tip of the iceberg with respect to their importance and frequency of consumption. More importantly, fish are very good sources of vitamin B12. For instance, smelts have 3.44 μg/100 g, perch have 1.90 μg/100 g, and smoked white fish have 3.26 μg/100 g. We argue that fish, in the form of small, dried minnow-sized lake fish under 300 mm in length, are the most important source of protein at Tlajinga 33 and the second most important source of vitamin B12 in the diet. While these might be best considered as flavorings in the cuisine, they obviously are very helpful to prevent megaloblastic anemia, an important ingredient in solving the “omnivore’s dilemma.”

The extensive lake and marshlands in the Tierra Fria were the most important wintering areas for migratory waterfowl, which were extremely plentiful before the lakes were drained over the four centuries following Spanish contact. Sahagun (1963:63–65), writing in the mid-sixteenth century, mentions 38 varieties of waterfowl, including ducks and geese, although they were only found in the Basin of Mexico during the winter months. Ten species of migratory waterfowl and one indigenous duck (*Anas idazi*) were recovered from excavations at Zohapilco on the lacustrine shores of the Chalco-Xochimilco Basin (Niederberger 1979), attesting to the availability of these dietary items from the sixth millennium BC through until the time of the Aztecs.

A unique aquatic creature, a salamander known to the Aztecs as *axolotl*, formed a key part of the edible resources of the Aztecs in the Basin of Mexico (Figure 13.2). Alexander von Humboldt, a nineteenth-century explorer of the New World who was instrumental in the European collection and study of the creature, described the Aztec consumption of the comestible as follows (quoted in Tate 2010:511):

> In the year 1245 (according to the chronology of the Abbe Clavigero) they arrived at Chapultepec. Harassed by the petty princes of Zaltocan … the Aztecs, to preserve their independence, withdrew to a group of small islands called Acocolco, situated toward the southern extremity of the lake of Tezoco. There they lived for half a century in great want, compelled to feed on roots of aquatic plants, insects, and a problematical reptile called axolotl, which Mr. Cuvier looks upon to be the nympha of an unknown salamander.

This salamander is found solely in the southern freshwater lakes of Chalco-Xochimilco of the Basin. It has three gill stalks, vividly colored pink, orange, or dark brown, which project from its head. It remains embryonic, living its life in water, and is capable of regenerating its limbs as well as its brain in the case of disease or injury (Tate 2010). There is plenty of ethnohistoric evidence that it was eaten as food in Aztec times. For instance, it appeared as an important symbol on pottery from before 1000 BC (Tate 2010), indicating it was important food during all prehispanic periods. Thus, this interesting animal is another example of a food source that would not have been thought of as food
by Europeans, along with the insects and rodents, but was heavily incorporated into prehispanic cuisine.

Remains of aquatic turtles were also recovered in the 6 mm screened samples. Unfortunately, the only reptile listed in the USDA vitamin B database is the green turtle, a marine turtle. It is anticipated that other reptiles should have similar vitamin B12 contents. The raw green turtle has a vitamin B12 content of 1.00 μg/100 g, suggesting that reptiles would be important sources of vitamin B12 as well.

Clearly, many of the aquatic resources that make up the prehispanic cuisine are recognizable to both Westerners and Mexicans, such as fish, turtles, ducks, and even crawfish, but other items, such as axolotl, spirulina, aquatic insects, their larvae, and eggs, would certainly not be considered food by the colonizing Europeans. Even today, if many of these were found in a meal served in a restaurant in Mexico, it would be sent back as a contaminated dish! Yet it was these dietary items, available in huge quantities, that provided the majority of the protein of the prehispanic Basin of Mexico diet. This is why we refer to them as “hidden.”

**Conclusion**

In retrospect, George Armelagos performed an invaluable service to the general public, as well to his academic audience, with his work on food and culture, and
these works were firmly grounded in the biocultural approach. If we consider the structure of cuisine as outlined by Armelagos, we indeed see how intensive agriculture, despite supporting the complex societies and large populations of the prehispanic Basin of Mexico for over 1500 years, would, through the narrowing of dietary diversity that it involved, have created needs to find new foods that fulfilled unmet important nutritional requirements. While there were important staples, such as maize and pulque, what was distinctive about this prehispanic cuisine was the wide variety of foods that were defined as edible and the diversity of nutritious flavorings that were added to these staples. These include chiles, tomatoes, and tomatillos, but also tiny fish, frogs, salamanders, turtles, insects both terrestrial and aquatic, aquatic birds, domesticated bird eggs, and spirulina. These foods exemplify the “omnivore’s dilemma,” as the people of the prehispanic Basin of Mexico might have been at first fearful to consider these substances as food, but soon they became fundamental parts of the cuisine. These foods created a balanced and easily accessible diet, which in many places persists today. Many of these ingredients would not have been considered food by European standards, and remain discredited and delegitimized as parts of a healthful diet following Western standards; nonetheless, they provided the inhabitants with a high-quality diet. The Prehispanic urban residents of the Basin of Mexico certainly had evidence of serious morbidity in paleopathological indicators, but these were due to other urban environmental problems of hygiene, rather than to protein and vitamin B12 deficiencies from their diet, even among the most humble.

Understanding the cuisine of the Prehispanic Basin of Mexico, and by extension the Tierra Fria of Central Mexico, requires a biocultural approach. The biological requirements of nutrition for human health, including the preference for sugar, salt, and fat, underlie how people use cultural definitions of what is edible, what are good flavorings, and how food should be prepared to fulfill these requirements. Researchers have been rediscovering the varied foods of the Prehispanic cuisine (e.g., Staller and Carrasco 2010) and recognizing how well the peoples of the Basin of Mexico and Central Mexico used the concept of cuisine to deal with the “omnivore’s dilemma” and the dominance of maize in the diet.

Acknowledgments

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PART IV
Biocultural approaches to infectious disease
CHAPTER 14

The specter of Ebola: epidemiologic transitions versus the zombie apocalypse

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Introduction

In March of 2014, a major outbreak of Ebola virus disease (EVD) was reported in the West African countries of Guinea, Liberia, and Sierra Leone (CDC 2015a,b). Over the next 17 months, the disease resulted in over 28,000 cases – 15,000 confirmed – and over 11,000 deaths. This was far more than the combined number of cases and deaths in the previous 19 epidemics of EVD in Central Africa that have been documented since the virus was first detected and identified in 1976. The epidemic also included 17 isolated cases outside of these three countries, two of which were health-care workers from the United States who had become infected in West Africa while treating patients and had then come home, only manifesting symptoms after they had returned.

Confounding efforts to control the epidemic, there have been a wide range of inappropriate responses to the West African Ebola epidemic: from apathy and inaction at one extreme, to terror and panic at the other. Of the two extremes, the terror response has been particularly troublesome, with communities and health-care workers refusing to provide assistance to the infected and presumed infected at local levels, and governments putting up resistance to providing humanitarian assistance at international levels. It has been argued that during epidemic and pandemic (global-level epidemics) emergencies, the stigma associated with the infectious disease is often worse than the infection itself (Barrett and Brown 2008). Unfortunately, the latest Ebola epidemic supports this claim.

The stigma and terror of Ebola have been represented with messages containing the most gruesome and exaggerated depictions of the disease. These include images of patients bleeding from their bodily orifices and rotting away while their internal organs dissolve. Fictional narratives have also played a role in these representations, with the zombie genre of popular horror movies providing a
prominent simile in many of these messages. The most famous of these is con-
tained in Richard Preston’s best-selling book *The Hot Zone*, about a small-scale
epidemic of Reston virus, a relative of Ebola, which occurred in the late 1980s
in a non-human primate quarantine facility in Reston, VA. At one point in the
look like a zombie.” At another point, he states “doctors began to notice signs of
mental derangement, psychosis, depersonalization, zombie-like behavior” in the
patients with Reston (Preston 1994:98).

As with many other books in this genre of sensationalized epidemics of infec-
tious disease, the zombie simile appears in *The Hot Zone* with a selective focus
on certain features while paying little or no attention to other important facts
about the disease. Missing from the horrific images is the fact that viral hem-
orrhagic viruses, like Ebola and Reston, are transmitted by blood and body flu-
ids, much like human immunodeficiency virus (HIV), and it is therefore fairly
difficult to become infected without close contact with infected fluids, unlike
infections that are spread by the highly transmissible respiratory route. Despite
rumors of it, there is no scientific evidence that Ebola has adapted a respiratory
route of transmission, though there were some documented cases of transmis-
sion through projection of large fluid droplets through sneezing, coughing, and
vomiting in instances where people were very close to extremely sick patients
(Martin-Moreno et al. 2014). Furthermore, it is highly unlikely that the virus
could easily develop an airborne capability through genetic mutation or through
natural selection. Other mutations of EVD’s DNA are far more likely, such as
to those genes involving virulence, which is the damage that the pathogen, or
disease-causing microorganism, causes to the host, and latency, which is the time
between when a host is first infected with the pathogen and when the host
becomes symptomatic. And although some patients develop a clotting reaction
that leads to hemorrhaging, this does not happen in all patients. Instead, the most
common symptoms are severe fever, head and muscle aches, fatigue, diarrhea,
and vomiting; diarrhea and vomit can contain the virus and are infectious fluids
in this disease (CDC 2015b).

However, with this new epidemic of Ebola in West Africa, 20 years after the
publication of *The Hot Zone* zombies have once again emerged into public dis-
course about Ebola, along with rumors of undead EVD patients. For instance,
voicing his distrust of medical authorities’ plea for calm with regard to the poten-
tial for the Ebola epidemic to spread to the United States, during a congressional
hearing in Dallas a Texas congressman, Blake Farenthold (R-Texas), stated that
“every outbreak novel or zombie movie you see starts with somebody from the
government sitting in front of a panel like this saying there’s nothing to worry
about” (Mascaro 2014). The statement was made in Dallas, where the first person
in the United States had died of the disease, and at the height of the Ebola epi-
demic in 2014, less than four weeks before the mid-term elections. During the
same month, a rumor spread internationally that three Ebola patients in West
Africa had risen from the dead (Eleftheriou-Smith 2014). Attempting to dispel
Chapter 14: Epidemiologic transitions versus the zombie apocalypse

this rumor, Xinhua, the Chinese government news agency, affirmed that Ebola is not a “zombie disease,” and that there have never been documented cases of Ebola sufferers becoming zombies and attacking people. “That can only happen in movies” they wrote (Sonnad 2014). But the agency also stated:

An Ebola sufferer may lose consciousness or faint, making him or her appear dead. But a few hours or even days later the patient may suddenly come to and enter an extremely violent state, tearing at and biting anything that moves, including people and animals.

Needless to say, the latter statements were not reassuring. Even when couched in scientific or medical explanations, the allusions to zombies or other exotic phenomena can greatly hamper efforts to prevent, detect, and control an infectious disease. We have seen this, for instance, in the ongoing pandemic of acquired immunological deficiency syndrome (AIDS). In the 1980s, during the early years of the pandemic, Haitians were initially blamed for the emergence of the disease, and the allusion to zombies was first employed. As one reporter wrote, AIDS among Haitians “was a clue from the grave, as though a zombie, leaving a trail of unwinding bandages and rotting flesh, had come to the hospital’s Grand Rounds to pronounce a curse” (Black 1986). As with AIDS, Ebola, and many other infectious diseases, such fears combine with undercurrents of racism, homophobia, and other prejudices to marginalize patient communities. In a negative synergy, this creates a major barrier for people who might otherwise seek testing and treatment for the disease, keeping them away from potentially life-saving care and risking transmission of the disease to others. In this manner, social stigma furthers the spread of infectious diseases.

To counter these kinds of alarming narratives, and to shed light on human determinants in the evolution of disease, George Armelagos and I published a text entitled *An Unnatural History of Emerging Infections* (Barrett and Armelagos 2013). This book takes a biocultural approach to infectious diseases, tracing the ways in which human culture – defined here as learned patterns of thought and behavior – can shape physical and social environments and thus affect the biological evolution of disease-causing microorganisms. These organisms, in turn, can shape the biological and social responses of human hosts. Such dynamics have occurred throughout human history and prehistory.

With a deep time perspective, our book examines three major disease events, known as epidemiologic transitions, which have occurred over the last 10 thousand years (see also Barrett *et al.* 1998). The first epidemiologic transition brought about a massive increase in the emergence of (as well as morbidity (sickness) and mortality (death) from) acute, epidemic infectious diseases, like measles, when human populations shifted from mobile foraging to agricultural intensification and increased sedentism during the Neolithic (c. 10 kya). The second transition brought about a major decline in mortality and morbidity from these infections and an increase in that from chronic non-infectious diseases, like cardiovascular disease and diabetes. This was associated with industrialization in high-income nations during the nineteenth century, and is ongoing in low-income developing
nations in a modified form. The third transition is occurring today, with origins in the 1980s, marked by an increase in morbidity and mortality from new, recurring, and drug-resistant infections. Problematically, these conditions are mutually interacting with the chronic non-infectious conditions within the modern global disease ecology.

The text addresses earlier Ebola outbreaks since the 1970s as examples of the third epidemiologic transition, generating lessons that could be applied to the recent West African Ebola epidemic. These lessons are derived from recurring themes that stretch from the Paleolithic (c. 2.5 mya–10 kya) to the present day. These are broad issues concerning subsistence, settlement, and social organization. This chapter briefly reviews these lessons and applies them to the recent Ebola epidemic with the hopes of furthering a more intelligent and productive response to this and other global health challenges.

**Case study: Ebola and the epidemiologic transitions**

**Emerging awareness**

Many authors writing about epidemiologic transitions use the model of the three transitions as a framework for teaching about “emerging” and “reemerging” infectious diseases. Emerging infections can be defined as infections that have newly appeared in a population or have existed previously but are rapidly increasing in incidence or geographic range (Morse 1995). In turn, reemerging infectious diseases can be defined as infectious diseases that are resurging in prevalence, having once been controlled, such as through vaccination or antimicrobial drugs (Morens et al. 2004). When I teach courses on global health to undergraduate and graduate students in public health and anthropology, and we discuss these phenomena, I usually begin with a question: “When does an infectious disease become an emerging infectious disease?” I want students to engage with the semantics of the term and understand its etymology. “Emerging” sounds a lot like “emergency,” the spontaneous appearance of something very bad, but with the added implication that it could quickly grow into something much worse. It also sounds exotic, a new and bizarre kind of danger. And finally, “emerging” sounds menacing, as if the harm is somehow intended: either deliberately guided by an unknown hand or deliberately enacted by the thing itself. Reemerging has similarly negative connotations.

Yet despite these ominous connotations, the term “emerging infections” was originally framed with the intention of raising thoughtful concern about these phenomena. A group of epidemiologists and medical researchers coined the phrase in the mid-1990s in response to three major infectious disease trends. The first was a major increase in the number of newly discovered infections. Twenty-nine new pathogens had been discovered in the 20 years leading up to 1993, including HIV/AIDS, Ebola, and highly pathogenic strains of *Escherichia coli* (*E. coli*) and cholera (Satcher 1995). That number has since expanded
considerably. A more recent comprehensive estimate reveals that 335 novel pathogens that can infect humans were identified between 1940 and 2004, with the majority having been detected since just 1980 (Jones et al. 2008).

The second major trend was the reemergence of infectious diseases thought to have been under epidemiological control. For instance, tuberculosis, long considered to be a receding plague of poverty, increased for the first time since the early twentieth century in the United States in the 1980s and early 1990s (Farmer 1997). This was part of a broader trend: an increase in age-adjusted mortality in the United States for infectious diseases between 1980 and 1992, and an overall increase in infection-related deaths in high-income nations (Pinner et al. 1996).

Although many of these trends have since declined in high-income nations, increases in morbidity and mortality from well-known and long-standing infections have leveled off the health gains made by many low- and middle-income developing nations (Bloom and Canning 2007).

The third trend concerned the increasing resistance of these emerging and reemerging infections to antimicrobial drugs. Since the early days of penicillin, bacteria have been steadily evolving resistance to antibiotics within a few years of their development and initial use (Normark and Normark 2002). Courtesy of existing, endogenous resistance genes, pathogens evolve antimicrobial resistance at far faster rates than their human hosts can develop new drugs, prompting some to argue that the world is approaching a postantibiotic era (Garrett 1994; Kåhrström 2013).

In response to these trends, in 1992 the United States Institute of Medicine published a seminal text, *Emerging Infections: Microbial Threats to Health in the United States*, featuring this novel term. The term also featured in the name of several major academic conferences in epidemiology and became the title of a new and prestigious academic journal, *Emerging Infections* (Lederburg et al. 1992). But although these efforts succeeded in raising public awareness of a major global health issue, important lessons were misunderstood or lost when the popular media translated them. Fear got the better of reason with the publication of books such as *The Hot Zone* and popular movies such as *Outbreak*, a 1995 American medical disaster film about an epidemic of infectious disease. These focused public attention on exotic new diseases from foreign lands and emphasized the importance of military-style interventions over well-established public health measures in quelling the epidemics.

Part of the translation problem lay with the terms “emerging” and “reemerging.” However well intended, these terms suggest that infectious disease outbreaks are sudden and spontaneous phenomena. But the history of disease tells us that this is not the case. To begin with, not all newly identified pathogens are actually new to the human species. For instance, retrospective studies of HIV in the blood and tissue samples of deceased patients revealed cases going back to 1959 (Zhu et al. 1998). The same methods revealed more than 2000 additional cases of legionnaire’s disease that predated its initial identification in 1976; these cases had been previously diagnosed as non-specific pneumonias (Meyer 1983).
For this reason, it is important to understand that a newly identified pathogen is not the same thing as a new pathogen. Moreover, an increasing number of these newly identified pathogens are at least partially due to new microbiological technologies for their discovery – a phenomenon known as detection bias – not just the emergence of new pathogen species.

Additionally, an infectious disease cannot “reemerge” in a population unless it was already assumed to be under control. Such assumptions are usually made in high-income nations that had previously reaped the benefits of abundant access to vaccines, antimicrobial drugs, and high-quality, salubrious or healthful living conditions. Low- and middle-income nations are less likely to make these assumptions when the diseases never receded in prevalence in the first place. Thus, it was overly optimistic in the 1950s, 1960s, and even 1980s when leading scientists predicted that the twentieth century would see “the virtual elimination of the infectious diseases as a significant factor in social life” (Burnet 1962:iii) or that there would be little need for infectious disease specialists in the next century (Petersdorf 1986:478). Incubating in poverty, it was only a matter of time before these same old infections returned to high-income nations, especially as globalization increasingly connects rich and poor communities while furthering the economic disparities between them.

A deep time perspective helps to prevent these kinds of misunderstandings. From this vantage point, we still see that the current wave of human infections is certainly an important global health problem, and that many of these diseases are indeed new to our species. But we also see that both the current and novel infectious disease can be explained by human activity patterns that can be traced back to prehistoric times. As such, the term “emerging” has less to do with the diseases themselves and more to do with an emerging awareness of a variety of ecological, political, and economic problems that have been previously ignored. Recognizing these problems will help us to better understand the evolution and spread of infections such as Ebola.

**Ebola and human subsistence**

If it were not for farming, the Ebola virus would never be much of a threat to humans. For millions of years, humans did not have much use for agriculture. Our species lived through hunting wild animals and gathering wild plants, growing food only as a supplement to a diet that was primarily, if not entirely, based on foraging. Studies of contemporary foraging societies have consistently shown that successful hunting and gathering strategies include a wide variety of food resources so as not to rely on a single resource in the face of seasonal and environmental uncertainty. For instance, the foraging !Kung San of the southern African Kalahari desert hunt 58 species of animals; they also gather 17 kinds of vegetables, 14 different fruits and nuts, 15 different berries, and 41 different roots and bulbs (Lee 1990). Prior to settlement and agricultural intensification, the foraging Aché of Paraguay hunted 56 animal species and gathered 40 species of plants,
as well as honey (Hill and Hurtado 1996). Studies of other foraging societies, the Australian Anbarra, the East African Hadza, and the Central African Efé, reveal similarly diverse diets (Jenike 2001). Such diversity ensures an adequate and comprehensive intake not only of calories, fat, and essential amino acids, but key micronutrients as well.

Comprehensive nutrition is essential for healthy immune function. The immune system is energetically expensive, mobilizing a great deal of glucose during the initial stages of infection, and protein energy during the latter stages. People with protein deficiencies who are more than 85% under their expected weight have compromised immune systems that are comparable to symptomatic AIDS patients (Schaible and Kaufmann 2007). Micronutrients are needed to maintain cell integrity in tissues where pathogens are most likely to enter the body: the skin, respiratory mucosa, and lining of the gastrointestinal tract. Consequently, infectious diseases are almost always found in people lacking these nutrients.

Around 10,000 years ago, human societies began shifting from foraging to intensive agriculture as their primary form of subsistence. This Neolithic transition or Agricultural Revolution independently occurred in several places over the next 8000 years, spreading until more than 99.99% of the world relied upon domesticated plants and animals as their primary sources of daily nutrition. This shift brought several important advantages, chief among them a major increase in available calories, primarily derived from cereal grains, and the ability to store food against seasonal shortages.

However, these advantages came at the expense of dietary diversity, a subsequent rise in nutritional deficiencies, and a concurrent rise in the emergence and prevalence of acute infectious diseases. Bioarchaeologists have studied the skeletal remains of a dozen ancient societies as they transitioned from foraging to intensive agriculture (Cohen and Armelagos 1984). These studies reveal much higher rates of nutritional and infectious disease stress among agricultural groups in comparison with their foraging predecessors. Although diet was not the sole factor (other major factors will be discussed later), skeletal evidence provides strong evidence that undernutrition was a major accomplice in the first major rise of infectious diseases as the primary cause of human mortality: the first epidemiologic transition.

Nutrition also played a major role when the same acute infections declined in high-income nations during the second epidemiologic transition. During industrialization in the eighteenth and nineteenth centuries, several of the world’s wealthiest nations experienced major declines in infectious disease mortality. This was particularly evident in England and Wales, where systematic records of births and causes of death were kept. These records show a major increase in life expectancy over the next 150 years (Omran 1971). But this was not mainly because people were living longer. Rather, more people were surviving to adulthood due to a decrease in mortality from childhood infectious diseases, like measles, pertussis (whooping cough), and smallpox – those same types of
acute epidemic conditions that had risen to prominence with agricultural intensification and remained as a major source of mortality for millennia. This same transition brought a major population increase, despite a decline in overall fertility. Several other European and North American countries experienced similar changes, and lower- and middle-income nations experienced similar, though less pronounced changes later in the twentieth century. These demographic and disease trends are also referred to as the “classic” epidemiologic transition (Omran 1971).

Many researchers have assumed that this transition was the result of new medical technologies, such as the development of antibiotics and vaccines. It is true that smallpox vaccination had a significant impact, especially in the earlier stages of the second transition (Mckeown 1976). But for the high-income nations which first experienced the transition, most of these declines occurred prior to the introduction of most major vaccines. Notably, they also declined prior to the discovery and distribution of any antibiotic, including penicillin.

In the near absence of these drugs, we must look for non-pharmacological determinants. While other factors, such as sanitation and housing, must have played significant roles, nutrition stands out among the candidates. This is primarily because the other factors varied over time and place, while nutritional improvements were consistently evident in other, dietary-related health trends such as increasing stature and declining age at first menstruation (Cole 2000). The co-occurrence of these trends in second transition nations strongly supports the nutrition argument, though it should be noted that it may not apply in low- and middle-income nations, where these changes happened after the introduction of antimicrobial medicines. Nevertheless, the first and second transitions provide important lessons for the role of nutrition in both the positive and negative sides of the epidemiological coin.

Turning our attention to the present day, it may be difficult at first to see how nutrition could play a role in the West African Ebola epidemic. We can reasonably assume that most of the infected American health-care workers were adequately nourished. But the infections in foreign health-care workers occurred during the later stages of the epidemic. When considering the earliest stages, the initial entry of the virus into a human population, we must focus on the vulnerability of the initial human hosts. Here, it is significant to note that the index case, or primary case, of the West African epidemic was an 18-month old Guinean boy from an impoverished village (WHO 2015). The child fits the common profile of undernourished and therefore immunocompromised people who often become the points of entry for pathogens making the initial leap from animal to human hosts (Anderson and May 1986).

The circumstances surrounding this index case point to another major factor in the epidemic’s emergence that is linked to human subsistence. The young boy lived in a remote village in the Guéckédou Prefecture of southern Guinea, an area known as the Forest Region (WHO 2015). Yet more than 80% of the surrounding forest has been destroyed by foreign timber and mining companies, resulting in
habitat disruption of local species. This includes the bat species that are thought to be a non-human reservoir of the Ebola virus (Pourrut et al. 2005). The boy was seen playing in a hollowed-out log that was populated with bats, and the genetic profile of the EVD strain that caused the West African epidemic makes it likely that animal-to-human transmission (rather than human importation) was responsible for the start of the epidemic (Gire et al. 2014).

Human–animal interactions have been implicated in the initial entry of many novel pathogens into human populations. We have seen this with the first epidemiologic transition, in which the domestication of animals brought humans into sustained contact with the potential hosts of non-human (i.e., zoonotic) infections (Weiss 2001). Most of the major infectious diseases that affect humans have their origins in non-human animals. Key examples include the measles virus, which evolved from the rinderpest virus in cattle, and the influenza virus, which originated in the guts of avian waterfowl that have either been variously domesticated themselves or have had regular interactions with other domesticated species (Alexander 2000; Furuse et al. 2010). In the ongoing third transition, there is evidence that the hunting of non-human primates for food, or bushmeat hunting, may result in animal-to-human transmission of novel blood-borne viruses (Wolfe et al. 2005). This practice is especially risky for humans, given the hazards of butchering closely related species with similar vulnerabilities to infectious pathogens. With this in mind, it is troubling to note that although non-human primates constitute 0.5% of all animal species, they have been the previous hosts and ongoing reservoirs of more than 20% of all human infections (Wolfe et al. 2007).

Bats are not primates, and they are not as closely related to humans. But the Guinean village situation shares many similarities with those communities engaged in bushmeat hunting insofar as they all represent recent settlements in remote areas. Residents of these settlements have migrated to earn a living from the larger scale resource extraction activities of timber production and mining. In this manner, the subsistence activities of the boy’s family placed him in close proximity with the bats, and larger economic forces drove his family into this mode of subsistence. Without considering these broader forces, any human–animal interactions, whether related to bats or bushmeat, could potentially degrade into just another exotic explanation. We will return to this issue when considering the role of social inequalities later in this chapter.

**Ebola and human settlement**

The biggest question about the West African Ebola epidemic is: why have there been so many more cases in this epidemic than in all of the previous epidemics? There are two potential places where we can look for the answer. The first is within the pathogen itself. Here, we can examine genetic sequences and biological traits and compare them with those of earlier viral strains. One trait worth examining is virulence. In previous Ebola epidemics, the viral infection produced
a very rapid progression of severe and clearly recognizable symptoms such that there was little opportunity for infected people to transmit the disease before either dying or recovering (Barrett and Armelagos 2013). Because of this high virulence, Ebola had little opportunity for onward transmission, making spectacular but brief flashes in human populations. These flashes are sometimes known as viral chatter, a phenomenon that occurs when a pathogen has evolved the necessary traits for animal-to-human transmission, but not yet to the degree that it can sustain transmission between human hosts (Wolfe et al. 2007).

Could it be that the strain responsible for the West African Ebola epidemic evolved to make us less sick, that it attenuated its virulence just enough so that humans could more easily and effectively transmit it to one another? Attenuation can certainly be an adaptive strategy for some pathogens, especially when the microbe can only survive within a single host species (Ewald 1983). When the pathogen can live in more than one host species, or sustain itself in non-physiological environments, such as through transmission by fomites, which are objects or materials that can carry infection, then increased virulence may be the more adaptive strategy insofar as the pathogen can disseminate more of itself (Ewald 1994). But evolutionary models are more complex than this, and the adaptive strategies must account for many additional factors (Bull 1994). Thus far, it appears that the Ebola strain responsible for the West African epidemic may be less virulent, but we must also account for differences in the health-care response and the overall sample size in this epidemic compared to the previous ones. This is the first time that researchers have observed transmission and virulence of any strain of EVD in a large human host population.

Setting aside the characteristics of the pathogen, we can turn to look in the second place: the host population. In the previous section, we considered within-host conditions with respect to nutritional status. But we have no evidence that the human hosts in West Africa were more or less malnourished than the Central African hosts of previous epidemics; indeed, we can reasonably assume that people in both regions are comparably poor and undernourished. But affected areas in West Africa are much more densely populated than those in Central Africa, and herein lies a potential explanation, one that can be illuminated by understanding the role of human settlement in the two previous epidemiologic transitions.

Returning to the Paleolithic, we know that the majority of foraging populations lived in small, widely dispersed bands that were at least seasonally nomadic. Hunting and gathering are not conducive to large and densely clustered populations. In the African savannas, where the earliest humans lived, contemporary hunter-gatherers require about 1 square mile per person to obtain an adequate diet from their local environments (Lee 1990). Such spacing requires that humans live in small, widely scattered groups, a principle that is supported in the archaeological record (Kelly 1995). A comparative study of 478 foraging
societies around the world reveals a median population of 30 people (Marlowe 2005).

When I teach this to students in my global health classes, I have them imagine that we are a band of Paleolithic hunter-gatherers. Our closest neighbors are 10 miles away, and we only see them a few times a year. I then have them imagine that one of us has somehow contracted a virulent and highly infectious disease. None of us has ever encountered it before and therefore, none of us would have any natural immunity. Under these conditions, the disease would quickly spread throughout our band, perhaps killing all or most of us. But even in this terrible scenario, there is little chance that we would infect our closest neighbors, with whom we rarely come into contact. The infection would be devastating for us, but it would not spread any further in the larger human population.

These settlement dynamics explain why acute infections would not have been prevalent in Paleolithic foraging societies. They also explain why the disease risk associated with game hunting, particularly of closely related organisms, like non-human primates such as found in modern bushmeat hunting and game hunting in the Paleolithic, would have little impact on these same societies. In contemporary times, even the most isolated communities that practice bushmeat hunting are nevertheless linked to larger social networks, especially if their settlement is due to large-scale, resource extraction industries. Not so in the case of Paleolithic foragers.

Comparing disease exposure in smaller versus larger and more densely settled societies, a classic study (Black 1975) found that several isolated indigenous Amazonian societies had comparable exposure to chronic viruses, such as herpes and Epstein–Barr virus, as suburban populations in the contemporary United States. But unlike their North American counterparts, the Amazonian groups had dramatically less exposure to acute infections, such as measles (Black 1975). A later study followed 19 unvaccinated Caribbean groups over 15 years, finding that measles outbreaks were self-limiting in populations of less than 500,000 people (Black 1966). The size and density of human settlements have a profound impact on the susceptibility of human populations to acute infectious diseases.

Finally, we can apply these settlement principles to historic examples. Specifically, we can examine how the changing living conditions experienced by industrializing, urbanizing societies may have impacted the decline of infectious disease mortality during the second epidemiologic transition. Until the mid-nineteenth century, urban areas in England and Wales expanded with little additional building and little change in basic infrastructure. Once again, nutritional changes most likely had the greatest impact on the declines in mortality from infectious disease during this initial period. But the steeper mortality declines occurred in the latter half of the 1800s, coinciding with major housing reforms (Burnett 1991). And the steepest mortality declines were seen when these housing improvements coincided with improved waste disposal and drainage, and increases in the availability of potable water. Applying these lessons to West Africa, we should not only think about the size and density of human settlements, but the manner in which they live.
Discussion and conclusion

An unequal conclusion
The lessons of epidemiologic transitions may be less exotic than the specter of zombie-like diseases in a spontaneously emerging pandemic. However, a global and deep time perspective reveals that these have been recurring themes in the evolution of human infections for the last 10,000 years. Moreover, it should be noted that social inequalities are inextricably linked to every one of these themes, especially in the global disease ecology of the present day. While we should take care not to valorize our Paleolithic past, it is nevertheless significant that small foraging groups do not lend themselves to the complex social hierarchies that we see in postagricultural societies. This is supported by studies of contemporary foraging groups, where essential living resources are more equally shared (Marlowe 2005).

Archaeology provides us with stark examples of social inequalities following the transition from mobile foraging to sedentism and agriculture, and even more so with the rise of state-level societies. For example, excavations of ancient Sudanese Nubian communities show an inverse relationship between life expectancy and the degree of political centralization, an important indicator of social inequality and power differences (Van Gerven et al. 1990). We can see social differences in the relative quality of graves and grave goods in the ancient, indigenous Dickson Mounds populations of North America following the intensification of agriculture. Here, excavations reveal that people buried in higher status graves had significantly greater life expectancies and fewer signs of nutritional and infectious disease stress than those buried in lower status graves. People tend to die the way they lived, and with social hierarchy, those lower in the hierarchy are in worse health, die younger, and do so under worse conditions.

Furthermore, these archaeological studies show that health inequalities are associated with declining health of populations as a whole. The same theme applies to mortality declines in the second transition, where we find that the reduction of health inequalities improved the status of entire populations, not just their poorest members. Extending this principle to the third transition, we can identify the best ways to prevent the emergence of new infections, such as Ebola, in high-income nations, by improving the health and living conditions of the most vulnerable populations in developing, low-, and middle-income nations.

Finally, it is only by taking a more holistic, biocultural approach to infectious diseases that we can discover and apply any of these lessons. It is not enough to simply examine the genetic make-up of viruses and bacteria, nor even the natural environments in which they occur. All infectious diseases are a product of host–parasite interactions in particular environments, and when the hosts are human, the disease environments are necessarily social and the products of human cultural activities. The biocultural lessons of Ebola will not only help us
to better understand the conditions that led to the recent West African epidemic, they will also help us to prevent the occurrence of future epidemics.

References


Notes

1 It should be noted that an index case of a disease may not be the actual first (primary) case of the disease. Rather, the index case is the earliest single case that can be determined by contact tracing methods. That said, the index case, and his or her subsequent contacts, provide important information about the earliest stages of an infectious disease epidemic.
CHAPTER 15

Beyond the differential diagnosis: new approaches to the bioarchaeology of the Hittite plague

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Introduction

Investigating the cause of an ancient epidemic requires gathering evidence from various disciplines to reconstruct the disease dynamics and fit clues from both ancient texts and human skeletons into population-based diagnostic models. In paleopathology, which is the study of ancient disease, differential diagnosis is generally applied to ancient skeletal individuals or samples to make inferences about bony lesions. This is accomplished by tallying all of the potential disease agents and eliminating them systematically based on similarities and differences to the study sample. In this chapter, we advocate expanding and incorporating the long established methods for differential diagnosis into population-based diagnostic modeling in order to investigate larger concepts of epidemic disease spread.

Specifically, we suggest an 11-step approach to investigating ancient epidemics wherein all possible causes are reduced to a single agent.

First, use historical texts from the specific time period of the epidemic(s) of interest to assemble evidence about the suspected disease’s dynamics and symptoms.

Second, use population-based diagnostic modeling to reduce the number of possible diseases that fit the description of the past epidemic(s) and use modern disease epidemiology specific to the given region to guide reconstruction of ancient disease dynamics in order to identify the most plausible disease.

Third, use theoretical models of ancient evolution of the disease, such as existing historical and molecular clock evidence, and the timeframe of the disease spread, to confirm the possibility that the selected disease could have been present in the region at the time.
Fourth, use historical descriptions of epidemics of the disease when it first appeared and of the disease’s impact on affected populations to confirm the capability of the hypothesized agent to cause the past epidemic(s) in question.

Fifth, use knowledge of the suspected disease vector’s behavior and ecology to confirm the past presence and behavior of the vector in question in the region.

Sixth, use reconstructions of ancient climate in the region to envisage how environments would impact the spread of the suspected disease.

Seventh, survey the published literature for established bioarchaeological methods that have been used to identify the suspected disease on skeletons from archaeological sites that are known to have been affected by the suspected disease, such as the analysis of ancient deoxyribonucleic acid (aDNA).

Eighth, compile data on frequencies of skeletal lesions from all published bioarchaeological reports in the region in order to estimate the disease’s spatiotemporal prevalence, or the proportion of the population that was infected over space and time, in the region.

Ninth, use established methods of paleopathological differential diagnosis in order to consider other potential diseases that could have caused the skeletal lesions in skeletal samples recovered from the region.

Tenth, analyze bone lesions present in individuals with antemortem, clinical diagnoses of the suspected disease curated in modern clinical skeletal samples from endemic areas, as well as skeletons from non-endemic areas, to identify skeletal indicators diagnostic of the disease.

And lastly, apply these refined indicators to the analysis of ancient skeletons recovered from archaeological sites in the region dating to the time of the ancient epidemic under consideration in order to determine the presence and prevalence of the suspected disease.

Using these 11 steps in the following sections, we present a case study of our investigation into the causes of the Hittite plague. A devastating epidemic hit the Hittite empire in 1322 BCE, which seemingly was carried by Egyptian prisoners of war captured along the Hittite–Egyptian border entering the Hittite capital (Bryce 1998; Singer 2002). The Hittites were an ancient civilization whose empire extended across Anatolia, or modern-day Turkey, between the seventeenth and twelfth centuries BCE. Many scholars have speculated about the disease responsible for this mysterious plague, but they have had no evidence with which to pinpoint the infectious agent. For example, a recent theory that the epidemic was tularemia, a severe infectious bacterial disease of animals (e.g., rabbits, hares, rodents) caused by Francisella tularensis, was subsequently refuted for lack of evidence (Martin-Serradilla and Guerrero-Peral 2008; Trevisanato 2007). In this chapter, we present a population-based diagnostic model approach embedded within a biocultural framework, which incorporates and considers both biological and cultural aspects of a given phenomenon, for solving this mystery. The paucity of Hittite burials from this time period (Emre 1991) has forced us to use Egyptian burials from the same time period recovered from the site of
Chapter 15: New approaches to the bioarchaeology of the Hittite plague

Amarna, Egypt, as a proxy or a representative sample that serves as a substitute for the absent sample, to identify the disease agent responsible for the Hittite plague.

Case study: investigating the cause of the Hittite plague

Step 1: Ancient Near Eastern texts

In the first step, historical texts from the time period of the epidemic are used to assemble evidence about the suspected disease’s dynamics and symptoms. The Hittite King Mursili II wrote a series of prayers in 1300 BCE pleading with the gods for relief from a widespread, 20-year epidemic that had already killed the two preceding kings and ravaged his subjects. The “Plague Prayers of Mursili II” reveal that this deadly epidemic was brought by Egyptian prisoners of war as they marched through the Hittite capital city (Singer 2002). However, for paleopathologists, the lack of recovered Hittite burials and the ancient Egyptian tendency to omit negative historical events in their records has made it difficult to identify the responsible disease.

Tumultuous events in Egypt leading up to 1322 BCE suggest that Egypt may have been stricken by the same epidemic disease as the Hittites. Specifically, Pharaoh Akhenaten suddenly changed the Egyptian religion and founded his new capital city of Amarna in a previously uninhabited area. Some scholars have attributed this abrupt religious and geographical shift to epidemic disease, perhaps even polio or bubonic plague (Kozloff 2006). Further dramatic changes followed in approximately 1332 BCE when Amarna was abandoned, scattering its occupants to the far reaches of the empire and, hence, possibly to the Egyptian–Hittite border. Along with the dispersal of people, any disease present at Amarna could also have been spread throughout the Egyptian empire, potentially affecting the Egyptian prisoners of war who were implicated as the source of the Hittite plague.

Step 2: Population-based diagnostic model of the Hittite plague

In the second step, population-based diagnostic modeling is used to reduce the number of possible diseases that fit the description of the past epidemic and use modern disease epidemiology for the region to guide reconstruction of ancient disease dynamics. A population-based diagnostic model of this epidemic must consider diseases thought to have plagued ancient Egyptians in addition to those diseases previously suggested by scholars to have caused the Hittite plague. Ancient Egyptian medical texts and well-preserved ancient Egyptian human remains are excellent sources for reconstructing ancient disease in the Near East. Paleopathologists have been working in Egypt for over a century, and
Table 15.1 Diseases potentially responsible for the Hittite plague.

<table>
<thead>
<tr>
<th>Disease</th>
<th>Mortality*</th>
<th>Demography*</th>
<th>Incubation*</th>
<th>Persistence*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Anthrax</td>
<td>High</td>
<td>All</td>
<td>1 day–2 months</td>
<td>Non-epidemic</td>
</tr>
<tr>
<td>Ascariasis</td>
<td>Low</td>
<td>All</td>
<td>None, often no symptoms</td>
<td>Non-epidemic</td>
</tr>
<tr>
<td>Bubonic plague</td>
<td>High</td>
<td>Higher risk in ages 12–45</td>
<td>7–10 days</td>
<td>Epidemic, or endemic with epidemic waves</td>
</tr>
<tr>
<td>Cholera</td>
<td>High</td>
<td>All</td>
<td>&lt;1–5 days</td>
<td>Epidemic/endemic</td>
</tr>
<tr>
<td>Hemorrhagic fever</td>
<td>High</td>
<td>All</td>
<td>2–21 days</td>
<td>Short-lived epidemics</td>
</tr>
<tr>
<td>Influenza</td>
<td>Low</td>
<td>Higher risk in infants, elderly</td>
<td>2 days</td>
<td>Seasonal epidemics</td>
</tr>
<tr>
<td>Malaria</td>
<td>High</td>
<td>All (on virgin ground)</td>
<td>10–15 days</td>
<td>Epidemic/endemic</td>
</tr>
<tr>
<td>Measles</td>
<td>High</td>
<td>Young children</td>
<td>10–12 days</td>
<td>Epidemic/endemic</td>
</tr>
<tr>
<td>Poliomyelitis</td>
<td>Low</td>
<td>Young children</td>
<td>7–10 days</td>
<td>Epidemic/endemic</td>
</tr>
<tr>
<td>Schistosomiasis</td>
<td>Low</td>
<td>Aquatic occupational risk</td>
<td>14–84 days</td>
<td>Endemic</td>
</tr>
<tr>
<td>Smallpox</td>
<td>Can be high</td>
<td>All</td>
<td>12–14 days</td>
<td>Epidemic</td>
</tr>
<tr>
<td>Typhoid fever</td>
<td>Low</td>
<td>Young adults</td>
<td>Weeks–years</td>
<td>Endemic</td>
</tr>
<tr>
<td>Typhus</td>
<td>Low</td>
<td>Domestic animal herding occupational risk</td>
<td>3–5 days</td>
<td>Non-epidemic</td>
</tr>
</tbody>
</table>

*General information on mortality, demography, incubation period, and persistence of the diseases sourced from the World Health Organization and Centers for Disease Control.

have established the existence of specific diseases at particular points in time. Similarly, solving the mystery of the Hittite plague has been a popular pastime of scholars who have championed a wide range of hypothetical diseases (see Table 15.1).

We use evidence of disease dynamics suggested by ancient texts to reduce the list of potential causes of the Hittite epidemic. Several details are key. For one, Mursili II blames the Egyptians for causing the plague, which means that the prisoners of war must have exhibited symptoms soon after they were brought into the city. The disease also spread quickly, infecting and killing the king, Suppiluliuma I, and his first son and successor, Arnuwanda II, within one year. Additionally, Mursili II identifies the age groups affected by the plague in his third plague prayer (Singer 2002:58):
For twenty years now people have been dying [in great numbers] in Hatti… Hatti has been very much oppressed by the plague. [If someone] produces a child, [the …] of the plague [snatches (?)] it from him. Should he reach adulthood, he will not attain old age. [And even if old age (?)] will be left for someone, he [will be oppressed (?) by] the plague. He will not [return] to his previous condition. When he reaches old age, [he will …], but he will not keep warm.

We know that the disease spread rapidly after the prisoners entered the city, and that infection with the disease was not dependent upon age or class. The texts do not mention specific symptoms, but we know the disease was deadly and persisted for 20 years. The prisoners showed no obvious symptoms until after entering the city, suggesting a long incubation period.

Next, we removed the diseases from Table 15.1 that do not fit the dynamic described by Mursili II. It is important to make uniformitarian assumptions about the nature of disease, specifically assuming that the disease-causing organisms have not changed in their behavior or virulence, even though we know that diseases can and do in modern times evolve in response to human-induced changes to their environment (Cohen and Crane-Kramer 2003). It is also possible that the disease responsible for the Hittite epidemic no longer exists or at least no longer infects humans. Nevertheless, we must make these assumptions because we simply do not have evidence of how each of these pathogens may have behaved differently in the past.

