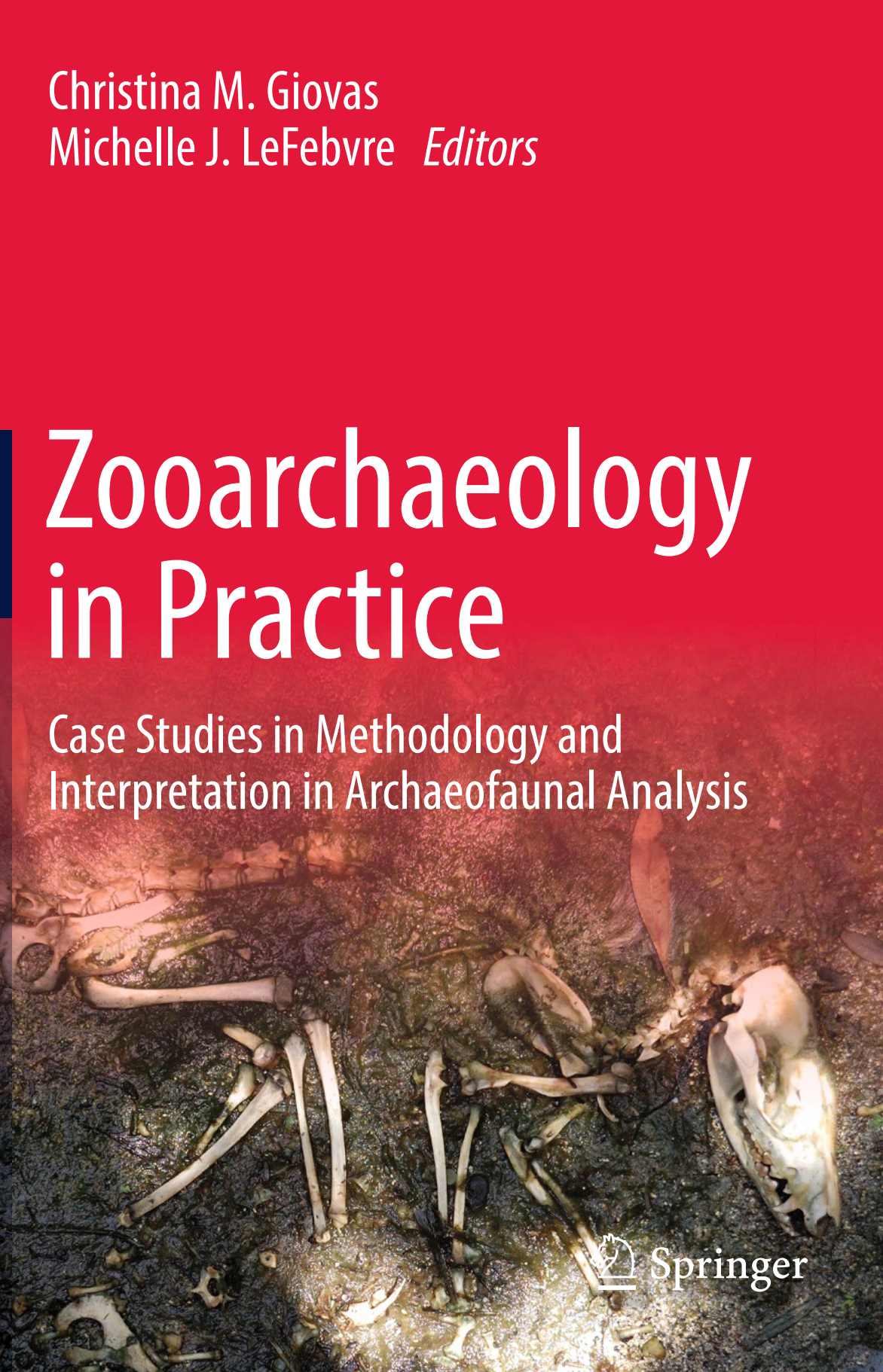
Christina M. Giovas
Michelle J. LeFebvre *Editors*

Zooarchaeology in Practice

Case Studies in Methodology and Interpretation in Archaeofaunal Analysis



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For DKG, SDD, and the others who inspire us to peer through the looking glass.

Acknowledgments

Zooarchaeology in Practice was born from a symposium on zooarchaeological sampling and methodological issues held at the 79th Annual Society for American Archaeology meeting in Austin, Texas, organized by one of us (CMG) and Aaron Poteate (University of Oregon). Its purpose was to foster a comparative perspective on key methodological debates in the field by drawing together practitioners with diverse perspectives and approaches. Many of those original symposium participants are contributors to this volume. Others joined as the book evolved. Aaron Poteate was instrumental in the early development of the volume, and while he was unable to shepherd this through to final publication, the pages here reflect his insights and efforts as much as our own. We are indebted to him for his contribution and thank also those who participated in the SAA session for the foundation of ideas they provided.

As Editors, we sought to unite depth of treatment with broad topical coverage into a single, integrated volume. Despite our best efforts, not all aspects of zooarchaeological practice could be covered, and the reader will note the absence of certain taxonomic and geographic areas (e.g., birds, East Asia). Notwithstanding, we saw an all-inclusive approach as neither feasible nor desirable. Rather, our objective for *Zooarchaeology in Practice* was to provide focused case studies and historical reference points that might serve as metaphorical lamps to light our way. We conceived of a volume that would (1) be of utility and significance to both beginners and seasoned professionals; (2) link methods to interpretive outcomes, offering a framework for methodological planning prior to research implementation; and (3) furnish scholars with a set of instructive approaches for addressing methodological challenges in their own research. If these objectives have been realized, it is due to the efforts of our authors. We are grateful to them for their innovative approaches to questions old and new, diligence through rounds of chapter peer review, and their patience. We also thank the many anonymous individuals who shared their expertise and valuable time as peer reviewers. Lastly, we wish to thank our editorial team at Springer, Teresa Krauss and Hana Nagdimov. They have provided invaluable assistance and support in the completion of this volume.

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Christina M. Giovas (Ph.D., University of Washington) is a Lecturer in Archaeology at the University of Queensland. Her research focuses on prehistoric fisheries, animal translocations, and the human paleoecology of island and coastal settings, particularly the Caribbean and Oceania. She has conducted fieldwork in the Lesser Antilles, Polynesia, France, and the Great Lakes and the Pacific Northwest regions of North America. Dr. Giovas is Associate Editor for the *Journal of Island and Coastal Archaeology* and serves on the Board of the International Association for Caribbean Archaeology. She joins the faculty of the Department of Archaeology at Simon Fraser University in 2018.

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Chapter 1
Methods, Methodology, and Zooarchaeology in Practice

Christina M. Giovas and Michelle J. LeFebvre

1.1 Methods and Methodology in Zooarchaeology

As a branch of archaeology, zooarchaeology has matured from purveyor of species lists to a dynamic sub-discipline that investigates all facets of past human relationships with animals. Today's practitioners seek to understand a bevy of issues at the interface of human-animal-environment interactions. Broadly, common research foci include subsistence and paleoenvironmental reconstruction (Barrett et al. 1999; Byrd 1996; Castel et al. 2006; Peacock et al. 2014), anthropogenic impacts on biodiversity and historical ecology (Corbett et al. 2008; Porcasi et al. 2000; Stahl 2008; Steadman 1995), cultural and social uses and significance of animals (Campbell 2014; Emery 2012; Kirch and O'Day 2003; Wallis and Blessing 2015), human manipulation of animals (e.g., translocations, management, domestication) (Giovas 2017; LeFebvre and deFrance 2014; Russell 2002; Thornton et al. 2012; Zeder 2015) as well as the application of zooarchaeological perspective in contemporary biological and ecological conservation (Grayson 2006; Lyman 2015; McKechnie et al. 2014; Newsome et al. 2010; Rosania 2012; Wolverton and Lyman 2012). To paraphrase Sykes (2014), zooarchaeology addresses archaeological questions through animal answers. More simply stated, zooarchaeology is archaeology. Here, in this introduction to a volume devoted to method and methodological principles, we highlight and discuss ongoing challenges to zooarchaeological practice and the path forward.