We were able to remove several diseases. Naturally acquired anthrax, most commonly the cutaneous form, tuberculosis, poliomyelitis, ascariasis, which is a parasitic roundworm infection, and schistosomiasis, which is a parasitic blood fluke infection, are unlikely to have been responsible for the massive death toll among the Hittites. This is because today they do not cause fast-spreading, deadly epidemics (CDC 2014; Hamborsky et al. 2015; WHO Expert Committee 2002; World Health Organization 2008). Conversely, viral hemorrhagic fevers, such as Ebola, are transmitted too easily and kill too many too quickly to ravage Hittites for 20 years (CDC 2015).

We also removed tularemia from our list. While it has been suggested as the cause of the Hittite plague (Trevisanato 2007), it was later discounted because of inconsistencies between known characteristics of the Hittite plague and modern epidemics of tularemia (Martin-Serradilla and Guerrero-Peral 2008). We add here that tularemia’s incubation period of 3–5 days and tendency to be occupation specific (e.g., shepherds) make it incongruous with transport by the Egyptian captives.

Lastly, we removed the diseases that do not fit the demographic profile; Mursili II wrote that the disease causing the Hittite plague did not discriminate against age or class. Therefore, we removed bubonic plague, influenza, and measles from our list (see demography column in Table 15.1) as they have a higher risk of infection for people between the ages of 12 and 45 years, infants and the elderly, and young children, respectively. Cholera certainly has the potential to cause a major, long-lasting epidemic, but it does not fit our model because it has
a very short incubation period of 1–5 days and its symptoms of severe diarrhea and dehydration would have been noticed as the Egyptians were marched from modern-day Syria to central Turkey. Smallpox is an excellent candidate as it affects all members of society, and the incubation period of approximately two weeks is long enough to allow travel to central Turkey before causing symptomatic illness or death. Nonetheless, smallpox was eliminated because we would expect to see its characteristic lesions – large fluid-filled blisters covering the entire body, which leave noticeable scars on survivors – mentioned in the Hittite texts. Typhoid fever, a bacterial infection, is another probable candidate as it was proposed as a cause of the Plague of Athens in 430–426 BCE (Papagrigorakis et al. 2006; but see critique by Shapiro et al. 2006). However, this disease is associated with poor sanitation, and the Hittites had strict rules regarding hygiene and cleanliness, especially concerning water, and most particularly for the king (Bryce 2004). This makes it unlikely for two kings to have died of typhoid. Lastly, we removed epidemic typhus, another bacterial disease, which is known to flourish under wartime conditions due to its spread by human lice. However, it is hard to imagine the king having been infected by lice directly from the prisoners of war. Typhus only survives within the living cells of lice or humans, so it is typically passed from bodily contact or from infested clothing (McQuiston 2016). Finally, we come to malaria, the last on our list of suggested sources. Malaria is caused by protozoal parasites of the genus Plasmodium transmitted by the Anopheles mosquito vector. There are at least four Plasmodium species known to affect humans, all differing in their disease ecology (see Table 15.2). The two species of major global importance which have the greatest impact on human health today are Plasmodium falciparum and Plasmodium vivax (Webb 2009). Malaria seems to fit all of the disease dynamic and population conditions of the Hittite plague, and was likely present in the ancient Near East. However, only the milder P. vivax species (Hershkovitz et al. 1991; Hume et al. 2003) has the ability to remain dormant in the liver of its host, and thus sustain itself during cold winter seasons, which are common in modern-day central Turkey, when its mosquito vector cannot survive. P. falciparum, the more deadly form of malaria, does not have this ability to relapse from the liver stage. Thus, warmer and wetter conditions than those found in modern-day central Turkey would be required for this species to have sustained the Hittite plague. Malaria does not discriminate against class, as demonstrated by recent ancient DNA studies of the Pharaoh Tutankhamun, who likely grew up at Amarna, Egypt, which revealed that he was co-infected with two strains of falciparum malaria at the time of his death (Hawass et al. 2010). Having eliminated all the other suggested causes of the Hittite plague, we probe further into the possibility of malaria being the culprit.

**Step 3: Theoretical models of malaria origin and spread**

In the third step, theoretical models of ancient evolution of the disease are used to confirm the possibility that the disease could have been present in the region
Table 15.2  Comparison chart of malaria species ecology*.

<table>
<thead>
<tr>
<th>Species</th>
<th>Global importance</th>
<th>Host</th>
<th>Incubation (avg.)</th>
<th>Relapse?</th>
<th>Fever wave freq.</th>
<th>Disease consequences</th>
<th>In utero infection?</th>
<th>Postpartum antibodies?</th>
<th>Required temp (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>P. falciparum</em></td>
<td>Major</td>
<td>Humans</td>
<td>12 days</td>
<td>No</td>
<td>Every 48 hours</td>
<td>Severe anemia, cerebral malaria</td>
<td>Yes</td>
<td>Yes</td>
<td>&gt;19</td>
</tr>
<tr>
<td><em>P. vivax</em></td>
<td>Major</td>
<td>Humans</td>
<td>15 days to 6–12 mo.</td>
<td>Yes</td>
<td>Every 48 hours</td>
<td>Increasingly severe anemia</td>
<td>Yes</td>
<td>No</td>
<td>&gt;15</td>
</tr>
<tr>
<td><em>P. ovale</em></td>
<td>Minor</td>
<td>Humans</td>
<td>17 days</td>
<td>Yes</td>
<td>Every 48 hours</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>P. malariae</em></td>
<td>Minor</td>
<td>Humans, Humans + African apes</td>
<td>18–40 days</td>
<td>No</td>
<td>Every 72 hours</td>
<td></td>
<td></td>
<td></td>
<td>(Tropical)</td>
</tr>
</tbody>
</table>

*Chart based on malaria species ecology from Webb’s (2009) Humanity’s Burden.
at the time of the epidemic. Most literature discussing the history of malaria cite Bruce-Chwatt and de Zulueta’s (1980) theory that falciparum malaria only arrived in Europe during the Roman Empire. They discount the textual and physical evidence of falciparum malaria, and insist that it could not have existed because they believed the *Anopheles* mosquito vectors were not present. Even in ancient Egypt where the warm climate and riverine urban landscape were undoubtedly well suited for malaria, de Zulueta (1987) claims that an effective mosquito vector – an *Anopheles* species whose biting behavior favors malaria transmission to humans – was absent.

Sallares and co-workers (2004) argue for a slightly earlier spread of malaria, possibly extending back to 700 BCE. They speculate that epidemics of falciparum malaria spread simultaneously with the migration of the mosquito, *Anopheles sacharovi*, into Greece and Italy from Tunisia. This hypothesis suggests that malaria spread gradually in Europe as these mosquitoes slowly migrated, but it does not consider that mosquitoes can, and often do in modern times, hitch rides on sea-faring vessels to arrive in new areas at the same time as their human hosts (Bataille et al. 2009; Guagliardo et al. 2015).

In contrast to historic reconstructions, genetic analyses indicate that falciparum malaria evolved in Africa anywhere between 5000 and 3 million years ago (Datta and Chauhan 2010), but the young age (less than 5000 years) of genetic variations that confer resistance or immunity to malaria suggests a more recent evolution of malaria, perhaps coinciding with the origins of agriculture between 10 000 and 5000 years ago (Hedrick 2012). This association with agriculture further suggests that malaria must have used the Nile River corridor with its early agricultural settlements to leave Africa for Europe and Asia.

**Step 4: Modern recorded malaria epidemics**

In the fourth step, historical descriptions of epidemics of the disease when it first appeared and its impacts in these early epidemics are used to confirm the capability of the hypothesized agent to cause the epidemic in question.

In reconstructing the past spread of malaria and modeling its population dynamics during past epidemics, we used historical records from well-documented epidemics. Historical malaria epidemics suggest generally devastating health effects in non-immune, naive populations experiencing the parasite for the first time. One such epidemic occurred on the north-west Coast of the United States in the 1830s. Detailed record keeping by the affected European settlers enabled historians to track down the exact person who carried the parasite on the specific ship that came into Portland, Oregon, in 1830 (Boyd 1999). With Oregon’s already substantial population of *Anopheles* mosquitoes, this one infected traveler spawned a five-year seasonal epidemic of malaria. Although Europeans were hard-hit during these yearly epidemics, the indigenous populations, who did not have access to the standard cinchona bark, or quinine, treatment, were ravaged by the disease (Boyd 1999). There is
no information as to which species of malaria caused the 1830s epidemic but in recent times, multi-year malaria epidemics caused by \textit{P. falciparum} entering a naive population have been well documented, such as in the Isthmus of Panama (Calzada \textit{et al.} 2008). There, during an epidemic in 2005, nearly half of the indigenous Kuna community of Chepo became infected before the Panamanian health officials could intervene (Shah 2010).

We employed the disease dynamics of these historical epidemics to identify the defining elements of past epidemics. Primarily, just one infected person migrating into a new area can spread malaria, as long as the area has a substantial anopheline mosquito population. Secondly, the absence of biological immunity plays a large part in the duration and virulence of the epidemic. Lastly, climate is an intrinsic factor in the ability of an epidemic of falciparum malaria to gain a foothold in a population, because it determines the dynamics of mosquito ecology.

\textbf{Step 5: Entomology of the malaria vector}

In the fifth step, knowledge of the suspected disease vector’s behavior and ecology is used to confirm the past presence and behavior of the vector in the region in question. The successful spread of malaria to new locations depends upon the existence of a substantial population of \textit{Anopheles} mosquito, and at least one human who is infected with malarial \textit{Plasmodium} (Sherman 1998). Each species of \textit{Anopheles} mosquito has its own preference for temperature and altitude range. Thus, different geographic locations tend to have different dominant malaria vector species. Some species do not enter man-made structures whereas others do, especially at night, making the latter a much more effective malaria vector than the former (Sherman 1998). Mosquitoes that prefer to bite humans instead of animals, known as anthropophilic mosquitoes, are much more likely to transmit malaria than those which prefer to bite other animals.

In the Near East, the dominant malaria vector species include \textit{An. sacharovi}, \textit{An. sergentii}, and \textit{An. superpictus} (Sinka \textit{et al.} 2010). \textit{An. sacharovi} is the most important malaria vector species in modern Turkey, and its current habitat ranges from coastal areas bordering the Mediterranean Sea in Greece, throughout Turkey, to coastal areas bordering the Black Sea. \textit{An. sacharovi} has several behavioral advantages for successful malaria transmission. It will breed in stagnant fresh water or brine, is found at elevations up to 1720 m, and has an incomplete hibernation during winter; thus, it is able to cause new cases of malaria all year round (Alten \textit{et al.} 2000). This year-round transmission is especially important when considering the plausibility of \textit{P. falciparum} malaria causing the Hittite plague because this parasite does not have the ability to remain dormant in the liver, unlike \textit{P. vivax} (Sherman 1998).

In sum, in order for malaria to have spread throughout the Near East, a substantial anthropophilic mosquito vector population size must have been maintained by optimal temperatures, elevation, and breeding grounds. Once these
conditions are met, transmission spawning an epidemic is possible when even a single human with malaria enters a new area.

Step 6: Paleoclimate of the Near East
In the sixth step, reconstructions of ancient climate in the region are used to envisage how environments would impact the spread of the suspected disease. Fossilized pollen and charcoal analyses from a lagoon in the Nile Delta indicate that the climate in the ancient Near East was very moist and humid from 6000 to 3500 BCE during the expansion of city-state societies (Bernhardt et al. 2012). After approximately 500 years of fluctuating rainfall, the climate became drier around 2800 BCE, likely involving droughts that negatively impacted ancient peoples (Kaniewski et al. 2013). This drier climate meant greatly decreased mosquito populations, probably only surviving in the Nile River floodplain and delta region. However, this drought was alleviated briefly by periods of increased rainfall between 1500 and 1100 BCE (Bernhardt et al. 2012). Thus, an increased mosquito population size and range in the Near East were possible during this wetter period that also encompassed the Amarna period and the Hittite plague.

Step 7: Skeletal indicators of malaria
In the seventh step, the published literature is surveyed for bioarchaeological methods that have been used to identify the suspected disease on skeletons from archaeological sites where the condition was present. Malaria is often dismissed in the differential diagnosis of pathological skeletal lesions by bioarchaeologists and paleopathologists because many think that the disease does not manifest itself upon the skeleton (Nunn and Tapp 2000; Roberts 2000). Genetic conditions conferring resistance to malaria, such as thalassemia and sickle cell disorder, have been suggested as causes of skeletal lesions such as porotic hyperostosis (PH) and cribra orbitalia (CO), porous lesions found on the cranial vault and eye orbits, respectively (Angel 1966, 1972). However, these genetic disorders, which are maintained at low frequencies, cannot explain findings of uniformly high rates of these skeletal lesions within ancient skeletal samples. Consequently, etiological theories have shifted toward iron deficiency anemia as the main cause of these lesions, and paleopathologists shifted their attention from the potential presence of malaria to dietary stress associated with agriculture (Stuart-Macadam 1987).

Attention slowly came back to malaria with advances in aDNA extraction from skeletal and mummified human remains. Many researchers have been successful in isolating the aDNA of *P. falciparum* in Egyptian mummified tissue and determining the presence of malaria (Bianucci et al. 2008; Hawass et al. 2010; Miller et al. 1994; Nerlich et al. 2008). However, this method is costly and therefore not routinely performed on entire skeletal assemblages. Thus, aDNA can be used to detect presence but not prevalence of the disease in a past population.
Rabino Massa and co-workers (2000) tested ancient Egyptian mummies for malarial aDNA. Of those positive for falciparum malaria, 92% had PH and CO. Their study provides a link between direct evidence for malaria and these lesions, which were previously associated with iron deficiency anemia. Further, Walker and co-workers (2009) reasoned that iron deficiency anemia, long held to be the main cause of PH and CO, could not in fact produce the bone marrow hypertrophy responsible for these lesions. Instead, they pointed to megaloblastic and hemolytic anemia. Megaloblastic anemia arises in individuals with a nutritional deficiency in vitamin B12, or folic acid, and hemolytic anemia arises in individuals with some genetic disorders conferring protection from malaria, as well as in individuals with a malaria infection.

Building on the previous two studies, Gowland and Western (2012) mapped and associated CO with the distribution of large populations of *Anopheles* mosquitoes, lower altitude, marshy environments, and higher incidence of historic “fever and ague,” an archaic term for malaria, across Great Britain. They found a correlation between malarial infection and CO, supporting the hypothesis that malaria manifests itself in the skeleton. Despite these results, much is still unknown about the etiology of these skeletal lesions. At the very least, multiple factors apparently lead to their manifestation, such as nutrition and parasitic infection, which could include malaria (Holland and O’Brien 1997; Walker *et al.* 2009; Wapler *et al.* 2004). Multiple lines of evidence must be employed to establish the skeletal manifestations of malaria for the purposes of differential diagnosis, including postcranial evidence of severe anemia and a demographic bias towards women and young juveniles in a given skeletal sample – malaria produces highest mortality in pregnant women, who lose acquired immunity during pregnancy, and children under the age of five (Gilles *et al.* 1969; World Health Organization 2007).

**Step 8: Spatial epidemiology of cribra orbitalia at Nile Valley archaeological sites**

**Methods**

In the eighth step, data on frequencies of skeletal lesions from all published bioarchaeological reports in the region are compiled in order to estimate the disease’s spatiotemporal prevalence in the region. The connection between CO and malaria suggested by previous studies (Gowland and Western, 2012; Rabino Massa *et al.* 2000) prompted the first author to survey CO frequencies in the ancient Nile Valley using published reports (Smith-Guzmán 2015a). This study tested Sallares and co-workers’ (2004) theoretical model for the spread of malaria up the Nile Valley and out of Africa using the variability of CO frequencies. This analysis surveyed reports from 29 ancient Nile Valley sites, representing 4760 individuals ranging from prehistoric to Christian periods (4400 BCE–1500 CE) and situated between upper Nubia and the Nile delta.
Results
Generally, high rates of CO (between 10.8% and 78.7%) existed at each of the sites, with an overall mean of 42.8%. The Nile Valley samples had greater overall rates of CO compared with CO meta-analyses from other regions. There was no significant correlation with geographical location or time, suggesting that high levels of hemolytic or megaloblastic anemia affected individuals in the Nile Valley equally from predynastic to Christian times. No association was found between the frequency of CO and the proportion of individuals under 18 years of age or the proportion of females versus males.

The gradual increase in CO over space and time that was hypothesized was not confirmed and the following interpretations were made. First, contrary to small-scale comparisons between Nile Valley sites, CO did not increase or decrease in frequency but stayed prominent over time. Second, the failure to associate the high CO rates with age suggests that the main cause was not age specific, like diet, exposure to parasites, or nutritional stress caused by weaning. Lastly, assuming that CO is indicative of malaria infection, an assumption derived from Gowland and Western (2012), then it must have been endemic long before the unification of Egypt. This interpretation is supported by aDNA evidence (Hawass et al. 2010; Nerlich et al. 2008; Rabino Massa et al. 2000).

These results rely on the assumption that the hemolytic anemia caused by malaria is responsible for high CO rates; the other causes of CO cannot be eliminated. A clinical comparison using a modern skeletal collection from an endemic malarial area is necessary to identify specific skeletal lesions associated with malaria using the differential diagnosis approach.

Step 9: Differential diagnosis for anemia in Egypt
In the ninth step, established methods of paleopathological differential diagnosis are used to consider other potential diseases that could have caused the skeletal lesions in samples recovered from the region. The high frequencies of CO indicating severe anemia (Hillson 1980) have prompted scholars to suggest a number of causes, including schistosomiasis, intestinal parasites, dietary deficiencies, brucellosis, and malaria. The presence of schistosomiasis in ancient Egyptians is well evidenced from preserved eggs in mummies, as well as from ancient textual references reporting characteristic symptoms such as bloody urine (Brier 2004). To test relationships between CO, PH, and schistosomiasis in the past, Alvrus (2006) compared CO and PH rates with tissue samples positive for an antigen indicating schistosome infection in ancient Nubians. She found a lack of association between these lesions and schistosome infection. This was particularly true for juveniles, who exhibited the greatest percentage of cranial with these lesions. Alvrus interprets this disparity as evidence that other factors were more important causative agents of anemia than schistosomiasis. However, as others have noted, individuals can be co-infected with
schistosomiasis and other diseases, increasing infection intensity and general anemia (Campbell Hibbs et al. 2011).

Hookworms, parasites which are common in modern tropical areas, cause blood loss, chronic diarrhea, and vitamin deficiencies, and are notorious causes of iron deficiency anemia (Hengen 1971). This type of anemia reduces the production of red blood cells, however, making it unable to cause the expansion of marrow space seen in PH and CO (Walker et al. 2009). The malabsorption of nutrients, particularly vitamin B12, due to chronic diarrhea can cause megaloblastic anemia and osseous expansion of marrow spaces. This prompted Walker and co-workers (2009) to suggest that megaloblastic anemia was the cause of PH and CO in some ancient contexts, such as the ancient North American south west. However, in the modern era, megaloblastic anemia due to vitamin B12 deficiency comprises a miniscule proportion of the total anemia worldwide (Kassebaum et al. 2014).

Brucellosis is a bacterial zoonotic infection commonly passed from domestic cattle to humans through ingestion of raw milk, and causes undulating fevers, as well as hemolytic anemia in some cases (d’Anastasio et al. 2011). Importantly, brucellosis existed in the ancient Mediterranean and Near East. Therefore, we postulate that anemia from brucellosis could induce marrow space expansion. However, modern epidemiological studies of regions where brucellosis is endemic indicate that its prevalence in humans tends to be low, affecting less than half as many humans as cattle, even among high-risk occupational groups such as dairy farmers (Lopes et al. 2010). Considering that not all brucellosis infections will result in anemia severe enough to cause skeletal lesions, it is unlikely that high rates of skeletal anemia can be attributed to brucellosis. Having excluded the above, the major cause of anemias in the Near East producing skeletal changes is most likely malaria.

Malaria is an unbiased infection – one that affects all members of a population – and causes hemolytic anemia, which has been linked with PH and CO. Malarial anemia is more severe in individuals without acquired immunity, including young children, pregnant women, and recent immigrants to a given region where malaria is endemic who have no acquired immunity. In addition to the classic model of skeletal anemia by expansion of marrow space, recent research has suggested that hemolysis during the schizogony phase of malaria infection – wherein parasites burst out of and destroy host red blood cells – may contribute to widespread porous skeletal lesion formation. This may occur due to release of acid phosphate, free heme, and the malarial pigment hemozoin from the red blood cells into the host’s bloodstream. This may lead to an imbalance in bone remodeling by stimulating osteoclasts, preventing bone resorption, while simultaneously impairing osteoblasts, preventing bone formation (d’Souza et al. 2011; Moreau et al. 2012). Furthermore, severe malarial anemia may induce extramedullary erythropoiesis, the production of red blood cells outside the bone marrow, which is known to cause thinning of bone cortex and coarsening of the spongy, or trabecular, bone (Al-Aabassi and Murad 2005).
**Step 10: Epidemiological approach to skeletal lesions through clinical samples**

**Methods**

In the penultimate step, bone lesions in skeletons with antemortem, clinical diagnoses of the disease from endemic regions and those from non-endemic regions are evaluated to identify diagnostic indicators with a high degree of certainty.

The first author compared skeletal lesions in a modern reference sample from Uganda, where malaria is holoendemic, or ubiquitous, to a similar modern sample from a malaria-free area (Smith-Guzmán 2015b). The goal was to record all porous lesions of the cranial and postcranial skeleton that might be associated with anemia (Djuric *et al.* 2008; Gowland and Western 2012; Rabino *et al.* 2000), but also other markers of specific or non-specific infection, such as periosteal reactions, which are areas of subperiosteal bone deposition; linear enamel hypoplasias, which are linear defects in the dental enamel caused by growth arrest from physiological stress during dental development in childhood; and periodontal disease, resorption of the bone tissue surrounding the teeth due to gum disease (gingivitis). The data collection proceeded in three phases: (1) individuals whose known cause of death was malaria or anemia, (2) individuals with other causes of death with the same age, sex, and tribal group as the malarial/anemic individuals, and (3) all remaining individuals with crania present. Because of this phased approach, the resulting data are comparable to modern epidemiological matched case/control studies and were analyzed as such.

**Results**

Five porous skeletal lesions were identified that appear more frequently in the Ugandan sample, especially in anemic individuals (Figure 15.1). These included CO, PH, and spinal porosity, consisting of porous lesions on the vertebral and sacral bodies; and cribra (porous lesions) on the humeri and femora. Frequencies of periosteal reactions were also higher in the malarial sample; however, linear enamel hypoplasias were conversely associated in this sample. Next, interlesion associations were examined, and epidemiological methods for determining the diagnostic certainty of a given lesion to a given disease condition (Boldsen 2001; Pinhasi and Turner 2008) were applied. Several lesions were confirmed as useful indicators of malaria: CO, humeral cribra, femoral cribra, spinal porosity, and periosteal reactions. These were combined into an outcome algorithm in order to diagnose individual skeletons for which their malarial status – negative or positive – is unknown. Based on this algorithm, if an individual has at least one of the cribrous lesions and either spinal porosity or periosteal reactions, the individual is diagnosed as positive for malaria. Without them, the individual is diagnosed as negative.
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Cribra orbitalia
Porotic hyperostosis
Humeral cribra
Femoral cribra
Spinal porosity
Periostitis
Alveolar resorption
LEHs

Non-anemic
Anemic

Figure 15.1 Comparison of skeletal lesions in Ugandans who died of anemia and those who died of other causes.

Step 11: Application of refined criteria to Amarna skeletons

Methods
In the final, 11th step, these refined indicators are assessed in skeletons recovered from archaeological sites in the region dating to the time of the ancient epidemic in order to determine the presence and prevalence of the suspected disease.

We analyzed 417 skeletons from the South Tombs Cemetery, which was utilized during the Amarna Period, 1349–1332 BCE, for the skeletal indicators of malaria identified above in order to determine the probability that malaria might have caused the Hittite plague. The cemetery is located in a dry channel, or wadi, next to the elite South Tombs carved into the cliffs. It was excavated in roughly four sections to sample the possible differential burial practices. These sections of the cemetery seem to have been populated in chronological order as follows: the oldest, the Wadi Mouth Site, Lower Site, Middle Site, and the youngest Upper Site. Excavations merged the Wadi Mouth and Lower Sites and they are considered as a single unit.

Results
Frequencies of skeletal indicators of malaria at Amarna tended to fall between those of the malarial and the non-malarial frequencies, as shown in Table 15.3.
Applications of the diagnostic outcome algorithm for skeletal indicators of malaria predicted a high prevalence of malaria amongst the Amarna skeletons, with around 50% of individuals showing signs of recent infection.

The frequency of malarial indicators at Amarna could mean several things. First, it could indicate an epidemic of malaria late in the site’s occupation, thereby affecting only a subset of the population in the cemetery. Alternatively, this could represent the difference between endemic and epidemic malaria. Epidemic malaria would tend to kill its victims before their bodies began to evidence severe malarial anemia, while endemic malaria would produce more chronic anemia. In order to elucidate the nature of malaria at Amarna, the demography of the site as it relates to disease patterns in modern endemic and epidemic malaria must be considered.

In the demography of the Amarna South Tombs Cemetery, the largest age group (160 skeletons or 44% of the sample) contains juveniles under the age of 16 (Figure 15.2). Further, 59% of the 206 adults of determined sex are female

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**Table 15.3** Frequencies of skeletal anemia at Amarna compared with modern malarial/non-malarial reference samples.

<table>
<thead>
<tr>
<th></th>
<th>Amarna</th>
<th>Malarial</th>
<th>Non-malarial</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cribra orbitalia</td>
<td>81 (40%)</td>
<td>33 (57%)</td>
<td>1 (2%)</td>
</tr>
<tr>
<td>Humeral cribra</td>
<td>5 (4%)</td>
<td>21 (24%)</td>
<td>2 (5%)</td>
</tr>
<tr>
<td>Femoral cribra</td>
<td>47 (17%)</td>
<td>37 (39%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Spinal porosity</td>
<td>32 (100%)</td>
<td>84 (89%)</td>
<td>9 (18%)</td>
</tr>
<tr>
<td>Periostitis</td>
<td>60 (19%)</td>
<td>51 (52%)</td>
<td>9 (17%)</td>
</tr>
</tbody>
</table>

**Figure 15.2** Amarna age-at-death frequencies by group.
Multiple burials, which increased incrementally over time during the cemetery’s use (Figure 15.4), were more likely to contain females than males. Stature for females also decreased incrementally over time (Figure 15.5), whereas male stature was more variable across the cemetery.

Several interpretations derive from these differences. First, the pattern of progressively more multiple burials suggests a gradual increase in the number of

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**Figure 15.3** Sex frequencies at Amarna’s South Tombs Cemetery.

**Figure 15.4** Frequencies of multiple burials by section of the South Tombs Cemetery at Amarna.
people dying simultaneously during the Amarna period. Second, since females tended to be buried in multiple burials more frequently than males, and they also declined in stature across the cemetery, we infer that the health of women at Amarna was impacted to a greater degree than that of men. Additionally, juveniles under the age of 16 are abundant at the site in general, with a greater proportion of those under the age of five (Figure 15.6). In sum, the demographic patterns at Amarna seem to indicate a health-related preferential mortality burden for women and children.

Figure 15.5 Female stature differences at Amarna by site.

Figure 15.6 Childhood age at death at Amarna.
Our Amarna data match most closely with endemic malaria, with a 50% estimated prevalence based on skeletal indicators of malaria and greater morbidity and mortality falling on non-immune juveniles and reproductive-age females. This interpretation is reinforced by our spatial comparison of CO, which shows that ancient Egypt yielded high rates of anemia throughout time and space, and by Tutankhamun’s multiple strain malaria infection. We plan to further confirm these findings of endemic malaria at Amarna by testing some of the anemic skeletons from the site for \textit{P. falciparum} DNA.

\textbf{Discussion and conclusion}

Through our case study, we have demonstrated that the climate, parasite and vector ecology, and historic data all suggest that at least one Egyptian prisoner of war taken to the Hittite capital could have harbored malaria in his veins, spawning the 20-year epidemic. Further, through spatial epidemiology and clinical evidence, combined with skeletal analysis of a sample from Amarna, we have presented evidence that malaria had a high prevalence and wide impact on the population living in the Egyptian capital city during the Amarna period and that the abandonment of Amarna and the scattering of its population could easily have supplied the infected individuals who initiated the Hittite plague.

We have shown that investigating an ancient epidemic must go far beyond the differential diagnosis of individual skeletons and employ population-based diagnostic modeling. Consideration must be given to the intrinsic intertwining of relationships between pathogen, vector, and host, as viewed within a biocultural framework. Evidence from many other disciplines including epidemiology, climatology, and history demonstrates that both biology and culture impact the way humans experience epidemic disease. Bioarchaeologists can say much more about ancient health and disease when we break outside of our discipline to incorporate knowledge and methods from related fields of study.

\textbf{Acknowledgments}

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CHAPTER 16

Paleoepidemiological and biocultural approaches to ancient disease: the origin and antiquity of syphilis

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Introduction

During Charles VIII’s siege of Naples, Italy, in 1495, a terrible new disease broke out among the French king’s troops and the prostitutes who accompanied them. Contemporary chroniclers described boils as big as acorns that burst and left scabs, terrible joint pain, rotting flesh, a revolting odor, and a high rate of mortality among sufferers. Overall, scholars agree that the disease they described represents the first recorded epidemic of acquired syphilis (Crosby 1972; Quétel 1990). Over time, descriptions of syphilis shifted from this highly virulent foe to a disease more closely resembling the infection that we are familiar with, which is chronic, debilitating, and highly destructive if it progresses to the final stage of infection, but typically progresses slowly (Quétel 1990).

At the same time, syphilis quickly spread around the world. By the turn of the twentieth century, for instance, approximately 10% of the residents of London, 15% of Parisians, and 20% of United States Army recruits were infected with syphilis (Hayden 2003). The bacterium responsible for syphilis, Treponema pallidum subsp. pallidum, was identified in 1905, and with the advent of antibiotics, the prevalence of syphilis plummeted throughout the twentieth and twenty-first centuries. Today, approximately 11 million people are infected with syphilis each year worldwide, with the highest number of cases reported in low-income nations (WHO 2012, 2013). Even in the United States, however, syphilis has been on the rise in recent years; between 2013 and 2014, the rate of reported primary and secondary syphilis increased 15%, to 6.3 cases per 100,000 people, and the rate of congenital syphilis rose 28%, to 12 cases per 100,000 live births (CDC 2015).
Since the first recorded epidemic, debate as to the origins and antiquity of syphilis has exercised disciplines as diverse as biological anthropology, history, and microbiology (Meyer et al. 2002). Although many explanations have been proposed for the disease’s history, there are two primary theories. Because the epidemic began shortly after the return of Christopher Columbus and his crew from the voyages of discovery to the New World, the theory that syphilis originated in the Americas had become common in popular and medical literature by the early sixteenth century (Crosby 1969). This view persisted over the next 400 years, undergoing various iterations during the twentieth century. It is now known as the Columbian hypothesis. The most recent version states that acquired syphilis evolved in the Old World from a non-sexually transmitted treponeme transmitted from the New World during early European expansion and colonization (Armelagos et al. 2005; Harper et al. 2008). This theory is supported by fifteenth- and sixteenth-century accounts of syphilis’s rapid spread throughout Europe, and the extreme virulence of the pathogen during the early years of the epidemic, which several scholars have argued indicates a new infectious disease exposed to epidemiologically “virgin soil” populations (Hudson 1963; Knell 2004).¹

In the nineteenth century, scholars began to critique this theory, with some arguing that syphilis was present in the Old World before Columbus’s return. These arguments crystallized into the Pre-Columbian hypothesis, which proposes that syphilis, or a closely related treponeme, was present in Europe prior to the 1490s (Hackett 1963, 1967; Holcomb 1934, 1935). According to this theory, the disease was very mild or confused with other similar conditions; it was only recognized as a distinct entity in the 1490s because of a surge in virulence (Waldron 2009) or improved medical and lay recognition of syphilis, possibly facilitated by the introduction of the printing press (Kampmeier 1984). Several researchers have given this explanation a biocultural twist by proposing that sexually transmitted treponemes evolved in response to the social, cultural, and environmental changes that humans have experienced since the Pleistocene, such as increased population density and urbanization (Brothwell 1981; Cockburn 1961; Hackett 1963; Wilcox 1972).

Due to concerns with the limitations of historical documents and ethnographic data, such as linguistic nuances and differences between Renaissance and modern medical criteria, and the incompleteness of the historical record, human skeletal material and its archaeological context have played a pivotal role in investigations of the origin and antiquity of syphilis (Roberts 1994; Siena 2005). Unlike most infectious diseases, syphilis and two closely related but not sexually transmitted infections, bejel (i.e., endemic syphilis) and yaws, leave distinctive skeletal lesions (Hackett 1976; Ortner 2003). Skeletons manifesting bone lesions indicative of infection with syphilis or the other treponematoses from both sides of the Atlantic have been brought into play in favor of both arguments for several decades.
In 1988, two bioarchaeologists and paleopathologists, Brenda Baker and George Armelagos, conducted a comprehensive review of the reported cases of treponemal disease from the New and Old Worlds. They documented an abundant number of indisputable New World pre-Columbian finds – which a similar review by Powell and Cook (2005) reaffirmed – but a complete absence of Old World cases. However, since then, numerous putative cases of Old World, pre-Columbian treponemal disease have been reported, leading some researchers to argue for the antiquity of syphilis and the treponematoses in the Old World (Brothwell 2005; Dutour et al. 1994), and muddying the waters as to where and when syphilis evolved.

Here, we discuss how an approach that is both paleoepidemiological and biocultural can be brought to bear upon skeletal and archaeological evidence for syphilis, clarifying the disease’s origins and antiquity. George Armelagos played a pivotal role in encouraging researchers to better understand diseases in antiquity by employing a biocultural perspective. This perspective, which conceptualizes biological and cultural components of a given phenomenon as inextricably intertwined (Zuckerman et al. 2011), provides a means to investigate the history of health and disease in bioarchaeology and paleopathology (Armelagos 1969). Likewise, paleoepidemiology has proved useful for elucidating the shared history of humans and their pathogens. Epidemiology deals with the incidence, distribution, and control of diseases and other factors relating to health. When applied to health in the premodern era, studied using skeletal evidence, it is known as paleoepidemiology. In paleoepidemiology, epidemiological concepts and methods are used to investigate disease determinants in past populations, relate disease to lifestyle and environment, and interpret the frequency and distribution of pathological skeletal lesions and the diseases that they represent relative to the ecological and cultural contexts of a given population (de Souza et al. 2003). Focusing on the origin and antiquity of syphilis, we demonstrate the unique insights into the history of disease and human health that biocultural and paleoepidemiological perspectives can grant.

**Background**

**Syphilis and the treponematoses**

Syphilis, yaws, and bejel, collectively known as treponemal disease, are caused by different subspecies of a spirochete in the genus *Treponema*. Syphilis is sexually transmitted and primarily affects adults, though a congenitally transmitted form of the infection exists (Singh and Romanowski 1999). Yaws, caused by subspecies *pertenue*, and bejel, caused by subspecies *endemicum*, are transmitted through skin-to-skin contact or shared utensils and drinking vessels, respectively, and are therefore most commonly transmitted during childhood, though symptoms can last well into adulthood (Hoeprich 1989). When not
treated with antibiotics, the treponematoses manifest over the course of several stages (Hoeprich 1989; Singh and Romanowski 1999), sometimes resulting in distinctive skeletal lesions (Ortner 2003).

Syphilis produces the best documented and most distinctly seriated set of signs and symptoms. The primary stage, which lasts from weeks to a few months, involves a chancre at the site of infection and systemic inflammation, but few, impermanent, and non-distinctive skeletal lesions (Singh and Romanowski 1999). The secondary stage, which begins two weeks to six months after infection, can cause a slew of signs and symptoms, ranging from rashes to fever, malaise, lesions on mucous membranes, baldness, meningitis, and transient, non-distinctive skeletal lesions. After approximately one year, sufferers enter latent (asymptomatic) infection, which can last for years to decades; during this stage, a small proportion of cases (~25%), experience the return of secondary symptoms. Infection resolves in most individuals after this stage, but in approximately 15–40% cases, tertiary stage infection sets in, sometimes several decades after initial infection. Tertiary infection encompasses cardiovascular involvement, such as aortic aneurysm; neurological involvement, causing nerve pain and psychosis (Singh and Romanowski 1999); and in circa 1–20% of cases, skeletal lesions (Resnick and Niwayama 1995). These lesions include periosteal reactions, or the addition of new bone on the external surface of a skeletal element, and osteitis, the same type of deposition within the marrow cavity. Osteomyelitis, an infection originating in the marrow, can occur, as well as gummata, or focused necrotic (dead tissue) gummy tumors (Ortner 2003). The progression and manifestations of yaws and bejel are largely the same as those of syphilis, though without well-documented tertiary neurological or cardiovascular involvement (Hoeprich 1989).2

**Diagnosing syphilis and the other treponematoses in skeletal material**

Choosing between the pre-Columbian and Columbian hypotheses requires that researchers be able to recognize evidence of syphilis and the other treponematoses in the skeleton and to distinguish between the skeletal lesions caused by each (Harper et al. 2011). These requirements are greatly complicated by two limiting factors. The first is that yaws, bejel, and syphilis all manifest with very similar lesions (Powell and Cook 2005); the majority of paleopathologists agree that the three variants cannot be distinguished from each other in skeletal material (Ortner 2003). This is primarily because the skeleton can only react physiologically in a few ways to insult. Successfully identifying cases of syphilis in the archaeological record would be ideal for resolving the debate over its origin and antiquity. However, because there is no reliable method for distinguishing between the treponematoses, investigations – including the one presented here – are limited to exploring whether there is evidence of pre-Columbian treponemal disease in a given skeletal sample (Harper et al. 2011). The second
complication, which also reflects the skeleton’s limited responses to insults, is that most of the skeletal lesions caused by treponemal disease are also found in other conditions. This means that, in most cases, it is impossible to confidently identify treponemal disease in skeletal material (Harper et al. 2011).

Evidence-based, scientific studies have identified various skeletal lesions that are consistent with treponemal disease, suggestive of it, and, more importantly, specific to it, meaning that they have a high probability of occurring only in treponemal disease. Lesions specific to treponemal disease include the final three stages of the caries sicca sequence, and bony expansions and nodes with superficial cavitation on the long bones, such as the femur or tibia (Hackett 1976). Caries sicca is a series of gummatous focal lesions that occur on the vault of the skull; over time, a combination of gummata, necrosis, pitting, osteitis, and excessive healing produces a very thickened skull with a “worm-eaten” appearance, covered in crater-like pits and star-like scars (Figure 16.1a) (Hackett 1976; Ortner 2003; Steinbock 1976). Expansion of a bone can be caused by osteitis or periosteal reactions, and it can wrap around the entire circumference of the bone. In treponemal disease, this expansion is combined with nodes, which are localized enlargements resulting from new bone deposition that can span half the length of a bone. In the diagnostic, or specific form, expansions and nodes are peppered with shallow cavities (Figure 16.1b) (Hackett 1976). When these two types of lesions are found within a skeleton, and especially when they are found on more than one bone in the skeleton (treponemal disease is systemic), it is highly probable that the individual was infected with \( T. \text{pallidum} \).

Lesions that are merely suggestive of treponemal disease include the first three stages of the caries sicca sequence, and expansions and nodes on bones that are rough or rugose, coarsely striated with pits, or finely striated. When these lesions are present, it is moderately probable that the individual had treponemal disease. Lesions merely consistent with treponemal disease, such as periosteal reactions, are found in treponemal disease, but also a large range of other conditions.

Figure 16.1 (a) Caries sicca lesions on the cranial vault. (b) Bony expansions and nodes with superficial cavitation on the long bones.
New directions in biocultural anthropology

**Treponemal disease in the archaeological record**
The body of evidence for treponemal disease in the archaeological record has increased over time, as more and more skeletons have been recovered and studied (Harper et al. 2011). Although relatively few published cases of putative Old World treponemal disease existed for Baker and Armelagos to review in 1988, dozens of cases predating Columbus's New World voyages, sometimes by thousands of years, have trickled in over the years. As of 2011, these were sprinkled across 54 publications. Many were presented in Dutour et al.’s 1994 volume, *The Origin of Syphilis in Europe: Before or After 1493?* Others have been described in a wide variety of venues, from peer-reviewed scientific journals to *National Geographic Research Explorations* magazine (Harper et al. 2011). Even so, this relatively small number of reports contrasts sharply with the bounty of cases from the New World. As Baker and Armelagos (1988) found, several strong pre-Columbian cases of treponemal disease in the New World had been documented by the late 1800s and early 1900s, but this number dramatically increased during the mid to late twentieth century. Reports of strong New World cases have continued to boom into the twenty-first century (Powell and Cook 2005). Some archaeological sites have yielded an estimated prevalence of treponemal disease of nearly 50% (Cook 1984; Powell 2003), and others have produced cases dating back as far as 7000 years BP (Hutchinson and Richman 2006; Powell and Cook 2005).

In 2005, paleopathologists Mary Lucas Powell, Professor Emeritus at the University of Kentucky, and Della Collins Cook of Indiana University decided to systematically review New World cases of treponemal disease, with the aim of empirically assessing their prevalence, manifestations, and distribution. They organized a standardized review of cases by many researchers, aggregating the results into a seminal edited volume, *The Myth of Syphilis*. Powell and Cook’s contributors documented dozens of indisputable cases of treponemal infection throughout the Americas, some dating back to the pre-Columbian New World. However, they also documented a high prevalence of treponemal disease at many of the surveyed archaeological sites and a young age for many of the affected skeletons. This profile, consistent with that documented by Baker and Armelagos (1988), is inconsistent with a sexually transmitted disease, which primarily affects adults. Together, the results from these reports indicate that treponemal diseases have been present in the New World for several millennia, most likely in an endemic, non-sexually transmitted form similar to modern yaws or bejel.

**The evolutionary tree of treponemal disease: genetic evidence**
These findings from skeletal evidence are highly congruent with those from genetic studies on the evolution of syphilis. In 2008, Kristin Harper and colleagues published a major phylogenetic analysis of the bacteria responsible for syphilis and the other treponematoses. They collected *T. pallidum* strains that had been gathered from affected communities across the globe, and used them to
construct a phylogenetic tree (Harper et al. 2008). This process was complicated by the fact that only five laboratory strains of *T. pallidum* subsp. *pertenue* and two strains of *T. pallidum* subsp. *endemicum* exist, and even the number of *T. pallidum* subsp. *pallidum* laboratory strains is quite limited, with most having been gathered in North America. Gathering new strains is difficult, as yaws is typically found only in remote, isolated communities, and bejel is incredibly rare, with only two cases reported in the last 20 years. Moreover, *T. pallidum* cannot be grown outside an animal host, complicating the study of this pathogen. Finally, *T. pallidum* strains are genetically very similar; the few informative genetic differences between the strains lead to a phylogenetic tree that lacks resolution.

Despite all of these complications, Harper and colleagues’ findings are highly evocative. They show that the closest genetic relatives to modern-day strains of syphilis are yaws-causing strains of *T. pallidum* collected from remote indigenous communities in Guyana, a nation in South America. Importantly, these strains were collected from children who manifested unusual yaws lesions; although the sores were found on parts of the body, such as the shins, which were characteristic of yaws, they looked more like the smooth chancres found in primary stage syphilis than the rough lesions characteristic of early yaws (Figure 16.2). The combination of genetic and clinical manifestations suggests that these Guyanese yaws strains occupy an evolutionary midpoint between modern yaws and syphilis strains. This suggests that *T. pallidum* subsp. *pallidum*, the cause of syphilis, evolved from a non-sexually transmitted pathogen, such as yaws, in the New World, and was transported by Columbus’s crew across the Atlantic, evolving into syphilis in the Old World.