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Careful consideration of the ways in which methods influence results has been a vital aspect of zooarchaeology's development (e.g., Blumenschine et al. 1996; Casteel and Grayson 1977; Driver 1992; Emery 2004; Grayson 1984; Hudson 1990; Klein and Cruz-Uribe 1984; Lyman 1994, 2008; Lyman and Ames 2004; Marean et al. 2004; Reitz et al. 2009). Filtering in from paleontology, taphonomy (Efremov 1940) and quantification (e.g., White 1953, 1954, 1955; see also review by Lyman (Chap. 2)) were early concerns in the nascent sub-discipline of the 1950s and 1960s, a time when most practitioners were moonlighting from the allied disciplines of zoology and paleontology. As the sub-discipline has matured, analytic techniques and publication platforms have evolved, presenting both new opportunities and new challenges for future practice. For instance, the introduction of zooarchaeology by mass spectrometry (ZooMS) (Buckley et al. 2009, 2010, 2014; Stewart et al. 2013; von Holstein et al. 2014; see also Buckley (Chap. 12)) and ancient DNA bulk bone metabarcoding (Grealy et al. 2015, 2016; Murray et al. 2013) offers unprecedented opportunities to identify traditionally non-diagnostic specimens on a large scale, but simultaneously poses issues for quantitative integration with assemblages analyzed using conventional morphological criteria and derived measures like the minimum number of individuals (MNI). Many of the tensions between advancement in methods and the capacity for existing methodological frameworks to absorb these are drawn out in the pages of this book (e.g., Jones (Chap. 13)).

At the same time, this volume reveals how a number of "older" methodological concerns—issues with taphonomy, quantitative units, specimen recovery (i.e., screening bias), and fragmentation—persist. How can it be that these problems have not yet been solved? Have zooarchaeologists failed to act upon the insights of six decades of methodological navel gazing? Are efforts to promote rigorous methods a sisyphean feat?

We believe the answer to these questions is an emphatic *no*. Yet, the reasons why certain methodological issues persist are complex. To understand better how and why this occurs, it is useful to remember the distinction between methods and methodology. Methodology systematically links a series of chosen research methods through a specific theoretical or conceptual framework for the purpose of interpretation. The (classic) case of screen mesh size and representative sample recovery illustrates the point to be made here. Several decades of studies demonstrate a simple principle: use of smaller-gauge mesh increases specimen recovery rates and taxonomic richness (Cannon 1999; Gobalet 2005; Gordon 1993; James 1997; Nagaoka 1994, 2005; Zohar and Belmaker 2005; but for exceptions see Emery and Thornton 2014; Vale and Gargett 2002). Yet, if smaller is better, why is fine-sieving not universally implemented? Sieving is a method for which each mesh size can be thought of as a specific technique. The application of sieving and the resulting data (material caught by the screen and subsequently analyzed) are informed by probability and sampling theory. Together, method (sieving) and linking theory (sampling and probability) collectively form a methodology. Discordance over the appropriate mesh size—and indeed whether fine-sieving is even necessary—constitutes a methodological issue. Such problems can arise in several ways: (1) when the selected method (mesh size) violates established principles derived from methodology (i.e.,

smaller mesh is better); (2) when a new conceptual component is introduced into the methodological equation (e.g., the feasibility of sieving is impacted by budget and schedule limitations, sediment characteristics, or water availability); or (3) when empirical evidence challenges underpinning theory (e.g., practical sieving studies that show no correlation between specimen recovery and sampling strategy). Because these catalysts are erratic and dependent on the context of application, they hold the potential to spark varying, iterative challenges to a given methodology—like a series of smaller fires within a much larger conflagration that zooarchaeologists are tasked with battling.

Two important conclusions logically follow from viewing methodological issues in this light. First, given the context-specific nature of many such issues, all-purpose methods/methodologies are generally not desirable. Couching methodological debates within the language of universal solutions does a disservice to the discipline. As technical methods and their objects and contexts of application change, so too must methodologies be flexible to accommodate these. This should not be confused with best practice guidelines for reporting standards, which provide a necessary foundation for assessments of data validity, interassemblage comparisons, and larger meta-analyses (Casteel and Grayson 1977; Driver 1992, 2011a; Lyman 1994; Wolverton et al. 2016; see also Jones (Chap. 13)). Second, ongoing challenges to a given methodology are an inherent component of their use and improvement, and hence methodological problems persist, sometimes seemingly without resolution. In his concluding remarks to this volume, Albarella offers the pointed insight that methodological review and refinement is a continuous endeavor. We agree. Increasingly diverse intellectual landscapes, research contexts, and goals present zooarchaeology with the critical challenge of balancing methodological flexibility, scientific rigor, logistical constraints, and analytical and theoretical goals.