When considered together, the potential South American origins of the strain that evolved into syphilis, Columbus’s voyages to the Americas in the 1490s, and the first documented epidemic of syphilis in 1495 strongly support the Columbian hypothesis. But why did acquired syphilis, which is sexually transmitted, evolve? Here, the biocultural approach provides a useful
New directions in biocultural anthropology

interpretive lens. Guyana, which is in northern South America, very close to the equator and the Caribbean, is tropical. In the past, indigenous communities typically did not wear much clothing – nor do many indigenous communities in the tropics today – which would have greatly facilitated skin-to-skin transmission of yaws, particularly during childhood. This contrasts sharply with the situation in fifteenth-century Europe. Europe has a mostly temperate climate, which in the fifteenth and sixteenth centuries led to individuals wearing multiple layers of clothing, typically made of wool, at any given time (Crowfoot et al. 2006). Importantly, the only time that most individuals experienced extensive skin-to-skin contact was during sexual activity. The fifteenth and early sixteenth centuries in Europe were also marked by the first evidence of large-scale, formal prostitution, meaning that sexual contact with multiple partners may have become much more common in large urban centers (Rossiaud 1988). It is therefore possible that the particular cultural conditions present in Europe when Columbus returned from the New World created selective pressures that *T. pallidum* had never encountered before. Perhaps the only opportunities for transmission occurred during sexual contact, selecting for strains of *T. pallidum* transmissible during sex. Cultural contact between the New and Old Worlds, with their radically different ecologies, behavioral patterns, and social mores, may have given rise to syphilis, the first truly globalized disease.

**Case study: biocultural and paleoepidemiological approaches to the origin and antiquity of syphilis**

Harper and colleagues’ (2008) findings on the phylogenetics of syphilis, combined with the results from Baker and Armelagos (1988) and Powell and Cook (2005), seemed to strongly support the Columbian over the Pre-Columbian hypothesis. However, the issue of the dozens of Pre-Columbian, Old World cases of treponemal disease that have been reported over the years remained. Unlike the New World cases, no standardized review had been conducted of these reported finds, leaving the Pre-Columbian hypothesis untested. Following in Baker and Armelagos’s footsteps, we conducted this much-needed review in 2011, revisiting and reevaluating all published cases of skeletal evidence for treponemal disease from the Pre-Columbian Old World. Importantly, we employed a paleoepidemiological perspective in our evaluation of the cases, and a biocultural one in our interpretation of the results.

**Materials**

We reviewed 54 published reports of pre-Columbian treponemal disease from the Old World published in the twentieth and twenty-first centuries. These represented 50 archaeological sites from Africa, Asia, Europe, and Australia.
(Harper et al. 2011). Although these reports came from a variety of venues, we only reviewed those that had been published in some form, as there is no unbiased way to find and assess unpublished reports. However, because the origin and antiquity of syphilis have been a source of vigorous debate for upwards of 500 years, it is likely that reports of New World pre-Columbian treponemal disease are almost uniformly published, making their way into the larger scientific discourse. We systemically evaluated each report of treponemal disease using standardized criteria for assessing the strength of the diagnosis and the pre-Columbian date. Each reported skeleton was individually and independently scored. When multiple cases were reported from a given archaeological site, each was ranked separately and the score for the whole site was assigned based on the case with the highest scores.

Methods
Evaluation criteria
We generated our diagnostic and chronological criteria using the published biomedical, paleopathological, geochronological, and archaeological literature. This literature, and how it translated into evaluative criteria, is discussed in greater detail in Harper et al. (2011). Importantly, although Powell and Cook (2005) created a set of criteria to evaluate New World cases, and other researchers have developed diagnostic objectives for evaluating cases of treponemal disease in other contexts (Waldron 2009), no comprehensive, scientific (i.e., evidence-based), standardized criteria exist for evaluating the diagnostic and chronological certainty of skeletal evidence for treponemal disease. Therefore, we created our own scoring system.

Diagnostic criteria
Our diagnostic criteria incorporated two fundamental concepts from epidemiology: sensitivity and specificity. The process of differential diagnosis in paleopathology is much like that of medical diagnosis in clinical medicine and disease screening in epidemiology; the aim is to determine whether a given individual is affected by a given condition and how common the condition is in a given population, respectively (Boldsen 2001). In the case of paleoepidemiology, sensitivity is the probability that an indicator used in diagnosis will be present in an individual affected by a given condition, whereas specificity is the probability that an indicator will not be present in an individual who is not affected by the condition of interest. As mentioned above, because our goal was to identify lesions that could confidently be attributed to treponemal disease, we employed criteria that prioritized lesions highly specific to this condition. This came with a trade-off, however, in that these lesions are not very sensitive, occurring in only a small number of individuals affected by the condition. Diagnostic criteria that do
not explicitly incorporate these concepts ignore the concept of diagnostic accuracy, and thus are not useful in determining paleopathological and paleoepidemiological trends with respect to specific disease conditions (Zuckerman et al. 2016).

Our evidence-based diagnostic criteria divided skeletal lesions into those consistent with, suggestive of, or specific to treponemal disease. As discussed above, lesions consistent with treponemal disease, such as periosteal reactions, are found in many other conditions. Suggestive lesions, such as the earliest stages of the caries sicca sequence, are found primarily in treponemal disease but also in a few other conditions. Specific lesions are those only found in treponemal disease, namely the last stages of the caries sicca sequence, and bony expansions with nodes and superficial cavitation on long bones. As treponemal disease is systemic, the highest scores were given to cases manifesting specific lesions on more than one bone, e.g., caries sicca on the skull and bony expansions on one or more bones of the lower, postcranial skeleton.

**Dating criteria**

When establishing a pre-Columbian case of treponemal disease, the certainty of the date is just as important as the certainty of the diagnosis (Harper et al. 2011). As is common in paleopathology, many reported cases of treponemal disease were dated using indirect evidence, such as associated artifacts, archaeological and architectural features, the skeleton’s provenience within an archaeological site’s stratigraphic profile or radiocarbon dating of associated organic matter, such as coffin wood. Although indirect dating is frequently used and minimizes damage to remains, it can generate time ranges with substantial error. For example, establishing accurate dates for the construction or use of archaeological and architectural features, such as burial mounds or church cemeteries, can be difficult. Artifacts, especially those with stylistic markers, can sometimes provide narrow date ranges, but dating with artifacts can also be problematic. Dates using coffin wood, for instance, can be misleading if wood is recycled (Schiffer 1986), and coins, jewelry, and tools buried with an individual may have been made long before his or her death (Schiffer 1987).

Direct radiocarbon dating of remains has been used for the past four decades to generate objective date ranges. In particular, accelerator mass spectrometry (AMS) radiocarbon dating, developed in the 1980s, generates highly accurate dates. However, even AMS radiocarbon dates must be interpreted carefully when a narrow date range is the goal. In addition to the analytical uncertainty incorporated into the 95% confidence interval accompanying the point estimates for dates (Higham et al. 2006), a diet rich in marine foods, such as fish or shellfish harvested from the ocean, can result in AMS radiocarbon dates for skeletal remains that are hundreds or even thousands of years too old. This is known as the “marine reservoir effect.” It is caused by delayed exchange rates between carbon dioxide from the atmosphere and bicarbonate in the ocean and the diluting effect of the mixing of water on the surface of the ocean with upwelling deep water that contains very “old carbon” (Cook et al. 2002; Hedges
Table 16.1 Scoring criteria employed, modified from Harper et al. (2011).

<table>
<thead>
<tr>
<th>Category</th>
<th>Score</th>
<th>Criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dating</td>
<td>0</td>
<td>Ambiguous date provided or date includes post-1493 period</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>Dating based on stratigraphic position, artifacts from other graves, stylistic markers on artifacts not associated with the reported skeleton</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>Dating based on artifacts closely associated with reported skeleton or pre-15th century grave features</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>Radiocarbon date of the reported skeleton in which 1493 falls outside the 95% confidence interval, but no $\delta^{13}$C values are available for date adjustment or the marine contribution to the diet was not originally incorporated</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>Radiocarbon date of the reported skeleton in which 1493 falls outside the 95% confidence interval after marine contribution to the diet has been taken into account</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>Radiocarbon date of the reported skeleton in which 1493 falls outside the 95% confidence interval after marine contribution to the diet has been taken into account and archaeological context (score 2) supports the date</td>
</tr>
<tr>
<td>Diagnosis</td>
<td>0</td>
<td>Lesions consistent with a non-treponemal process (e.g., non-infectious disease)</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>Lesions consistent with treponemal disease on one or more elements of the skeleton (e.g., periosteal reactions)</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>Lesions suggestive of treponemal disease on a single skeletal element: stage 1–3 caries sicca lesions or finely striated nodes and expansions; coarsely striated and pitted expansions; rugose nodes and expansions</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>Lesions suggestive of treponemal disease on multiple skeletal elements</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>Lesions specific to treponemal disease: stage 4–6 caries sicca lesions or nodes/expansions with superficial cavitation on a single skeletal element</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>Lesions specific to treponemal disease found on multiple skeletal elements or in the presence of lesions suggestive of treponemal disease on other skeletal elements</td>
</tr>
</tbody>
</table>

and van Klinken 1992; Molto et al. 1997). However, AMS radiocarbon date ranges can be adjusted for this effect by estimating the marine contribution to a given individual's diet. This is accomplished through the use of stable isotope data, specifically $\delta^{13}$C values from bone, which reflect marine dietary contributions. Our dating criteria (Table 16.1) incorporate all of the issues and adjustments necessary for direct and indirect dating.

Results

The 54 papers that we evaluated comprised 50 archaeological sites and dozens of cases, which yielded diagnosis and dating scores ranging from 0 to 5. Six sites were from Africa and 13 from Asia, while 31 were from Europe, showing a geographical imbalance in reporting. With regard to diagnosis, one of the most troubling findings was that 20% of the papers that were evaluated, even very recent papers, made a diagnosis of treponemal disease based solely upon non-specific lesions, such as periosteal reactions. Thirty-three percent of the papers, however, did base their diagnosis on diagnostic lesions. With regard to
New directions in biocultural anthropology

Figure 16.3 Maps depicting (a) all reported cases of pre-Columbian treponemal disease in the Old World, (c) those cases with a certain diagnosis (score ≥4), and (c) those cases with both a certain diagnosis (score ≥4) and a radiocarbon date with a 95% CI interval that ends before 1493, after adjusting for the marine signature (dating score ≥4). Modified from Harper et al. (2011). Reroduced with permission of American Journal of Physical Anthropology.

dating, even though a reliable date is very important to the debate over the origins of treponemal disease, we found that many of the papers – 39% – did not describe dating methods in any detail. Importantly, in many reports, cases with a certain diagnosis yielded radiocarbon dates that, when adjusted for the marine reservoir, presented date ranges that overlapped with the end of the fifteenth century, in some cases by several hundred years. In the end, only 6% of papers (n = 3) described cases that were securely dated to the pre-Columbian period.

When combined, the diagnosis and dating scores for the papers yielded two remarkable findings. First, only 11 cases possessed both a certain diagnosis and a radiocarbon date, and the 95% confidence intervals of the radiocarbon dates for all of these cases clustered around and overlapped 1493. Instead of presenting evidence of pre-Columbian treponemal disease, as many of the authors of the original papers argued, we argue that these cases instead provide support for the Columbian hypothesis; they demonstrate that the earliest identified cases of treponemal disease in pre-Columbian Europe cluster around the period immediately following 1495. The second major result is depicted in Figure 16.3. The 54 reports yielded dozens of putative cases of pre-Columbian, Old World treponemal disease, as shown in Figure 16.3a. But although we found a number of cases with a very strong diagnosis of treponemal disease, as shown in Figure 16.3b, and a number with a secure pre-Columbian date, we did not find a single case that had both a certain diagnosis and a secure date (Figure 16.3c). When combined with the first finding, this finding leads us to question whether syphilis did indeed appear in Europe before Columbus sailed the ocean blue.

Discussion

Our evaluation demonstrated that, as of 2011, there was not a single published report of pre-Columbian treponemal disease that had both a certain diagnosis and a radiocarbon date that positioned it firmly within the fifteenth century or before. Here it is important to invoke the old trope, “Absence of evidence
is not the same as evidence of absence.” But why is there no evidence of pre-Columbian treponemal disease in the Old World? There are a number of possible explanations for this phenomenon, as we discuss in detail elsewhere (Harper et al. 2011). For instance, perhaps diagnostic skeletal lesions occur so rarely in treponemal disease that they have been overlooked in some geographical areas. This explanation seems reasonable for some parts of the Old World, such as sub-Saharan Africa and Asia, which have received little attention from paleopathologists. However, it can hardly be true of places such as the United Kingdom, where tens of thousands of skeletons have been analyzed and yielded not even one securely dated and diagnosed case.

Many explanations for the absence of Old World pre-Columbian treponemal disease, however, are best evaluated using a biocultural approach. One such explanation revolves around demographic patterns in the pre-Columbian Old World. Some researchers have argued that because tertiary stage treponemal infection can take years, even decades, to develop, lower life expectancies in the past may have cut many infections short, precluding the development of diagnostic lesions (Watts 1997). Demographic evidence on patterns of life expectancy in Europe in the premodern era shows that life expectancy was fairly low from the Neolithic until the mid-nineteenth century: around 35 years of age (Wrigley and Schofield 1981). However, no evidence exists that the Old World experienced any great change in longevity immediately after the close of the fifteenth century. Early modern Europe witnessed a number of economic, political, and cultural shifts, but none greatly affected life expectancy; large-scale, sustained increases in longevity only occurred in the mid-nineteenth and twentieth centuries (Steckel 1999; Steckel and Floud 1997; Wrigley and Schofield 1981). These shifts were associated with industrialization, modernization, and great improvements in urban and public health infrastructure throughout the Old World that reduced deaths from childhood infectious diseases, such as smallpox and measles. This reduction in early life mortality resulted in coincident increases in longevity (see Chapters 14, 17, and 18). Thus, shifting demographic patterns in the Old World cannot explain our finding away. That Old World archaeological sites from the early sixteenth century onwards yield considerable evidence of treponemal disease, despite the fact that individuals in those communities were living no longer than their ancestors, undermines the argument that the absence of pre-Columbian cases of treponemal disease in this hemisphere is a result of short pre-Columbian life expectancies.

Another argument against the Columbian hypothesis is that syphilis may have been confused with leprosy prior to the 1500s. Several researchers have argued that in the pre-Columbian United Kingdom, especially, individuals infected with syphilis may have been grouped with those suffering from leprosy (Roberts 1994; Stirland 1991). This lumping of diagnostic categories could explain why syphilis was not recognized as a disease until the end of the fifteenth century. Leprosy, now known as Hansen’s disease, is a chronic bacterial infection that, in the long term, can cause destruction of the feet, face, and hands, much like
syphilis. Importantly, it was also highly stigmatized in the past, just as syphilis was, causing ostracism and isolation of sufferers. If the two conditions were confused with each other, sufferers may have been grouped together in hospitals and public institutions, known as leprosaria, intended for those with leprosy.

Historical and archaeological evidence does not support this argument, however. Historical evidence shows that, in many regions, physicians in the late medieval period were able to distinguish between leprosy and syphilis almost immediately, even as the disease initially spread across the Old World in the 1490s and early 1500s (Harris 1996; McGough 2005; Mitchell 2003; Oriel 1994). For instance, in Italy, physicians and chroniclers compared syphilis and leprosy for classificatory purposes, but their writings, as well as contemporary death and hospital records, reveal widespread recognition of the emergence of a new disease and uniformly clear criteria for distinguishing between it and other conditions, including leprosy (Arrizabalaga et al. 1997; Carmichael 1990). Records show that the same was true in other parts of the Old World, such as France, Scotland, and England (Foa 1990; Quétel 1990). This makes it unlikely that practitioners would have been unable to distinguish syphilis – if it existed – from other diseases prior to the 1490s. In addition, excavations of pre-Columbian leprosy hospital cemeteries have yet to produce any cases of treponemal disease (Crane-Kramer 2002; Møller-Christensen 1969). Future excavations and analyses of skeletons from leprosaria will shed further light on this issue, but as of this time, little empirical support exists for the argument that premodern diagnostic criteria conflated syphilis and leprosy, masking syphilis in the populace – and the archaeological record – until the 1490s.

Conclusion

Overall, the scope of archaeological evidence for pre-Columbian treponemal disease yields several clear conclusions. First, it is essential for researchers to report possible cases of treponemal disease as clearly as possible, using diagnostic criteria that are based on lesions specific to treponemal disease, and dating methods that are as accurate as possible and, in the case of radiocarbon dating, that take into account reservoir effects and other sources of error. Transparent reporting and rigorous analysis allow other researchers to evaluate cases independently and compare cases from different regions and time periods (Roberts 1994). This is the only approach by which paleopathology and paleoepidemiology can advance as scientific fields (Zuckerman et al. 2016).

Second, some regions of the world – namely sub-Saharan Africa and large expanses of Asia – must be further investigated before the book on the history of treponemal disease in the Old World can be shut (Harper et al. 2011). However, the dozens of reported cases with neither secure dates nor certain diagnoses from well-studied regions of Europe paint a clear picture: there is no secure
archaeological evidence that treponemal disease was present on this continent prior to the 1490s and the voyages of discovery.

These results mesh interestingly with the genetic data discussed above. They are consistent with genetic data indicating that syphilis, or its progenitor, arose in the New World. However, they are inconsistent with genetic data that suggest that the non-venereal treponematoses – yaws and bejel – have a long history in the Old World (see Harper et al. (2008), contra Mulligan et al. (2008)). The reported pre-Columbian evidence from Europe also butts up against large skeletal samples from England, Russia, Japan, Lithuania, Latvia, Denmark, Hungary, and other nations that overlap 1493 and have yielded many certain cases of treponemal disease that date to the period after but not before this significant date (Jankauskas 1994; Marcisk 1994; Møller-Christensen 1978; Rokhlin 1965; Rokhlin and Rubasheva 1938; Suzuki 1984).

As in epidemiological and biocultural studies of modern populations, isolated findings mean very little until they are explored and confirmed by identifying patterns across multiple, diverse samples. We eagerly await – and anticipate evaluating – the publication of more cases of reported pre-Columbian treponemal disease. As of this time, however, the scarcity of evidence prior to 1493 and great wealth of it afterwards cannot be explained away by geographical, demographic, or medical issues. Instead, our findings support the hypothesis that treponemal infection was not present in pre-Columbian Europe. Syphilis must be seen as one of the first pathological products of the process of globalization that began with the Columbian Exchange and the uniting of the Western and Eastern hemispheres.

The same biocultural approach that is gradually elucidating the history of syphilis may also be applied to other conditions, such as tuberculosis, leprosy, and cancer, which manifest upon the skeleton and are visible in the archaeological record, to learn more about the presence and prevalence of various pathologies at different times and in different places. As we learn more about the sensitivity and specificity of various skeletal lesions for different conditions,4 as new diagnostic methods for use in skeletal materials are developed, including molecular tests; as new sequencing techniques are able to produce information about the molecular evolution of pathogens obtained from ancient remains (e.g., Rasmussen et al. 2015); and as more and more skeletal remains are thoroughly investigated and carefully reported, new opportunities for learning more about the health of past populations will arise. Paleopathology and paleoepidemiology are entering their own era of “big data,” and the biocultural approach will be necessary to make sense of the impending influx of new information from many sources.

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**Notes**

1 However, for critiques of the assumption that virulence in a host declines over time, see Ebert and Bull (2003), Levin and Bull (1994) and Read (1994).
2 But see Román & Román (1986) for a discussion of the possibility of such involvement.
3 These estimates have been based on consistent, suggestive, and specific lesions, not just suggestive and specific ones, meaning that the actual prevalence may be lower.
4 See Weston (2008, 2009) for examples of a rigorous examination of lesion specificity.
PART V
Biocultural approaches to understanding population dynamics
CHAPTER 17

Population and disease transitions in the Åland Islands, Finland

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Introduction

Biocultural anthropology strives to integrate both the biological and cultural dimensions of humans into a unified research approach. It sits at the intersection of culture, biology, and the environment. Hruschka et al. (2005:4) define biocultural anthropology as “a critical and productive dialogue between biological and cultural theories and methods in answering key questions in anthropology.” These questions, according to Lende (2012), all revolve around anthropology’s core question of “What does it mean to be human?” He adds to this core question five basic areas of biocultural research:
1. What is the nature of human variation?
2. How do social structure, political economy, and inequality shape human life?
3. How did we evolve as biocultural beings?
4. How does enculturation happen?
5. How does science, both as a form of knowledge and a form of ideology, shape our lives and govern and mark off how we are similar and different?

A graphic way to view this biocultural holistic anthropological approach or model is to think of three circles (culture, biology, environment) intersecting in a Venn diagram with the research emphasis focused where all three circles overlap. For further discussions of the nature of biocultural anthropology and examples of biocultural research, see the following: Armelagos (1990, 1998, 2004, 2008), Armelagos and Harper (2005), Armelagos and Barrett (2013), and Armelagos et al. (2005).

Some researchers have argued that there is a widening chasm between cultural and biological anthropology because of an emphasis on subdiscipline diversification and specialization (Goodman and Leatherman 1998). Biological anthropologists have often ignored sociocultural processes (e.g., political, economic) that affect human biology, and likewise sociocultural anthropologists have paid little attention to how natural environments and culture have impacted the biological dimensions of humans. It has even been suggested that biocultural anthropology
could reunite the fragmented subdivisions of anthropology (Khongsdier 2007). This reunification could be achieved only if biocultural research becomes inclusive, flexible, methodologically useful, theoretically sound, and truly holistic. In sum, doing successful biocultural research is extremely difficult, and attempts often fall short of expectations. These outcomes should not deter anthropologists from employing this integrative approach, which readers can see deployed throughout this volume.

In order to fully understand human variation, adaptation, and evolution, there must be a melding of culture and biology within an environmental framework. Local-level ecologies can be ideal settings in which to conduct biocultural research because good data sets are often available and the size of the population or culture can reduce the complexity of the relationships among variables. Keeping with this focus and using archival and historical sources, this chapter explores demographic and epidemiologic changes or transitions in the Åland Island archipelago of Finland, spanning a 200-year time period (AD 1750–1950). These local population and disease changes will be placed within the larger regional context by comparing and contrasting Åland’s transition with the transitions that took place in both Finland and Sweden during the same time period. In addition, the chapter documents and discusses the changes over time in causes of death, especially infectious disease mortality, and changes in the age at death, and explores some of the possible sociocultural factors influencing these changes and transitions.

**Background**

**Demographic and epidemiologic transitions**

**Demographic transition**

The demographic transition is a central concept in demography that is both a description of the timing of the historical decrease in the numbers of births and deaths and a controversial theory that attempts to explain these mortality and fertility declines and the ensuing changes in population composition, namely age and sex distribution, and size (Caldwell 1976, 2006; Coleman and Schofield 1986; Kirk 1996; Landry 1933, 1934; Lee 2003; Notestein 1945; Thompson 1929). In its most basic form, the demographic transition is a shift from high mortality and fertility to low mortality and fertility. It must also be noted here that a number of anthropologists, especially Armelagos (1990) and Armelagos and colleagues (1996), argue that the first demographic transition – and ensuing epidemiologic or disease transitions – was really the increase in population sizes in prehistory that accompanied the subsistence change from a hunting, gathering, foraging lifeway to one of food production (i.e., the Neolithic Transition) approximately 10,000 years ago. This early transition resulted in larger and denser sedentary population groupings, in villages and towns, whose
populations then experienced increases in nutritional and infectious disease mortality.

The first formulation of what has now become known as the demographic transition theory or model began with Thompson’s (1929) description and classification of the world’s populations based primarily upon mortality, fertility, and population growth patterns that had occurred in the late nineteenth and early to mid-twentieth centuries. He identified three groups based on rates of population growth. Group A were countries that exhibited low death rates, rapidly declining birth rates, and a decreasing rate of natural population increase (e.g., most of Western Europe north of Spain and Italy). Group B consisted of countries where birth rates were coming under control, death rates were declining more rapidly than birth rates, and natural population increase was rising (e.g., southern and central Europe). Group C included many countries where both birth and death rates were subject to little, if any, voluntary or socioeconomic control. These populations were controlled by the Malthusian positive effects of famine, disease, and war (e.g., Russia, Japan, India, Africa, and South America).

Thompson (1929) did not view his classification in terms of a transition from one group to the next, nor did he apparently think his description constituted a theory (Kirk 1996). The idea of populations transitioning from one stage to the next came a bit later in the writings of Landry (1933, 1934, 1987) and Notestein (1945). Landry spoke of \textit{la révolution démographique}, identifying three population regimes that he labeled primitive, intermediate, and modern. The primitive regimes were characterized by natural fertility (i.e., no deliberate birth control of any kind; see Henry 1953, 1979, and Bledsoe et al. 1994) and high mortality, with the mortality being regulated by periodic epidemics and famines. The intermediate regimes saw the beginnings of restrictions or controls on marriage and fertility, and the modern regimes were typified by late nineteenth- and twentieth-century France and Sweden, exhibiting low fertility and low mortality. These regimes and their associated fertility, mortality, and population increase rates were similar to those discussed by Thompson, but apparently neither knew of the other’s work. Although similar, Landry’s characterization of each of these three regimes was more extensive, detailed, and causally related than those Thompson provided for the mortality and fertility declines. Landry suggested that the mortality declines were related to better treatments for diseases, improved hygiene, vaccinations, and general improvements in the standard of living. Like other researchers, he found it more difficult to explain fertility declines, opting for some forms of birth restrictions, such as contraception, suggestively linked to the economic costs of children, previous birth experiences of the mother, and child-care costs and experiences.

While initially proposing three stages – incipient decline, transitional growth, and high growth potential – Notestein (1945) identified declining mortality as the major factor in the transition of populations and in the projections of worldwide population growth. According to Kirk (1996), Notestein’s description and analysis is now considered as the classic formulation of the demographic transition.
So, in its standard formulation today, the demographic transition theory consists of the following stages.

1. **Pretransition or preindustrial**: marked by high and fluctuating or variable mortality and fertility; characterized all human populations across the world prior to the eighteenth century when changes first started to take place in Western Europe.

2. **Early industrial or expanding**: traditional regimes exhibiting declining mortality and fertility (with mortality typically running ahead of fertility, resulting in population growth); characterized by Western Europe in the nineteenth century.

3. **Mature industrial or late expanding**: displaying low mortality and low, possibly fluctuating fertility; characterized by much of Europe and the United States during the late nineteenth and early twentieth centuries.

4. **Postindustrial or low stationary**: exhibiting both low mortality and fertility, natural increase stable or very slowly increasing; characterized by developed countries such as Japan, Italy, and Germany by the late twentieth century.

5. **Second demographic transition**: birth rates are very low, often below death rates, the populations are aging and declining in size, some populations exhibit subreplacement fertility with the total fertility rate (TFR) below 2.1. The TFR is the number of children that a woman would give birth to if she were to survive from birth to the end of her reproductive period while reproducing in accordance with the prevailing age-specific birth rates. A TFR of 2.1 is considered replacement level. This fifth stage has been added to the model to take into account the current population dynamics being experienced by many countries in Western Europe and the United States where population sizes are decreasing (Lesthaeghe 2011; Lesthaeghe and van de Kaa 1986; Valkonen et al. 2008; van de Kaa 1987).

**Epidemiologic transition**

Understanding that the patterns of disease and health in human populations are basic features of population change, Omran (1971) integrated epidemiology with demography in what he called the epidemiologic transition. His goal was to model historical changes in the causes of death over time, not changes in overall mortality. The primary goal of this theory was to explain both the determinants and consequences of changes in mortality patterns over time. Omran (1971) put forth five propositions.

**The theory of epidemiologic transition begins with the major premise that mortality is a fundamental factor in population dynamics (p. 511)**

Historical demographic research has documented that declining mortality is generally followed by declining fertility. Lower death rates, lower birth rates, and the ensuing increase in life expectancy then produce a new and different age
structure in the population. On the other hand, a different age distribution would be produced if the birth rates remain unchanged while the death rates decline. These different age distributions could then be visually represented as altered population pyramids.

**During the transition, a long-term shift occurs in mortality and disease patterns whereby pandemics of infection are gradually replaced by degenerative and man-made [sic] diseases as the chief form of morbidity and primary cause of death. Three major phases were then identified by Omran: the Age of Pestilence and Famine, the Age of Receding Pandemics, and the Age of Degenerative and Man-Made [sic] Diseases (pp. 516–517)**

Omran portrayed the initial or first phase as one in which there is high and fluctuating mortality, short life spans, and variable but unsustained population growth, noting that (p. 512), “Caught between the towering peaks of mortality from epidemics and other disasters and the high plateaus of mortality dictated by chronic malnutrition and endemic diseases, life expectancy was short and human misery was assured.”

As noted above, Armelagos and colleagues (e.g., Armelagos and Barrett 2013; Armelagos and Harper 2005; Armelagos et al. 2005) have argued that the first epidemiologic transition actually took place in prehistory about 10,000 years ago. As many cultures across the world shifted from a hunting and foraging lifestyle to one of food production, featuring domestication of plants and animals, they experienced a number of demographic and epidemiologic changes. With the rise of villages, population mobility decreased, population sizes and densities increased, and individuals came into closer and daily contact with domesticated animals. In addition, the storage of food attracted unwelcome animals such as rats and flies. Human and animal wastes became an issue, with water sources becoming contaminated. All of these changes created a new disease ecology or landscape that saw the emergence and intensification of waterborne diseases, such as cholera and intestinal parasites, and diseases of zoonotic origin (from other animals), such as anthrax, brucellosis, and tuberculosis. In addition, a number of nutritional diseases linked to a less diverse diet, such as iron deficiency anemia, scurvy or vitamin C deficiency, increased in frequency. As civilizations emerged and trade and human movements increased, this collection of diverse diseases became either endemic or epidemic as they moved across the geographical expanses, establishing themselves across the world. This then became the phase Omran called the Age of Pestilence and Famine.

During the second phase, the Age of Receding Pandemics, mortality declines increasingly over time as epidemics become less and less prevalent and life expectancy rises from about 30 to 50 years of age, thus changing the age
structure of populations. Populations now exhibit sustained growth patterns, eventually displaying an exponential rate of increase. The infectious diseases of the first phase give way to chronic and degenerative diseases, such as cardiovascular and cancers. As industries develop and expand and urban living commences, new environmental hazards appear to play major roles in the causes of death.

Explaining these temporal changes in the causes of death is challenging and often tenuous. Many explanations have been offered. These include changes in the relationship among host, pathogen, and the environment, both natural and sociocultural. They also include improvements in the standards of living; public health enhancements, such as sanitation systems, medical innovations, and pasteurization; improved nutrition; and lastly, changes in fertility patterns and better child-care practices.

In the third phase, the Age of Degenerative and Man-Made [sic] Diseases, infectious disease mortality, in the form of epidemics, as the primary cause of morbidity and mortality, is replaced by degenerative and anthropogenic causes of death. As mortality rates continue to decline, life expectancy rises above 50 years of age, and fertility becomes a more prominent factor in population growth over time.

**During the epidemiologic transition the most profound changes in health and disease patterns obtain among children and young women (p. 521)**

Omran (1971: 521–526) provides historical demographic data from England, Wales, Chile, and Japan to illustrate the declines in infant mortality rates (IMR), childhood mortality, and maternal mortality. The timing of these declines is different for each of these countries, but the probability of death by age and sex diminishes steadily over time. These age and sex changes in mortality, coupled with a reduction in fertility, generate a population pyramid that reflects an ever-growing larger proportion of older individuals in the populations.

**The shifts in health and disease patterns that characterize the epidemiologic transition are closely associated with the demographic and socioeconomic transitions that constitute the modernization complex (p. 527)**

This proposition nicely ties the two transition theories – demographic and epidemiologic – together in a unified model of historical population change. As McKeown (2009:4) very succinctly notes:

> This proposition in some ways bridges the other propositions in that, consistent with the third, it is characterized by lower fertility and longer birth intervals, and in keeping with the second and fifth propositions, it is posited that improved socioeconomic status leads to better nutrition and sanitation, which in turn improve health and reduce morbidity and mortality.
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Peculiar variations in the pattern, the pace, the determinants and the consequences of population change differentiate three basic models of the epidemiologic transition: the classical or Western model, the accelerated model, and the contemporary or delayed model (pp. 532–533)

After examining the temporal mortality patterns of many populations across the world, Omran (1971:533–534) presents what he calls “distinctive core patterns of the epidemiologic transition.” The classical model characterizes the experiences of most of Western Europe that exhibit slow declines in mortality followed later by declines in fertility as modernization ensues. The accelerated model is exemplified by Japan, and exhibits an accelerated pace of transition to arrive at a mortality level of 10 deaths per 1000 population. The delayed or contemporary model fits the experiences of many developing countries that recently, since World War II, have begun a general mortality transition while retaining high levels of infant and maternal mortality rates. In addition, fertility rates in these countries remain high.

Coupling the demographic transition model with the epidemiologic transition model (Figure 17.1) provides an integrated picture of temporal changes in the disease landscape, such as causes of death, and associated population changes,

![Figure 17.1](image-url) The components, stages, and characteristics of demographic and epidemiologic transitions.
including mortality, fertility, life expectancy, natural increase in population size, and age distributions, in many populations across the world, but especially those in Europe and the United States.

Critiques and criticisms of these theories have revealed explanatory limitations, oversimplifications, timing problems, philosophical concerns, and other issues (e.g., see Caldwell 2001; Gage 2005; Knodel and van de Walle 1979; McKeown 2009). However, Coale (1973) notes that the generalizations and predictions articulated in the demographic transition model remain – societies experiencing modernization will go through a demographic transition. The exact timing of transitions and the sociocultural and economic features, both before and after the transition, remain elusive in most instances. Researchers have proposed numerous causes for the demographic and epidemiologic transitions, both sociocultural and biological. These include medical advances and interventions, such as immunizations and therapies; interaction between hosts and pathogens, such as the evolution of virulence and immunity; reduced exposure to pathogens brought about by public health measures, including clean water and milk supplies, improved food handling, and quarantine of the sick; economic improvements; enhanced diet and nutrition of the host; individual responsibility for one’s health, such as personal hygiene and lifestyle changes; and family planning (Caldwell 2006; Coale 1984; de la Croix et al. 2009; Galor 2005; Harper and Armelagos 2010; Lee and Reher 2011; McKeown 1976; Reher 2011). McKeown (1976) argues that improved diet and nutrition was the main cause, while many other researchers suggest that there are multiple causes, both biological and sociocultural in nature, intersecting at the same time. Research has also made it abundantly clear that the causes of change are often population, culture, and time specific. Current research that examines the causes, and variation within those causes, of the second epidemiologic transition is clearly articulated and discussed in a recent collection of articles edited by Zuckerman (2014).

**Case study: Åland archipelago**

Understanding long-term disease patterns and their linkages to demographic, environmental, and cultural features is important in today’s ever-changing epidemiological landscape. As we witness the emergence and reemergence of disease after disease (e.g., Ebola, severe acute respiratory syndrome or SARS, measles, and methicillin-resistant *Staphylococcus aureus* or MRSA) and watch as a new strain of influenza spreads across a nation, continent, or the world, a clear understanding of the factors associated with disease spread, and the possible methods of containment, is vital to our future health and well-being. If we can document, understand, and model the dynamics of historical disease outbreaks, whether local or global, we are better prepared to react to future epidemics and pandemics. The biocultural approach in anthropology, coupled with a temporal
perspective, can provide us with the tools to explore and understand disease
dynamics while at the same time giving us clues for how to effectively control
and contain these disease outbreaks.

The Åland archipelago is an excellent location to examine these temporal
changes in disease outbreaks and to explore their underlying factors. Historical
and demographic data for the archipelago are complete, detailed, and accurate.
In addition, the islands are relatively isolated, making it easy to define the popu-
lation and trace changes in the population composition and structure over time.

In this case study, I use historical demographic and epidemiological data
gleaned from the extensive archives of the Åland Islands, Finland. The Åland
archipelago is situated between Finland and Sweden and is bounded by the
Baltic Sea to the south and the Gulf of Bothnia to the north (Figure 17.2). The
Åboland archipelago and Finland lie to the east while the Sea of Åland and
Sweden lie to the west. The archipelago consists of about 6600 islands and
skerries, which are small, rocky, uninhabitable islands. At the beginning of the
twentieth century, only 158 of these islands were inhabited, and by 1975 that
number had dropped to 70 (Mead and Jaatinen 1975). The archipelago has
been inhabited for centuries, but the population data we use in this case study
start in the eighteenth century.

The earliest evidence of human occupation of the Åland archipelago, identi-
fied as the Comb Ceramic culture, dates to around 4000 BC. The Bronze Age,
c. 1500 BC, appeared in Åland about the same time it did in Finland and other

Figure 17.2 Map showing location and parish subdivisions for the Åland Island archipelago.
parts of Scandinavia. Judging from archaeological data, the Bronze Age period of Åland was densely populated, but toward the termination of the age (c. 500 BC) the scarcity of remains suggested that the population had gradually declined, reasons unknown. It was not until about AD 600 that the population began to increase. This increase was due to considerable immigration of farming peoples from Sweden to the islands. The archipelago became densely populated from AD 800 to AD 1100 because of its location along Viking trade routes (Dreijer 1968). Legend has it that Eric IX of Sweden, also known as Eric the Saint or Eric the Lawgiver, occupied the islands during the twelfth century, establishing Christianity throughout the entire archipelago. From about 1300 to 1600 the islands were a focus of a number of raids and battles, all centered around Kastelholm castle in the parish of Sund, as Sweden consolidated its control over the Baltic. Åland had, during this time period, a peasant economy composed of agriculture, stock raising, and fishing (Dreijer 1968).

In 1699, August II of Saxony united Russia, Poland, Saxony, and Denmark-Norway in a common cause to overthrow the Kingdom of Sweden. For Åland, this time period was a disaster because most of the inhabitants were Swedish. The arrival of a Russian fleet in 1714 and the subsequent occupation of the islands prompted a mass exodus of most of the island’s inhabitants, about 7000 persons, to Sweden. The Peace of Nystad in 1721 returned control of the islands to Sweden.

The first relatively accurate estimate of Åland’s population size was given as 6000 individuals in 1720, and by 1750 the island contained about 9000 individuals (Mielke et al. 1987; Radloff 1795). The archipelago’s annual growth rate from 1721 until 1800 was about 0.9% per annum and then 0.5% during the nineteenth century. These growth rates were similar to those for Sweden (0.5% and 0.8%) but less than those for a relatively rapidly growing Finland (1.3% and 1.0%) during the same time periods. Åland’s lower growth rates were due to a smaller natural increase – basically births minus deaths – which was also checked by emigration during the nineteenth and twentieth centuries, finally reaching about 20000 inhabitants at the turn of the twentieth century (Historillinen tilasto 1983; Mielke et al. 1987; Pitkänen 1977, 1980; Radloff 1795).

The Åland Islands are divided into 16 administrative units, or kommuner (see Figure 17.2). The rural kommuner correspond to the 15 old church parishes, which were established prior to the 1650s. These parishes were originally Roman Catholic, but became Lutheran during the Reformation of the Swedish-Finnish church. The kommun of Mariehamn, which is the only urban parish, was established in 1861. The actual separation of Mariehamn from the parish of Jomala became final in 1905 when Mariehamn received a rector of its own, but the actual act of legislation was in 1900.

Primary data for this case study were gleaned from the parish records kept by the Lutheran ministers of each of the 16 parishes. During the seventeenth century, ministers sporadically kept track of their parishioners and certain religious acts, such as baptisms, marriages, and burials, but it was not until the Swedish
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Ecclesiastical Law of 1686 mandating uniform record keeping that ministers took on this role with more regularity. This study will rely most heavily on the burial, or death, records which consist of the date of death and burial, the name of the individual, his or her occupation or social position, place of residence at time of death (i.e., parish, village, and often house or farm number/location), age at death, and cause of death. Besides these vital events records, population (census) and population change tables are used to document population size and composition changes (Pitkänen and Nieminen 1984).

As with many historical data sets, the records used in this study must be viewed with some caution because of a number of potential biases. These include possible gaps in recordings, loss of whole record sets, records representing only certain time periods, changes over time in what information was actually recorded, illegible handwriting, and idiosyncrasies of individual record keepers. The records used in this study, and the Finnish and Swedish archival sources in general, are of exceptional quality and relatively complete from 1751 to the present (see Pitkänen 1980). For the Åland records, there are a few gaps, primarily occurring between 1750 and 1770, caused by fire and water loss or by recording peculiarities of some parish ministers. None of these inconsistencies follow a pattern and should not be construed as a systematic bias affecting inferences or interpretations. And, in some cases, the same data may be obtained from multiple sources (e.g., birth records and household composition records). Another caution for researchers using archival records is their accuracy and inclusivity. That is, there may be a policy or a practice of excluding people considered to be marginal by the record keeper or the culture (e.g., social, racial, and sexual minorities). For some of the records used in this study, the accuracy of diagnosis of specific causes of death listed in the death and burial records (döde och begravne) may cause some problems. For example, one cause of death may actually include a number of different diseases, or multiple names may be used for a single disease. The diagnoses were made by either the parish minister himself or the family of the deceased. Thus, nosological (the science of classifying diseases) determinations are not always accurate and must be viewed with caution.

Results

The timing of the demographic transition

The annual time series depicting crude birth rates, crude death rates, and population growth are presented in Figure 17.3. Crude rates are calculated by dividing the number of events, in this case the number of deaths (or number of live births) per year, per 1000 population estimated at midyear. Crude birth and death rates generally decline between 1750 and 1950. From year to year, the changes are typically small, but there are a few major aberrations that correspond to periods of war and epidemic encounters. There are large upward spikes in the crude death rate in 1765, 1779, 1808–1809, and 1854 and downward spikes in births in 1773 and 1809. The records show that two of the upward spikes, 1765 and 1779,
are attributable to severe smallpox epidemics while typhoid, typhus, or relapsing fever was responsible for the peak in 1789. As discussed above, the three possible causes of death in 1789 illustrate the difficulty of accurately determining the cause of death in historical data sets. The very large peak in mortality in 1808–1809 was probably caused by typhus, typhoid, and dysentery. The accompanying decrease in births occurred during the War of Finland when Russian and Swedish troops occupied the archipelago (Mielke and Pitkänen 1989). According to the parish death and burial records, the large upswing in deaths in 1854 was caused by cholera and scarlet fever, which are relatively easily differentiated disease entities because of the very different symptoms they cause.

Increases in population size are shown in relative terms, derived from the midyear population figures, superimposed on the crude rates over the same time period. As can be seen in Figure 17.3, the population slowly increased in size from 1750 to 1808 when it dropped because of the war. As is seen in the figure and as documented by Mielke and Pitkänen (1989), there is an ensuing slow recovery after the war. The rate then accelerates greatly after 1860 as a result of the demographic transition (stage 2) taking place in Åland, with mortality decreasing rapidly and fertility remaining high. Thus, Aland experiences a rapid natural increase in population numbers.

It is interesting to note that the crude birth and death rates are not uniformly declining over the 200-year time period. Instead, the rates of decline are sharper – note the steeper slope of the line – in the late 1800s. These changes
in declines can be explored more formally and statistically by fitting a sequence of linear regression models and scanning the time series for breakpoints, in this case dates, or changes in the slope of the lines. Linear regression is a statistical method that assesses the association between two variables by fitting a line to the observed data points, in this case the year and birth or death rates. This analysis provides us with a year that can then be associated with the temporal change in the number of deaths and births. In Figure 17.4, the observed crude rates and the statistically predicted values are represented. This procedure scans the time series to find breakpoints in a two-stage process. Candidate year points for slope changes are identified in a first pass. That procedure generally results in more “bends” in the predictive model than are strictly necessary. Cross-validation concepts are used to eliminate breakpoints that appear not to contribute a substantial amount of predictive power (Friedman 1991; Milborrow 2014; R Core Team 2014). The parameter estimates for these models are summarized in Table 17.1.

The regression or MARS analysis (see Figure 17.4 and Table 17.1) finds slope changes for deaths occurring in 1810, 1860, and 1895 and for births in 1845, 1870, and 1930. The change in slope for deaths in 1810 is attributable to the aftermath of the War of Finland and can be interpreted as the beginning of the demographic transition, with death rates decreasing before a decline in birth rates. The additional change in death rates in 1860 and the change in slope of the birth rates in 1870 indicate that stage 2 of the demographic transition had clearly occurred. Here, it followed the pattern of traditional regimes that experienced
staggered declining mortality and fertility, with mortality typically running ahead of fertility, resulting in population growth. The earlier slope change in births in 1845 identifies a short period when birth rates increase slightly in Åland before dropping. Birth rates again increase slightly starting in 1930. In 1895, the slope of the death rates also changes slightly, not dropping as fast as it initially did with the initiation of the demographic transition.

**Discussion**

**Explaining the demographic transitions**
The timing of Åland’s demographic transition is similar to those that occurred in both Sweden and Finland. In fact, Eckstein et al. (1999) place the date for...
the transition in Sweden occurring with the 1856 birth cohort. Sweden experienced an initial decline in mortality following the Finnish War or Winter War, from February 1808 to September 1809, with fertility dropping in the last quarter of the nineteenth century. Total fertility rates fluctuated between 5.0 and 4.0 between 1750, finally dropping below 4.0 just before the twentieth century began. Much of the decline in mortality occurred among children. In the mid-eighteenth century, 40% of all children died before reaching age 10, but by 1850 that figure had dropped to 25% (de la Croix et al. 2009; Lutz 1986; Malmberg and Sommestad 2000; Schultz 1985).

Following Omran’s (1971) model, during the first stage of the epidemiologic transition in Finland, mortality was very high, peaking during epidemics, wars, and famines. Epidemics of smallpox, paratyphoid, and typhoid, as well as occasional outbreaks of other infectious diseases such as typhus, cholera, and dysentery, shaped the epidemiological landscape during this time (Kannisto et al. 1999; Turpeinen 1979a). Typhoid fever is caused by the bacterium *Salmonella enterica* serotype *typhi*, while paratyphoid is caused by *Salmonella enterica* serotype *paratyphi* A, B or C. Both are transmitted by food or water that has been contaminated by fecal material.

The crude death rate in Finland during the period 1751–1800 was 28.0, during 1801–1850 it was 26.5, and during 1815–1900 it was 24.3. There was then a major decline after 1900 with the rate dropping to 15.9 during 1901–1950. TFRs remained high (5.886 to 4.888) during the eighteenth century and most of the nineteenth century. Remember that the TFR is the number of children that a woman would give birth to if she were to survive from birth to the end of her reproductive period while reproducing in accordance with the prevailing age-specific rates. The TFR fell rapidly over the period from 1876 to 1925, finally dipping to 2.724 in 1926–1950. IMRs, or deaths between birth and one year of age per 1000 live births, also declined after 1880 (Turpeinen 1979a). According to Turpeinen (1979a,b), the reasons for these transitions included improvements in the standard of living, such as wage increases, personal hygiene advances, the construction of piped water supplies and sewer/drainage systems in urban areas and the passage of health legislation, coupled with increases in literacy. All these cultural changes reduced the exposure to and transmission of diseases. One public health campaign that is thought to have had a great impact on IMR was that which promoted the advantages of breastfeeding. Breastfeeding, with its nutritional and health advantages, may have played a part in reducing infections among infants and young children, but the real benefit may have been the fact that this practice reduced the need to give children other foods that could be easily contaminated (Pitkänen 1983; Turpeinen 1979a,b).

During the 1600s and 1700s, many deaths among infants and young children can be attributed to outbreaks of smallpox. With the introduction of smallpox vaccination in the early 1800s in Finland and Sweden (and Åland in 1805), smallpox deaths decreased remarkably, thus playing a role in this reduction as well, especially when infant mortality dropped from 17.1 to 9.4 and then to
5.4 during the respective periods of 1776–1800, 1801–1825, and 1826–1865 (Björkstén 1902, 1908; Mielke et al. 1984; Pitkänen et al. 1989; Turpeinen 1979a).

**Epidemiological and age changes**

The observed number of deaths from a select number of identifiable infectious diseases is presented in Figure 17.5. This figure combines the deaths due to measles, pertussis or whooping cough, scarlet fever, smallpox, and typhus. The predicted values from the regression procedure, MARS analysis, are also included in the figure. In 1875, there is a break in the line or slope change in which deaths due to infectious diseases are substantially reduced. This break point is found at year 1875, no matter whether we treat the outcome data as normally distributed or not (i.e., either Gaussian or Poisson). Although not illustrated, if we exclude deaths due to smallpox in the analysis, there is a statistically significant drop in smallpox deaths after 1810 accompanied by a major shift in the age at death for smallpox victims (Jorde et al. 1989; Mielke et al. 1984; Pitkänen et al. 1989). This is attributable to the introduction and consistent use of smallpox vaccination in the archipelago. The age shift in smallpox deaths after 1810 is rather dramatic. Between 1750 and 1810, 90% of the deaths were among children from birth to 10 years of age with only 10% among those older than 10 years. After 1810, the pattern shifts with 56% of the deaths occurring among those less than 10 years old and 44% among those older than 10 years. To better investigate this age shift,
we further look at the death rates over the entire time period broken into two age groups.

Figures 17.6 and 17.7 show the observed and predicted death rates (per 1000 population) from 1750 to 1900 for those less than 10 years old and those 10 and older, respectively. For those less than 10 years old, the regression analysis provides both predicted values and break points over the 150-year time series. We attribute the first slope change in 1811 to the effects of a rather efficient smallpox vaccination program in which 26,065 infants and children (proportion vaccinated was 95.4%) were vaccinated from 1812 to 1880 (Jorde et al. 1989; Mielke et al. 1984; Pitkänen, et al. 1989). The slight upswing in deaths among those less than 10 years old in 1841 is possibly due to the increased effects of a combination of infectious diseases, including pertussis, measles, typhus, and typhoid but especially cholera and scarlet fever. It is interesting that there is a comparable upswing in deaths at this same time among those 10 years and older (see Figure 17.7). The exact cause(s) of this slight upswing in mortality at all ages is not known. Analyses often reveal findings that cannot be immediately and easily explained, and this is one such example that needs to be addressed in future research. This increased mortality may be related in some manner to the economic effects of the trade barriers imposed by Sweden on Åland from 1838 to 1855 following the Crimean War that established the islands under Russian

![Figure 17.6](image-url)  
Figure 17.6 Observed and predicted changes in deaths of children less than 10 years of age along with slope changes.
control. Figures 17.6 and 17.7 then show a decrease in deaths due to infectious agents, first (slope change in 1856) among those less than 10 years followed by the older age group in 1861. These decreases fit nicely within the timing of the demographic transition in Åland and coincidently with the lifting of the trade embargo imposed by the Russians between 1809 and 1856. How all of these features interacted to cause these changes awaits further research.

Temporal changes in infant mortality rates give us an additional window into the disease dynamics and epidemiologic and demographic transition within Åland (Trapp et al. 1983). Yearly infant mortality rates were generally very high and widely fluctuating between 1750 and 1839, ranging between 230 and 400/1000 births. Around 1840, the rates began a relatively steady decrease. Rates ranged from 120 to 240 per 1000 births until 1905 when there was another decrease, with rates fluctuating between 40 and 120. It is also interesting to note that there was extreme yearly variation in rates between 1750 and 1810, after which the rates show much less variation and a smoother, steadier decline occurs. This change occurs right after the War with Finland (1808–1809) and also corresponds with the introduction of an efficient smallpox vaccination program. After the War with Finland, Russia imposed a trade embargo on Åland that was not lifted until 1856. As noted above, this historical event corresponds

Figure 17.7 Observed and predicted changes in deaths of children 10 years and older along with the changes in slopes.
to a decrease in deaths among children less than 10 and those 10 and older (see Figures 17.6, 17.7).

High infant mortality rates during the middle to late eighteenth century in Åland suggest that the general health was not good. In fact, Åland’s infant mortality rates were much higher than the rates in both Sweden and Finland during both the eighteenth and nineteenth centuries, suggesting that living conditions were harsher in Åland. Infant mortality in Finland declined 23% between 1751–1760 and 1871–1880. This is attributed to a combination of improved childcare practices and the propagation of breastfeeding (Pitkänen 1983; Strömmer 1969; Turpeinen 1979b), as noted above.

The demographic transition theory hypothesizes that a reduction in infant and child mortality is an essential precondition for a fertility decline (Preston 1978). In addition, some researchers (e.g., Eckstein et al. 1999; Hondroyiannis and Papapetrou 2002) have empirically found that a decline in infant and child mortality is an important factor in explaining the onset of a fertility decline. On the other hand, other researchers argue that the mortality decline explanation is inconsistent with the historical evidence and theoretically a weak explanation. They argue that a decline in infant mortality rates is not a trigger for a fertility decline but that the more important causes are related to the economy, more specifically, the rise in demand for labor induced households to invest more heavily in their offspring (Doepke 2005; Galor 2005; Galor and Moav 2002; Galor and Weil 1999, 2000; Lutz 1986; Murphy 2009). These differing opinions and inconsistent research results suggest that demographic transitions across the world are complex and possibly multi-triggered changes that have numerous precipitating factors, demographic and sociocultural.

**Conclusion**

This chapter broadly illustrates how useful the biocultural approach can be in formulating and answering questions of anthropological interest related to historical demography and historical epidemiology. More specifically, it demonstrates how useful it can be for understanding the dynamics of the demographic and epidemiologic transitions. Demographic and epidemiologic transitions have often been used as frameworks for exploring and explaining population and disease changes over time. These transformations occurred at different times and at different rates in many populations and countries. Their causes are controversial and probably unique in many instances. Gradual economic changes, improvements in preventive and curative medicine, improvements in sanitation and water supplies, changes in personal hygiene, enhancements in nutrition, improvements in child health and care (e.g., promotion of breastfeeding practices), and general improvements in living standards have all been invoked as possible causal factors.
Researching the causes of these transformations has proved an elusive challenge. Some researchers prefer one or more of these explanations to others, often arguing for a primary causal factor. There is still controversy concerning which of the factors are most important and which may be secondary. I have avoided this debate here, and instead suggest that there may be unique and variable causes for different populations, cultures, and time periods. I have, however, presented a biocultural case study of a demographic and epidemiological transformation to document the changes in both the structure of the population and the disease landscape in the hope that the study will provide additional insights into these types of transformations.

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Chapter 17: Population and disease transitions in the Åland Islands, Finland


New directions in biocultural anthropology


Radloff, F.W. (1795) *Beskrifning öfver Åland* (Description on Åland), Åbo, Finland.


Introduction

The hygiene hypothesis proposes that within high-income, economically developed nations, such as the United States, the increasingly widespread lack of exposure during early life to a variety of environmental microorganisms predisposes humans to chronic inflammatory disorders (CIDs) in adulthood (Björkstén 2009; Strachan 1989; 2000). CIDs are long-term diseases that involve an inflammatory immune response; those implicated in the hygiene hypothesis are allergic and autoimmune diseases, ranging from asthma, allergic rhinitis (hay fever), and atopic dermatitis (eczema), to inflammatory bowel disease (IBD), multiple sclerosis (MS), and insulin-dependent diabetes mellitus or type 1 diabetes (T1D) (Rook 2010). Numerous types of microorganisms are also included, such as helminths (parasitic worms), many chronic viruses and bacterial infections, and non-pathogenic microorganisms known as pseudo-commensals. These are omnipresent, do not actually replicate in humans, and are consumed every day in exposed populations. They include environmental saprophytes, which obtain nutrients from dead organic matter (e.g., fungi), and lactobacilli, non-pathogenic microorganisms that are found in soil, untreated water, and fermented food (Rook 2010). Several researchers have also found that human gut microbiota, the bacterial community of the gut, have immunomodulatory effects, and have linked microbiota composition to greater incidence of CIDs in individuals and populations (Maslowski and Mackay 2011).
Environmental microorganisms are ubiquitous in non-westernized, non-urbanized, and non-hygienic environments, and presumably have been throughout mammalian – and therefore human – evolution (Rook 2010). The hygiene hypothesis contends that because of this, humans are not just immunologically tolerant of these microorganisms but are evolutionarily dependent on them; exposure during early life, ranging from gestation to childhood, is critical to the development of a well-functioning immune system. Specifically, early exposure may be crucial for building regulatory immune responses that prevent the development of autoimmune diseases, such as rheumatoid arthritis, by maintaining the body’s immunological tolerance of self-antigens (Rook 2010), the substances on the outside of human host cells that signal that they are part of the host.

The hygiene hypothesis is situated within epidemiologic transition theory. This theoretical framework is a descriptive model for the large-scale changes in global patterns in the causes of mortality in human populations throughout history (Omran 1977). The original, “classic” epidemiologic transition is a replacement of a high burden of mortality from infectious disease, primarily acute, epidemic “childhood” diseases, such as smallpox, pertussis, and measles, with one of chronic, degenerative, and mostly non-communicable diseases (NCDs). NCDs include cancer, diabetes, and cardiovascular disease, among others. The classic transition coincided with industrialization in the eighteenth and nineteenth centuries in Western Europe and the United States (Omran 1977), but many developing, low-, and middle-income countries (LMICs), such as Ecuador and Guatemala, are still undergoing a modified transition (Marinho et al. 2013). This involves a moderate to high burden of mortality from NCDs, associated with economic development, but also a comparable burden of acute infectious diseases, due to high degrees of social inequality and less access to health care (Marinho et al. 2013). Armelagos and colleagues were the first to recognize that this was not the first global shift to affect human health; placing the model within an evolutionary context, they recognized a “first” transition, associated with agricultural intensification during the Neolithic, and a third, which has been ongoing since the 1980s (Barrett et al. 1998). This adapted framework repositioned the “classic” transition as the “second epidemiologic transition.”

In this evolutionary context, industrialization and modernization represent a large-scale trade-off in human health. In high-income, developed nations, sanitation systems, treated water, and pasteurization of food and beverages, complemented by improvements in personal hygiene and medical advances, such as vaccination, precipitated the second transition, lowering mortality from acute infectious diseases. However, these practices also reduced, and in some cases eliminated, human contact with less pathogenic environmental microorganisms. Viewed through the hygiene hypothesis, this shift may have produced widespread immunoregulatory failure, causing the cascade of CIDs.
now sickening high numbers of people in many countries (Zuckerman and Armelagos 2014).

For several decades, epidemiologic transition theory has served as a guiding framework for understanding relationships between patterns of health and disease in human populations in relation to economic growth and development and environmental change. In particular, it is used to model dynamics between economic, social, demographic, and ecological factors, and the evolution and spread of disease (Armelagos and Barnes 1999), as well as explaining major trends in the human disease-scape over time. It therefore can grant insight into ultimate, fundamental causes (versus more immediate, proximate causes) of a given trend, and therefore potential solutions. Consequently, it has become paradigmatic in public health policy, demography, economics, and, pioneered by Armelagos and colleagues, biological and medical anthropology (Harper and Armelagos 2010; Zuckerman et al. 2014). However, it has had much less impact in epidemiology and clinical medicine (Fleischer and McKeown 2014; Sullivan 2003). Overall, this is because epidemiologists and physicians are generally concerned with the study of a single disease, or a limited number of conditions, in a particular population or patient. Identifying a causal pathogen or a new condition requires attention to its specific properties, such as symptoms or statistical risk factors. This translates into conceptualizing diseases as singular entities attributable to proximate causes, rather than components of broader health trends (Harper and Armelagos 2010).

Our objective here is to demonstrate how epidemiologic transition theory placed within an evolutionary context, specifically that of the second epidemiologic transition and the hygiene hypothesis, can be used to beneficially inform practice in clinical medicine and public health. We promote the view, fundamental to evolutionary medicine, that human health can best be understood – and contemporary health conditions best resolved – using the long-range lens of evolutionary history, with specific attention to how humans have adapted to changing environmental conditions over millennia.

To do so, we interpret epidemiologic transition theory, the hygiene hypothesis, and evidence of past health within the biocultural approach. There are many definitions of this perspective but overall, it conceptualizes biology and culture as being dialectically intertwined (Zuckerman and Armelagos 2011). It explicitly considers interactions between social, cultural, and physical environments and how they produce and mediate human adaptation, biology, and variation (Zuckerman and Armelagos 2011). Using this framework, we discuss how empirical knowledge of relationships between economic growth, environmental change, and human health in the past can be used to better comprehend contemporary health problems, specifically CIDs. We demonstrate the application of this approach with a case study focused on how scientific information on the hygiene hypothesis can inform practice in clinical medicine and public health for preventing and treating a specific CID – inflammatory bowel disease (IBD).


**Background**

**Epidemiologic transition theory**

Epidemiologic transition theory models the changes in patterns of causes of death (cause-specific) mortality that accompanied the demographic transition. The demographic transition represents the declines in mortality and fertility, and the resulting increases in life expectancy and population growth, that accompanied industrialization in the eighteenth and nineteenth centuries (Thompson 1929). As originally formulated (Omran 1971), epidemiologic transition theory identifies sequential changes in cause-specific mortality across the demographic transition (see Figure 18.1). Stage 1, the “Age of Pestilence and Famine,” during the preindustrial period, features high mortality, primarily from infectious disease epidemics. Stages 2 and 3, the “Age of Receding Pandemics,” encompass a shift from epidemic to endemic or “always present” diseases, and corresponding declines in epidemic mortality. Stage 4, the “Age of Degenerative and Man-Made (sic) Diseases,” involves increased mortality from NCDs via age-related degenerative processes, and “man-made” (anthropogenic)

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**Figure 18.1** The model of demographic and epidemiologic transitions, as conceptualized by Omran (1971) and Thompson (1929).
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causes. These causes include accidents as well as the nutritional and behavioral patterns associated with modernization, such as sedentary lifestyles (Omran 1971) and calorie-rich but low-nutrient and low-fiber diets (Popkin 1994). The line between infectious conditions and NCDs has been blurred by increasing recognition of the inflammatory, infectious causes of many chronic conditions, such as cervical cancer (Walboomers et al. 1999), but this complication only emphasizes the importance of historical and evolutionary relationships for understanding contemporary trends in human health (Zuckerman et al. 2014).

Epidemiologic transitions
The Paleolithic baseline

As Armelagos and colleagues recognized, human populations have experienced multiple epidemiologic transitions, each coinciding with profound changes in their environments and economic strategies. The Paleolithic, stretching from approximately 2.6 million years ago to 10,000 years before the present, is an appropriate baseline for understanding these shifts. Multiple lines of evidence, from genomic analyses of humans and pathogens to ethnographic studies, indicate that the human disease ecology of the Paleolithic was rich with environmental microorganisms, but likely few other forms of pathogen exposure, especially from epidemic diseases (Harper and Armelagos 2013).

For comprehending human disease ecology, epidemiologic transitions, and the hygiene hypothesis, it is useful to group microorganisms into two categories—heirloom and souvenir. Heirloom species have been in long-standing evolutionary relationships with humans, originating amongst our anthropoid ancestors and infecting hominins and eventually humans for millennia (Sprent 1969a,b). Souvenir microorganisms are newer acquisitions. They are typically zoonotic, diseases that can be transmitted from animals to humans, and are contracted through exposure to environments with existing zoonotic reservoirs or vectors, agents of disease transmission such as mosquitoes (Sprent 1969a,b). During the Paleolithic, small group sizes and low population density would have limited the number of heirloom species affecting hominin and human populations, particularly epidemic diseases, like measles, which need large host populations for sustained transmission (Dunn et al. 2010). Nonetheless, some heirloom conditions relevant to the hygiene hypothesis, including helminthic parasites, such as pinworms (*Enterobius vermicularis*), chronic viral infections, such as herpesviruses and papoviruses (*Papilloma*), and bacterial infections, such as *Helicobacter pylori*, *Salmonella*, and *Staphylococcus*, would have thrived in these settings (Rook 2010).

Ethnographic evidence from modern-day foragers and archaeological evidence also suggests that Paleolithic communities were likely exposed to several other kinds of pseudo-commensals. For instance, intense, life-long contact with soil, untreated water, and decaying vegetable matter, as well as food fermentation, would have greatly exposed them to *Lactobacillus* (Rook 2010). They were also likely characterized by a large and highly diverse gut
microbiota (Bengmark 2000). Ancient gut microbiota in bog bodies, frozen remains, and mummies have been reconstructed in several studies (e.g., Cano et al. 2000; Rollo et al. 2007), revealing high phylogenetic diversity. Investigations of the phylogenetic diversity of the gut microbiota in modern-day foraging societies, specifically the Hadza of Tanzania, have also revealed higher levels of microbial richness and biodiversity than found in both modern, urban humans and farming communities in the same region (Schnorr et al. 2014).

Extrapolating from these lines of evidence, Paleolithic communities may have experienced high levels of immunological regulation. In the context of the hygiene hypothesis, it is anticipated that daily, life-long contact with all of these microorganisms renders the Paleolithic into an immunological baseline, characterized by immunological pathways finely tuned to prohibiting CIDs (Zuckerman and Armelagos 2014).

The first epidemiologic transition
Human disease ecology, economic strategies, and environments altered profoundly during the Neolithic and the associated first epidemiologic transition, but likely in ways that only increased and diversified human contact with microorganisms (Zuckerman and Armelagos 2014). Throughout the Neolithic, humans domesticated plants and animals, shifting from foraging to horticulture, pastoralism, and agriculture, became increasingly sedentary, and increased in population size and density.

As Armelagos and Barnes (1999) first noted, several epidemiological consequences of this shift are relevant to the hygiene hypothesis. Animal domestication increased human exposure to a wide range of zoonotic pathogens, such as orthomyxoviruses (e.g., influenza B and C), paramyxoviruses (e.g., measles, mumps, smallpox), and rotaviruses; in low-income developing nations, nearly all children are seropositive for rotavirus, suggesting that it might also play some role in the hygiene hypothesis (Rook 2010). The development of agricultural practices, like irrigation and the use of digging sticks, would have increased exposure to helminths (Campbell Hibbs et al. 2011) and pseudo-commensals (Zuckerman and Armelagos 2014). Decreased dietary diversity and nutritional adequacy would also likely have increased frequencies of metabolic diseases and altered immunocompetence (Chandra 1999), making humans more susceptible to diverse pathogens (Zuckerman and Armelagos 2014). Underground food storage, the use of fermentation, and increased risks of spoilage in stored food would also have increased human exposure to a wide range of pseudo-commensals, including yeasts, molds, and bacteria (Zuckerman and Armelagos 2014). Findings of a high degree of gut and dermal (skin) microbial diversity in modern horticulturalists in comparison to Western urban populations (Clemente et al. 2015) may also indicate that early agriculturalists possessed rich gut microbiota.

Several studies have also found a “farm effect” in modern populations: associations between long-term, early life exposure to non-pathogenic “cowshed” bacteria, molds, and plant material found amongst livestock
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and their environments and reduced risk of CIDs, like asthma, in traditional farming communities (von Mutius and Vercelli 2010). This suggests that the emergence of life-long exposure to livestock and their environs during the Neolithic, independent of zoonoses, may have exerted an impact on human disease ecology, immunological functioning, and the incidence of CIDs.

As Neolithic populations gradually increased, a novel demographic and epidemiologic regime emerged. Larger population sizes, reduced mobility, and greater population density, particularly starting 2000–3000 years ago, enabled many infectious diseases, particularly zoonoses, to evolve into acute, epidemic and eventually endemic infections. This precipitated Omran’s “Age of Pestilence,” featuring increased morbidity and mortality from epidemic and endemic infectious diseases, such as smallpox, particularly among infants and children, and reduced life expectancy (Dobson and Carper 1996). This regime likely persisted until the nineteenth century for many communities, as up until very recently, most humans were rural agropastoralists.

In sum, the first transition may have involved increased mortality and decreased longevity (Cohen and Armelagos 1984; but see Gage and DeWitte 2009), but it likely only intensified the life-long contact that humans had maintained with environmental microorganisms for millennia, strengthening this co-evolutionary relationship and producing immune systems even more finely regulated for preventing CIDs (Zuckerman and Armelagos 2014).

The second epidemiologic transition

This epidemiologic and demographic regime characterized most human populations until industrialization began in the eighteenth century. Industrialization ushered in an unprecedented era of environmental, social, and demographic change, and radically altered the disease ecology of most human populations (Armelagos et al. 2005). These changes reduced exposure to pathogens and the risk of death from infectious conditions in developed nations (Gage 2005). They precipitated the second epidemiologic transition, marked by declining mortality, both overall and from epidemic and endemic diseases, and greater longevity. As longevity increased, and populations in developed nations aged in modernized, urbanized, and westernized environments, the burden of mortality shifted to NCDs and chronic diseases (Gage 2005).

Despite decades of research, the cause of this decline, specifically in infectious disease mortality, remains contentious (Gage 2005; Zuckerman 2014a). McKeown (1976) famously proposed that a rising standard of living, specifically improvements in per capita nutritional consumption from improved economic conditions, bolstered resistance to infections, but this has been discredited (Szreter 2002). While the causes of the decline likely vary by region, culture, and time period (Zuckerman 2014b), researchers now recognize that public health measures, namely sanitation, improvement of urban infrastructure, public housing, reduction of crowding, and pasteurization of foods and beverages, played a major role in reducing mortality (Szreter 1988). Medical
advances, such as vaccination, the germ theory of disease, and improvements in hygiene, exerted a delayed, complementary effect (Cutler and Miller 2005).

Over the last 200 years, high-income developed nations have continued this trend, and LMICs have moved towards it, experiencing improvements in public health, urban infrastructure, and sanitation. LMICs have enjoyed a higher standard of living, reduced exposure to pathogens, and more hygienic environments (Gage 2005). However, following the hygiene hypothesis, these changes also drastically altered human relationships with environmental microorganisms; those in developed and, increasingly, developing nations have moved from environments that are covered in “dirt” to those which are overly “clean” (Ashenburg 2007; Smith 2007). From roughly the 1950s onwards (Bach 2002), researchers have documented an “allergy epidemic” of increased rates of CIDs in most high-income developed nations and many LMICs (Munoz-Lopez 2006).

The “allergy epidemic”: CIDs in the modern world

**Increases in the incidence and global distribution of CIDs**

The occurrence of many CIDs, including allergic conditions such as asthma, rhinitis, and atopic dermatitis, and autoimmune conditions such as IBD, MS, and T1D (Rook 2010), has increased dramatically since the 1950s. In the United States, for instance, the prevalence of childhood asthma increased from 4.6% in 1985 to 7.5% in 1995, to 9.1% in 2007 (see Figure 18.2), representing 6.7

![Figure 18.2](image-url)  
*Figure 18.2* Asthma prevalence among children 0 to 17 years of age in the United States, in 1980–2007, based on data from the National Health Interview Survey. Figure shows an increase from 3.6% in 1980 to a peak of 7.5% in 1995. Asthma attack is defined as those experiencing >1 asthma attack in the previous year.
million cases in this year (Akinbami et al. 2009; CDC 2011; Eder et al. 2006). The prevalence of atopic dermatitis has doubled or even tripled in developed nations since the 1980s, now affecting 15–30% of children and 2–10% of adults (Beiber 2008). T1D has become a major public health problem in Europe and the United States, with increases in incidence of approximately 3–4% per year in Europe (1989–2008) (Patterson et al. 2012), and roughly 2.3% per year (1978–2004) in the United States (Maahs et al. 2010). While part of the increase may be due to improved diagnostics and access to medical care, this cannot explain the dramatic rise that has occurred in just a few decades, particularly for diseases like MS that are conspicuous and easily diagnosed (Okada et al. 2010).

The distribution and incidence of CIDs are not uniform across regions, populations, or nations. In fact, analyses of the distribution of CIDs reveal interrelated geographic, social, and epidemiological phenomena (Okada et al. 2010). For instance, a north–south gradient exists for immune disorders in North America (Wallin et al. 2004), Europe (Bach 2002), and China (Yang et al. 1998). A west–east gradient exists in Europe, with the incidence of some CIDs, such as T1D, much greater in Eastern than Western Europe (Green and Patterson 2001).

Asthma exhibits particularly striking patterns of global prevalence, with a trend towards more developed, westernized nations having the highest rates. For instance, between 1999 and 2004, at least 20% of sampled adolescents in the United States, Australia, and the United Kingdom manifested asthma symptoms, but only 2–3% in Taiwan, Ethiopia, and India (Asher et al. 2006). Several explanations for this have been proposed, such as genetic differences between populations in susceptibility to different conditions, as well as differences in medical resources between nations. However, many studies have now convincingly shown that the geographical distribution of CIDs is roughly a mirror image of the geographical distribution of several infectious diseases, such as hepatitis A virus (HAV), gastrointestinal infections, and parasitic infections (Okada et al. 2010).

The “old friends” hypothesis
Since the late 1980s, numerous cohering lines of evidence have strongly indicated that aspects of social and physical environments, namely development, modernization, westernization, and the attendant reduction or elimination of exposure to both infectious diseases and environmental microorganisms, are driving the rise of CIDs (Zuckerman and Armelagos 2014). Evidence for this dynamic comes from studies of the geographic distribution of CIDs and infectious diseases, animal models of CIDs, and, to a lesser extent, clinical intervention studies (Okada et al. 2010). The latter are discussed in the case study below. Overall, these demonstrate an inverse relationship between incidences of CIDs and infectious diseases – which are effectively proxies for environmental microorganisms.

Animal models have clearly and fairly consistently established this dynamic (Okada et al. 2010). For instance, many studies have shown that autoimmune diseases in strains of mice and rats genetically engineered to be susceptible to these diseases develop them earlier and at a higher rate among rodents bred and
housed in special pathogen-free environments than those in more conventional, “dirty” lab environments (Bach 2002). This has been found to be particularly true of T1D, with a low burden of infectious disease translating into a high burden of CIDs (Bach 2002; Like et al. 1991). A similar dynamic has been documented for gut microbiota; for example, mouse models have shown that supplementing gut microbial diversity with specific bacteria, such as *Bacterioides fragilis*, produces a protective effect against experimentally caused ulcerative colitis, a form of IBD (Mazmanian et al. 2008).

As stated above, the hygiene hypothesis posits that the lack of exposure to environmental microorganisms – as well as alterations in the composition of gut microbiota – during the early life of humans in modern, industrialized environments prevents the development of immunoregulatory pathways that inhibit the development of CIDs. Over the course of mammalian evolutionary history, daily, life-long contact with these microorganisms has resulted in co-evolved dependence between them and humans, wherein exposure is developmentally critical for immunological regulation. In effect, these microorganisms have become our “old friends” (Maizels et al. 2012; Rook 2010; Rook and Brunet 2005b). But how does this work?

Some aspects of this dynamic are well understood (Lott et al. 2015); others remain murky. What is known is that helminthic infections, such as from pinworms, as well as inflammatory allergic reactions, like asthma, involve an allergic type 2 immune response (Else et al. 1994); however, the exact underlying mechanism remains unclear (Pulendran and Artis 2012). Type 2 responses are initiated by and provide protection against helminthic infections; they also promote both acute and chronic inflammatory responses to other pathogens (Lambrecht and Hammad 2012; Maizels et al. 2012; Paul and Zhu 2010; Pulendran et al. 2010). On a cellular level, type 2 responses involve induction of CD4+T helper cells (TH2), a type of T-lymphocyte immune cell that plays an important role in the immune system by initiating the activity of other immune cells involved in adaptive immunity. When the antigen of a given cell, whether from a helminth or pseudo-commensal, is detected, it activates dendritic cells (DCs). DCs present the detected antigen to T-cells specific to those antigens, fine-tuning the type of immune response that the human host then generates, either a type 1 (TH1), which has not been implicated in the hygiene hypothesis, or a TH2.

Rook (2007, 2010, 2012; Rook et al. 2014) has proposed that when antigens from environmental microorganisms – our “old friends” – are detected, DCs mature into regulatory DCs (DCreg), a highly specialized form of DCs that regulate innate and adaptive immunity. These drive regulatory T-cell (Treg) responses to the antigens. They also have the effect of modulating the immune system, including suppressing TH1 or TH2 responses. Suppression of these responses, particularly the TH2 response, effectively self-checks the immune system to prevent excessive inflammatory reactions, namely allergies and autoimmune diseases. According to Rook (2010; Rook et al. 2014), the activation of Treg cells
causes two mechanisms that can rein in excessive inflammatory reactions. The first is that continuous exposure to environmental microorganisms and gut microbes results in constant secretion of regulatory cytokines, which are short proteins involved in cell and autocrine signaling. This signals dendritic cells that exert bystander suppression and dampen additional immune responses. The second is when the high numbers of DC_{reg} lead to an increased processing of self-antigens, which are the antigens present on gut microbiota, and the “natural” allergens present in a given human’s environment, such as pollen. In effect, the immune system has been trained to be less sensitive and not react with an allergic response to every common antigen that it encounters, such as those found on allergens like pollen, peanuts, and animal dander.

Rook and Brunet (2005a) proposed that when antigens from our “old friends” are not continuously encountered, particularly in early life, this protective process does not occur. In an unexposed or underexposed individual, T_{reg} cells are not triggered, causing defective specific and bystander suppression, and a pathological T_{H2} response. In response to allergens, this manifests as allergies. In response to self-cells, it manifests as autoimmune conditions. In a population of such unexposed or underexposed individuals, the prevalence of CIDs rises (Rook and Brunet 2005a). It is possible, however, that other, currently unrecognized processes may be at work. More work remains to be done on understanding this critical process (Licona-Limón et al. 2013; Pulendran and Artis 2012). Nonetheless, it is clear that there is a strong relationship between economic development, westernization, modernization, exposure to environmental microorganisms, gut microbial diversity – particularly in relation to heavy current use of antibiotics (e.g., Russell et al. 2012) – and declines in helminthic burdens, and the incidence of CIDs (Okada et al. 2010). This dynamic makes it unsurprising that humans in developed – and many developing nations – are experiencing dramatically increased incidences of CIDs (Molodecky et al. 2012; Wills-Karp et al. 2001).

Case study: applying the hygiene hypothesis to practice in public health and clinical medicine

While the underlying mechanisms remain subject to intense research, there is a clear relationship between modern, Western environments, exposure to environmental microorganisms, and the incidence of CIDs. This means that this interplay can be used to inform practice, including the prevention and treatment of disease, in public health and clinical medicine. This aim falls under the umbrella of translational medicine or translational science. In these fields, findings from scientific research are translated into practice, including new diagnostic tools, therapies, medical procedures, policies, and public education (Woolf 2008). Translational medicine is an effort to move scientific knowledge from “laboratory bench to bedside” and does so through a variety of interdisciplinary venues, with (particularly in public health) a focus on bringing together
multiple strategies to make sure that proven tools are actually implemented to improve community health (Woolf 2008).

The case study presented here is a demonstration of translational medicine, specifically of how scientific findings from research on the hygiene hypothesis have been applied to practice in clinical medicine and public health. Translational research focused on the hygiene hypothesis is distinctly different from that typically conducted in clinical medicine and public health, which is focused on one or a few disease conditions, and scientific research conducted on living animals or humans. This is because, as discussed above, the hygiene hypothesis is rooted in an evolutionary, ecological, and ultimately biocultural approach to understanding human health. Researchers working on the hygiene hypothesis examine broad trends in patterns of disease across the temporal, regional, and cultural scape of human history to understand both the biological and social underpinnings of these trends in past as well as present populations. Knowledge on these ultimate causes, as discussed here, can be applied to treating and preventing disease in human populations. Scientific findings on the relationship between exposure to environmental microorganisms and the incidence of CID, and variation in this pattern across human history during the first and second epidemiologic transitions have been translated into clinical and public health interventions. Here, we focus on one particular aspect of this: the potential for helminthic therapy for IBD, which includes the intentional infection of patients with helminthic parasites.

**Results**

**Inflammatory bowel disease**

Globally, millions of people suffer from IBD, which comprises a group of remitting and relapsing chronic inflammatory disorders affecting the gastrointestinal tract, including Crohn’s disease and ulcerative colitis. Approximately 3–4 million people have Crohn’s disease or ulcerative colitis (Heylen et al. 2014), and roughly 1.6 million are affected by these conditions in the United States (Loftus et al. 2014). IBD produces symptoms including abdominal pain, rectal bleeding, diarrhea, fever, weight loss, and fatigue (Braus and Elliott 2009), which can greatly impact a patient’s quality of life (Xavier and Podolsky 2007). There are many treatments available for IBD, including immunomodulators and antibiotics, but there is currently no cure for the disease (Pedersen et al. 2014). Similarly, the cause of IBD is unknown, but many researchers have proposed that the mechanism is a loss of immunological tolerance of normal gut microbiota (Braus and Elliott 2009; Podolsky 2002; Scharl and Rogler 2012).

Diagnoses of IBD increased dramatically starting in the 1950s, particularly in high-income developed nations, such as the United States (Lapidus 2000). There are both biological and cultural forces behind this trend. As Heylen and colleagues (2014) note, several scholars have tied the increase to a particular type of reduced exposure to environmental microorganisms, specifically
helminthic infections. The improvements in hygiene and sanitation, medical advances, such as anthelmintics (i.e., “de-wormers”), and regulation of food industries that accompanied industrialization and development have led to the near eradication of helminths (Elliott et al. 2007; Feillet and Bach 2004). For example, the prevalence of hookworm infections in North American schoolchildren declined from 65% in 1910 to less than 2% in the 1980s (Elliott and Weinstock 2012). And in support of the hygiene hypothesis, a vast body of epidemiological, experimental, and clinical evidence shows that helminthic infection exerts protection against immune-mediated diseases, like IBD (Heylen et al. 2014). Elliott and Weinstock (2012) have suggested that, in turn, a lack of helminthic exposure in developed and many developing nations contributes to susceptibility to IBD. The mechanism by which helminths exert this protective effect is not completely understood (Loftus et al. 2014), though it is known that helminths release helminth-derived immunomodulatory molecules into their hosts, which may suppress immune responses (Ruyssers et al. 2008).

**Why helminthic therapy for IBD?**

Why would helminths be useful for treating the kind of inflammation in the human gut that is found in IBD? Helminths have colonized mammals, hominins, and now humans throughout evolutionary history and, consequently, have co-evolved along with their hosts (Dunne and Cooke 2005). While different species of helminths may induce different immune responses in their hosts, these reactions are highly similar (Jackson et al. 2009). During helminthic infection, human hosts experience a strong TH2 response, involving the secretion of numerous types of cytokines and the activation of DCs alongside many other immune cells to provide protection against colonization (Allen and Maizels 2011; Maizels et al. 2004; Salgame et al. 2013). To survive this onslaught, helminths evolved immune mechanisms such as the induction of T_{reg} cells and the production of their regulatory cytokines, which leads to an even more immunosuppressed state in the host (Elliott et al. 2005; Maizels et al. 2012; Taylor et al. 2012). Innate immune cells, such as phagocytes, which engulf and absorb invading organisms, also play an important role (Heylen et al. 2014) in the initial response towards helminths, as they and their products skew the subsequent adaptive immune response towards a TH2 and a T_{reg} response. This suppresses the inflammatory responses involved in IBD (Khan and Fallon 2013; McSorley and Loukas 2010; Ruyssers et al. 2008).

**Clinical intervention with helminthic therapy**

Many clinical trials have been performed to assess whether helminthic infection could be used to treat IBD (see Heylen et al. 2014 for a review). Overall, as with clinical intervention studies aimed at treating other allergic and autoimmune diseases with helminths, the results have been mixed (Heylen et al. 2014; Okada et al. 2010). So far, clinical intervention studies have involved patients consuming eggs of *Trichuris suis* (*T. suis*), the pig whipworm, and the human hookworm,
Figure 18.3 Helminths that have been used in trials to treat IBD. (a) *Trichuris suis*, the pig whipworm. (b) *Necator americanus*, the human hookworm.

*Necator americanus* (*N. americanus*) (see Figure 18.3). Across nearly two dozen studies, starting in 2003, patients treated with these helminths have experienced an overall improvement in symptoms, often without side effects – though in some studies, some patients experienced no effects while others experienced worsened symptoms – with repeated doses of eggs often producing sustained clinical improvement in symptoms (Heylen et al. 2014). After these studies produced promising results from *T. suis* treatment in particular, the US Food and Drug Administration (FDA) requested the development of *T. suis* under
good manufacturing practice and clinical trials of the treatment (Heylen 
 et al. 2014). Recently, a large, randomized, double-blind (neither researchers nor
 patients know who is receiving treatment and who is receiving a placebo)
 placebo-controlled clinical trial was initiated to test the safety and efficacy of T.
 suis therapy in patients with Crohn’s disease. Unfortunately, preliminary results
 show no statistically significant improvement in those treated versus those given
 a placebo, though patients with severe Crohn’s did experience an improved
 response (Lu et al. 2013).

 As of this time, helminthic therapies for IBD are only available in clinical trial
 settings. More research, in animal models and in clinical trial settings, is needed
 to validate the treatment and eventually commercialize helminthic therapy for
 IBD (Heylen et al. 2014). However, Heylen and colleagues note an interesting
 DIY twist: some IBD patients, unwilling to wait for the approval of these ther-
apies, are taking matters into their own hands and treating themselves with
 helminths (Weinstock 2012). In particular, Crohn’s patients seem to be pur-
 chasing helminths on the internet, infecting themselves, and then reporting and
discussing their experiences in online forums (Flowers and Hopkins 2013).

 Discussion and conclusion

 Over the past 10 000 years, humans have engaged in a rapid transformation from
 foraging in relatively small groups to being embedded in an industrialized, glob-
 alized society. During this process, we have profoundly altered the large-scale
 patterns of health and disease that have characterized human societies for millen-
nia. But even though many of us have moved past our humble origins in “dirty”
environments, we still bear the biological and cultural markers of our evolution-
ary beginnings. We seem to be inexorably intertwined with our “old friends”
and decreasing our contact with them as a byproduct of economic development,
westernization, and modernization may have produced calamitous effects on
human health, as seen in the modern-day “allergy epidemic” and high incidences
of CIDs faced by many developed and developing nations.

 As originally recognized by Armelagos and Barnes (1999), when viewed
within the perspective of the hygiene hypothesis, employing epidemiologic
transition theory, and framed by a biocultural approach, it is becoming
increasingly evident that economic development and the social transformation
represented by modernization may have produced an enormous change in
patterns of human morbidity. By removing ourselves from contact with parasites
and environmental microorganisms, and altering the composition of our gut
microbiota, we may have rendered our immune systems dysfunctional, unable
to distinguish between normal and harmful stimuli. Sanitation, improved
hygiene, pasteurization, widespread antibiotic use, and the “cleansing” of mod-
ern environments, ostensibly rendering them more healthful, may have had
just the opposite effect. We have co-evolved with our “old friends” for millennia,
and the sudden interruption of this long-standing relationship through rapid economic and cultural change may have done more harm than good. Humans in developed and some developing nations may have inadvertently traded protection from epidemic infectious diseases, and the devastatingly high mortality they wrought, for the more insidious destruction of a high incidence of CIDs and correspondingly greatly reduced quality of life.

While humans in developed and developing nations may be bearing the brunt of this trade-off, the evolutionary lens and biocultural framework of the hygiene hypothesis and epidemiologic transition theory may not just yield an explanation for this trend. Through practice in public health and clinical medicine, it may produce a resolution to it. Human societies will not be shifting back to “dirty” environments, replete with poor sanitation, unpasteurized “raw” foods and beverages, and stifled antibiotic use in the name of reducing the incidence of CIDs any time soon. But, as translational medicine is bringing to light, though it may sound paradoxical, the severity of CIDs, such as IBD, may be lessened by reintroducing “dirt” into our lives in the form of parasites, specifically helminths. This type of therapy could only be conceptualized through a biocultural approach, whether implicit or explicit, digging back into our evolutionary past and considering the biological, pathological effects of recent economic and social changes. This approach enables the recognition of and consequent engagement with the ultimate causes, rather than the symptomatic results, of modern patterns of health and disease. Focusing on IBD alone, in the future, helminthic therapy may be used to decrease the rates of the disease in both developed and developing nations, slowing the seemingly ever-increasing march of this disease, and potentially other CIDs in modernized, westernized urban areas.

This is not to suggest that all new medical treatments must derive from the application of helminths or other microorganisms. Instead, as Armelagos and colleagues (Armelagos et al. 2005; Harper and Armelagos 2010) have argued, the biocultural approach, and evolutionary models like the hygiene hypothesis and epidemiologic transition theory, should be employed as interpretive frameworks in the face of emergent large-scale epidemics or steadily increasing rates of diseases. We are the products of our long-term history and our past environments. By considering these, as well as where, when, and how humans evolved, and how environmental change and economic transitions have affected health, morbidity, and mortality, it is possible to get a fuller understanding of how certain conditions arose and have changed over time.

The use of a biocultural approach has already resulted in deeper understandings about our current disease-scape, as well as evolutionarily informed treatments for increasingly common medical problems. Further application of the biocultural approach may allow for further understandings of other disease conditions and epidemiologic trends. Since our health and well-being are linked to our past, and therefore to our biocultural evolution, it makes sense that novel and informative treatments involve reexamining the past in order to look forwards towards our future.
References


Chapter 18: The hygiene hypothesis and the second epidemiologic transition


CHAPTER 19

An emerging history of indigenous Caribbean and circum-Caribbean populations: insights from archaeological, ethnographic, genetic, and historical studies

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Introduction

The Caribbean region has long fascinated anthropologists because it bore witness to pre-Columbian human migrations and interactions for several millennia (Curet and Hauser 2011; Schurr 2010; Wilson 2007) and European colonization and forced movement of African peoples to the area over the past several centuries (Curtin 1969; Hulme 1992; Rawley and Behrendt 2005). It is the location where Columbus’ ships first reached what became known as America (Crosby 2003; Morison 1939) and Europeans first contacted indigenous populations (Rouse 1992). Having settled the larger Caribbean islands such as Hispaniola, Spaniards such as de Soto used them as bases from which to explore south-eastern North America in search of riches (Galloway 2006). During the seventeenth to nineteenth centuries, the region became a central focus of European efforts to extract natural resources through the use of indigenous and African slave labor (Hulme 1992; Rogozinsky 1999). It is also where successful rebellions against colonial rule took place in Jamaica in 1739 and Haiti in 1804 (Geggus 2001; Girard 2011; Kopytoff 1978). Eventually its constituent island colonies gained independence in the twentieth century and began their own nation-building process (Augier et al. 1960; Chamberlain 2010; Henry and Stone 1983; Knight 2011). This complicated history has produced the diversity of peoples and cultures that exists in the Caribbean region today.
The Bermuda islands (Bermuda) are located nearly 650 miles east of Cape Hatteras, North Carolina. While not technically part of the Caribbean proper, Bermuda was instrumental to the English colonization of and expansion in the Atlantic, including the trans-Atlantic slave trade (Jarvis 2002, 2010). In this way, Bermuda can be thought of as a circum-Caribbean island. Bermuda was completely uninhabited until the Virginia-bound *Sea Venture* crashed upon its shores in 1609 (Woodward 2009). Upon discovering its fertile ground, the British began settling the islands, only two years after the colonization of Jamestown in Virginia (Jarvis 2010). Its strategic role in the transatlantic trade meant that Bermuda was inextricably linked to the European colonization and exploitation of the Caribbean region. In being the first English colony to forcibly import its labor by trafficking in enslaved Africans, white ethnic minorities, and indigenous Americans (Jarvis 2010; Lefroy 1981; Smith 1976), Bermuda also gave rise to a culturally and genetically complex community that is unique among New World populations.

Because of their geographic extension between North and South America, the Caribbean islands and their living inhabitants are key to unraveling the complex processes and timing of the peopling of the region (Figure 19.1). The initial presence of human populations within the region has been dated to approximately 7200 years before present (ybp), based on evidence from the Banwari Trace site in Trinidad (Harris 1973; Sued-Badillo 2003; Wilson 2007). On the northern side of the island chain, marked by sites on Cuba, Hispaniola, and Puerto Rico (Fitzpatrick 2011; Hagg 1964; Willey 1956), the earliest signs of human settlement date to an independent migration event that took place between 8000 and 5000 ybp. Within the northern Lesser Antilles and Barbados, human occupation dates back as far as 5000–3000 ybp (Fitzpatrick 2011). Both archaeological and

![Figure 19.1](image_url)
linguistic research suggests that, for the remaining islands of the Caribbean, a series of migrations likely originating from South America and ending just prior to AD 1500 resulted in a human presence throughout the region and on nearly every island (Allaire 2003). Possible sources of these population expansions to the Caribbean include migrations north through the southern Lesser Antilles from northern South America or, alternatively, directly to the Greater Antilles from either the Yucatan or the Florida peninsulas, followed by subsequent southward migrations (Allaire 1980, 2003; Callaghan 2001, 2003; Davis and Goodwin 1990; Fitzpatrick 2006, 2013; Granberry 2013; Rouse 1986; Wilson 1997). By contrast, indigenous groups never settled the remote island of Bermuda, some 900 miles north east of the Bahamas archipelago (Gaieski et al. 2011).

As a result of these different expansions and subsequent interactions, at least eight different ethnic groups were present in the Caribbean at the time of European contact. These included the Guanahatebay in Cuba, the Macorix of Hispaniola, the Ciguayo of Hispaniola, the Lucayo (also referred to as Lucayan Taíno) in the Bahamas, the Ciboney of Haiti, Jamaica, and Cuba, the Classic Taíno in the Dominican Republic, Puerto Rico, the Virgin Islands, and the Leeward Islands, and the Kalipuna and the Karina Caribs in the Windward Islands of the Lesser Antilles (Granberry 2013; Mol 2007). The exact cultural, biological, and linguistic relationships among these historical populations are still not well understood. European colonization of the Caribbean, including the transatlantic slave trade, culture assimilation, disease, and genocide, has had a lasting and damaging effect on indigenous Caribbean peoples across the region (Patterson 1991; Rogozinsky 1999). In order to extract the most labor and resources from the colonial territories, on many islands European colonists systematically dissolved indigenous Caribbean communities, effectively legislating them out of the historiography of the region (Forte 2005, 2006; González 1988; Hulme 1992; Toro-Labrador et al. 2003). Despite the colonial-era population decline (Allaire 1980; Boucher 1992), several contemporary indigenous communities still persist on several Caribbean islands. While archaeological, ethnohistorical, and linguistic data provide crucial perspectives on the peopling and history of the Caribbean Basin, many questions regarding the timing and origins of the initial migrations and the impact of European colonization on indigenous Caribbean communities remain unanswered.

**Case study: exploring Caribbean genetic history**

Over the past five years, our multi-institutional team of anthropologists has worked with several populations from the broader Caribbean region to explore their genetic ancestry and links to the other inhabitants of the region. These groups include the Naguake Community of Puerto Rico, the First Peoples Community of Trinidad and Tobago, the Garifuna of St Vincent and the Grenadines, and the St David’s Islanders of Bermuda. A major goal of this research was
clarifying the migration and settlement histories of indigenous populations of the Caribbean, whose exact genetic roots were poorly understood from a genetic standpoint. We were also interested in describing the biological and cultural impact of European colonization and the transatlantic slave trade on the genetic make-up of contemporary Caribbean communities. In order to accomplish this, we employed a biocultural perspective, which addresses both the biological and cultural aspects of a given phenomenon. Each indigenous descendant community was keenly interested in learning more about its own biological history and ancestry using the new genetic tools available to them. Our work revealed that, while generally experiencing a similar process of population formation over the past several hundred years, each community had its own unique history – both pre- and post-Columbian – that was reflected in the pattern of genetic diversity seen within it.

**Methods and materials**

To clarify the genetic heritage of circum-Caribbean populations, we analyzed portions of the genome that provide useful information about migration history and phylogeography of human populations. These included the maternally inherited mitochondrial DNA (mtDNA), which accumulates mutations that define specific maternal lineages, some dating back thousands of years (Pakendorf and Stoneking 2005). The paternally inherited Y-chromosome also accumulates mutations through time that produce distinct paternal lineages in human populations (Jobling and Tyler-Smith 2003). Autosomal DNA, which is contained in chromosomes 1–22 and the X-chromosome, reflects the biparental inheritance of genetic markers (Li et al. 2008; Schaffner 2004). By screening an individual’s genome for thousands of these markers, we can use the resulting data to estimate the proportional ancestry of this individual (Bryc et al. 2010).

In other words, we can use the geographic concentration of different markers from various parts of the world to predict the areas from which an individual’s ancestors came. By examining the different parts of the genome, we can learn different aspects of human evolution and migration, including the effects of social organization and kinship on patterns of genetic diversity in human groups (e.g., Dulik et al. 2011; Schurr et al. 2012).

For each study, DNA samples and genealogical information were collected from individual members of several self-identified native descendant communities. All samples were collected with permission of the Penn IRB #8, the University of Notre Dame IRB, the National Ethics Research Committee of St Vincent and the Grenadines, the Ministry of Health, Wellness and Environment in the Republic of Trinidad and Tobago (hereafter Trinidad), the Bermuda Hospitals Board, the Santa Rosa First Peoples’ Community (FPC) and the St Vincent Garifuna Community. In the laboratory, we used a variety of sequencing and genotyping methods to characterize sequence variation in the Caribbean populations. Descriptions of these methods can be found in the papers reporting the
different studies (Benn Torres et al. 2015; Elhaik et al. 2013; Gaieski et al. 2011; Vilar et al. 2014).

**Results**

**Puerto Rico**

We worked with individuals living in south-eastern Puerto Rico and the island of Vieques to investigate their putative genetic ties to Taíno ancestors. The majority of the participants in this study were members of the Naguake Community of eastern Puerto Rico, which includes 36 contiguous barrios in eight municipalities. This organization is currently seeking state recognition as an indigenous base community on the island (ancient Borinquen). It is also now teaching the Arawak language and Taíno culture in schools and conducting outreach with other native descendant communities throughout the Caribbean and northern South America, as well as seeking other ways to disseminate knowledge of Taíno heritage to all Puerto Ricans.

Our analysis illuminated Puerto Rican history and that of the Naguake Community in a number of ways. First, we found that 60–65% of all Puerto Rican individuals had Native American mtDNAs belonging to haplogroups (lineages)\(^2\) A2, B2, C1 and D1 (Table 19.1). The remaining individuals had mtDNAs from sub-Saharan Africa (L0–L3), with a minority of these belonging to West Eurasian (Europe) lineages (Vilar et al. 2014). Of the Native American lineages, A2 and

<table>
<thead>
<tr>
<th>Haplogroup</th>
<th>n = 111</th>
<th>n = 326</th>
<th>n = 43</th>
<th>n = 12</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Bermuda</td>
<td>Puerto Rico</td>
<td>St Vincent</td>
<td>Trinidad</td>
</tr>
<tr>
<td>A2</td>
<td>&lt; 1.0</td>
<td>29.8</td>
<td>16.3</td>
<td>41.7</td>
</tr>
<tr>
<td>B2</td>
<td>–</td>
<td>4.3</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C1</td>
<td>&lt; 1.0</td>
<td>22.1</td>
<td>20.9</td>
<td>16.7</td>
</tr>
<tr>
<td>D1</td>
<td>–</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L0</td>
<td>13.0</td>
<td>1.5</td>
<td>7.0</td>
<td>–</td>
</tr>
<tr>
<td>L1</td>
<td>14.0</td>
<td>9.8</td>
<td>4.7</td>
<td>–</td>
</tr>
<tr>
<td>L2</td>
<td>14.0</td>
<td>3.7</td>
<td>30.2</td>
<td>16.7</td>
</tr>
<tr>
<td>L3</td>
<td>24.0</td>
<td>10.7</td>
<td>20.9</td>
<td>16.7</td>
</tr>
<tr>
<td>L4</td>
<td>3.0</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>M33</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>8.3</td>
</tr>
<tr>
<td>H</td>
<td>9.0</td>
<td>3.7</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>J</td>
<td>13.0</td>
<td>3.7</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>K</td>
<td>2.0</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>R</td>
<td>1.0</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>T</td>
<td>2.0</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>U</td>
<td>3.0</td>
<td>7.1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>V</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>W</td>
<td>1.0</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>X</td>
<td>–</td>
<td>&lt; 1.0</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>
C1 were the predominant types occurring in Puerto Ricans, with B2 and D1 occurring at much lower frequency (Vilar et al. 2014). A2 was the most frequent of the four indigenous lineages, as was observed in previously published information for Puerto Ricans (Martinez-Cruzado 2010; Martinez-Cruzado et al. 2005), although we did not observe any clinal or geographically varying distributions of these mtDNAs in our sample set (Vilar et al. 2014). From a haplotype standpoint, A2 was quite diverse, as it exhibited several sublineages that appeared elsewhere at appreciable frequencies (A2z in Cuba (Mendizabal et al. 2008); A2k in Colombia (Tamm et al. 2007) and Venezuela (Castro de Guerra et al. 2012; Gomez-Carbello et al. 2007); A2f3 in Mexico (Kumar et al. 2011; Sandoval et al. 2009; Vilar et al. 2014). Similarly, C1 mtDNA belonged to primarily two sublineages, C1b2 and C1b4 (Vilar et al. 2014), both having their origin in northern South America (Achilli et al. 2008; Perego et al. 2010; Tamm et al. 2014) and being dispersed into the Caribbean with the ancestors of the Taíno and later Arawak and Carib peoples.

These results demonstrate that the majority of the maternal lineages found in modern Puerto Ricans were indigenous in origin, even after more than 500 years of colonization and historical demographic reductions of Taíno populations at the hands of the Spanish colonists (Fewkes 2009; Rodriguez-Ramos 2010; Siegel 2005). The diversity and geographical distribution of the A2 lineages suggest they may have originated from two distinct sources: the Yucatan Peninsula through Cuba and Hispaniola to Puerto Rico, and from the Orinoco River valley of South America up through Trinidad and the Lesser Antilles. While they are of differing ages, the C1b2 and C1b4 lineages likely originated in South America, although they may have arrived in Puerto Rico at distinct times and as a product of distinct migratory waves.

By contrast, none of the Puerto Rican male participants had indigenous Y-chromosomes belonging to haplogroup Q, the major paternal lineage in the Americas (Vilar et al. 2014) (Table 19.2). Nearly all of these paternal lineages had their roots in Europe, North Africa, and sub-Saharan Africa (E, G, I, J, R1a, R1b), indicating that they were brought to Puerto Rico by migrating Europeans or enslaved Africans. These findings confirmed a trend seen in other parts of the Caribbean where indigenous Y-chromosomes were replaced in native descendant communities due to male-biased European colonization and the slave trade (e.g., Benn Torres et al. 2008; Deacon et al. 2012; Mendizabal et al. 2008; Miljkovic-Gaćić et al. 2005; Simms et al. 2013), with indigenous males dying from warfare, disease, and slavery (Patterson 1991).

When the autosomal DNA of Puerto Ricans was screened for 150,000 ancestry informative markers (AIMs) or single nucleotide polymorphisms (SNPs) using the GenoChip,1 evidence of Native American genetic ancestry was found in circa 10–20% of the genomes of all participants (Elhaik et al. 2013; Schurr et al. unpublished data). Thus, despite the loss of indigenous Y-chromosomes because of European colonization, there was clear evidence for indigenous genetic ancestry
Table 19.2  Y-chromosome haplogroup frequencies in indigenous Caribbean communities

<table>
<thead>
<tr>
<th>Haplogroup</th>
<th>n = 54 Bermuda</th>
<th>n = 121 Puerto Rico</th>
<th>n = 18 St Vincent</th>
<th>n = 5 Trinidad</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q-L54</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Q-M3</td>
<td>1.9</td>
<td>–</td>
<td>16.7</td>
<td>20.0</td>
</tr>
<tr>
<td>B</td>
<td>3.7</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>E1a</td>
<td>1.9</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>E1b1b</td>
<td>27.8</td>
<td>15.7</td>
<td>44.4</td>
<td>60.0</td>
</tr>
<tr>
<td>E1b1a</td>
<td>3.7</td>
<td>17.4</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>G2a</td>
<td>3.7</td>
<td>5.8</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>I1</td>
<td>5.6</td>
<td>5.0</td>
<td>11.1</td>
<td>–</td>
</tr>
<tr>
<td>I2a</td>
<td>3.7</td>
<td>3.3</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>I2b</td>
<td>1.9</td>
<td>0.8</td>
<td>5.5</td>
<td>–</td>
</tr>
<tr>
<td>J2a</td>
<td>–</td>
<td>5.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>J2b</td>
<td>1.9</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>R1a</td>
<td>7.4</td>
<td>0.8</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>R1b</td>
<td>37.0</td>
<td>44.6</td>
<td>22.2</td>
<td>20.0</td>
</tr>
<tr>
<td>T</td>
<td>–</td>
<td>1.7</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

in all Puerto Rican individuals, regardless of the mtDNA or Y-chromosome background that they had. This result is similar to those found by previous studies of autosomal DNA variation in Puerto Rico, which used a somewhat different set of autosomal markers to assess admixture proportions in this population (Moreno-Estrada et al. 2013).

These findings were quite exciting for the Naguake Community members, who had long held the view that they were the descendants of Taíno people. The results reinforced their views of themselves as having genetic roots in the recent indigenous past, and deeper connections to all prehistoric Caribbean peoples, as well.

Lesser Antilles (St Vincent and Trinidad)
Similar research was conducted in collaboration with the Santa Rosa FPC of Trinidad and Garifuna Community of St Vincent. For both populations, some 35–45% of their members had indigenous mtDNAs, with all of these haplotypes belonging to haplogroups A2 and C1 (Benn Torres et al. 2015) (see Table 19.1). Interestingly, the Santa Rosa FPC had different frequencies of these two lineages from the St Vincent Garifuna, with A2 being higher in the former and C1 in the latter, with limited sharing of haplotypes, as well. This trend suggested that the two islands became genetically differentiated from one another prior to the arrival of Europeans in the region, lending supporting to the idea that indigenous Caribbean people were genetically diverse prior to the arrival of African and Eurasian peoples. These results also support a multiple migration model for the peopling of the Caribbean. Otherwise the majority of the remaining mtDNAs were of sub-Saharan African ancestry, with the Santa Rosa FPC also
exhibiting haplogroup M33 haplotypes from South Asia. This is most likely due to
intermarriage with South Asian women. South Asian people initially arrived in
Trinidad as indentured laborers beginning in the nineteenth century (Laurence
1994).

Unlike our results for Puerto Ricans, we found indigenous Y-chromosomes
in several of the males from both the FPC and the Garifuna (Benn Torres et al.
2015) (see Table 19.2). This observation was a noteworthy finding because of
the near absence of haplogroup Q Y-chromosomes in the rest of the Caribbean,
an exception being Cuba (Marcheco-Teruel et al. 2014). It also suggested that
these haplotypes, which belong to Q-M3, the most common paternal lineage in
the Americas (Schurr 2004), had persisted in the face of significant cultural and
linguistic loss in the Caribbean, as well as the demographic reduction occurring
in the Lesser Antilles due to European conquest.

The remaining Y-chromosomes for the FPC and Garifuna belonged largely
to European haplogroups, with a minority of African haplogroup E1b1a hap-
lotypes also appearing among them (Benn Torres et al. 2015). No South Asian or
East Asian paternal lineages were observed in these two groups, despite known
indentured laborers mixing with native derived groups (Ramdin 2000), possibly
due to sample size effects.

As with the Puerto Ricans, we analyzed autosomal SNP variation in the Santa
Rosa FPC and Vincentian Garifuna using the GenoChip. Based on preliminary
data, it appears that these two native descent groups have, on average, 12–23%
indigenous ancestry, regardless of their mtDNA or Y-chromosome haplogroup
background (Benn Torres et al. unpublished data). These findings were similar
to those observed for Puerto Ricans, and indicate the persistence of indigenous
genetic ancestry in Lesser Antillean populations.

The mtDNA and Y-chromosome data were reported to the Santa Rosa FPC and
Vincentian Garifuna, whose cultural heritage leaders have co-authored a paper
with us that summarizes these data (Benn Torres et al. 2015). The results largely
affirm what these communities knew about their histories, namely ancestry from
and continuity with indigenous Caribbean people. The FPC already exists as a
nationally recognized native group but this is not yet the case for the Garifuna of
St Vincent, who are seeking recognition as a native diasporic population, due to
their removal from their homeland some three centuries ago (Kim 2013; Leland
2014; Palmer 2014).

**Bermuda**

Bermuda has been part of the circum-Caribbean world for over five centuries.
Unlike Puerto Rico and the Lesser Antilles, Bermuda was not originally set-
tled by Native American populations prior to its colonization by Europeans. The
Bermudian population began to take form in 1609, during the early colonial
period, when the islands were settled by the English to establish a trading post
in the Atlantic Ocean (Craven 1937). While the first discoverers of the islands
were European, Bermuda was soon occupied by people of Native American,
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African, and European descent, leading to a highly mixed population. This was the by-product of slavery, indentured servitude, exploration, and commercial opportunism. Bermuda eventually became a stopping point for ships sailing to North America and the Caribbean bearing cargo from Europe and a transit point for ships returning to Europe with goods and foods produced in the Americas. Thus Bermuda has had an important but underappreciated role in the emergence of globalization and international commerce (Jarvis 2002, 2010).

We worked with Bermuda’s St David’s Island community (Islanders), whose history fairly closely mirrors that of the Bermuda islands as a whole. A large number of Islanders consider themselves to be descendants of the Native Americans who were enslaved following early American wars with indigenous New Englanders – specifically, the Pequot Wars (1634–1638) and King Philip’s War (1675–1676). They contend that their indigenous American ancestors were shipped to Bermuda at various times during these conflicts and put to work as slaves (Calloway 1997; Fickes 2000; Schultz 2000). Existing apart from other communities in Bermuda for many generations, St David’s Islanders have passed down an oral history of descending from native forebears and being biological and culturally distinct from other Bermudians.

Based on the history of Bermuda and the their putative links to the Wampanoag and Pequot peoples of New England, we began working with the St David’s Islanders to explore its population and genealogical history. We specifically sought to investigate the genetic evidence that might support the community’s putative links to native North Americans.

Our work initially revealed a population of mixed African and European ancestry, with only a trace of indigenous ancestry being evident (Gaieski et al. 2011). One individual had a native A2 haplotype and another a Q-M3 Y-chromosome, but otherwise African mtDNA haplogroups predominated among the St David’s Islanders, and West Eurasian Y-chromosome haplogroups were most common amongst the men (see Tables 19.1 and 19.2). These results were not wholly surprising in light of the demographic history of the Bermudian population, and the fact that the genealogies of the St David’s Islanders showed complicated interrelationships between families (Gaieski et al. unpublished data). Yet these initial results generally affirmed the community’s assertion of having some indigenous ancestry and potential connections to seventeenth-century native populations of New England.

We subsequently analyzed autosomal SNP variation in Bermudians using the GenoChip to expand our understanding of the genetic history of the St David’s Islanders. Our results indicated that most participants had 4–9% Native American ancestry, regardless of their mtDNA or Y-chromosome haplogroup status, while showing a largely African and European genetic ancestry (Elhaik et al. 2013; Schurr et al. unpublished data). These results were consistent with our initial genetic findings, and with data from an analysis of allelic diversity at the
D9S1120 locus (Schurr et al. unpublished data), which showed several individuals with short alleles typically found only in Native American populations (Schroeder et al. 2007, 2009).

When we reported these results to the St David's Islanders, they generally found them very interesting. Although the extent of indigenous ancestry varied by person, the data confirmed the Islanders' understanding of their having descended from or having biological links to indigenous populations of the Americas. In this regard, the indigenous autosomal contributions may have come from some of the earliest inhabitants of the island (i.e., enslaved Native American peoples), and/or possibly from intermarriage with Afro-Caribbean individuals having some indigenous genetic ancestry. Regardless, St David's Islanders know they have a complex genealogical and genetic history, and now have genetic affirmation of indigenous roots, as well.

Discussion

Population history and reclamation of heritage
The population histories outlined above provide a bioculturally informed understanding of the settlement of the circum-Caribbean region and the genetic heritage of its populations. The genetic data are helping to reconstruct the ancient migration history of the region and also define the biological and cultural impact of the European and African presence on indigenous populations of the Caribbean islands. Through the use of genetic approaches, we have gained knowledge about the biological affinities of these Caribbean communities, and learned how they use genetic information, that we have jointly discovered, to heighten their own sense of identity and reckon with their historical connectedness to indigenous, African, and European populations.

Despite generations of marginalization and relative neglect, these groups retain a strong sense of their native identity. In fact, most are now seeking some form of official recognition as native descendant communities by the governments of the islands on which they reside. The Vincentian Garifuna are claiming St Vincent (Yurumein) as their homeland and seeking compensation from the British for the disenfranchisement and displacement from their original home. In this regard, they can potentially use genetic data to help demonstrate that indigenous people and their descendants have not disappeared from St Vincent. They have also reached out to Garifuna communities across the Caribbean in an effort to build solidarity with them and share their cultural and linguistic traditions, some of which have been lost on St Vincent itself. The Santa Rosa FPC has gained status as an native descendant group on Trinidad and Tobago, and in 1976 incorporated itself as a limited liability company, thereby becoming the only collective of indigenous people with national recognition in the country (Forte 2005; Ingram 2008). The Puerto Rican Naguake community is also seeking state recognition.
as an indigenous heritage group, and is using the new genetic data to demonstrate its connection to Taíno ancestors, thus continuing a native presence on the island. In fact, Naguake was declared by resolution an Indigenous Base Community by the Humacao and San Lorenzo municipal governments (Resolution Num. 42, Series 2010-11, Autonomous Municipality of Humacao; Resolution Num. 15–OT, Series 2013–14, Autonomous Municipality of San Lorenzo). These declarations were based in large part on the results of our genetic research conducted in the community between 2010 and 2014. Bermuda’s St David’s Islanders celebrate their native ancestry by holding a biannual powwow on the island, and by engaging in a revival of their cultural traditions. Furthermore, several federally recognized New England native groups accept the Islanders as their “lost cousins,” even inviting them to participate as featured guests in their own powwows (Bermuda Gazette 2013, 2015).

Overall, these communities are strategically employing multiple sources of information – ethnographic, cultural, linguistic, archival, oral historical, and genetic – through a uniquely biocultural lens in order to elucidate their own histories and assert their status as the descendants of the first peoples of the Caribbean or, in the case of Bermuda, relatives of the native communities of New England.

It should further be emphasized that the success of these studies comes from collaboration between local communities and researchers. Such collaborations take time to develop, but are essential for ensuring that primary stakeholders in these studies – the indigenous communities themselves – are fully informed about the nature of the research and the results of the genetic exploration of their samples. In addition, these joint investigations of history and ancestry can yield new insights into questions of population history and ancestry by including perspectives from indigenous communities that have previously been excluded from consideration. Moreover, through their engagement with researchers, members of indigenous communities gain knowledge about scientific research, genetic methods, and anthropological evidence which, in turn, offers them new perspectives on their histories and provides novel information for educating younger people in their communities.

**Conclusion**

**Biology and identity**

As illustrated in the preceding discussion, the Caribbean is very diverse from a population history perspective, and is now home to people with biological ancestry tracing to the Americas, Africa, Europe, North Africa, and South and East Asia, among other places. This fact is quite evident in our genetic research with native descendant communities from Bermuda, Puerto Rico, and the Lesser Antilles. In fact, aside from Bermuda, the region has always been a diverse place, being home to numerous different indigenous groups at the time of
European contact, which emerged through a series of demographic expansions from northern South America and perhaps elsewhere. Unfortunately, much of this pre-Columbian diversity remains poorly documented from an ethnographic and genetic perspective. We therefore hope that our work will contribute to a broader understanding of this history and population diversity.

What existed of the pre-Columbian world has been profoundly changed in the past several centuries. Native American populations have undergone transformations in terms of their language, culture, genetics, and social organization since European contact, and the rapid twenty-first century changes are accelerating the pace of cultural exchange and amalgamation. Throughout the contemporary period many indigenous communities have disappeared, been absorbed into new groups, remained largely isolated from colonial populations, and/or reemerged within new historical circumstances. Despite these facts, several of these indigenous groups have persisted and are now seeking to reclaim and revitalize their heritage, cultural practices and languages, and are using biological information to help guide these efforts.

From a biological point of view, Caribbean populations have genetic ties to African, indigenous American, and European peoples. But culture has exerted an intertwined influence; the nature and extent of these ancestral contributions have also been shaped by colonial practices of marriage and social integration of mixed ancestry individuals, which ultimately created complex phenotypic variation on every island of the Caribbean. In recognition of this fact, our work in the Caribbean further demonstrates that genotypic and phenotypic variation does not necessarily correspond with conventional or folk theories of race. Moreover, our work affirms previous studies that have examined relationships between culture, social structure, race, and biology (Bryc et al. 2010; Guo et al. 2014). Overall, our findings further reveal the tremendous demographic, cultural, and biological complexity that has characterized the circum-Caribbean since the beginning of contact and colonization, and continued into the modern era of escalating globalization.

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Notes

1 This SNP genotyping array was designed for anthropological genetic research, having over 130,000 highly informative autosomal and X-chromosomal SNPs ascertained from over 450 worldwide populations, including those analyzed by the Genographic Project Consortium.

2 In the mtDNA, we search for mutations or markers that define different branches of the human mtDNA phylogeny or tree. Specific markers or single nucleotide polymorphisms (SNPs) define different branches of this tree, being markers of genealogically related haplotypes, and can be classified into haplogroups, or maternal lineages, using an alphanumerical nomenclature (van Oven and Kayser 2009). The deepest and most diverse branches of the mtDNA tree are found in Africa, due to it being the place of origin of modern humans, while haplogroups found outside Africa derive from macrohaplogroups M, N, and R, which ultimately evolved from African L3 (Behar et al. 2008). Similar to the mtDNA tree, we search for mutations or markers that define different branches of the human Y-chromosome phylogeny or tree. Different markers define different branches of this tree, and are classified into haplogroups using an alphanumerical nomenclature (Karafet et al. 2008; Y-chromosome Consortium 2002). The deepest branches of the tree are found in Africa (A, B) while most haplogroups or paternal lineages found outside Africa (C-R) arose and were spread through modern human expansions, with C, D, and F being some of the older branches that evolved from B before being dispersed outside Africa and E being a lineage that expanded in both Europe and Africa (e.g., Cruciani et al. 2004).

3 We learned about the possible Bermudian connection to indigenous populations from New England through working with the Seaconke Wampanoag tribe in Massachusetts (Zhadanov et al. 2010).

4 In addition to broader sampling of contemporary Caribbean populations, data from ancient DNA studies (Lalueza-Fox et al. 2001, 2003; Mendisco et al. 2015; Schroeder et al. 2015) will help to show the pattern of genetic variation that existed prior to European entry into the region.
CHAPTER 20

Explorations in paleodemography: an overview of the Artificial Long House Valley agent-based modeling project

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Introduction

A long-standing question in Southwestern archaeology and demography has centered on the depopulation of communities that occupied the Colorado Plateau between roughly AD 200 and AD 1300 (Cordell and Plog 1979; Dean et al. 1985; Gumerman and Gell-Mann 1994; Kohler et al. 2010). The Colorado Plateau generally refers to the Four Corners region where Utah, Colorado, Arizona, and New Mexico join. During the early part of this period, horticulturists, the Basketmakers, expanded into the region and developed settled communities. After AD 600, the Basketmakers transitioned from pithouses to semi-permanent, above-ground structures and became more engaged in the intensive production of local crops, principally maize, beans, and squash. Archaeologists refer to these later groups as Ancient or Ancestral Pueblo or Anasazi, and the period AD 700–1300 saw their rapid population growth. These groups became increasingly dependent on agriculture as time went on, and maize (corn) was the single most important crop. In addition, cultural elaborations took place in productive technologies – including highly decorated pottery styles – as well as in religion, and in social organization (see Powell and Smiley 2002, Ware 2014, and Cordell and McBrinn 2012 for further discussion).

Beginning around AD 1150, severe droughts plagued the Southwest and by AD 1300, much of the Colorado Plateau region was abandoned (see Cameron and Tomka 1993; Dean et al. 1985; Nelson and Schachner 2002). The archaeological evidence for abandonments includes sites and clusters of sites that were
deserted over a short period of time and the cessation of further construction. The long-standing central issue, then, is to what extent did the droughts force Pueblo peoples out of the region and what other factors might have been involved? In addition, why did people still leave, often for protracted periods of time, areas in which environmental evidence suggests continued habitation by small numbers of people or groups should have been possible?

This central question obviously leads to many others, such as the role of violence and conflict (Haas and Creamer 1993), the inadequacy of nutrition, as well as the presence of stress, disease (Martin et al. 1991; Nelson et al. 1994) and other factors in the disappearance of ancestral Puebloan populations from the Colorado Plateau. In addition, social and political factors, such as the inability to carry out ritual functions with reduced population sizes or the contraction of social networks previously used to overcome resource shortfalls, may have further precipitated the wide-scale abandonment (Blinman 2008; Dean et al. 1985; Plog 1986). Since at least the late nineteenth century, amateurs and professional archaeologists alike have researched this region and its numerous sites and posed several theories. Over the years, stronger inferences and improved explanations have emerged, but answers to how the pieces all fit together, and how some areas may have differed in experience from others are still being sought.

The complexity of the region’s prehistory is now more widely acknowledged and at the same time deemed more interpretable through use of a variety of approaches. As research techniques and methodologies have become more sophisticated, the evidence for past events is stronger. By using a biocultural approach, archaeologists and bioarchaeologists have come to realize that in combining the history of health and disease, population transitions, and evidence for conflict and trauma with the material culture and ethnohistory of various communities and regions, more complex and accurate explanations are possible that were inaccessible to researchers in the past. As high-speed computers became available to researchers in the 1970s, new avenues opened that involved the management and manipulation of large amounts of data, plus the opportunity to experiment with various ways of modeling demographic and cultural processes to test hypotheses in ways not before possible. In this chapter, we describe one such computer modeling approach and provide some examples of how we are combining modeling with biocultural inferences to address the growth and abandonment of a particular subregion in the Colorado Plateau. The purpose of our project, and indeed this chapter, is to develop more complete understanding of how climate change, population dynamics, and biocultural factors all interacted to produce the prehistory of the Colorado Plateau.

Beginning in the mid-1990s, new computer-based techniques were explored to see whether they could supplement traditional archaeological methods. The first of these projects, originally called the Artificial Anasazi (AA) project and now the Artificial Long House Valley project (ALHV), uses agent-based computer
simulation to model realistic farming practices and population growth at the sites and locales represented in the archaeological record of the Long House Valley in northeastern Arizona (Figure 20.1). Agent-based simulation is a computer modeling technique that places individual agents (representing people, groups of people, or other analogous entities) on a space. Simple rules for behavior are built
into the model and allow the agents to engage in different activities of interest to the modeler. The AA model and similar simulations (see later in this chapter; also Kohler et al. 2010) incorporate bodies of data about the Four Corners region collected over the years by archaeologists, paleoclimatologists, bioarchaeologists, and others. Gumerman and Kohler (1996:14) commented that using computer simulation to vary and manipulate features of the archaeological landscape and its inhabitants allows us to “rewind the tape” of population history; in effect, to estimate the internal and external factors that could produce the observed results.

It is important to remember, however, that agent-based modeling is only one method that can be used to understand the past and it should not be used to replace traditional approaches. Models involve important simplifications of real-world processes that require assumptions about how the processes work. Ideally, these assumptions are based on a full understanding of the processes being modeled, but sometimes a lack of relevant data requires that they be based more on logical scenarios derived from incomplete information. Agent-based models such as the one described here are also very time-consuming to develop. The construction of a suitable model for anthropological problems necessitates taking a strong biocultural approach, both to guarantee that the aspects of human behavior and biology related to the essential questions being studied are incorporated appropriately into the model and to ensure that any assumptions made are reasonable given the questions being addressed. More traditional approaches, such as skeletal analyses and environmental reconstruction, provide the underlying data and important inferences about human behavior necessary to ensure that the model adequately represents the scenario being modeled. Without the contributions from more traditional approaches, models are at great risk of reflecting the mind of the developer, not the reality of the scenario.

The Long House Valley is located in the Kayenta area of northeastern Arizona, and was occupied as early as around 7000 BC until AD 1300, at which time the valley was abandoned. The sites in the valley were intensively archaeologically surveyed for the study period from AD 800–1300; in addition, environmental and climatic data were collected. Population estimates were derived using long established methods for sites in this region and elsewhere (see Chamberlain 2006; Layhe 1981; Zorn 1994). Pollen studies, which revealed periods of greater and lesser precipitation, and hydrological studies helped to determine local-scale changes in the environment that influenced agricultural productivity at different locations in the valley. These empirical data, described in Dean et al. (2000) and Axtell et al. (2002), provide the means to model variations in the primary demographic parameters and estimate the total rates of growth. Based on births, deaths, and migration, these estimates ranged up to 1.2% per annum. As an example, a rate of 1.2%, if sustained, would mean that the population would double approximately every 58 years.
Background

Computer simulation and the study of ancient populations
Joshua Epstein and Robert Axtell, two original members of the AA project and pioneers in the use of computer simulations to study human social processes, have pointed out that some researchers in recent decades have called the social sciences the “real” hard sciences. Social processes, such as the demographic, economic, and cultural behaviors of humans, are complex, vary greatly in space and time, and are not governed as much by the defined rules of the natural world as in chemistry or physics. Methodologies for natural phenomena do not readily translate into formulas for studying the complex processes of biocultural change in humans, and controlled experimentation on humans is difficult, sometimes impossible, and often unethical (see Epstein and Axtell 1996:1–2).

Computer simulation has been used since at least the 1960s in the social sciences to address complex questions about past human experience. Simplifying assumptions are made about very complicated social behaviors and then, through the simulation, these assumptions are tested over time and space to predict a documented history or prehistory. The results can then be compared to conclusions archaeologists, historians, and other social scientists have made about the social or biological processes in question. Simulation does not necessarily provide definitive answers, but it can be very helpful in understanding the plausibility of hypotheses, and perhaps even suggest their likelihood (see Axelrod 1997; Doran and Gilbert 1994; Epstein 1999; Gumerman and Kohler 1996; Kohler and van der Leeuw 2007; Swedlund et al. 2014).

Prior to the 1990s, computer simulations in the social and biological sciences often treated individuals, communities, or populations in static ways. For example, in demographic models each individual being modeled may have been given the same probability of fertility, mortality, and migration. Results could vary due to stochastic (random) processes, but the models tended to be very limited in their ability to incorporate behavioral variation, and results were strongly determined by the values of base variables of the model. In the mid- to late-1990s new simulation methods were developed that allowed more adequate representations of some of the complexities of human social behavior, such as individual variation in responses to situations such as exposure to infectious disease. These advances were partially a consequence of readily accessible and powerful high-speed computers, and partially because of new ways of thinking about how to efficiently simulate human and animal behaviors (see Kohler and Gumerman 2000).

Agent-based simulation is the most common computer modeling technique in the social sciences. Generally, such models consist of an environment, a set of agents (discrete individuals or groups), and rules to govern interactions among agents and between the agents and the environment (Epstein and Axtell 1996). The rules are algorithms (or procedures) that determine whether an agent expresses
a given behavior at a given point in time; this expression of behavior can be influenced significantly by random effects. For example, in an agent-based demographic simulation of a human population, each reproductive-aged female has a chance of giving birth at any age during the reproductive time span, and this event can depend on random effects as well as changing external conditions, including nutritional status or number of other children. This means that each female in the simulated population can have a different timing and number of births. However, within the simulation, the realized fertility of individuals is set to be consistent with what is known from ethnographic observations. Similar constraints based on ethnographic evidence are also imposed for mortality, marriage, immigration, or other agent behaviors. Below, we illustrate how agent-based models have been used to help understand population growth and distribution in our study region.

Case study: the Artificial Long House Valley (ALHV) Project models

The models developed in the original AA Project were written using a software program, Ascape, developed specifically to facilitate agent-based modeling in the social sciences (Epstein and Axtell 1996). The goal of the first model, the AA model, was to compare and contrast its results with the known archaeological and paleoenvironmental record of Long House Valley (e.g., Axtell et al. 2002; Dean et al. 2000). Ideally, the AA model was meant to aid in understanding how population-level demographic interactions led to the observed trajectory of population growth and decline apparent in Figure 20.2. The AA model focused on household-level decisions made about where to farm and when to move in light of changing climatic conditions evidenced in the paleoenvironmental record.

In the late 1990s, the original project members initiated the development of a second Ascape model, but this model was never completed; completion and extensions of this model are the focus of our most recent work. This model, which we have named the Artificial Long House Valley (ALHV) model, centers on the behaviors of individuals in a household rather than the entire household as a single unit, although decisions about where to farm and when to move are still made at the household level. In both models, the total population size (the number of households) is tracked by the model across time and compared to estimates of population size derived from archaeological evidence recovered from Long House Valley. For example, in the Southwest United States, archaeologists can estimate population size at a given point in the history of a site by characteristics such as the site’s overall size, number of rooms and hearths, and the size of middens. These can be translated into the number of individuals and households using methods that have been tested and validated for many regions and time horizons.
Figure 20.2 Population growth rates in the Long House Valley, AD 800–1350. The archaeological data are based on archaeological estimates over the entire period. The curves in gray fit an exponential growth model to the three time periods corresponding to growing populations in the region. The early and late periods are characterized by similar growth rates ($r = 0.006$ versus $r = 0.005$), while the middle period indicates a time of accelerated growth ($r = 0.012$).

Structure of the AA model
The environment of the AA model was designed using detailed paleoenvironmental data from Long House Valley. These data include Palmer Drought Severity Indices (PDSI) (measures of available moisture in the soil) for the region, and estimates of groundwater and levels of erosion at different locations in the valley as they changed throughout the occupation period of the valley. These data were combined to provide an estimate of the overall potential maize productivity available in each cell of the model space (maize is used as a proxy for all sources of nutrition) for each time step (= one simulated year). Cells with similar maize productivity were grouped into seven different types of environmental zones. The agents of an agent-based model need only be distinct entities, and in ethnography and archaeology, the household is frequently considered the most fundamental unit for social, economic, and ritual activity. Thus, in the AA model, the agents are households, and all decisions and actions operate only on households. Each agent is endowed with basic attributes (e.g., life span and nutritional requirements) as well as attributes essential to a horticultural way of life (e.g., movement capabilities and storage capacities). The model rules that determine how agents interact with the environment and with each other are constrained by ethnographic reality.
Activities each time step in the AA model

Determine the yield in each cell (beginning of step) → Simulated and historic settlements in the current step are placed on map

Die

No spots available

Spots available

Find farm and settlement

Give corn to daughter

New household ← Parent household

Yes

No

Is the household fertile, and if so, does it meet the criterion for reproducing?

Die

No spot available

Try to move

Spot available

Yes

No

Is there enough food for the coming year?

No

Yes

Does corn supply of household satisfy present needs?

No

Yes

Die

> Death age

= Death age

Determine present time step’s harvest and add to household’s stores

Figure 20.3 General structure of the original AA model. The model space is 80 × 120 cells with each cell representing a 100 m × 100 m space. Farms can be placed on any productive cell, but only one farm is allowed per cell. Households are placed on unfarmed, less productive cells near farms, with multiple households allowed per cell.

Because the AA model is a household-level model, the life cycle of households is modeled, not the life cycles of the individuals within each household. Figure 20.3 gives a simplified view of this general process. The model begins with a complicated set-up process that first builds the space (an 80 × 120 cell world, with each cell representing a 100 m × 100 m piece of land). The initial model also determines the soil productivity for each cell using the environmental data, creates households and places them randomly on the space, makes and appropriately spaces the adjacent farms, estimates the initial harvest for each household, and places both simulated households and archaeologically verified households on the model space. At each time step, all households follow a similar procedure (see Figure 20.3). If at any step a household does not have enough resources
to meet its nutritional needs, it dies and is removed from the space. Households can also die if they have reached a user-specified maximum age. If resources are adequate and a household has not reached this age, it determines whether there is enough food to survive the coming year. If there is insufficient food, it tries to move, but if a suitable cell cannot be found, it dies or migrates out of the valley (which removes it from the simulation). If there is a cell available that will provide the needed resources (either the present or a new cell) and the household is within the fertile period (the time during which it is allowed to produce a “daughter” household), then it reproduces with a certain probability.

Note, though, that this is reproduction of a household, better thought of as fissioning (one household divides into two), not reproduction of the individuals within the household. New daughter households then need to find suitable locations for their own farm in order to survive. The choice of location for this farm plot is determined by a decision-making algorithm that considers where the parent household is located as well as the environmental resources available in a potential farm plot. Once a farm plot is identified, the daughter household finds a location for itself on the space that is near the identified farm location. If this is successful, the new household is added to the population and the model moves on to the next time step.

Figure 20.4a shows a map of the Long House Valley during a simulation of the AA model, with the locations of both simulated and archaeological households indicated. Figure 20.4b compares the number of simulated and archaeological households during a single run of the model. As this figure shows, simulations of the AA model are capable of reproducing the peaks in population size observed in the archaeological data reasonably well, although the model is not able to reproduce all details of the archaeological data. For example, repeated simulations using the same values that produced Figure 20.4b do not adequately reproduce the archaeological data prior to the first peak (AD 1050) and they have not been able to replicate the thirteenth-century abandonment of the valley.

Structure of the ALHV model
One of the major limitations of the AA model that may at least partially explain this lack of fit is that in real populations, births and deaths occur at the individual level, not the household level. Individuals reproduce and die, and at rates that vary with age. For example, in the base set of parameters for the AA model, a household is assumed to have a chance to fission when it reaches 16 years of age, corresponding, in principle, to the maturation of the eldest child (at an age suggested by ethnographic data). Since individuals are not explicitly modeled, this fissioning process involves the “birth” of a new household, not a single individual.

Recognizing that the demographic birth and death processes affect individuals within households, not the households themselves, the ALHV (Artificial Long House Valley) model was developed. This model incorporates constant age-specific fertility and mortality schedules derived from paleodemographic
data from neighboring Black Mesa and ethnographic data from the greater Southwest to better represent realistic patterns of population growth and decline. The ALHV model is intended to operate at the individual level, in contrast to the household-level demography of the AA model. The agricultural cycle and rules of behavior with respect to farming activities remain analogous to those used in the AA model, however. Therefore, this model has household-level decisions about farming activities, but individual-level demography.

Results
Simulations of the AA model produce population counts similar to those estimated from the archaeological record (Figure 20.4.b), but to better understand the behavior of the model and simulation results, we conducted extensive sensitivity analyses to determine the relative influence of the different environmental and demographic variables underlying the model. Sensitivity analysis involves varying specific parameters, both singly and in combination, that drive the model in order to assess how responsive the model is to changes in these parameters. Parameters are variables whose values are determined from either data or from assumptions derived from the modeler’s knowledge of the situation being modeled; they are thus under control of the modeler. The sensitivity analyses also allow determination of which parameter values provide the best fit to the available archaeological data. For our analyses, we completed 500 simulations for each of the parameter values of interest and used the averages of these runs to compare changes in model output. Ranges for the values of model parameters were decided based on the values that provided the best fit to the archaeological data as determined by the members of the original modeling group (Axtell et al. 2002) as well as ranges chosen by Janssen (2009) and Stonedahl and Wilensky (2010) for additional analyses.

Figure 20.4 Output from simulations of the AA model. (a) Map of the simulated Long House Valley near the time of maximum population size. White squares designate household farms, which are densely distributed throughout the prime agricultural land (darkest gray) at this time. (b) Graph of archaeological (black) and simulated (gray) household counts between AD 800 and AD 1350 exhibiting a “good fit” of the model to data. The model parameters were chosen to maximize the probability that the fit between the model and data is adequate, although specific runs are highly variable and can result in, for example, early extinction, presence of only one peak, overshooting both peaks, etc. Analyses presented in Janssen (2009) indicate that the general pattern is driven by environmental characteristics that influence “harvest parameters” and determine the carrying capacity of the land.
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(a) 

(b) 

Year (AD)

Households

Simulation data

Archaeological data
In addition to the detailed environmental data used to determine the productive capacity of each maize-growing zone through time, the AA model also relies on two additional parameters designed to more realistically estimate actual maize yields. The first, harvest adjustment, is a measure of how much of the potential yield is actually realized for a particular area in a particular year. For instance, a harvest adjustment value of 0.60 means that 60% of the estimated yield for that year was available for consumption and storage. The second parameter, harvest variance, provides a means to simulate differences in crop yields for different farms within the larger environmental zones. The quality of a particular farm plot is calculated by increasing or decreasing the base percentage yield (determined by harvest adjustment) by a small randomly determined amount.

Note the pattern in the archaeological data (see Figure 20.2): population size peaks around AD 1100, declines, and peaks again around AD 1250, before abruptly declining near AD 1300. A well-fitting model will capture this basic picture. Sensitivity analyses reveal that the AA model is especially sensitive to variation in harvest adjustment (see, for example, Figure 20.5). The value for harvest adjustment remains constant for all farm plots throughout the entire model run, so as this value increases, more of the productive potential is realized for each plot of land. In the model, the decision to choose a farm plot is based on its calculated productive potential, so higher values of harvest adjustment result in greater numbers of farm plots available to households. This allows households to survive and reproduce longer, thereby generating a larger number of households overall. Moderate harvest adjustment values produce

![Figure 20.5](image_url) Results of simulations using low, moderate, and high values for harvest adjustment with archaeological population estimates for comparison.
the best fit to the archaeological record because they result in neither over-
or underestimates of productivity and the resulting household counts (see Figure 20.5).

The AA model is less sensitive to changes in the value of \textit{harvest variance} because this parameter essentially just leads to minor modifications of the calculated yield, which is determined largely by the underlying environmental data and the value of \textit{harvest adjustment}. Intermediate values of \textit{harvest variance} produce the best fit to the archaeological data, but even for these best-fit values, the model consistently underestimates the number of households for the first peak while producing household counts close to those generated from the archaeological record for the second peak.

Both \textit{harvest adjustment} and \textit{harvest variance} affect the timing of the peaks in the simulations by affecting the rate at which the simulated population grows. For almost all values of both parameters, we observe a delayed first peak and a consistently early second peak. This is also evident in comparisons of the results of our analyses to those reported by Axtell \textit{et al.} (2002). We find that, for the default values they chose (a \textit{harvest adjustment} of 0.60 and a \textit{harvest variance} of 0.40), the model is reasonably good at capturing the size of both peaks, but is inadequate for capturing the timing of either peak.

This can be explained by a number of factors. The \textit{harvest adjustment} and \textit{harvest variance} parameters determine the valley’s carrying capacity for households during any given period, but the \textit{actual} number of simulated households is directly influenced by the rates of household reproduction (“fissioning”). Household reproduction in the AA model is a function of three modeled components of fertility. The first parameter, \textit{fertility}, is the probability that a household will reproduce itself in any given year during its fertile span. The second, \textit{fertility age}, is the age at which a household becomes fertile, and the third, \textit{fertility ends age}, is the age at which household fertility ceases. Note that the difference between \textit{fertility age} and \textit{fertility ends age} is the length of the fertile span of a household.

Another result revealed by our sensitivity analyses is that the length of the household fertile span strongly influences the probability that simulated populations go extinct before AD 1300, which is the approximate date of abandonment for the region observed in the archaeological record. In order for households to survive consistently through the simulation period, the household-level reproduction rate must be greater than one. In other words, during their fertile span households must reproduce at a rate sufficient to generate at least one daughter household. Simulations suggest that, for \textit{fertility} of 0.125 (the default value used by Axtell \textit{et al.} 2002), the fertile span must be greater than or equal to 16 years to ensure that the population-level growth rate is high enough to sustain the population. Other values of \textit{fertility} lead to different estimates of the critical fertile span needed to ensure populations are sustained.
Varying the three fertility parameters also reveals interesting patterns of population growth, further illustrating the importance of the underlying environmental variables. In simulations where FERTILITY is high or the fertile span is lengthened by either an earlier FERTILITY AGE or later FERTILITY ENDS AGE, the simulated populations grow unbounded until they reach the carrying capacity of the landscape during a particular year. Figure 20.6 shows the results of simulations where the population reaches this carrying capacity. Varying these fertility parameters also affects the timing of peaks. Our results indicate that a FERTILITY of 0.125 is clearly the best value for capturing the AD 1200–1299 peak, and a good value for capturing the AD 1050–1149 peak. A FERTILITY of 0.140 produces the best fit to the archaeological data over the entire length of the simulation (i.e., the simulations reproduce the archaeological population counts much better in non-peak years; therefore, even though the peak years are not estimated well, the curve overall is a better fit). All values of FERTILITY AGE produce relatively good fits for the timing of both peaks, while only the highest values of FERTILITY ENDS AGE capture the timing of the first peak well and no values capture that of the second peak. The effects of FERTILITY AGE and FERTILITY ENDS AGE on peak timing are a function of shortening and lengthening fertile spans and the subsequent effects of span length on the rates of population growth.

Simulations of the ALHV model lead to very different population growth patterns (see Figure 20.7 for a typical run of the ALHV model). Initial sensitivity analyses of this model indicate that population growth has been decoupled from

![Figure 20.6](image-url)

**Figure 20.6** An example of simulations where population estimates reach the carrying capacity of the landscape. The tops of the peaks have leveled off because the population cannot grow larger than the carrying capacity.
underlying environmental constraints, meaning that simulations are now driven solely by demographic parameters. Although the environmental conditions are still used in household decisions about where to farm, the crop yield estimates determined by the `HARVEST_ADJUSTMENT` and `HARVEST_VARIANCE` values for each farm plot do not affect individual households in the ALHV model. This is because the present version of the model is not yet formulated correctly and does not have individuals or households consuming any grown or stored maize. As a result, households are not relocating when their stores get too low (because nothing is depleting the stored maize) and individuals are not dying of starvation due to inadequate maize productivity. When the probability of fertility is high (i.e., the fertile spans are longer than a generation and the age-specific fertility rates are high), the population grows without bound until every productive farm plot on the landscape is filled (Figure 20.8). Once this occurs, households and the individuals within them die or leave the simulation because they cannot find a place to live or farm. We expect that once the environmental constraints are included in the ALHV model, the effects of these constraints will be similar to those seen in AA sensitivity analyses (i.e., the productive capacity, not available space, will limit population growth).

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**Figure 20.7** Typical output from simulations of the ALHV model. The vast majority of runs exhibit a pattern of exponential growth (consistent with the assumption of constant age-specific birth and death rates), followed by a steep decline as the region becomes agriculturally unproductive. Patterns of population growth are independent of the environmental characteristics that influence “harvest variables.” Note: the archaeological data curve is identical to that shown in Figures 20.2 and 20.4b, but the vertical scale has changed so that all simulated data can appear on the plot.
You might now ask, “Why didn’t you make the AA model do what you want the ALHV model to do? Why does it take so long to change the ALHV model so that it will incorporate the environmental constraints?” When developing a new model, it is very important to start with a relatively simplified model so that the effects of the different parameters on the model can be determined, allowing the modeler to assess the specific aspects of the model that are most important. This can generate insights into the importance of different behaviors and interactions.
among real people. The AA model was developed at the household level because the archaeological data available only provide information on households, not on their members, and, as mentioned earlier, the processes related to farming affect entire households. Since the primary goal of the AA model was to test whether an agent-based simulation that was designed to reflect real behaviors could lead to population histories that approximated what was observed in the archaeological data, reaching this goal required modeling how the numbers of households changed over time, which provided simulation data that were of the same general type as the archaeological data.

So why does it take a long time to adapt the AA model so that the model can look at individual-level behaviors? In short, modeling is a very time-consuming process and the necessary changes are more complicated than they might appear. For example, to include unique individuals within a household, agents that represent people in addition to agents that represent households must be included. All the “people” must recognize that they belong to a particular household and all the households must recognize which “people” are part of their “family.” A way for “people” to age as time passes and to marry (i.e., find a suitable mate, “build” a new household, move to that household, and set up an associated farm) must also be built in. Then a method must be designed for them to reproduce and eventually die. In addition, the mechanisms that allow households to die when the people in them die or move away must be included, as well as adaptations to the household reproduction method (fissioning) so that all the individuals assigned to the household are reassigned to either their present household or the new one. What seems to be a straightforward process is actually much more complicated than it appears, and this is true of many of the behaviors you might want to put in a model.

**Discussion**

**Linking simulations to real life**

Simulations of well-designed agent-based models can elucidate much about the characteristics of prehistoric populations and how they might have been affected by changes in fertility, mortality, agricultural productivity, climate change, or other factors. The knowledge derived from the analysis of simulation results must still be linked back to the populations on which the model was based in order to make sense of the results, however. What is known about the Long House Valley population?

Unfortunately, there are no analyses of human remains from the Long House Valley sites because they were intensively surveyed but not excavated. There are, however, extensive analyses of human remains recovered from the adjacent Black Mesa site by the Black Mesa Archaeological Project (Martin et al. 1991). Martin and her colleagues conducted detailed demographic and paleopathological analyses on over 160 burials dating from Basketmaker II (200 BC to AD 200),
Early Pueblo (AD 800–1050) and Late Pueblo (AD 1050–1150) periods. Black Mesa was abandoned at about AD 1150, approximately 100–150 years earlier than Long House Valley.

Exhaustive paleopathological analysis revealed, among other things, distinctive dental pathologies including dental caries (cavities), antemortem tooth loss, which is often associated with high rates of dental caries, dental attrition (tooth wear) (Molnar 1971), and linear enamel hypoplasias (LEH) (Goodman and Rose 1990). Dental caries and antemortem tooth loss are typically linked to agriculturally based diets high in carbohydrates like maize (Schollmeyer and Turner 2004) and dental attrition is most often related to consumption of rough textured food, often the result of processing techniques (Watson 2008). Linear enamel hypoplasias, which result from the disruption of enamel formation during tooth development, can be a strong signal of nutritional or dietary stress or infections (Goodman and Rose 1990). Martin and colleagues also found that a majority of adult skeletons in the Black Mesa skeletal collection had healed cranial lesions due to porotic hyperostosis (PH). In light of recent research, which indicates that PH is an indicator of general poor health and linked to nutritional deficiencies, chronic and acute infections, and underlying environmental and social issues like poor sanitation and unequal access to food (Walker et al. 2009), the results suggest that poor environmental quality and inadequate nutrition were common for the region during the period.

Martin and colleagues divided the 160 skeletons into Early Pueblo (AD 800–1050, n = 49), and Late Pueblo (AD 1050–1150, n = 111) samples. The Early Pueblo sample represents a growing population on the mesa during an extended period of generally good climatic conditions. The Late Pueblo sample represents a period when droughts and other unfavorable climatic conditions likely led to resource stress and, eventually, the abandonment of the mesa circa AD 1150. Strikingly, virtually all of the dental pathologies were higher in frequency in the Late Pueblo period than in the Early (see Figure 20.9), potentially suggesting an increased reliance on maize over other food resources as well as higher incidences of infectious diseases that lead to LEH formation. The frequency differences between Early and Late Pueblo for PH are not significant, but the important observation here is that the lesions are at comparatively high frequency in both periods, affecting 87% of individuals, and the severity of the lesions is higher in the Late Pueblo period.

These findings indicate a population subject to a high degree of nutritional stress with chronic health problems throughout the total occupational period on Black Mesa (Martin et al. 1991). This stress increased through time and was possibly a factor contributing to the abandonment of Black Mesa as environmental conditions gradually worsened throughout the Colorado Plateau region. On Black Mesa, where perennial water sources were not available and people relied on variable and unreliable precipitation for agriculture, the effects of long-term drought would have been dramatic (Euler et al. 1979; Gumerman 1988). Some of the survivors in the Late Pueblo period would very likely have moved into
the Long House Valley where they had social and kin networks, and this may have increased the nutritional challenges for the Long House Valley residents (Gumerman and Euler 1976).

How does this knowledge help our simulations? The main conclusion from the skeletal evidence is that during the period covered by our simulations, and especially near the end of that period, the Black Mesa peoples may have been in relatively poor health, at least partially from nutritional stress. Although the bioarchaeological analyses of the Black Mesa skeletons revealed only non-specific indicators of biological disruption, studies on skeletal collections throughout the Southwest have produced evidence for high infectious disease burdens, especially diarrheal and helminthic infections (Martin et al. 1991; Nelson et al. 1994; Reinhold 1988). Therefore, it is likely the Black Mesa populations were also characterized by increased infectious disease burdens.

Feuding and raiding were also widespread throughout the contemporaneous Southwest and many scholars believe that the levels of violence and civil conflict in some areas rose to those considered to be organized warfare instead of simply low-level interpersonal violence (see Haas and Creamer 1993; Kuckelman 2012; LeBlanc 1999; Lekson 2002). In the Kayenta area, there is virtually no evidence for warfare, raiding, or significant violence (Dean 2010, contra Haas and Creamer 1993). Martin (1997:63–64) reports that the Black Mesa skeletons showed trauma possibly indicative of interpersonal violence, but no evidence for
raiding and warfare. The explanations for variable levels of violence in the prehistoric Southwest include differences in environmental regime, demographic profiles, social complexity, technological differences, and differing historical trajectories (Dean 2010).

Bioarchaeological analyses of the Black Mesa skeletons suggest that our simulations should focus on the stressors of food supply, nutrition, drought, environmental degradation, and disease as well as the primary demographic processes and their effects on the trajectory of these prehistoric populations. Future work will focus, in part, on adapting the model to deal with these additional factors.

It is important to note, however, that the skeletons are from Black Mesa, not from Long House Valley, while the model is designed for the population of Long House Valley. Black Mesa is directly adjacent to Long House Valley and so there were abundant opportunities for interaction between the groups; archaeologists have also found evidence for close connections between the two areas (Fernstrom 1976). Furthermore, our work in progress shows strong correlations between periods of severe drought, which would have been felt more acutely on Black Mesa, and increases in population at Long House Valley, with the timing of the largest of these population increases corresponding to the abandonment of Black Mesa around AD 1150.

Can our simulations help us to understand the results from analysis of the skeletons from Black Mesa? Not yet. The current models do not provide data that can be directly compared to the results of skeletal analyses. Once individual-level demography is incorporated into the ALHV model, however, it will be possible to compare the results of paleodemographic analyses completed by Martin et al. (1991) to demographic data from the simulations. Comparing key demographic measurements such as life expectancy at birth, mean age at death, and population age distributions will provide important information about the populations that once lived in Black Mesa and Long House Valley.

The AA and AHLV models do provide an excellent base for building extended models to address how infectious diseases, nutritional stress, and the presence or absence of warfare may have influenced local populations. The skeletal analyses have already revealed the important influence of these factors on the people in the region but because these factors operate most strongly at the individual level, we need a truly individual-level model to further link the results of skeletal analyses to simulation results and explore these factors in greater detail. The ALHV model is designed to facilitate these explorations, but it is still a work in progress.

**Conclusion**

In the past 20 years, great strides have been made in addressing questions about abandonment of the Colorado Plateau through the use of agent-based modeling. These advances relate both to refining methodologies and testing the plausibility of inferences made on the broad patterns and on site or regionally specific
distinctions. Two projects, the present study in the Long House Valley of northern Arizona and surrounding area and one based in the Four Corners area and focused on Mesa Verde (e.g. Kohler et al. 2010), are using agent-based modeling as an adjunct to other archaeological approaches. That two different projects have turned to agent-based modeling – creating two “test-beds” as it were – presents exciting opportunities to compare complementary approaches and hypotheses. Despite several years of experimentation with these models, there is still much to learn.

Agent-based modeling is not a substitute for bioarchaeological and demographic research; rather, it is a complement to such work – one that allows us to take empirical findings and explore their possible causes and outcomes. Agent-based simulation poses both challenges and benefits. The original modeling of the late 1990s was incomplete on the individual level of analysis. Our research described here has clarified several problems and potential resolutions using sensitivity analysis, and points to new ways to revise and test the models.

We have learned that it is possible to produce a good approximation of the archaeological estimates of population growth and dispersal, and, through sensitivity analyses and other means, we can identify which parameters are most influential in these processes. As we continue to refine our models and hypotheses, we expect to learn much more about the relative importance of the different hypotheses that have been advanced to explain the abandonment of the region, such as nutritional stress, infectious diseases, warfare, and kin-related issues like finding suitable marriage partners. We also intend to develop a model linking Black Mesa to Long House Valley, both because much of our knowledge of the Long House Valley climate and population is derived from analyses of materials from Black Mesa and because there is good evidence that the two populations were very closely associated. Without a good model for both populations, any explanations of the population history of Long House Valley will be incomplete.

With their ground-breaking book *Paleopathology at the Origins of Agriculture* (1984), Cohen and Armelagos brought together scholars researching the rise and evolution of agriculture in a number of populations and locations around the world. Cohen and Armelagos argued that although agriculture was responsible for the growth of human populations globally and even the rise of civilization itself, it did not come without serious costs, including the compromised health of agriculturists. Lessons learned from this and successive works still resonate, and point to the importance of a rigorous biocultural approach to understanding the struggles of human populations in the past. As a pioneer in paleopathology and paleodemography, Armelagos was always encouraging of new approaches and analyses to gain insights into the causes of morbidity and mortality, including the research described here. Our goal going forward is to continue on with the spirit Armelagos would have inspired to make further contributions to our growing knowledge regarding the growth and abandonment of Ancient Pueblo sites on the Colorado Plateau.
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PART VI

Biocultural approaches to inequality and violence
CHAPTER 21
Biocultural perspectives in bioarchaeology

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The patterns of pathology may reveal cultural patterns which are not apparent from the archaeological record… one of the most important aspects of paleopathology is the study of the culture of the populations concerned.

(Armelagos 1969:255)

Introduction

Over the course of the twentieth century, the study of human skeletal remains transformed from a mostly descriptive enterprise, focused on noteworthy clinical oddities and the bony manifestations of diseases, to a fully anthropological specialization within the discipline of biological anthropology. No longer merely concerned with the individual skeleton as a clinical type specimen, bioarchaeologists have sought to better understand the variable ways in which social and cultural processes in antiquity affected the health and well-being of ancient peoples (Armelagos 2003; Buikstra and Beck 2006; Larsen 2015). Moreover, by excavating human remains themselves and working in direct collaboration with archaeologists and ethnohistorians (researchers who interpret historical and ancient texts), bioarchaeologists have been able to produce deeply nuanced analyses of ancient human remains and their cultural contexts. Consequently, this integrated biocultural bioarchaeology has significantly advanced what is known of urbanization, inequality, economic practices, warfare, religious ideologies, cultural exchange, and other aspects of life in the past. It has also directly challenged many of our modern sensibilities about the past: that agriculture represented universally beneficial progress (Armelagos 1969; Cohen and Armelagos 1984), that the quality of everyday life declined in the wake of state collapse (Armelagos 1969), and that slaves in the northern United States were treated better than their counterparts in the south (Blakey 2001), among other topics and insights. It therefore provides a critical counterpoint to “top-down” narratives of history that often reflect the perspectives and
agendas of those in power; using individuals and their populations as the units of analysis, bioarchaeologists are able to provide “bottom-up” insights into the lived experiences and identities of the privileged and the disenfranchised alike (Agarwal and Glencross 2010).

This chapter provides a brief introduction to biocultural bioarchaeology, using several seminal research projects as illustrative case studies. We also discuss our own collaborative research into indigenous life on the northern coast of Peru during the centuries following the Spanish invasion and colonization of western South America. Our own research is strongly informed by a biocultural perspective, one that approaches the humanity as a rich feedback loop of physiological and cultural processes, all occurring within an array of natural and constructed environments across time and geographic space. Our research combines multimethod skeletal analysis, mortuary analysis, and cultural theory to study this integral tableau in a little explored temporal and geographic context.

Background

Analytical foundations: an overview
Before jumping fully into a discussion of seminal research in biocultural bioarchaeology, it is important to first introduce some of the methods most commonly employed in the discipline. This is because the sorts of questions that a bioarchaeologist can pose in a given study of human remains are constrained by the remains themselves: what elements of the skeleton are preserved, whether any soft tissues are present, whether the archaeological context provides any insights into their cultural and temporal context, and what kinds of analysis are permitted by the country or municipality that curates the remains. In that sense, new methods, or the combination of different methods, often allow new kinds of questions; while the methodologies do not drive the theories that underlie a biocultural analysis, in the context of bioarchaeology they certainly frame how those theories are applied.

Paleodiet
The study of paleodiet is a critical component of research on archaeological populations. Studying the ways in which different human groups procure and/or produce their food from their respective environments provides clues about technological advances, economic networks, and relationships between subsistence and cultural dynamics of small groups and large populations alike. The fact that subsistence and diet encompass fundamental aspects of both biological well-being and cultural processes (Roosevelt 1987) underscores the importance of using a biocultural focus when reconstructing and interpreting aspects of paleodiet (Armelagos 1987, 1994). A host of methodologies and analytical perspectives is used to investigate subsistence and diet from a biocultural perspective. Importantly, making a distinction between subsistence – the
food resources that groups pursue and/or produce – and diet – what members of these groups actually consume – allows researchers to examine not only group-level behavior but also individual variation in consumption that might reflect gender (Craig et al. 2009; Hastorf 1996), age (Turner et al. 2007), status (Ambrose et al. 2003), or other aspects of social identity.

Isotopic reconstructions of diet in archaeological samples constitute an important and now common area of bioarchaeological research, studying the relative importance of constituent food types to individual diets. An isotope is a variant of an element that differs in the number of neutrons in the nucleus, which changes its atomic weight. In biological systems, lighter isotopes, those that have fewer neutrons in the atomic nucleus, enter more easily into physical or chemical reactions such as digestion, tissue formation, and respiration, than their heavier counterparts. This results in differing abundances of different isotopes for the dominant elements in ecosystems, and foodwebs in particular. Many of the elemental isotopes in foodwebs undergo predictable changes in their proportions as plants are consumed by animals, which are then consumed by other animals. As more of the light isotope is consumed by processes of metabolism and excretion at every step in a foodweb, more of the heavier isotope is left behind. This increase in the relative abundance of the heavy isotope is known as enrichment, and the process by which that enrichment occurs is referred to as fractionation.

Studying the processes of fractionation in the tissues of different plants and consumers can be used to not only characterize existing foodwebs, but reconstruct ancient ones as well. The absolute differences in the proportions of different stable (non-radioactive) isotopes used to reconstruct the diets of organisms in foodwebs are extremely small. Because of this, the ratios of these isotopes are typically expressed in parts per thousand, or per mil (‰), in delta (δ) notation relative to an established geological or environmental standard (reviewed in Ambrose 1993; Schwarcz and Schoeninger 1991). Moreover, different bodily tissues develop at different stages during life. Some tissues, such as tooth enamel and hair, become metabolically inert after they form, while others, such as a bone, undergo continuous metabolic turnover throughout life. These different tissues thus preserve the isotope values from common elements such as carbon, nitrogen, and oxygen, incorporated at different points during an individual’s life. Consequently, studies that incorporate isotopic analysis of multiple preserved tissues (most commonly bone and tooth enamel, though occasionally hair or other soft tissues preserve as well) are able to reconstruct the types of foods consumed and the types of environments inhabited over the course of individuals’ lifespans (see Price and Burton 2010). The two elemental isotope ratios most commonly utilized for studying paleodiet are carbon-13 relative to carbon-12 (δ^{13}C), and nitrogen-15 relative to nitrogen-14 (δ^{15}N).

Isotopic studies of ancient populations have provided critical insights into prehistoric subsistence such as those related to movement between regions (Aufderheide et al. 1994; Turner et al. 2010; White et al. 2009) and shifts from nomadism to sedentism (Benfer 1990). Changes in subsistence have also been
related to aspects of state formation and consolidation, including increased maize production and consumption (Finucane et al. 2006; Sandness 1992), access to meat (Hastorf 2001), gendered and status-based access to high-status foods (Hastorf 1996; Ubelaker et al. 1995), and shifting relationships with imperial cores over time (Slovak 2007).

**Paleopathology**
The study of pathological conditions – lesions, signs of disrupted growth, and other skeletal symptoms of stress – has a long history in biological anthropology, and remains one of the foundations of bioarchaeology (Grauer 2012; Larsen 2015). It also has a long history of lively debate, from what causes particular conditions such as porotic hyperostosis (reviewed in Turner 2015), porous lesions on the cranial vault, to whether the field is sufficiently grounded in evolutionary and biocultural perspectives (Zuckerman et al. 2012) or whether it is too atheoretical and descriptive (Armelagos and Van Gerven 2003). Some of the most commonly studied pathological conditions are summarized in Table 21.1; more in-depth discussion of these and other conditions can be found elsewhere (Buikstra and Ubelaker 1994; Goodman et al. 1984). When employed with a biocultural framework that draws on scholarship in skeletal biology, medical anthropology, and epidemiology, analyses of these conditions can provide significant insights into the health and well-being of ancient populations. These insights are particularly enriched when they are examined in contexts of ancient inequality, cultural complexity, and culture change.

**Social identity**
Studying the ascribed and achieved identities of living peoples in ethnographic context is itself a complex endeavor, never mind reconstructing the identities of peoples who have long since faded into antiquity. To estimate the identities of archaeological individuals, bioarchaeologists rely on a combination of data, all of which provide different types of answers to the question “Who was this person?” These lines of evidence include proxies of genetic ancestry such as the dimensions and morphological traits found in the permanent dentition, or even ancient nuclear or mitochondrial DNA. Of equal importance is material culture, i.e., the styles of interment from which individuals are recovered and the objects found in association with their bodies, and associated time period or cultural phase.

Finally, a different combination of isotopes from those of carbon and nitrogen described above can be used to estimate the geographic origin of individuals and track their movements between geographic regions during their lifetimes (Price and Burton 2010). Isotopic ratios of strontium ($^{87}$Sr/$^{86}$Sr) and lead ($^{208}$Pb/$^{204}$Pb) serve as proxies of local geology, because isotopes of both elements are incorporated from local bedrock and ore deposits into soils. Plants absorb strontium isotopes from soils, where they thereby enter into and cycle through foodwebs (Price et al. 2002). Lead isotopes are inhaled or ingested directly by animals
Table 21.1  Commonly studied pathological conditions in human skeletal remains.

<table>
<thead>
<tr>
<th>Pathological condition</th>
<th>Description</th>
<th>Cause(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Porotic hyperostosis and cribra orbitalia</td>
<td>Spongy-appearing lesions on the external surface of the cranium and/or the upper margins of the orbits</td>
<td>Chronic anemia resulting from B vitamin deficiency, iron deficiency, parasitic infection, and/or hypoxia</td>
</tr>
<tr>
<td>Linear enamel hypoplasia</td>
<td>Horizontal lines apparent on the enamel surface of the dentition, particularly the anterior teeth</td>
<td>Interrupted growth during tooth crown formation resulting from diarrheal diseases, high fevers, and/or other signs of systemic stress</td>
</tr>
<tr>
<td>Osteomyelitis</td>
<td>Rough, uneven apposition of new bone on the shafts or other surfaces of bones, sometimes with cloacae (holes for pus drainage)</td>
<td>Bacterial infection that spreads to infect bone cells and often becomes systemic</td>
</tr>
<tr>
<td>Periostitis</td>
<td>Striated apposition of new bone on the shafts of limb bones, especially the tibia</td>
<td>Inflammation of the periosteum (outer membrane of bones) due to infection or localized activity-related stress</td>
</tr>
<tr>
<td>Caries</td>
<td>Cavity lesions, often darkly stained, on the surface of the tooth; may be accompanied by abscessing of the surrounding bone (bony holes for pus drainage)</td>
<td>Corrosion of the enamel from bacterial activity on the tooth surface, often penetrating the dentin and resulting in infection of the root and surrounding jaw; often associated with starch-heavy diets</td>
</tr>
<tr>
<td>Osteopenia/osteoporosis</td>
<td>Tell-tale thinning of the cortical layer of bone and loss of spongy trabecular bone (visible if the bone is sectioned or on radiographs); bone is often uncharacteristically lightweight</td>
<td>Loss of bone density due to calcium deficiency and/or inactivity</td>
</tr>
<tr>
<td>Fracture</td>
<td>Any breakage of bone, whether healed or active at the time of death, caused by impact trauma</td>
<td>Accidental injury or interpersonal violence</td>
</tr>
<tr>
<td>Growth stunting</td>
<td>Shorter than expected limb bones relative to the rest of the skeleton, or an estimated skeletal age that lags behind estimated dental age</td>
<td>Systemic stress, usually from malnutrition, chronic infection, or a combination of the two</td>
</tr>
</tbody>
</table>

from air-blown soil and dust particulates (Kamenov 2008). Oxygen isotopic values ($^{18}$O/$^{16}$O or $\delta^{18}$O) reflect the isotopic composition of the water that an individual drank and metabolized into their bodily tissues during their life; the composition of that water is shaped by the temperature, aridity, seasonality, and other aspects of the local environment (Price and Burton 2010). These isotopic variables are thus instrumental in identifying recent immigrants to a site, as well as foreigners who had long since settled in the region where they
were found. When analyzed together, a combination of genetic, geographic, and cultural data can be used to better understand not just identity on an individual level, but also the complexities of identity among groups and whole societies (Knudson and Stojanowski 2008).

This holistic and integrated approach is also critical in order to avoid a reductive or narrow definition of identity, or one that employs long debunked concepts of biological race, discussed in more detail later in this chapter. One that has been particularly contentious in evolutionary approaches to paleopathology is the study of biodistance using skeletal and dental non-metric/discrete and metric traits. Using biodistance analysis, researchers can potentially infer patterns of disease exposure, dietary adaptation, and gene flow through integrated analyses of traits and pathological lesions in different populations (Ortner 2011:7), though analyses thus far have mainly focused on integrated analyses of biodistance and trauma (Sutter and Verano 2007). These analyses have been decried as “return[ing] to old questions of racial history (often cast in terms of biological distance)” and inattentive to both the anatomical functions and environmental malleability of skeletal and dental traits (Armelagos and Van Gerven 2003:60). They have also been defended as holistic and reasoned methodologies, as “many regional histories (and cultural transformational processes) have been further enhanced by an appreciation for the genetic structure of the populations involved” (Stojanowski and Buikstra 2004:2). Indeed, the applications of biodistance analysis have moved well beyond the typological, race-based analysis of traits and toward a more theoretically rich examination of phyletic variation, i.e., subtle evolutionary change within populations that might shed light on lineages or local ancestry – as one component of identity among many (Corruccini and Shimada 2002; Stojanowski 2010; Stojanowski and Schillaci 2006; Stojanowski et al. 2007; Sutter 2000; Sutter and Verano 2007).

**Biocultural bioarchaeology**

Notably, several of the studies referenced below are drawn from the same large, well-preserved skeletal sample from two site complexes in what is now Sudan: Wadi Halfa and Kulubnarti. Almost 800 exceptionally well-preserved skeletons were excavated from the Wadi Halfa area in the 1960s as part of a salvage archaeological excavation before the region was flooded by the High Aswan Dam (Hassan 2007); over 200 additional skeletons were recovered several decades later in a similar excavation of the Kulubnarti site (Van Gerven et al. 1973). This combined collection of human remains spans roughly 8000 years, from the Mesolithic through medieval Christian periods, and has also become the most thoroughly researched skeletal sample in the world. It also serves as a prime example of how a bioarchaeological approach that combines myriad rigorous methodologies with a focus on both biocultural evolution among populations and individual variation in diet, activity, and disease can revolutionize our view of the past.


**Imperial decline in ancient Nubia**

Archaeologists have long assumed that the decline and collapse of state-level societies is consistently associated with declines in health and well-being. However, a seminal study by Armelagos (1969) challenged this tenet. Specifically, Armelagos’s in-depth paleopathological analysis revealed that the two centuries following the end of the Meroitic kingdom in AD 350 were not periods of cultural decline and instability. Instead, it appeared that the intermediate X-Group (AD 350–550) experienced improved health – slightly lower frequencies of fracture and other signs of violent trauma, and slightly higher average ages at death (i.e., longer average lifespans) – relative to the earlier Meroitic period (350 BC–AD 350). This was an important contribution because it used empirical data from human remains to critique the notion that large-scale states reliably brought stability to the regions that they dominated, and that discord and suffering followed their decline, akin to Europe’s *Pax Romana* and subsequent Dark Ages (Ferguson 2004).

The Nubian remains from Wadi Halfa indicated that aspects of everyday life actually improved in the hinterland regions of the Meroitic kingdom in the absence of its domination. A later isotopic study of Wadi Halfa remains (White and Schwarcz 1994) revealed significant changes in diet among X-Group individuals relative to earlier Meroitic and later Christian phases. In particular, X-Group individuals appear to have consumed significantly more millet and sorghum, which corresponds with archaeological evidence of lower water levels in the nearby Nile River and suggests a significant change in subsistence practices following the Meroitic decline. Moreover, skeletal analysis of the Wadi Halfa remains (White and Armelagos 1997) revealed significantly higher frequencies of osteopenia, or reduced bone density, among the X-Group females relative to earlier Meroitic and later Christian phases. This bone thinning did not appear to be linked to a poor diet, however, as there was no difference in carbon or nitrogen isotopic values among females with versus without osteopenia. Instead, these results suggested physiological factors such as pregnancy or stresses affecting kidney function as the more likely causes. These studies and others like them have helped to highlight the importance of combining estimates of diet and estimates of nutritional adequacy to gain a fuller understanding of how cultural shifts affected health outcomes across different time periods.

**Up-ending the racial paradigm in Nubia**

Part of the impetus behind developing the biocultural approach in biological anthropology as a whole is a desire among researchers to move beyond the sordid history of the field and its ties to the race-based (pseudo)science of the eighteenth and nineteenth centuries (Brown and Armelagos 2001). For centuries, European scientists concerned themselves with describing and categorizing groups of people as if they were subspecies or biological types. They measured the dimensions of living heads or archaeological skulls and used
these data and terms like “Negroid,” “Mongoloid,” and “Caucasoid” to argue (conveniently) for the inherent superiority of white Europeans (Gould 1996).

A shift toward a biocultural perspective first developed in the mid-twentieth century. It stemmed from a declining interest in description and racial classification in anthropology, largely in reaction to how race-based research was used by the Nazis to justify genocide during World War II (Armelagos and Goodman 1998; Blakey 1987; Zuckerman et al. 2012). Biological anthropologists became interested in the shifting focus toward populations rather than type specimens that was taking root in evolutionary biology (Warren 1951), and the emphasis on the functional and adaptive aspects of human variation that was part of what became known as “the new physical anthropology” (Washburn 1951, 1953).

This view of human races as biologically meaningful categories, from which one could explain not only physical variation such as skin pigmentation or body size, but behavior and capability as well, nonetheless persisted in biological anthropology. Carlton Coon’s (1962) *The Origin of Races* even argued that human races were subspecies that branched from separate populations of *Homo erectus*. Archaeological research was also used to argue that these biological differences manifested in the technological sophistication, or supposed lack thereof, found at archaeological sites worldwide (Maceachern 2006). When impressive architecture or technological advances such as metallurgy were uncovered at Native American and African archaeological sites, such sophistication was interpreted as the work of prehistoric European “Moundbuilders,” in the case of the Americas (Echo-Hawk and Zimmerman 2006), or light-skinned “Semitic” immigrants in the case of East Africa (Maceachern 2006:82; Trigger 1994).

Such was the assumption in studies of cultural evolution along the Nile River in Nubia, until it was empirically challenged by the work of bioarchaeologists analyzing the large sample of human remains from Wadi Halfa and Kulubnarti. Researchers sought to address the suggestion that advances in agricultural technology and architecture in the region were due to the arrival of a lighter-skinned group of immigrants, possibly from the Mediterranean region, rather than the work of indigenous Nubians. Bioarchaeologists quantified aspects of the cranial morphology (Van Gerven et al. 1973, 1977) and dentition (Greene 1972) in Meroitic, X-Group, and Christian-era (350 BC–AD 1300) skeletal samples, and concluded that the same biological population had continuously occupied this region of Nubia. This finding ran contrary to the widespread assumption that a Negroid-Caucasoid admixed group replaced an earlier, less culturally complex “Negroid” population which had abandoned the region.

This was a highly significant study in that it empirically refuted race-based interpretations of Nubian cultural evolution – namely that cultural complexity was the result of people with European ancestry arriving in the region. Instead, it pointed to *in situ* cultural evolution among a homogenous indigenous African population, using the very analyses (measuring skulls) that had been used for so long in perpetuating racial typologies. The key difference was that, by employing a biocultural framework, these researchers focused on the functionality of
the dentition and facial musculature rather than merely describing the traits themselves. By recognizing that teeth and the surrounding facial bones are principally a toolkit for chewing food, Van Gerven and colleagues suggested that the changes in skull features between the Meroitic and Christian eras resulted from changes in their diet; softer foods relieved a selective pressure on more robust facial features. This attention to functionality and the links between biology and behavior directly undermined a lingering racial paradigm using rigorous methodologies and a broader, biocultural lens of interpretation.

This large, multivariable, and diachronic research program on Nubian populations has inspired similar research programs in bioarchaeology. Investigating temporal trends in health, disease, diet, and mobility in other global regions and time periods is now the norm for many bioarchaeological studies (Stojanowski 2010). For example, Clark Spencer Larsen and colleagues have conducted long-term studies on human remains recovered from coastal Georgia and Florida. The collective aim of these studies was to assess the impacts of the transition from foraging to farming and the effects of European contact and colonization on indigenous Native Americans. Larsen and his team (Larsen 2001; Larsen et al. 2000, 2001a,b) conducted comparative analyses of biological stress markers in bones and teeth, including stable isotope reconstructions of diet and residential mobility, measures of biological distance, and limb robusticity (an indicator of load-bearing and activity-related stress). Larsen and colleagues similarly expanded the scope of their study of postcontact populations to include those across North, Central, and South America, Hawaii, and Oceania, producing an influential edited volume describing the varied effects of European colonization on different indigenous populations (Larsen and Milner 1994). The studies in this volume empirically demonstrated the ways in which European diseases and oppressive colonial policies devastated Native American populations and the lasting effects of these processes on their economies, diets, population mobility, and overall fates. Importantly, though, the volume was careful not to imply that the effects of European domination on Native populations were uniform. Instead, the constituent studies discussed the ways in which colonial policies differentially impacted particular subgroups, such as women (Reinhard et al. 1994), or how they changed through time (Cybulski 1994).

**Case study: understanding European contact in the Americas**

An important gap in this otherwise excellent comparative analysis of American colonialism was an inclusion of South American populations, prompting us to initiate a collaborative bioarchaeological research project of colonial-period Peru, in the north-west region of the continent along the Andes mountain range (Figure 21.1). In particular, we are interested in understanding the effects of Inca domination (AD 1450–1532), followed by Spanish conquest and colonization
(AD 1532–1821), on the diets, residential mobility, nutritional status, disease prevalence, and cultural evolution of populations who lived in the Lambayeque Valley Complex on the desert north coast of what is now Peru (Klaus 2008; Klaus and Alvarez-Calderón in press; Klaus and Tam 2009, 2010; Turner et al. 2012). Unlike other coastal valleys to the north and south, the Lambayeque region contains five river drainages and a diversity of rich microenvironments. Archaeological research has found evidence of complex cultural organization in this arid region starting about 2800 BC (Alva Meneses 2012). The Lambayeque Valley Complex was an epicenter of both Early Moche (AD 100–350/400) and Late Moche (AD 550–750/800) chiefdoms (Alva and Donnan 1993; Shimada 1994, 2000), during which time a particular style of material culture and mortuary treatments emerged that has been attributed to the Muchik ethnic group (Klaus and Shimada 2003). The Lambayeque Valley then became the heartland of the influential Middle Sicán theocratic state and a hinterland of the
highland Wari Empire, ca. AD 550–1000. By the late fourteenth century, the predatory Chimú Empire centered to the south incorporated Lambayeque into its territory. At this time, the Lambayeque Valley Complex probably contained a third of all land under cultivation and a full third of the human population of the entire Peruvian coast (Kosok 1965).

During the fifteenth century, the region was annexed into the highland Inca Empire, the largest and most complex indigenous state ever to exist in the Western hemisphere. However, this domination was short-lived; the Inca state reigned for only a century before it was destroyed by the Spanish invasion in AD 1532 and the subsequent conquest of the region. The Spanish exploited both the singular agroeconomic potential of the region and indigenous labor for centuries before Peru’s eventual emancipation as an independent republic in 1821. Importantly, throughout all the centuries in which control was imposed from outside the Lambayeque Valley – direct or indirect, coastal or highland – it appears that the local population maintained some form of the Muchik ethnic identity rooted in the early Moche period (Klaus and Tam 2015).

**Methods and materials**

Drawing on the integrated approach of biocultural bioarchaeology, we have incorporated an array of analytical perspectives to investigate the effects of the imposition of Spanish colonial rule on indigenous diet and health on the northern Peruvian coast over the course of the colonial period (AD 1532–1760). Our research methods include isotope biochemistry, osteology, and mortuary analysis. These are used to reconstruct aspects of diet, disease, demography and mobility. Further, we interpret our data in comparison to similar analyses of earlier archaeological sites in the region, as well as published analyses of historical written accounts in surviving Spanish chronicles (Ramírez 1996; Rubiños y Andrade 1936). We also incorporate anthropological theories of identity, ethnicity, adaptability, and social stratification (for example, Knudson and Stojanowski 2010). In doing so, we are able to open a new window into the lives of Andeans whose existence was turned upside down by the arrival of the Spanish, and provide new insights into how they adapted, adjusted, and endured within the new socioeconomic realities of the centuries that followed.

Our collaborative research is focused on two sites in the Lambayeque Valley, San Pedro de Mórrope and Eten (Figure 21.2), that may have been administered in different ways by Spanish colonial officials (Klaus and Alvarez-Calderón in press). Under Spanish control, the Lambayeque Valley became an important center of agricultural and pastoral production. However, unlike other regions of the Andes, Lambayeque lacked a Spanish chronicler and this has limited direct insights into the effects of colonialism on the region’s Muchik populations (Ramírez 1996). Nonetheless, ethnohistoric sources indicate that while the disruption wrought by the Spanish during the sixteenth century was minimal,
within a century the region had been transformed (Ramírez 1996). Lambayeque was reorganized into expansive haciendas focused on monocropping sugarcane and alfalfa production in order to manage vast herds of cattle and pigs. Muchik communities were forcibly resettled into towns called reducciones; these communities were densely populated and rigidly controlled by the Spanish, and in many cases, established in areas with substandard water sources and marginal land (Ramírez 1996). In colonial Lambayeque, the environment was degraded by agricultural intensification and overgrazing, and damage to the pre-Hispanic irrigation canals led to desertification of the land at the valley’s fringes. Indigenous political systems that promoted reciprocity and redistributive networks were dismantled, and the Muchik were forced into a proto-capitalist economy in which they were structurally disenfranchised (Klaus 2008).
As was the case in Mesoamerica and southern regions of North America, the Spanish aimed to maximize their extraction of natural resources by coercing indigenous labor while converting the indigenous peoples into tax-paying Christians. However, the contact-era bioarchaeological research in North America described above highlights how varied the degrees of change in diet, demography, disease burden, and identities were in different parts of the continent, and even between nearby regions. Therefore, a central aim of our research is to reconstruct patterns of diet, demography, disease, and trauma among the human remains from these two sites, San Pedro de Mórrope and Eten, to examine the effects of Spanish policies between the Early (AD 1532–1620) and Middle/Late (AD 1620–1760) Colonial periods.

Moreover, we also aim to compare these patterns between the two sites. Mórrope abuts the Sechura desert and its landscape is characterized by saline and nutrient-poor soils and water insecurity. Ethnohistoric accounts (Rubíños y Andrade 1936) portray Mórrope as a marginalized Muchik community burdened first by conflicts over water access and then by Spanish labor demands. In contrast, Eten’s landscape is rich in resources, including water and both terrestrial and aquatic biodiversity. Paleobotanical evidence from colonial Eten reveals the presence of maize, beans, chenopods such as quinoa, peppers, oranges, bananas, gourds, potatoes and other tubers, guanabana, and algarrobo fruits (Castillo 2011). Faunal evidence indicates the presence of sheep, goats, cuy (guinea pigs), dogs, rabbits, ducks, pigs, cows, and seabirds, as well as Donax sp., crabs, and fish (del Alcazar 2011; Puse 2012). Eten may therefore have been a more attractive site to the Spanish for economic extraction and political administration of their indigenous subjects.

**Results and discussion: paleodiet, paleopathology, and identity in colonial Lambayeque**

The results of our analyses have identified several interesting trends. Our carbon isotopic data (δ^{13}C; Figures 21.3, 21.4) indicate a diet at Eten that was dominated by C_{4} resources (Turner and Klaus 2015). C_{4} resources include cereal grains like maize and amaranth (kiwicha), meat from grass-eating herbivores such as llamas, and marine resources. C_{3} plants utilize a different photosynthetic pathway, and include grains like quinoa, vegetables like potatoes and squash. C_{3} resources also include the meat of animals that eat C_{3} plants. In comparison, the individuals at Mórrope had more variation in their diets and, in general, a more mixed diet of C_{3} and C_{4} plant and animal resources but protein from lower trophic levels. Nitrogen isotopic values from bone collagen, which primarily reflect the source of protein in the diet, are also distinct between Mórrope and Eten. Individuals from Eten had higher mean δ^{15}N values overall, suggesting that they were consuming a greater proportion of their dietary protein from terrestrial and aquatic animals such as llamas, cuy, and fish, rather than from plant sources such as legumes or protein-rich grains (Turner and Klaus 2015).
Our paleopathology data (Table 21.2) indicate that, at Mórrope, rates of non-specific periosteal infection and childhood anemia were high (over 46% and over 53%, respectively); individuals who died as children or adolescents also experienced growth stunting, compared to skeletal samples from earlier time periods in the region (Klaus and Tam 2009). In contrast, frequencies of enamel hypoplasia are unexpectedly low. Instead of reflecting better health,
though, this may have been produced by a shift towards higher mortality among children. This spike in childhood mortality would indicate an increase in the types of stressors that individuals did not survive and from which they had no chance to recover. This interpretation – that fewer signs of skeletal stress might actually indicate more severe and lethal stressors – is known as the Osteological Paradox (Wood *et al.*, 1992). The prevalence of degenerative joint disease (DJD) was elevated in multiple joint systems in Mórrope, and this is consistent with the ethnohistoric descriptions of intense physical labor extraction. High frequencies of tooth caries and teeth lost antemortem (before death) among the Mórrope sample suggest a dietary shift towards greater reliance on starchy cultigens (Klaus and Tam 2010). This is because starches feed the bacteria that live on the

### Table 21.2 Summary pathological condition frequencies and prevalence at Mórrope and Eten (broken down by time period) (adapted from Klaus and Alvarez-Calderón, in press).

<table>
<thead>
<tr>
<th>Pathological condition</th>
<th>Mórrope (\frac{N_{\text{affected}}}{N_{\text{total}}};% \text{ affected})</th>
<th>Eten (\frac{N_{\text{affected}}}{N_{\text{total}}};% \text{ affected})</th>
<th>(\hat{\text{OR}}^{*})</th>
<th>Interpretation**</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enamel hypoplasias</td>
<td>37/155 (23.9%)</td>
<td>95/363 (26.2%)</td>
<td>1.13</td>
<td>1.13 times more common in Mórrope; no significant difference</td>
</tr>
<tr>
<td>Porotic hyperostosis</td>
<td>165/309 (53.4%)</td>
<td>65/379 (17.2%)</td>
<td>5.69</td>
<td>5.69 times more common in Mórrope; significant difference</td>
</tr>
<tr>
<td>Non-specific periostitis</td>
<td>28/60 (46.7%)</td>
<td>17/106 (16.0%)</td>
<td>5.75</td>
<td>5.75 times more common in Mórrope; significant difference</td>
</tr>
<tr>
<td>DJD – shoulder</td>
<td>95/139 (68.3%)</td>
<td>39/107 (36.4%)</td>
<td>3.80</td>
<td>3.8 times more common in Mórrope; significant difference</td>
</tr>
<tr>
<td>DJD – elbow</td>
<td>80/115 (69.6%)</td>
<td>61/121 (50.4%)</td>
<td>2.17</td>
<td>2.17 times more common in Mórrope; significant difference</td>
</tr>
<tr>
<td>DJD – wrist</td>
<td>23/53 (43.4%)</td>
<td>17/98 (17.3%)</td>
<td>4.02</td>
<td>4.02 times more common in Mórrope; significant difference</td>
</tr>
<tr>
<td>DJD – knee</td>
<td>76/123 (61.8 %)</td>
<td>34/98 (34.7%)</td>
<td>3.73</td>
<td>3.73 times more common in Mórrope; significant difference</td>
</tr>
</tbody>
</table>

* \(\hat{\text{OR}}\), or common odds ratio value, for each pathological condition. This summary statistic measures overall prevalence differences between the two samples.

** Differences are at 1% significance; this means that the probability that these differences are due to random chance is less than 1%.

DJD, degenerative joint disease.
surfaces of teeth and secrete acidic compounds that break down tooth enamel and initiate decay (Hardie 1982; Holloway 1983).

In contrast, the Eten sample exhibits lower frequencies of all of the same indicators compared to Mórrope (see Table 21.2); however, they do exhibit higher frequencies of fractures, suggesting that at least some of the people of Eten engaged in physically hazardous behaviors (Klaus and Alvarez-Calderón, in press). A lower frequency of caries and teeth lost antemortem suggests a diet in Eten that was less dominated by starchy carbohydrates. This interpretation is supported by the nitrogen isotopic evidence ($\delta^{15}$N) from bone collagen summarized above, which suggests that individuals at Eten consumed more of their dietary protein from terrestrial animals and fish. This dietary difference, particularly in the source of dietary protein, may have played a role in the lower prevalence of pathological conditions at Eten, and likely reflects the richer resources of Eten’s environment.

If we look not just at variation between the two sites but variation between the Early/Middle and Middle/Late Colonial sequences from both, equally interesting patterns emerge. While the residents of Mórrope appear to have had worse health outcomes than the residents of Eten, this does not mean that the Eten population enjoyed a more comfortable existence across the entire colonial period. Paradoxically, Mórrope’s marginal environment may have actually buffered its population from some of the most catastrophic effects of the Spanish presence, because the Spanish had less interest in establishing economic production at Mórrope than they did at Eten. Multiple waves of epidemic diseases ravaged Peru’s north coast in the late sixteenth and seventeenth centuries (Buikstra and Cook 1980), and zooarchaeological evidence indicates a significant rat population in Eten (del Alcazar 2011) which may have carried infectious diseases with them. Several of the mid-sixteenth century burials in Eten appear to be mass graves (Duday 2009), while several others were double interments. There was no evidence of chronic poor health in any of these skeletons, which could actually suggest that individuals died quickly, possibly from an acute epidemic like smallpox, before they could manifest any skeletal symptoms. In contrast, there are no burial contexts at Mórrope that suggest mass graves or multiple interments (Klaus 2008), suggesting that patterns of mortality at Mórrope may have been different from those at Eten.

A recent study (Garland 2014) examined microscopic defects within the tooth enamel, known as Wilson’s bands, to reconstruct early-life stress in a small sample of individuals from Eten between the Early and Middle/Late Colonial periods. Internal enamel microdefects, such as Wilson’s bands (Figure 21.5), have been used as indicators of a broad range of infant, juvenile, and maternal stresses, often stemming from infection or nutritional deficiencies and often linked to infants’ supplementary feeding and weaning from breast milk (Fitzgerald et al. 2006). Enamel is laid down in incremental layers that follow daily circadian rhythms, and does not remodel after it forms. Therefore, any disruptions in enamel formation due to stressors such as diarrheal or febrile (fever) diseases
Garland’s (2014) analysis revealed a higher prevalence of Wilson’s bands among the Early Colonial period individuals than among those associated with the Middle/Late Colonial periods. This result could suggest that the Muchik population at Eten may have begun to adapt to Spanish occupation and were able to access adequately nutritious food and sufficiently clean water for successful infant supplementary feeding. Alternatively, it could be argued that children in the Early/Middle Colonial period were surviving stress and disease events, whereas the children of the Middle/Late Colonial period were dying before skeletal signs of stress could manifest; this echoes aspects of the Osteological Paradox described earlier (Wood et al. 1992). Interestingly, Garland (2014) also compared the frequencies of Wilson’s bands to the age at death for each individual to see if early-life stress was associated with a shorter lifespan among the Eten sample. A similar study (Armelagos et al. 2009) identified a similar association between linear enamel hypoplasias and age at death in a range of archaeological samples from different continents and time periods. Garland’s (2014) analysis found that the majority of individuals with observed Wilson’s bands at Eten perished within 12 years of birth; conversely, the majority of individuals without observed Wilson’s bands died after the age of 12.

These Wilson’s band results suggest that stressors endured during infancy and early childhood among the Eten sample, when tooth crowns are forming, had long-term implications for their overall health and well-being. These stressors
likely included supplementation of maternal breast milk with contaminated water and/or nutritionally inadequate foods; oxygen isotope results may provide some support for this interpretation. We found no significant difference in mean bone carbonate oxygen isotope values between Eten and Mórrope. However, at Eten the average bone carbonate oxygen isotope value among the individuals associated with the Early Colonial period differs slightly but significantly from those associated with the Middle/Late Colonial period (Turner and Klaus 2015). This suggests that at some point during the colonial periods, individuals at Eten shifted in their patterns of water consumption, which would be consistent with the possibility that voluntary migration and/or forced population resettlement drew a greater diversity of people into Eten's crowded and unsanitary reducciones.

All of these results suggest that while Spanish conquest and colonization of the Lambayeque Valley Complex resulted in profound upheaval to the social and economic lives of indigenous groups in the region, the biological effects of this upheaval were not uniform. Moreover, because our analyses draw on a number of methodologies and incorporate archaeological and ethnohistorical context, we have been able to identify subtler signs of stress in the colonial period, such as the possibility of epidemics at Eten, and reduced lifespans due to stress, as well as more obvious ones, such as the dramatic frequencies of skeletal pathology overall. Importantly, we have been able to interpret the results of these multifaceted analyses in a way that allows us to better understand the ways in which sociopolitical processes became written on the bodies of indigenous Lambayeque communities through time.

**Conclusion**

Bioarchaeology has come into its own as a fully biocultural discipline, and is contributing exciting research to understandings of human health, culture, and behavior through time and space. By employing the biocultural approach, bioarchaeologists have sought to give a voice to those who so often passed anonymously into history, and have done so with a combination of methodological rigor and anthropological interpretation. In this chapter, we have introduced some of the seminal research in this field and described our own ongoing research as well, and hope that readers will dive further into this stimulating and dynamically biocultural area of inquiry.

**Acknowledgments**

We would like to thank Molly Zuckerman and Deb Martin for graciously inviting us to contribute to this volume. The work discussed here was supported by the Wenner-Gren Foundation for Anthropological Research, the National Science
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**Notes**

1 See Larsen (2015) for an in-depth review.

CHAPTER 22
The poetics of violence in bioarchaeology: Integrating social theory with trauma analysis

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Violence is the term used rhetorically, not analytically, and its most constant meaning is that it signals acts whose legitimacy is itself an object of conflict.

(Stewart and Strathern 2002:9)

Introduction

The word “violence” is loaded with meaning. Language fails to adequately capture the concepts and meanings embedded in this eight-letter word. The role of violence theory in the scientific community is to try to ascertain the causes and consequences of violence. For the philosopher, violence theory exists to examine the concept of violence, not violence itself, and, for the moralist, the aim is the practical elimination of violence by changing the world (Burgess-Jackson 2003). To my mind, these three realms are not mutually exclusive, but it is important to distinguish between them for, although they inform one another, they have uniquely specific goals, and, when their disciplinary boundaries are not observed, confusion arises.

The use of social theory and violence theory, particularly in bioarchaeology, has become increasingly more popular (Agarwal and Glencross 2011; Klaus 2012; Martin and Harrod 2015; Martin et al. 2012; Pérez 2012; Pérez et al. 2008; Sofaer 2006; Walker 2001). However, too often violence theory is used as an adjective to describe a type of violence rather than as a mechanism for exploring the concept of violence that is bound to the place and time of a specific event. Ideas like genocide, structural violence, symbolic violence, and cultural violence are tacitly used to identify anomalies in the archaeological past such as trauma or health disparities. Sometimes bioarchaeologists and archaeologists infuse violence theory into their work without understanding the nexus of these social theories. Merely reading and citing prominent scholars in the field, such as Johan Galtung or Paul Farmer, falls woefully short of understanding structural violence as a mechanism for deciphering trauma pattern recognition on skeletal
remains, epidemiological distributions of disease within a skeletal sample, or reconstructing maternal mortality rates.

Structural or indirect violence can best be understood in relation to direct or personal violence. Direct violence involves a concrete person or actor committing the violence, while indirect violence does not in any meaningful way (Galtung 1969:170–171). Klaus (2012:35) has argued for “careful and critical use of structural violence in bioarchaeological analysis.” Most bioarchaeologists utilize a biocultural framework in their analysis of violence, but the inclusion of social theory is an important dimension as well. Here, I critique the use of violence theory as it has been employed in bioarchaeology by exploring the poetics of violence. That is, this approach explores the logic of violence and its reproductive characteristics as they relate to a specific time and place. This chapter will explore the necessity to recognize and situate the use of violence theory within often contested conceptual borders like force, power, and violence (Hanssen 2000).

Background

Bioarchaeology and the study of violence

Violence is a key feature in human interactions. Its presence has a long and profoundly complicated history in our species (Bocquentin and Bar-Yosef 2004; Kelly 2000; Martin and Harrod 2015; Schmidt and Schröder 2001). Violence has been discussed in terms of our evolutionary make-up (Ahlström and Molnar 2012; Wrangham and Glowacki 2012) and as an extension of aggression in primates. As Knauft (1991:391) noted, “This raises an important larger question: what is the overall trajectory of violence and sociality in human evolution?” This is a question that I do not have the space to answer here.

Throughout human history, periods of relative peace have been marred by eruptions of interpersonal or institutional violence. Bioarchaeology offers an extremely useful approach to the classification and interpretation of traumatic injuries, evident on the skeleton or in preserved soft tissues, that are often indicative of conflict and violence. Bioarchaeology accomplishes this by bridging the chasm between biology and the social and environmental dimensions of the populations being analyzed. When interpreting skeletal evidence of violent trauma, the challenge lies in trying to decipher the complexity, variability, and ambiguities in the total picture of the population’s mortuary behavior. The population’s relationship to abandonment, migration, conflict, resource scarcity, ethnic identity, settlement patterns, and other factors is then considered to understand the social conditions necessary for violence and warfare to occur.

The effects of violence on the body

Disease and death are the outcome of an accumulated set of biological, behavioral, and cultural processes, so it makes sense that understanding how people
in the past came to be infirm or die involves a complex linkage of an interrelated set of variables. Age, sex, gender, ethnic group, occupation, marital status, political affiliation, socioeconomic status, and access to social support, health care, resources, and power compose a constellation of interacting factors that temper and affect how dangerous or deadly acts of violence are. After death, the mortuary component of an archaeological site provides an abundance of data, and from the “where, how, and why” of the treatment of a corpse or corpses, a range of culturally appropriate activities may be deciphered. Human bodies can be buried, left unburied, reburied, displayed, hidden, sacrificed, articulated, disarticulated, defleshed, dismembered, painted with ochre, hung from rafters, stored in containers, and utilized in ceremonies.

Because bioarchaeologists must reconstruct the illnesses and deaths of past people from their skeletal remains (which may be embedded in systems of violence), they are essentially “third party interpretations.” Mummendey and Otten (1993) have noted that third party interpretations of violence are almost impossible to make without knowing the mindsets of the perpetrators and the victims. This is because violence has specific and often unique cultural meanings associated with it and should never be reduced to its physicality when trying to understand its use (Scheper-Hughes and Bourgois 2004). Violent acts often exemplify intricate social and cultural dimensions and are frequently defined by these same social contexts. Disease, like violence and death, is never random in a population. The distribution of non-genetic diseases is almost always an outcome of inequalities (often a form of structural violence) among members of a group in terms of food and medicine, shelter and housing, potable water, protection from physical insults (in the form of microbes or abuse), hygiene, and exposure to environmental stressors (Cohen 1989). Like disease, episodes of violence and warfare are also seldom random, and have also been linked to inequality, political economic stratification, and differential access to resources, which can become heightened in periods of unpredictability and environmental degradation (Ember and Ember 1997; Ferguson 1997; Knauft et al. 1991; Sluka 1992).

**Violence theory**

When thinking about the application of violence theory to the interpretation of archaeological skeletal remains, I am reminded of the problem of defining and conceptualizing violence in the social sciences in general, which has been very aptly commented on by Zygmunt Bauman (1995:139).

Virtually all writers attempting to come to grips with the phenomenon of violence find the concept either under-, or over-defined, or both. They also report in other writers (if they do not display themselves) an amazing reluctance, or ineptitude, to resolve the confusion and put things straight. Above all, they find in the texts they read plenty of understatures and half-truths, a lot of embarrassed silence, and other signs of shame-facedness.
With all of these apparent contradictions, how are we to identify and explain violent behavior? To begin with, it is important to clarify which explanatory model you are using and why it is relevant to the analysis at hand. There are times when a researcher is less concerned with the causes and consequences of violence than with the logic of violence.

Even within the scientific analysis of a first-order level of inquiry of violence (i.e., a murder investigation), there are multiple starting points that must be clarified at the outset. Due to the length constraints of this volume, I provide only a very truncated example of one concept, “power,” which is central to the idea of direct and indirect structural violence (Galtung 1969:170–171). One of the most common and heavily referenced definitions of power in the social sciences, and anthropology in particular, is Foucault’s (1978:91–92) which is worth quoting here in its entirety.

[Power] must be understood in the first instance as the multiplicity of force relations \textit{immanent} in the sphere in which they operate and which constitute their own organization; as the process which, through ceaseless struggles and confrontations, transforms, strengthens, or reverses them; as the support which these force relations find in one another, thus forming a chain or a system, or on the contrary, the disjunctions and contradictions which isolate them from one another; and lastly, as the strategies in which they take effect, whose general design or institutional crystallization is embodied in the state apparatus, in the formulation of the law, in the various social hegemonies.

Foucault’s definition of power serves as a lens to view the bioarchaeologist’s use of structural violence in terms of systemic violence. Systemic violence refers to violence that has become so common within a society that its practice at both the institutional and individual level serves to maintain it. This idea of systemic violence can further be placed into particular paradigms such as creative, moral, and destructive power as discussed in Vahabi’s (2004) \textit{The Political Economy of Destructive Power}.

Whatever explanatory model is used to consider violence, I believe it must be placed within a system of “poetics,” meaning that the violence being explained must be considered within the time and place of its commission. The defleshed, dismembered, broken, and chopped-up bones found at some sites in the pre-Hispanic greater south-west (AD 900–1250) tell a unique story that is tied to a specific place and time (Pérez 2012). The remains from La Quemada, Mexico (AD 500–900), evidencing cutmarks and trauma pattern recognition consistent with dismemberment, indicate a strong likelihood that ancestor veneration along with the ritualized destruction of enemy remains accounts for the multiple mortuary behaviors present (Nelson \textit{et al.} 1992; Pérez 2002, 2012; Pérez \textit{et al.} 2000, 2008). The specific types of trauma seen on these remains were not produced by inhuman sociopaths but followed a cultural logic and were performative events. The poetics of these performances are bound to a specific history and cultural meaning for a particular group of people occupying a unique place in time and space (Whitehead 2004:73–74). Thus these “generative schemes” (Bourdieu 1977) are given meaning through
what Whitehead (2004:60) refers to as historically entrenched configurations of symbolic and social behavior that inform individual agency through symbols and icons. The term “poetics” serves to focus our understanding of violence as being the core cultural expression of an essential and complex component of a society (Whitehead 2004:68).

**Violence theory in bioarchaeological models of violence**

Martin and Harrod (2015:120) offer an extremely useful model for thinking about a bioarchaeology of violence that integrates three levels of analysis on violence in antiquity: skeletal data, contextual data, and social theory. I would suggest a slightly different model for employing the use of violence theory within a bioarchaeological approach to violence. Using a stacked Venn model (Figure 22.1) illustrates the importance of each of the concepts in identifying and understanding violence in the archaeological past. In this configuration, you see the importance of each of the categories in building the base required to inform the core idea. The understanding of violence in the past gets stronger as we move through each level towards the core. Each idea is only as strong as the evidence that comes before it.

The use of violence theory as an interpretive tool is only as strong as the skeletal and contextual data. Violence theory is further complicated by the necessity to embed it within a system of poetics. Structural violence cannot be understood as violence unless we understand it in terms of systemic violence. This

![Figure 22.1 Alternative model for a bioarchaeology of violence.](image-url)
involves examining who occupies the structures, how they were formed and maintained, and how they are part of a recognizable system that is excessive, expressive, and symbolic (Pawlett 2013). Finally, we must ask, what are the conditions under which the structures in systemic violence are permitted to move to direct/physical violence? Rarely does systemic violence reach the level of physical violence without it being concealed within ideological justifications, like warfare and sacrifice.

**Case study: the Sierra de Mazatán massacre**

In order to illustrate the concepts outlined above, I explore the poetics of violence, both direct and structural, experienced by the Yaqui in Mexico in the early twentieth century. This analysis focuses on the skeletal remains of 13 individuals, 12 of which were collected from a massacre site, Sierra de Mazatán, in Sonora, Mexico, by Aleš Hrdlička, a prominent physical anthropologist, in 1902. This has been published in greater detail in a recent work (Bauer-Clapp and Pérez 2014). The Mexican army was responsible for the massacre on June 8, 1902, killing at least 124 Yaqui men, women, and children in reprisal for a raid, represented as an “Indian uprising,” conducted by the Yaqui during the same year.

In order to understand how and why these people were brutally murdered, it is important that the analysis not be seen as episodic but rather placed in a complex system of power relationships including but not limited to force, coercion, compulsion, domination, terrorism, torture, punishment, oppression, and immorality. These can best be understood through the sociopolitical and economic realities the Yaqui faced. The violent brutality of their deaths extends beyond the tearing of flesh and splintering of bone caused by the Mexican Mauser rifles; their bodies are both metaphorically and factually the site of oppression. They represent the physical expression of violence personified by the violence of an ingrained system of structures in a particular historiography that operated with legitimacy and impunity.

The Yaquis’ deaths helped to reinforce structures of oppression through a nexus of policies, symbols, and economies that create and maintain hierarchies of privilege and power. Judith Butler’s work, *Bodies that Matter* (1993), is particularly useful for understanding this dynamic. According to Butler (1993:3), the “exclusionary matrix by which subjects are formed thus requires the simultaneous production of a domain of abject beings, those who are not yet ‘subjects,’ but who form the constitutive outside the domain of the subject.” That is to say, what are the structures of oppression that create the “abject” – those who inhabit a position in life that is “unlivable” and do “not enjoy the status of the subject” and the “subject” as a being “constituted through the force of exclusion and abjection” (Butler 1993:3). The interpretation of the skeletal evidence of violence in the 13 massacred individuals, along with a discussion of the structural violence involved in the repatriation of the skeletal remains of
Figure 22.2 Map of relevant locations in north-western Mexico.

*los guerreros* (“warriors”) to the Yaqui in 2009, illustrates how as “subjects” the positions of *los guerreros* were dictated by the dominant cultural apparatus that was reinforced, regulated, and regenerated through a web of violence driven by policy and the political bureaucracy of the United States and Mexico.

**A brief historical context**

The Yaqui are the indigenous people of the modern-day state of Sonora in northern Mexico (see Figure 22.2). In the late nineteenth century, the Yaquis also occasionally migrated or were deported to the south-western United States and developed permanent settlements in Arizona. In 1939, the Yaqui of Mexico were granted official recognition by the Mexican government and gained title to a small portion of the land in Sonora which they considered to be their home territory. The Pascua Yaqui tribe of Arizona were federally recognized by the US government in 1978 (Bauer-Clapp and Pérez 2014). Yaqui identity in modern Mexico and the United States centers on maintaining cultural autonomy and control over their territory. This is an ongoing struggle that has persisted since European contact in 1533 (Molina 2000; Sandoval 2009). For a detailed overview of the Yaqui from Spanish contact through Mexican independence and the 1902 Sierra de Mazatán massacre, see Bauer-Clapp and Pérez (2014).

Postcolonial struggles in Sonora mirrored postcolonial political and economic changes throughout Mexico. These changes were aimed at accelerating assimilation of autonomous indigenous groups under the Mexican government. Communal land holdings were dissolved and debt peonage laws were strengthened, both of which facilitated the expansion of haciendas (Meyers *et al.* 2008). Haciendas were predominantly owned by European-descended individuals or families who employed or enslaved indigenous peoples to produce surpluses for export (Meyers and Carlson 2002; Meyers *et al.* 2008).

By 1902, all Yaquis were required to carry passports as identification; any individual caught without one was subject to arrest and deportation to haciendas
in the Yucatán, executed immediately, or sent to labor camps or haciendas in Sonora. More than 2000 adults were deported under these policies; children of the deported were placed as servants with local families or left to die (Hu-DeHart 1974). Hu-DeHart (1974:83) observes that these procedures had tragic consequences, which were all the more devastating because the family had been such a strong cultural institution for the Yaqui.

The forced labor, deportations, and splitting up of families resulted in several rescue-style raids on haciendas in Sonora by Yaqui warriors. On May 31, 1902, the *New York Times* reported:

YAQUI INDIANS ON WARPATH.
Kill the Governor of a Ranch and Make Several Raids.
TUCSON, Arizona, May 30.
The Yaqui Indians are again on the warpath. On Tuesday a band of Yaquis visited La Carmen, a hacienda near Hermosillo, and killed the governor of the ranch and a servant, besides carrying off the provisions and taking away the best stock on the place. Another band visited the ranch of Don Juan Maytorena, near Guaymas, and raided it. The occupants escaped when they saw the Indians approaching. Several other haciendas were visited and robbed. The situation is serious.

The Sierra de Mazatán massacre
The bioarchaeological research for this case study focuses on the skeletal remains of 12 Yaqui individuals killed in the above-mentioned massacre. Yaqui fighting around Sierra de Mazatán began to receive coverage in US newspapers on June 5, 1902. The *New York Times* ran a story entitled “Yaqui Indian Uprising,” which mentions the Yaqui fighting in the Mazatán Mountains specifically. The article estimated that there were 1000 “well-armed” Yaqui in the foothills and that the Mexican soldiers were outnumbered and short of arms and ammunition. On June 8 this interpretation was denounced by General Torres, commander of the Mexican Army in Sonora and leader of the Mexican forces in the massacre at Sierra de Mazatán, in another *New York Times* article, “No War with Yaqui Indians,” in which Torres insists that only minor skirmishes are occurring. This reflects that during this period in Mexican history, both the President of Mexico, Porfirio Diaz, and General Torres had vested interests in maintaining regional stability – or at least the image of stability – to maintain the influx of foreign capital into Sonora.

The massacre at Sierra de Mazatán represents state-sanctioned violence in response to a rescue raid conducted by the Yaqui. Events surrounding the massacre were recorded by Hrdlička, who was traveling in Mexico, conducting research for the American Museum of Natural History (AMNH) under the auspices of the Hyde expedition. Three weeks after the massacre, Hrdlička traveled to the site and found the bodies of the Yaqui lying where they had fallen. For Hrdlička’s (1904:65–66) brief but detailed account of the events, see Bauer-Clapp and Pérez (2014). The Mexican Army’s official account of this encounter, recorded by General Torres, lists the Yaqui fatalities as 78 men, 26
women, and 20 children, with 234 taken as prisoners. Torres reports only one injury and no fatalities among the Mexican troops (Troncoso 1977).

Hrdlička (1904:66) visited the Sierra de Mazatán massacre site to obtain material for the AMNH’s collections, but was only able to obtain remains from 12 individuals, as extensive damage had been done to most of the skulls, “whether from a peculiar effect of the Mauser cartridges or from the closeness of the range.” He also collected weapons, articles of clothing, and jewelry. On his way to Sierra de Mazatán, Hrdlička had also passed the body of a Yaqui man, executed the day before, hanging from a tree. Days later, he collected the man’s cranium – the 13th individual in the sample – after the body had been cut down and partially burned.

In 1904, Hrdlička reported on his trip to Sonora in an article, “Notes on the Indians of Sonora, Mexico,” in the *American Anthropologist*. He noted the 12 skulls in a table highlighting cranial measurements derived from them that are designed to identify “tribal differences in the various body dimensions,” and argued that “when these [differences] can be eliminated or explained, there is good prospect of reducing all the numerous ethnic divisions” present in the people of Sonora (Hrdlička 1904:86), a reflection of nineteenth- and early twentieth-century physical anthropology’s devotion to using anthropometry to create racial classifications of past and modern humans.

**Bioarchaeology data on the Sierra de Mazatán massacre**

The bioarchaeological analysis focused on cranial remains from 12 individuals from Sierra de Mazatán and postcranial remains from the executed, hanged individual in Sonora (Table 22.1), which are referred to as los guerreros (the warriors). The remains were curated at AMNH from 1902 until their repatriation in 2009.

Of the 12 individuals from Sierra de Mazatán, five exhibit clear evidence of perimortem trauma. In the analysis of perimortem trauma related to the 1902 encounter, data from #99-3972 were excluded, as this individual was the executed man and thus not involved in the event.

For the purposes of this chapter, I will focus on the perimortem trauma identified on the crania of these individuals. What follows below is a brief description of trauma associated with the crania collected at the Sierra de Mazatán massacre.

**Projectile trauma**

Two individuals exhibit projectile trauma consistent with a gunshot wound. One (#99-3973) was likely shot while kneeling or lying on the ground, based on the location and angle of the entrance wound. The bullet entered the right side of the skull and exited the left side just behind the ear. The extensive trauma produced around the entrance wound is consistent with a high-velocity contact wound to the head. In a second individual (#99-3974), the bullet entered the left side of the skull just behind the ear and exited near the right eye. The entrance
Table 22.1 Trauma and pathology analysis of crania from the 1902 Sierra de Mazatán massacre. Source: Bauer-Clapp and Pérez (2014:180).

<table>
<thead>
<tr>
<th>Accession number</th>
<th>Trauma</th>
<th>Pathologies</th>
</tr>
</thead>
<tbody>
<tr>
<td>99-3972</td>
<td>Charred cranium</td>
<td>Healed porotic hyperostosis</td>
</tr>
<tr>
<td>99-3973</td>
<td>Projectile trauma R parietal boss</td>
<td>Healed porotic hyperostosis</td>
</tr>
<tr>
<td>99-3974</td>
<td>Projectile trauma L mastoid; blunt-force trauma L side of occipital</td>
<td>Healing cribra orbitalia; 18 LEH on 11 teeth</td>
</tr>
<tr>
<td>99-3975</td>
<td>Healed broken nose; healed fracture on frontal</td>
<td>Healed porotic hyperostosis</td>
</tr>
<tr>
<td>99-3976</td>
<td>Healed broken nose</td>
<td>Possible periostitis on mandible; two LEH on two teeth</td>
</tr>
<tr>
<td>99-3977</td>
<td>Possible healed depression fracture on sagittal suture</td>
<td>Possible healed porotic hyperostosis; nine LEH on five teeth</td>
</tr>
<tr>
<td>99-3978</td>
<td>Multiple sites of sharp force trauma/cutmarks</td>
<td>One LEH on one tooth</td>
</tr>
<tr>
<td>99-3979</td>
<td>Blunt force trauma R side of occipital and R temporal</td>
<td>Healing porotic hyperostosis; three LEH on three teeth</td>
</tr>
<tr>
<td>99-3980</td>
<td>Blunt force trauma on occipital</td>
<td>Healed porotic hyperostosis; Three LEH on three teeth</td>
</tr>
<tr>
<td>99-3981</td>
<td>No trauma exhibited</td>
<td>No pathologies exhibited</td>
</tr>
<tr>
<td>99-3982</td>
<td>No trauma exhibited</td>
<td>Lipping on 5th lumbar vertebra and body of sacrum</td>
</tr>
<tr>
<td>99-3983</td>
<td>No trauma exhibited</td>
<td>Healing porotic hyperostosis and cribra orbitalia; two LEH on one tooth</td>
</tr>
<tr>
<td>99-3984</td>
<td>Multiple cutmarks</td>
<td>Healed porotic hyperostosis; 12 LEH on eight teeth</td>
</tr>
</tbody>
</table>

wound is consistent with a high-velocity round entering the skull with minimal deformation due to rapid penetration and absorption of the kinetic energy of the bullet by the entrance wound (primary fracture).

**Blunt force trauma**

Two individuals exhibit evidence of blunt force trauma. One (#99-3980) exhibits two fractures: one on the occipital bone (near lambda) and one radiating fracture extending up and around the right parietal bone nearly to the coronal suture. The shape and dimensions of the fracture are consistent with the butt of a Mauser rifle, as measured by the author from an example in the National Firearms Collection at the Smithsonian Museum of American History. The Mauser rifle was standard issue for the Mexican Army at this time. Individual #99-3979 exhibits evidence of blunt force trauma on the right occipital and temporal bones. This individual also exhibits at least three radiating fractures and additional fractures on the opposite side of the cranium. The severity of the fractures on both of
these skulls suggests the assailant was striking the victim with a heavy weapon propelled with great force.

**Sharp force trauma**
Three individuals exhibit evidence of sharp force trauma, with a total of 23 cutmarks identified. For each incidence of sharp force trauma, the location, position, length, width, depth, shape, and direction were recorded. Afterwards, a vinyl polysiloxane impression was made of the cutmarks. Positive casts were then produced creating an exact replica of the cutmarks. These in turn were thin-sectioned and examined microscopically. Microscopic analysis allowed identification of the geometry of the cutmarks as well as verification of the maximum depth and width, and determination of the amount of soft tissue present on the remains at the time of processing.

Of the three individuals, one incident of perimortem sharp force trauma was identified that is likely related to the massacre. In this individual, the cutmarks are clustered around the right side of the cranium near the external auditory meatus. Two of these cutmarks were produced by a slicing motion; the cutmark pattern and location suggest that the ear was cut off around the time of death. The other two individuals exhibit cutmarks that appear to be associated with Hrdlička’s collection of the remains; he removed the crania with a machete. One individual exhibits a chop mark located on the left lateral aspect of the posterior portion of the ascending ramus, which was likely produced during removal of the cranium. Additional cutmarks on the two individuals appear to be related to Hrdlička’s efforts to deflesh his specimens after his return to AMNH.

**Interpretation of the traumatic injuries**
One key aspect of violence is that the symbolic aspects of violence have the potential to create both order and disorder, depending on the specific social context within which the violence is expressed (Galtung 1990; Sluka 1992). This is one of the paradoxes of violence, as noted by Schinkel (2010). Most cultures, in the modern era and historically, feel that their safety lies in their ability to control violence using violence. Sluka (1992:28) refers to this apparent paradox as the dual nature of conflict; violence and conflict often have the ability to unite, create stability, and be progressive while at the same time generating the antithesis of these positive forces.

The skeletal trauma on the 12 individuals from Sierra de Mazatán was consistent with tactics used by the Mexican military at that time. The patterns and characteristics of the ballistic and blunt force trauma all correspond with Mexican-issued 7 × 57 Mauser high-velocity rifles. While many people, cross-culturally, fear and abhor violent acts that they see as senseless, they are more than willing to condone the legitimate, state-sanctioned use of violence to promote social control and economic stability (Turpin and Kurtz 1997). As demonstrated by Hrdlička’s account and the remains from Sierra de Mazatán,
this form of legitimate violence was employed by the Mexican government to bring a halt to the “problem” of Yaqui raiding and resistance in the early twentieth century.

**Contextual data on the Sierra de Mazatán massacre**

The bioarchaeological data were analyzed in context with four additional lines of contextual evidence to categorize the participation of various groups and individuals in the June 8 event at Sierra de Mazatán. These include the material culture collected from Sierra de Mazatán by Hrdlička, supporting historical documents, Hrdlička’s journal and photographs, and existing literature on the Yaqui of Sonora. These lines of evidence suggest that the encounter between the Mexican Army and the Yaqui should be classified as a massacre rather than a battle. The Yaqui were overpowered by the Army and had significantly fewer and less sophisticated weapons than the soldiers. Historical research suggests that the Yaqui were outnumbered by an army with vastly superior firepower, thus the level of trauma evident in Hrdlička’s records, the material culture, and the skeletal remains become further evidence for a massacre of the Yaqui by the Mexican Army rather than a battle fought with relatively equal resources on both sides.

**Yaqui repatriation**

After the analysis of the skeletal remains was completed, this information was brought to the attention of Robert Valencia, the Vice Chairman of the Yaqui tribe, who in turn brought it to the Pascua Yaqui tribal council. This started the process of repatriation, including a formal request to the AMNH for repatriation of the Yaqui skeletal remains and associated material culture, which culminated in the AMNH agreeing to return the materials to the National Institute of Anthropology and History (INAH) in Mexico, who in turn agreed to transfer them to the Yaqui. The transfer of control/ownership occurred during a formal signing ceremony in New York at the AMNH in the fall of 2009. After the ceremony, the Yaqui delegation brought the remains back to their homeland, to the towns of Guadalupe, Tucson, and Rio Yaqui, which involved a cavalcade of ceremonial dancers, an American Legion color guard, and prayers at a community church, allowing the descendent community to pay homage to their relatives.

In talking to several elders from Guadalupe, Vice Chairman Valencia was informed that even though my fellow researchers and I had made presentations to the community prior to the return of the remains and items of material culture, community members were unable to hold back their emotional outbursts and displays of mourning upon the return of the remains, which represented a mixture of both sadness and joy at the return of los guerreros. This can be interpreted as evidence of historical trauma, a psychological phenomenon also known as intergenerational posttraumatic stress disorder, historical grief, postcolonial stress disorder, and “soul wound.” Historical trauma is a form of intergenerational trauma, which refers to the cumulative emotional and
psychological wounding, exceeding an individual lifespan and extending across generations, that involves traumatic experiences in the past exerting negative consequences in the present (Haskell and Randall 2009; Prince 1985; Sotero 2006). For the Yaqui, the return of the materials – and the evidence of direct violence that they carried – caused a materialization and manifestation in the present, especially for the elders, of all the narratives that their parents and elders had told them about the violence that had been perpetrated against the Yaqui by the Mexican government in the past. This is in part due to the fact that memories of violence are negotiated through systems of cultural frameworks and mediated by the collective consciousness of a given community. These intense emotional responses were repeated in Tucson and Rio Yaqui. Entire families came together as elders tried to explain this painful history to their children, grandchildren, and great-grandchildren. The tribal psychologist reported the effect on the community as overwhelming.

The repatriation of los guerreros to the Yaqui also had a tremendous impact beyond the descendent community via coverage and discussion of the event in countless blogs, web sites, and news articles. This is because the cooperation and speed of this particular international repatriation was unprecedented in the three decades since repatriation of indigenous remains became implemented under the Native American Graves Protection and Repatriation Act (NAGPRA), a law that was passed as Pub. L. 101-601, 25 U.S.C. 3001 et seq., 104 Stat. 3048 in 1990. However, it was not precedent setting. This is because one of the principal reasons that the repatriation was allowed was because the materials were not considered to be archaeological material by either the AMNH or INAH, but rather were seen as representative of a historical massacre site and thus constituted a human rights issue. Because of this, the AMNH did not give the material from Mexico to a culturally affiliated, federally recognized tribe in the United States as part of NAGPRA, and the INAH did not return archaeological material to a Mexican tribe.

For the Yaqui, the repatriation had a profound impact on the community, reopening old wounds and traumatic memories. The social reality of the Yaqui was affected by the lives, deaths, and prolonged burial and grieving process for members of their past, los guerreros. Their repatriation stirred narratives and memories of violence that had a profound impact on contemporary Yaqui, affecting current and future generations of people through an indirect experience of the violence that their mothers, fathers, and grandparents had directly experienced.

**Conclusion**

The approach taken by this chapter is at its heart biocultural, and demonstrates how bioarchaeology can be inherently anthropological. Here, I have explored why it is necessary to interrogate, recognize, and situate the use of violence
theory within contested conceptual borders, and how it can be applied to multiple lines of evidence from past lives. The contextual data regarding the story of los guerreros Yaqui demonstrate not just the direct, physical violence endured by the Yaqui but also the symbolic violence of history. Here, Foucault’s (1978:91–92) concept of power is brought to light in terms of the systemic violence that was produced by the writings of Hrdlička, the Mexican government, and the US and Mexican press. All had performative powers to establish laws and normalize the cultural and structural violence that was being perpetrated by the Mexican government against the Yaqui, demonstrating the dynamic between the concepts of direct and indirect violence (see Galtung 1969:170–171). More was at play here than denial. As official rhetoric worked to conquer the mental space of Mexican citizens, a coercive discourse was brought into play to try to eliminate aspects of a traumatic “lived past” for the Yaqui people. The repatriation of los guerreros serves as a grim reminder of the historical trauma and tremendous sacrifices made by the ancestors of the Yaqui people.

Using the stacked Venn model (see Figure 22.1) illustrates the importance of each of the concepts in identifying and understanding the violence experienced by los guerreros Yaqui. The evidence of trauma exhibited by the individuals demonstrates an aspect of the structural and direct violence experienced by the Yaqui in the nineteenth and early twentieth centuries. Combining the bioarchaeological with the contextual data enables a consideration of the political, social, and economic factors involved in the deaths of los guerreros. In addition, while I am mindful of the need to refrain from characterizing these individuals’ lives based on the circumstances of their deaths, I can conclude that the 12 individuals collected from Sierra de Mazatán in 1902 were victims of a violent massacre perpetrated by Mexican troops. Our understanding of the violence committed against the Yaqui grows stronger as we move through each level towards the core.

Each idea is only as strong as the evidence that comes before it. Thus the use of violence theory as an interpretive tool is only as strong as the skeletal and contextual data. Oppression and persecution of the Yaqui continued through the Mexican Revolution and beyond. The last armed conflict between Yaquis in the United States and the US Army occurred in 1918; in 1927, the Yaquis of Sonora engaged in their last major battle with the Mexican Army and lost. While Yaqui tribes on both sides of the border have been granted recognition by their respective federal governments, the Yaquis characterize their past as a “long history of struggle” (Molina 2000:98). The bioarchaeological analysis and the 2009 repatriation activities brought this heritage of Yaqui resistance and resilience to younger generations, making the past – and its trauma – a dynamic part of the present.

The violence experienced by the Yaqui in the nineteenth and early twentieth centuries constituted an attempt by the Mexican government to reconfigure their social environment. This type of structural violence must never be viewed as a transitory, punctuated, and isolated event with no lasting effects. Instead, this sort of violence becomes a determining factor that shapes future realities for
both individuals and their cultures through the imposition of social, political, and economic structures, imposed by the dominant (in this case colonial, Mexican) powers. Thus we must examine the cultural realities of the Yaqui during this period by their daily practice and not as some static historical event. In short, by necessity, the Yaqui violence must be embedded within a system of poetics.

As stated above, the use of a bioarchaeology of violence that integrates three levels of analysis on violence in antiquity – skeletal data, contextual data, and social theory – is critical to an accurate portrayal of violence in the past. Here, it is critical for understanding how to categorize the participation of various groups and individuals in the June 8, 1902 massacre at Sierra de Mazatán. This includes the need to explore evidence of antemortem stress and trauma to counter the tendency to categorize the entire life history of these individuals based on their roles (e.g., victim, perpetrator) during the June 8, 1902 event. Keeping in mind Klaus’s (2012:37) warning to avoid categorizing victims of structural violence as “passive,” multiple lines of evidence were utilized, relying heavily on skeletal and contextual data (Martin and Harrod 2015:120), to understand the life histories of these 13 people, not just the circumstances surrounding their deaths.

Acknowledgments

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References


CHAPTER 23

Broken bodies and broken bones: Biocultural approaches to ancient slavery and torture

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Introduction

In thinking about violence in the modern world, there is a tendency to link violence to causal factors such as genetics (biology), droughts or climate (environment), or poverty, inequality, migration or overpopulation (culture) (see for examples popular books by Diamond (2012) and Pinker (2011)). Anthropologists utilizing a biocultural approach, such as the authors in this volume, are hard pressed to explain any human behavior in terms of solely biology, environment or culture.

Rather, we view most all human behaviors as affected by a wide range of interacting biological, cultural, and environmental factors. And we acknowledge that it is a two-way street: just as biology, environment, and culture can affect human behavior, human behavior also has an effect on biology, environment, and culture. But this makes explaining why humans do what they do a difficult and complicated task. However, the use of a biocultural approach makes the task easier. Patterns and associations that emerge within given cultures at particular moments in time can be explained by locating the defining factors that are strongly linked with certain behaviors (see case studies in Martin and Osterholtz 2016).

For example, violence such as warfare, raiding, and interpersonal fighting cannot be causally linked to phenomena such as male testosterone (Assari et al. 2014), droughts (Harrod and Martin 2014) or poverty (Haugen and Boutros 2014) although there is often the tendency to suggest that violence increases with these kinds of biological, environmental, and socioeconomic factors. However, statistically associating one variable with another only reveals that they are related, not that one variable causes another; correlation is not causation (Wakeford 2015). Associations are a good place to begin in unraveling the underlying
forces that shape human behavior. Associations should be seen as the beginning of the analytical process, not the end result.

Violence is a difficult behavior to define and quantifying and qualifying it across different cultures at different points in time is challenging (see Chapter 22). Direct physical violence that causes bodily harm is the most common kind of activity labeled as violence, but the meaning that different cultures provide for why there is violence is quite variable (Martin and Harrod 2014). Are boxing and welter-weight fights violence? Is female genital mutilation violence? Is warfare violence? Is slavery violence? Is causing physical or psychological pain to an individual violence? Asking these questions for different time periods in different cultural contexts may produce different answers.

Anthropologists and others tend to operationalize a broad and inclusive notion of behaviors that constitute violence. We have operationalized a definition of violence for the past that takes many different factors into consideration: Violence is the diverse set of bioculturally embedded processes that employ power and force to harm others through physical violence and death, and through non-lethal tactics involving intimidation, pain, domination, fear, and subordination (often through symbolism), or through structural violence and the restriction of access to necessary resources. It involves victims, perpetrators, and witnesses. It can strengthen and create identities, and it can violate and destroy them. Culturally meaningful rituals and public performance make it a self-perpetuating phenomenon (Martin and Harrod 2014:3).

Physical violence and harming other individuals are part of the idea of violence but it is not the complete definition. Just as harmful and insidious to human well-being are the effects of political or social ideologies that benefit some segments of the population and deny resources to others. This is referred to as structural violence and it is less visible than physical violence, but it hurts, harms, and injures individuals and groups nonetheless (Farmer et al. 2006; Galtung 1990). Studying trauma on human remains from the past is a form of bioarchaeological “witnessing” of violent events that help us to sharpen our understanding of the history of violence in human groups and the motivations for using violence (Schepet-Hughes and Bourgois 2004). Through bioarchaeological study of trauma in archaeological remains, people who suffered and died at the hands of others have a chance to tell their story.

George Armelagos wrote the final summary chapter for a book entitled Social Violence in the Prehispanic Southwest (2008) that he called “Devouring ourselves.” Several of the chapters focused on whether or not anthropophagy, also referred to as cannibalism, was practiced in the prehispanic Southwestern region of the United States in the period encompassing AD 900–1450, and Armelagos focused upon this critical issue. Armelagos (2008:216) stated that:

... there is evidence of various forms of violence in the ancestral Pueblo ... world that reveals a complexity that we are only now beginning to understand.
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He took issue with the fact that many researchers in the region had assumed that the inhabitants of the American Southwest used “rampant brutality” and cannibalism as a form of social control that would instill fear in anyone considering going against the powerful elites. The interpretation, however, was based on scant evidence that primarily consisted of skeletal remains with cutmarks and burning. He concluded that more recent studies utilizing a biocultural approach, such as those in the 2008 edited volume, provided a more nuanced and likely set of explanations for the kinds of evidence on the bones. In these new biocultural interpretations, social control and violence may not have played a role at all in the cutmarks and burning seen on the human bones. More parsimonious explanations include such things as mortuary rituals, ceremonial preparations of the dead, and veneration of ancestors because these kinds of behaviors would also leave cutmarks and burning. He also argued that as scholars, we must question our own biases that we may inadvertently bring to studies of ancient violence. He concluded that:

... the site-specific cases and ethnographic data allowed [researchers] to address epistemological issues and to examine the politics of interpreting violence in the past from different perspectives and approaches (2008:219).

Shining a light on these complex behaviors reveals the ways in which violence is deeply embedded in social ideologies and political-economic structures. Additionally, this viewpoint examines the way in which violence is used as a form of social communication and social control.

Here, we pick up on these themes introduced by Armelagos and continue to interrogate the role of violence in past societies. Using a biocultural approach, we can see that violence is embedded with meaning at both biological (damage to physical bodies and neurological processes) and cultural levels. This produces individual, household, community, regional, and interregional ripples of effect. This chapter focuses on systems of culturally sanctioned violence that relied upon slavery and torture as part of everyday activities that were bound up in cosmological, political, and economic systems that used violence. Public torture of captives may signal to the witnesses that justice is being served by punishing those who would try and do the community harm. Captivity and enslavement of individuals are often an important part of the economic system whereby slaves are used to work the fields and produce trade items. Both of these activities can only be carried out by using force and violence yet they are important parts of community viability.

We draw on the American Southwest, the region encompassing Utah, Colorado, Arizona, and New Mexico, because of the intensive archaeological study that has been ongoing there since the 1960s, including the volume on social violence (Nichols and Crown 2008) that Armelagos was instrumental in shaping. While the chapter uses case studies from the past, they are chosen precisely because they reveal important understandings that help us see the slavery, torture, and executions that are happening today in a broader and
more encompassing way. Bioarchaeology can make important contributions to understanding the ways in which violence is used today to produce and maintain particular kinds of social orders.

**Background**

There are two truisms to culturally sanctioned violence. One is that violence begets violence. Raiding for women, children, goods, and resources has been practiced across the sociopolitical spectrum, from foraging groups in the Mesolithic to settled agriculturalists in the Neolithic (Boehm 2011). Archaeologists Maschner and Reedy-Maschner explained how violence begets more violence as it relates to raiding with this meme: raid, retreat, defend, repeat (1998). A group is attacked; it may fend off the attackers but lose individuals and resources in the process, and so begin plotting a revenge attack that will cause death and loss of resources to its enemies.

Another truism is that culturally sanctioned violence solves perceived problems that people have. Ember and Ember (1997) examined 186 preindustrialized cultures using the Human Relations Area Files which contain detailed ethnographic information on human groups from around the world. They statistically examined the reasons people give for the use of warfare and violence. Some of the reasons that were statistically significant were the fear of disasters and when resources were unpredictable. The use of violence is largely socially and culturally sanctioned, meaning that it is deemed important and necessary in certain circumstances. Violence that is not sanctioned by cultures are those acts that are considered deviant or illegal. Every culture has an elaborate ideological basis for rules, laws, and structures that dictate when various forms of violence are to be carried out, by and against whom. Often these rules and laws are made and enforced by those who have accrued enough wealth and power to have them carried out.

Violence can be studied in past populations by examining the bones and teeth that are preserved. Bioarchaeology is the branch of biological anthropology that uses the integrated analysis of human remains (osteology) along with any archaeological, forensic, and medical data that can provide additional information about the individual as well as the context within which the bones were found. Using standardized skeletal analyses established by biological anthropologists (e.g., Buikstra and Ubelaker 1994; Larsen 2015), human remains can reveal a great deal about the kinds of violence individuals suffered from (see later under Methods). Direct physical violence (both non-lethal and lethal) often leaves changes on bones that can be analyzed using techniques similar to those that coroners and medical examiners use to figure out why and how someone died in police investigations.
Bioarchaeological evidence of interpersonal violence

Interpersonal violence, defined as violence committed by a human or humans against another at close range, has been documented going back thousands of years. Knüsel and Smith (2013) provide 34 case studies of ancient violence from around the world. Raiding for captives and for resources has a very long history as well. Cameron (2011) surveys the archaeological evidence for raiding, captive taking, and slavery and finds that there is abundant ethnohistoric and archaeological data to show it has been part of the human experience for thousands of years. As she demonstrates, the worldwide scale of captive taking is broad and deep in societies of every political-economic level on every continent. In early non-state societies, the goal of collective violence and warfare was in fact likely specifically to gain captives, who often were used as a form of wealth to gain power and control over resources.¹

Torture, as a particular type of violence that produces prolonged pain and intentional suffering but not death, is harder to analyze based solely on human remains. For places where there are both written records and good archaeology, torture is widespread. For example, in early Roman and Grecian times (400 BC–AD 400) as well as throughout medieval Europe (fifth to fifteenth centuries), various forms of punishment and torture are well documented (Innes 2012).

Case study: slavery and torture in the prehispanic Southwest

One of the goals of anthropological research is to understand and explain human behavior and human variation. In this case, we want to understand the biocultural impacts of prolonged periods of physical violence and abuse, with a focus on public torture and execution, at the hands of others in the prehispanic Southwest in the United States. What was it like to be a captive or an enslaved person in AD 1100? What was it like to be a victim – as well as the perpetrator and the witnesses – of torture and execution in a public setting in AD 900? What were the underlying reasons for this kind of social violence? In these case studies, we work with ideas and theories about the ways in which both lethal and non-lethal violence are used to subdue and exploit people, but also the very public and therefore culturally sanctioned ways that these forms of violence communicate particular kinds of values and meaning to the witnesses.

Methods

The methods used here to analyze human remains include a number of standardized and scientific measures and observations that have been fine-tuned within bioarchaeology (White et al. 2012). The metric and non-metric characteristics of skeletons can reveal age, sex, stature, physique, pathology, and habitual activities (Jurmain 2013). As discussed above, there are many ways to examine the extent of trauma on human remains. Traumatic lesions encompass a broad
range of clinical classifications that include fractures, crushing injuries, wounds caused by weapons and other devices, dislocations, and an assortment of degenerative problems such as exostoses, osteochondritis dissecans, and spondylolysis (Walker 2001). These types of injury are primarily caused by physical force or by contact with sharp or blunt objects. The cause of traumatic lesions can often be determined by analyzing the intensity and direction of the force. Interpretations concerning trauma are generally more direct than other kinds of pathologies, especially if the age, sex, and health status of the individuals are known. Also, the degree to which a trauma has healed provides a clue to the relationship between the event and the possible contribution of the trauma to morbidity and mortality.

Fractures in long bones, ribs, and vertebrae are the traumatic lesions most frequently reported in the paleopathology literature (Merbs 1989) and the most easily assessed. Fractures can be classified into a number of categories ranging from microstress fractures to greenstick breaks to comminuted and complete breaks. Martin and Harrod (2014) define a depression fracture as one produced by a force applied to just one side of a bone whereas compression fractures are produced when there is force from two sides; however, these distinctions can be challenging to make in archaeological specimens but usually depressions in the cranium are referred to as depression fractures. Depression fractures usually result from a blow to the head with a blunt object.

In archaeological specimens, fractures and traumatic lesions in the process of healing or with complete healing are fairly straightforward in diagnosis. However, when traumatic events occur around the time of death, it can be difficult to distinguish the perimortem bone damage from postmortem changes. Although numerous researchers have attempted to isolate the differences between perimortem and postmortem breaks, without other information regarding the context of the burial and the nature of the death, it is almost impossible to make firm diagnostic interpretations (White 1992). For example, although bone crushed from the blow of a blunt object will shatter differently when it is fresh versus later when it is dry, recovery of all of the pieces of bone is necessary for distinguishing the timing of the breaks. The amount of bone beveling and the type of fracturing (spiral versus straight) have been used as important indicators of the timing of the traumatic event; however, in reality these are related to plasticity of the bone at the time of the event. Another example of problematic diagnosis is that the non-union of a fractured end of a long bone could be interpreted upon recovery as an amputation if the distal end is not also recovered.

Specific types of trauma can prompt a direct inference about behavioral patterns. Certain activities predispose individuals to certain types of accidental or intentional trauma. Moreover, various forms of interpersonal violence (warfare, scalping, mutilation, lacerations, cannibalism) and surgical intervention (trephination, amputation) can sometimes be specifically identified (Merbs 1989; White 1992). Fractures of the forearm (radius and ulna) can reveal information about the activities of the group. A common fracture seen in many archaeological specimens is at the distal end where the wrist is located and these are generally
referred to as Colles fractures. They result when an individual who is falling extends the arms in order to break or soften the fall. Fractures that occur farther up along the forearm may result from the raising of the arm in front of the face to ward off a blow (these are called parry fractures).

Bioarchaeology of the prehispanic American Southwest: slavery

Bioarchaeological research on human remains from the ancient American Southwest represents a substantially long period of time, from about AD 800 up to the colonial period (circa AD 1500) and into the present. The Southwest is one of the most well-studied regions in the United States today due to the generally good preservation of habitation sites, artifacts, and human remains (Cordell and McBrinn 2012). Residents of the prehispanic Southwest, who were settled in agricultural communities, were descended from hunter-gatherer (archaic) groups that were in the area as long ago as 6500 BC (Cordell and McBrinn 2012). Imagine living in one of the agricultural communities spread throughout this region around a thousand years ago. You are in a high Colorado Plateau desert at an elevation about 5000 feet above sea level. The temperature is mild and pleasant most of the year. For instance, situated near present-day Farmington, New Mexico, there were a series of farming communities on the La Plata River, very close to the place where three rivers, the Animas, the La Plata, and the San Juan, converge. Archaeologists now refer to the remains of the communities as the La Plata sites. This area is called the Tóta by the Navajo people living there today, which means “between the waters.” In the late Pueblo II period (circa AD 1000–1200), this region was a relatively good place to be a high desert farmer because of the increased agricultural potential of the more fertile areas near the rivers.

In the 1990s, a team of bioarchaeologists and archaeologists worked on excavations from this region for several years, producing a bioculturally framed, synthetic report in 2001 (Martin et al. 2001). Many surprising finds arose from the analysis of the 68 burials and hundreds of disarticulated human remains from the Tóta. For example, because this area is relatively good for farming compared with more dry areas to the north and south, the archaeologists assumed that the human remains would reveal healthy and well-nourished people. The bioarchaeological team was led by two PhD students of George Armelagos who were trained in the biocultural approach to the study of human remains: Debra Martin and Alan Goodman. The biocultural manner in which they carried out the data collection and analysis yielded some startling findings.

Of the 68 burials, there were 28 children, 19 adult females, 15 adult males, and six unassigned adults. Preservation of the skeletal remains was poor to good across the burials, so some yielded more information than others. A subset of the 14 adult women between the ages of 20 and 40 had healed fractures; that is, they showed the healing of bones that had once been broken. Many of these healed fractures were on the cranium, and a number of the females with these had more than one trauma, known as injury recidivism. The type of healed cranial
depression fractures that they had were most likely due to blunt force trauma. They also had a variety of healed fractures in the lower body, including several with localized trauma to the joints, such as one female who exhibited a healing dislocated hip joint. When compared to the women with no healed fractures, these individuals also exhibited more skeletal indicators of poor overall health in the form of periosteal reactions, which are non-specific indicators of stress, and nutritional deficiencies. These findings are described in great detail in Martin (1997) and Martin and colleagues (2001, 2008). This pattern of healed trauma, the cases of pathology, and the increased frequency of traumatic dislocations and arthritis were clear signs that these females’ lived experiences were quite different from those of some of the other females in the group. The kinds of sustained injuries, health problems, and burial suggest these females were captives who were mistreated and abused.

When the burial reports prepared by the archaeologists who excavated the burials were reviewed, another surprise was in store. At one of the La Plata sites, Barker Arroyo (LA 65030), there were 19 females for whom there was contextual information on their mortuary configuration. Specifically, five females with no evidence of trauma were buried in a semi-flexed position with grave offerings of ceramic bowls and this is a pattern seen throughout the ancient Southwest (Figure 23.1). In contrast, 14 women had healed cranial depression fractures and other indicators of poor health and they were positioned on their backs, or in haphazard positions, as if thrown into the abandoned pit structures that they were recovered from (Figures 23.2–23.4). Figures 23.2 and 23.3 depict two of these individuals. Also, there were two adult females (one around the age of 20

Figure 23.1  Female, age 25, no skeletal evidence of trauma. Pit structure 1, upper fill. LA 37595, B1. Courtesy of Robert Turner, Office of Archaeological Studies, Department of Cultural Affairs, Santa Fe, NM.
Figure 23.2 Female, age 33, cranial and postcranial trauma evident on the skeleton highlighted. Pit structure 1, lower fill. LA 65030, B9. Courtesy of Robert Turner, Office of Archaeological Studies, Department of Cultural Affairs, Santa Fe, NM.

Figure 23.3 Female, age 20, cranial and postcranial trauma evident on the skeleton highlighted. Pit structure 1, lower fill. LA 65030, B8. Courtesy of Robert Turner, Office of Archaeological Studies, Department of Cultural Affairs, Santa Fe, NM.
years and one in her 30s) found alongside a 10.5 year old child of unknown sex in the lower fill of a pit structure (see Figure 23.4). Use of the pit structures for burial was not unusual; these pits were part of the normal architecture of the time and were used for a variety of functions. However, positioning of the individuals was highly unusual; archaeologists suggested that when they first exposed these individuals, they looked as though they had been thrown into the structures. Their analysis of the stratigraphy of the burials also suggested that they died at around the same time and were interred at the same time, all without grave offerings.

Putting all these data sets together – the archaeological artifacts, the skeletal analysis, and the mortuary pattern – we deduced that these women were likely captives who were taken from another group. Archaeologists had long suspected that the ancient Southwest region was rife with small-scale warfare and raiding (Kohler and Turner 2006; LeBlanc 1999) and these females seem to embody the effects of different kinds of violent interactions. Some of their head injuries likely came from the raiding itself. Cameron (2011) has documented that during raiding, often women and children are the preferred captives, because the women can aid in household and agricultural labor and the children also could be valuable workers. This pattern is documented by Cameron to be common in many cultures around the world that raided for women so it is not surprising to find it in the ancient Southwest. Years of hard labor would result in the kinds of joint trauma and pathology found on their bodies. That they were recovered from burial contexts so different from those of other females at the site also suggests that their social status within the group as a whole was
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quite different from that of the other non-pathological and more typically buried females.

A neuropathologist, Bradley Crenshaw, of the University of Massachusetts at Amherst, who works with living people who have sustained head wounds serious enough to cause cranial depression fractures, examined the 14 La Plata women with accumulated trauma. He suggested that the women had been hit hard enough to sustain some short- and long-term effects from neurological damage (Martin et al. 2008). Damage to the brain during blunt force trauma occurs first at the “coup,” which is the place where the force is applied. It can also occur at a second place, the “contra-coup,” where the brain slams into the skull on the opposite side from where the blow occurred. Many different side effects can result, depending on where on the brain the injuries were sustained and how forcibly the brain was hit. For example, the 33-year-old female in Figure 23.2 survived a crushing blow to the top of her head. Crenshaw analyzed all of her injuries and pathologies and hypothesized that she would have had life-long behavioral challenges. Specifically, due to the location and status of her injury, she may have had problems with migraine headaches, dizziness, motor control, balance, and general coordination. As seen in Figure 23.2, she also had a dislocated hip, which may have resulted from some of these motor control and balance problems.

As this brief example shows, using a biocultural approach and multiple lines of evidence from biological reconstructions of poor health and cultural reconstructions of mortuary context, the bones tell a story of individuals literally being worked to the bone, dying young, and receiving no special death rituals (Martin et al. 2010). These multiple lines of evidence suggest that these women were captives who were forced to work hard and when they died, they were not afforded the burial treatment of the males and other females from the site. Documentation of the ways in which repetitive activity and trauma leave signs on the skeletal material can only shift into strong interpretations of lived experiences in the past when all lines of evidence are brought together.

Bioarchaeology of the prehispanic American Southwest: hobbling, torture, and pain

In thinking about the social role that violence plays and the performative nature of violence, we only need look to the site of Sacred Ridge in the southwestern portion of Colorado. Around AD 800, at least 33 men, women, and children were killed. These people belonged to the Ancestral Pueblo groups who lived throughout the ancient Southwest. They predated the La Plata groups by about 300 years and were living about 50 miles north of the La Plata region. The individuals who were killed were likely related to each other and had grown up in the area, based on dental and cranial non-metric biodistance analyses and isotopic reconstructions of residential history (see studies in Perry et al. 2010). The valley they inhabited provided rich farmland and easy access to water, and likely served as a focal point for regional feasting activities based on the faunal and
ground stone assemblages that have been recovered (Potter and Chuipka 2007). The massacre assemblage dates to the Pueblo I period, a time of aggregation and intensification of agriculture, but little identified violence – at least prior to the analysis of the assemblage described here (Kuckelman et al. 2000). The site of Sacred Ridge was abandoned around the time of this massacre, since the latest radiocarbon dates, dating to around AD 800, are from the assemblage (Potter and Chuipka 2007). Bioarchaeological analysis of the assemblage revealed that the individuals were systematically disassembled, progressing from intact bodies to masses of bone and tissue that were deposited in a pit structure.

Their disarticulation and processing were systematic but that is not the focus here. Instead, we focus on the damage of the foot bones due to hobbling and torture. The foot bones were analyzed along with the rest of the skeletal assemblage (Stodder et al. 2010). During the analysis, it became clear that the feet of some individuals had been subjected to both hobbling and torture while they were alive. For example, one of the conjoins, reconstructions consisting of two or more fragments or elements representing an individual’s foot, designated FOO-002, is that of an adult male who exhibits all of the perimortem taphonomic indicators of hobbling and torture of the feet. All surfaces of this individual’s foot bones, the tarsals, metatarsals, and phalanges, exhibit damage consistent with beating and cutting. In particular, the dorsum (top) of the foot, specifically the tarsals, shows evidence of crushing, indicative of two distinct blows to the ankle once the foot was reconstructed (Figure 23.5). On the sides of the foot, the tarsals and metatarsals show a pattern of crushing and cutmarks that would have severed the tendons stabilizing the foot and are interpreted as hobbling (injuries that would have stopped an individual from being able to freely move or flee). On the lateral aspect of one of the tarsals, the calcaneus, the bone is missing with buckling around the edges of the missing cortex, indicating perimortem damage. On the medial aspect, cutmarks are visible on the calcaneus (not visible in Figure 23.6). The plantar (sole) surfaces of the foot elements and conjoins, including FOO-002 (Figure 23.6), have areas of peeling of the outer cortex of the metatarsal shaft and crushing consistent with beating the soles of the foot.

Beating the soles of the foot has a long history and continues to be used today as a form of torture for several reasons (Rejali 2009). First, it is extremely painful. Second, due to the anatomy and physiology of the foot, beating the soles of the feet is unlikely to cause visible damage to the foot. In modern contexts, this allows for photos of the victim to be made showing no or minimal damage while causing exceptional pain and limiting physical mobility. The sole of the foot is covered by a very thick aponeurosis (Gray 2000), a band of thick, soft tissue which acts as a barrier, blocking blood seeping to the surface of the skin during trauma. Blood instead pools underneath the aponeurosis, and these clots may become loose and travel in the bloodstream to the heart or brain, causing injury or death (e.g., Treat et al. 2004).
Key to understanding the importance of hobbling (visible as crushing and cut-marks on the medial and lateral aspects of the calcaneus) and torture (visible in the form of crushing and peeling on the plantar surface) in a social perspective are the twin roles of pain and performance. The performative aspects of torture and hobbling have been explored at length for the Sacred Ridge assemblage (e.g., Osterholtz 2012, 2013, 2014b). To summarize, the bodies were processed consistently regardless of age at death of the individual or sex. In short, all individuals were subjected to the same systematic disarticulation and fragmentation. When the same act is repeated over and over again by multiple individuals, as suggested by slight variation in the location of the impacts due to handedness or differences in strength between individual processors, group identity is created and reinforced amongst the aggressors, here the processors (Osterholtz and Harrod 2013). The performance therefore constitutes a series of intentional acts perpetrated by aggressors for a specific audience – the witnesses – upon a subjected group – the victims.

The relationships between these three groups can be seen as a power structure, but it must be remembered that it is a fluid power structure. The victim group is easily identified archaeologically and the aggressors can be inferred based on
the presence of the victims but are not present archaeologically – their presence is inferred based on the presence and processing of the victims, but the identities of the witnesses are more fluid. From a theoretical perspective, witnesses can be members of the aggressors’ group going through initiations. In this scenario, they are negotiating their place within the social group, possibly through participation in the massacre. The witnesses may also be members of the victims’ group who were used as examples. Specifically, it may be more effective to hobble just some individuals in front of the group as a mechanism for overall social control.

This is largely due to how we, as humans, respond to the pain of those whom we care about. In a study of 650 parents of school children, Goubert and colleagues (2008:277) found that children’s pain had a significant impact on the emotional state of parents. In particular, for parents “imagining their child in pain induces a blend of self-oriented emotions (distress) and other-oriented emotions (concern).” Empathy, the ability to try and feel what it feels like when someone
else experiences physical or emotional pain, is a crucial element to understanding the human condition. Singer and colleagues (Singer et al. 2004:1158) used functional magnetic resonance imaging (fMRI) to map areas of brain activity involved with the experience of pain, both as experienced by the individual being imaged as well as that experienced by others witnessed by or described to the individual being imaged. Their study group consisted of romantic couples, as “couples are likely to feel empathy for each other.” They found that only part of the pain network is activated when empathetically experiencing the pain of a loved one; the authors conclude that at least part of the pain network is automatically activated when witnessing someone one cares about experience pain. What they found was that individuals can experience someone’s pain when it is witnessed. The ability to feel another person’s pain is the basis for empathy and that empathetic response is more pronounced amongst people we are closest to.

For the examination of the role of pain in social control, it is Singer and colleagues’ second conclusion that is of interest: the ability to empathize carries with it the ability to predict likely consequences of the action being experienced by another. It is this function of empathy that allows pain to be used as a mechanism for social control. Understanding that the activities being experienced by a portion of a social group could be visited upon the rest of the group, in conjunction with an empathetic reaction allowing for at least some of the pain pathways to be activated. This produces a nuanced and rich understanding of how the physical activities of torture translate into social consequences.

Heightened emotional intensity, empathetic responses, and a feeling of powerlessness to change the situation would have been experienced by all the victims and witnesses. This would have all come together and created a power relationship between the aggressors and the other two groups. For those individuals in the aggressor group, group cohesion would have been strengthened through common activity and repetition. For those in the witness group, they would have been exposed to a power relationship based on the control of pain. The causing of or, even more importantly, the withholding of pain creates a dependency between the witnesses and the aggressors. The witnesses become fully aware that they are at the mercy of the aggressors and are more likely to alter their own behavior in order to spare both themselves and their loved ones physical and emotional trauma.

The analysis of hobbling and torture at Sacred Ridge begins with the identification of marks on bone but ends with a very poignant view into the beginnings of a massacre. Hobbling would have likely occurred at the beginning as a way to physically and psychologically control the victim group and to create psychological dependency between the aggressors and witnesses. After this relationship was constructed, processing (in the form of disarticulation, dismemberment, and commingling) of the victims was systematic and thorough. By the end of the processing event, it would have been impossible to identify someone amongst the victims as human let alone as a specific individual. For example, in no instance
could facial bone be associated with a cranial vault – they were broken into pieces too small to refit. Through the careful layering of psychological research, ethnographic and specialized studies, such as the biodistance studies, the behaviors involved in creating the assemblage can be examined.

The actual meaning of the creation of this assemblage and others like it is open to debate. The intense time commitment for the creation of the assemblage as well as the creation of similar assemblages about 100–200 years later in other parts of the Southwest suggests that this type of activity had deep roots and historical persistence and was very important socially. Martin and Osterholtz (2015) have discussed the behavior creating this type of assemblage as involving elements of renewal and kretaphenous violence (witchcraft execution). What is clear from examination of these assemblages is that they are complex and should be viewed in relation to time period, social processes, and cosmology. Given the long-term presence of assemblages of this type (they extend into the historic period in the Southwest), they may be seen as a mechanism for memory creation, tying previous populations to the current ones. We see these assemblages as activities of renewal, revitalization, and a performance of cosmology that would assist in the creation and negotiation of group identity and individual status.

Discussion

A biocultural approach to understanding the human costs of these kinds of activities has been useful in providing scientific data on the ways in which violence permeates social systems. As Perez documents (Chapter 22), culturally sanctioned violence is largely structural in that it is part of everyday living; people do not necessarily “see” the violence as something unusual or wrong. Structural violence makes things like slavery and torture look and feel normal. As we demonstrate here, moving from the bones of those who suffered at the hands of others, to the manner in which they were interred, to the larger social, political, and economic milieu in which these people lived can provide information on how violence operated in the past, shedding light on how it may operate in the present.

Another important strand in bioculturally oriented bioarchaeological research on violence is that it provides a way to see violence as more than just a way to hurt or kill people. Violence is often like a theater performance, in that perpetrators commit it against victims to communicate fear, subordination or some other message to those witnessing the performance. In this way, how slaves are treated and how captives are tortured is performative, and this impacts the witnesses. Pain is inherently relatable, so the examination of pain is a way to humanize culturally sanctioned violence such as that seen at Sacred Ridge, where the scale of the massacre has a tendency to overwhelm individual observations.
Although pain is notoriously difficult to document and score objectively, neuroscientists have examined the role of pain and empathy, particularly as it pertains to the experience of pain when witnessed by loved ones. These studies show that pain is a shared experience between those experiencing it and those witnessing. For bioarchaeologists, who cannot effectively document the experience of pain because it is both culturally defined and mediated, these studies can be illustrative of the human experience of pain. There is no reason to think that the experience of empathy would have been substantially different in the past. Even when we cannot objectively score the presence or degree of pain, we can be convinced of the presence of empathetic responses. Parent–child and romantic partner relationships are typically studied for pain research as those relationships are assumed to have a greater degree of empathy between the participants. For instance, Goubert and colleagues (2008) found that parental responses to pain either helped or exacerbated the experience of the child experiencing pain. If a parent was overly dramatic about the pain experienced by the child, the child experienced greater pain-related distress. These parents also experienced more parenting stress, anxiety, and depression than those who used humor and distraction as coping mechanisms.

The role of empathy must also be examined in relation to the role of the performance. Performance has the ability to reinforce group identity. It also involves heightened emotional situations that might intensify empathetic responses. This relationship between heightened reactions and stress is hinted at by Goubert et al. (2008), when they note that catastrophizing pain intensifies stress in both the person feeling the physical pain and those witnessing the pain.

**Conclusion**

George Armelagos was on to something when he wrote the landmark publication entitled ‘Bioarchaeology as Anthropology’ arguing that the study of the past was crucial to the overall study of human behavior. He stated that, “We are enriched when essential insights drawn from the past provide a prologue to the future. Understanding the successes and failures of our ancestors helps us to understand how we live and how we die. Bioarchaeology … should search for relevance to contemporary life. The experience may help us understand ourselves more deeply” (2003:38). Studies of ancient trauma and violence provide not only a window to the past, but a way to imagine our future as well. Bioarchaeology is forging ahead into this new area of study in part because of pioneers such as Armelagos who continually demonstrated the value of the past for the future. The data from the bioarchaeological record on slavery and torture show patterns in trauma and injury that provide important insights into the ways in which violence is used to inflict pain and suffering in the service of larger political, social, and ideological agendas.
References


Chapter 23: Biocultural approaches to ancient slavery and torture


Notes

1 See Cameron (2011) for archaeological reconstructions that support this.
2 The report is available at www.nmarchaeology.org/assets/files/archnotes/242.pdf
3 See Osterholtz (2012, 2013, 2014a) and Stodder et al. (2010) for more details.
4 For a full explanation of the series of events, see Stodder et al. (2010).
5 This brings up an interesting cultural understanding: that we will be more empathetic towards those with whom we have a closer social or familial relationship than with those we have no relationship with. In examining literature on pain, this appears to be an underlying assumption for all of the research.
6 See Osterholtz (2012, 2013, 2014a,b) for more information.
PART VII

The next generation
CHAPTER 24

Concluding thoughts: a bright future for students trained in using a biocultural perspective

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Introduction

Anthropology provides three ways in which to approach understanding humans in their diverse cultural and physical environments. First, it is the only discipline that provides time depth. This is very important because many problems, such as disease and violence, have long and diverse histories that are crucial to understand in order to provide interventions and prevention. Second, anthropology is the only discipline that demands that research produced within its boundaries compares and contrasts different cultures with respect to various behaviors. This helps to identify what is most distinctive about cultures, but also what cultures share. The third is that anthropology demands integration across knowledge domains and interpretations that are holistic. While other disciplines have heeded the call to be interdisciplinary and to work outside their normally bounded fields of interest, anthropology is by default interdisciplinary, holistic, and integrative. As can be seen from the case studies in this volume, anthropologists utilizing the biocultural approach draw upon all the subdisciplines within anthropology, including archaeology and linguistics, biological, and cultural anthropology. But many of the chapters go far beyond these borders, drawing upon methods, theory, and data from clinical medicine, epidemiology, nutrition, geosciences, demography, ecology, entomology, forensics, and health sciences.

For example, sociologists and psychologists often frame questions about violence in deterministic ways: Why are men so violent? Why are blacks more violent than whites? Most anthropologists would say that these are not good ways to frame these questions because they invite single-answer responses, such as hormones, genetics or socialization. While it is seductive to think that there could be one major causal factor that explains why males use violence or black
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communities have higher rates than white communities, it is far more complex than just biology, or just culture. Anthropologists, as seen in this volume, ask the question differently: What perceived problems does violence solve for the perpetrators in particular contexts? That is, if violent behavior is the answer, what was the question? This reframing of how violence can be studied provides a way to collect information that includes all aspects of biology and culture within particular natural and social environments. This biocultural approach can be seen over and over again in the case studies presented in this volume.

A biocultural research question is very specific but it is also all-encompassing. Imagine trying to organize a research study wherein you have data from a number of different analyses, such as the studies dealing with infectious disease and epidemics in this volume. You have biological and genetic data, such as age at death, sex, health prior to death, and perhaps biochemical data illustrative of diet but you also have archival data from historic documents and medical records, and information on economic contexts and politics processes from the time period. It would be very difficult to keep so many points of information within one interpretive framework, yet that is precisely what a biocultural model provides. That is, it is used to keep multiple and complex factors organized, in the interpretive picture, and operationalized.

The biocultural model also provides ways in which to comprehend how environmental, biological, and cultural factors interact, and which factors are most important in unpacking and explaining the type of human behavior or phenomenon that is of interest. Above all, biocultural research is a path towards holistic and integrative interpretations that engage with real-world problems.

Teaching, pedagogy, and ethics

A recent article in the Chronicle of Higher Education provided ideas about what makes a professor really effective (Jenkins 2015). Beyond being well prepared, there is evidence that professors should also be passionate, present, and mutually engaged with their students in the classroom. Good professors do not provide facts; rather, they model how they and others go about doing research and solving problems. Students are emphatic that they want teachers who are passionate and excited by what they are teaching, and who themselves are engaged in research that they find absorbing and productive. Students seem to learn best when they are engaged and invited to discuss and debate alternatives to the status quo, for example.

What undergraduate and graduate students will remember from their courses at university is not any particular set of facts. These details will be progressively lost from their memories as they move further out from their lives on campus into their careers. Instead, they will remember moments in which they were able to think through a complex issue and have a well-argued opinion that they could back up with facts. These are “light-bulb” moments, and it is hoped that some
of the case studies in this volume might provide that kind of experience. These case studies reflect the work of scholars who are committed to making the world a better place through studies that are carefully and rigorously carried out. They are passionate about their work and its real-world applications and implications.

As can be seen in several chapters throughout this volume, often this research requires multiple episodes of fieldwork in order to observe and collect data and this happens over many years. Chapter 2 by Thomas, for instance, details the lessons that he learned, the maturation of his thinking, and sometimes radically differing perspectives that he adopted during more than 50 years of fieldwork in communities in Peru. These chapters model for students how to reason through complex issues and the kinds of methods that generate data that can be used to solve problems. These are relevant to any comprehension of how research within anthropology works, as well as how one might undertake fieldwork, operationalize anthropological theory, and do anthropological research that is deeply relevant to today’s communities.

Many of these case studies either hint at or take head on the ethical implications of doing the kind of research presented here. In some chapters, ancient indigenous skeletons are probed to better understand why violence was used, but at the same time, descendant communities of Native Americans, also experiencing violence in the modern era, would prefer that scientists did not study their ancestors (see Chapter 23). In others, indigenous communities welcome anthropological geneticists, eager to learn more about biological history, the identities of their ancestries, and the formation of their communities (see Chapter 22). Importantly, leaders in these indigenous communities put this knowledge to work, using the genetic findings to gain federal recognition of their tribes and associated rights and privileges, and gain better control over their heritage (see Chapter 19). In others, it is evident that while biocultural studies were being carried out to understand development and adaptability, local communities were under siege by oppressive political forces that were not being studied or even perceived by the researchers (see Chapters 2 and 3). In several chapters, we learn about the direct effects on human well-being of overt acts of racism at the individual and community level (see Chapters 4–7).

The authors address the ethics of racist behavior not by demonizing the racists, but by showing all the ways in which this type of violence is both structural (within the societal laws and rules) and normalized. The biocultural approach, by incorporating consideration of political-economic factors as well as other structures that buffer some people while exposing and abusing others, is a powerful tool for articulating the context for what ethical research entails, as well as for thinking about the ethical implications of not doing the kinds of research that identify the proximate and ultimate causal factors.

In summary, biocultural approaches within anthropology are really a model for interdisciplinary learning and research that is conducted with a variety of scientific, data-based research strategies.
The past as a guide

Rebecca Solnit is a philosopher and nature writer who has pondered the trope that “the past is crucial for understanding the future” (Solnit 2013). Historians have beaten home the more cynical version of this trope, which can be expressed as “those who don’t know history are doomed to repeat it.” But Solnit sees things a little differently. She emphasizes that it is not single moments of time in history that are informative, but that understanding the longer arc of history is what is important. She sees the long arc of history as a means to an end. In a compelling quote for the ages, she points out that “the past doesn’t need us. The past guides us; the future needs us” (Solnit 2013). The past, be it the 2014 epidemic of Ebola in West Africa (see Chapter 14) or historic African-American burials (see Chapters 6 and 7) or ancient Native Americans (see Chapter 23), can be used to better monitor and observe the implications of things that cause human suffering over a period of time.

This kind of research helps us to keep problems under systematic review by comparison across time or space. In the chapters on infectious disease and contemporary health issues (see Chapters 4, 5 and 14), it is clear that the long arc of history helps us locate the problem and understand its development and impact. The biocultural perspective interrogates all aspects of a problem, and as such, can present a more nuanced and complex picture. This information, in turn, can perhaps be used to limit or even prevent these processes and their outcomes for contemporary and future societies. In this way, the lives of those in the past, and the suffering that many experienced, are not in vain. Importantly, this usefulness – the employment of knowledge to better the lives of contemporary humans and preemptively better those of future generations – is what makes anthropological research not only meaningful but also ethical.

A bright future for biocultural scholarship

Are there jobs for students trained in biocultural anthropology? Yes, there are. There are anthropologists in both academic and non-academic settings whose specific talents and skills are derived from exposure to biocultural research. While it may say something about the darker times we are living in, the American Anthropological Association (AAA) has data that suggest it is a great time to be an anthropologist in terms of career opportunities. In businesses, corporations, non-profits, international health programs, international development programs, museums, social services, criminal justice, health care, ecology and sustainability programs, and government agencies, anthropologists who can work in multilingual, multicultural, and multivocal settings are being recruited quickly.

All the anthropologists in this volume worked as graduate students with George Armelagos or were colleagues of George’s during his career. One of
the main themes to emerge when they reminisced about those times with him is how much fun it was and how exciting it was to find a particular area to do research in. As you can see from the diverse topics covered in this volume, students working with George and those collaborating with him chose diverse regions, cultures, and time periods to work in. Thus, what really drove their training and research was the questions they were asking. This is a very different approach to graduate training versus other disciplines where it is the method or topic that drives the research. You can learn more about the diversity of anthropological research from the web sites and educational materials of professional anthropological organizations, like the American Anthropological Association (AAA), the Society for American Archaeology (SAA), the Society for Applied Anthropology (SfAA), and the American Association of Physical Anthropology (AAPA).

In George’s lab and on his research projects, it was the question that was important. Who survives an epidemic of infectious disease? Who is most at risk to die a violent death? What is the burden of illness in those who are poor? Why are different societies affected by different kinds of disease? How do human bodies adapt to the environments in which they live? What are the effects of racism on health? What can we learn from studying skeletal remains from historically oppressed groups? What can genetic data tell you about the effects of cultural change on populations in the past? For an anthropologist, finding the answers to these kinds of questions can draw on a range of data sets from archaeological remains to medical records, and from ethnographic interviews to reading the bones of ancient skeletons.

More and more, we hear that students who wish to solve the world’s problems must be versatile scientists who can think outside the box. Undergraduates and graduate students who receive exposure to anthropology and to biocultural ways of thinking about problems in the world will be more than ready to work on complex issues in any number of cultural and environmental settings.

In this volume, we hoped to invite you, the reader, to see the ways in which one scholar who dared to pioneer a new approach led to a generation of problem-solvers who now work in diverse settings, from traditional academia to non-academic settings, such as health programs and advocacy groups. One of the potential strengths of the biocultural approach is its diversity and inquiry-based approach. This makes for good teaching and good learning, but also for forward motion in producing the next generation of scholars, researchers, aid workers, physicians, activists, and others who will be needed to promote justice for humans, animals, and the environments that they live in and to work towards the repair of the planet. Lofty goals, but those of us who worked under and with George Armelagos saw first-hand how the power of one could accomplish much in a lifetime. The 43 scholars involved with writing the case studies in this volume are a testament to the influence that one good advisor, mentor, and colleague can have on the world.
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Notes

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