Importantly, neither of the observations noted above releases us as zooarchaeologists from our responsibility to address areas of practice where we have made limited progress (compare, for example, Driver 1992 with Driver 2011a, b and commentary therein) or where methodological approaches could be strengthened. Looking to address a blend of persistent and emerging issues, a number of scholars have called for improved methodological transparency, explanation, and reporting, and increased quality assurance in zooarchaeology (Driver 2011a, b; Wolverton 2013; see also Driver 1992; Gobalet 2001). The calls have been especially blunt with respect to taxonomic identification, which Lyman (2002, p. 18) has described as the "most fundamental first step of zooarchaeology". At their core, such appeals are about strengthening confidence in zooarchaeological methodology, results, and the reliability of its conclusions.

This volume speaks to that objective. In practice, zooarchaeologists, like other researchers, rely on a set of context-appropriate methods developed through disciplinary dialogue and engagement. However, the current publication structure supporting this dialogue—primarily academic journals heavily focused on data presentation—limits in-depth synthetic treatments of methodological issues from a variety of perspectives. *Zooarchaeology in Practice* was conceived to advance methodological introspection and discussion beyond this stricture by addressing the

elements of sound analytical practice through a collection of case studies bound under a single cover. The 15 chapters that follow explore the ways in which zooarchaeological data are shaped by methods of practice and the interpretive impact of these effects at varying scales. Emphasis is not placed on promoting particular methodologies or research designs. Rather, contributions are geographically, temporally, culturally, and taxonomically diverse and offer instructive approaches to problems in both traditional and emerging areas of methodological concern.

1.2 Zooarchaeology in Practice

Part I of this volume concerns primary data collection (involving identification and simple counts, such as the number of identified specimens (NISP)) and secondary analysis (involving derived quantitative units and measures, such as MNI). Methodologically, this research stage is significant as the first opportunity for the potential introduction of post-excavation analytic bias. Lyman (Chap. 2) examines the historical roots of the minimum number of individuals, a now fundamental quantitative unit in zooarchaeology, and reveals in this history an early and critical disciplinary awareness of unit performance in relation to analytic function. LeFebvre and Sharpe (Chap. 3) examine the nature of zooarchaeological specimen identification, its epistemological underpinnings in analogical inference, and the interpretive challenges associated with this, especially in the era of big data and evolving platforms for data dissemination. Giovas considers how identification protocols in archaeofish analysis, specifically the decision of which elements to include, impact quantifications and reconstruction of fishing behavior. Her analysis pinpoints sources of equifinality and differential bias, allowing useable data to be gleaned from studies which might otherwise be considered entirely compromised. Together, these chapters illustrate how unit selection, with respect to both taxonomic level and quantification, impact interpretation at multiple scales and remind us that we must carefully consider at all times how these articulate with our target analytic variables.

Using site specific case studies, Part II offers fresh perspectives on longstanding analytic challenges related to taphonomy, screen size, specimen fragmentation, attrition, and sample size. Chapters 5–8 demonstrate that when assemblage taphonomy and its relationship to site formation processes and stratigraphy is overlooked, especially from a quantitative perspective, the interpretive value of zooarchaeological data may be compromised and incompatible with desired research goals. Rainsford and O'Connor's (Chap. 5) detailed discussion of "contextual taphonomic analysis" emphasizes the interplay of pre-deposition behaviors, in-ground diagenesis, and post-excavation biases that need to be considered, ideally on a site by site basis, when designing and implementing excavation strategies, conducting analysis, and planning for specimen curation. Faith and Thompson (Chap. 6) and Fisher (Chap. 7) similarly explore differential bone survivorship and probable links to attrition (Faith and Thompson) and density-mediated destruction (Fisher). In each

case, the authors argue for great methodological diligence when discerning between cultural and natural causation for assemblage taxonomic and/or elemental composition and abundance (e.g., carcass transport (Faith and Thomson), optimal foraging (Fisher)). Jerardino (Chap. 8) carries forward the theme of taphonomy with a new model for recognizing and quantifying possibly differential rates of shell deposition and fragmentation. The experimental nature of the model encourages methodological innovation and provides an analytical template for taxonomically broader studies of shell, and ostensibly bone, fragmentation adaptable to a diversity of archaeological contexts. Together, these contributions demonstrate why zooarchaeologists and archaeologists alike would do well to value taphonomic information as data inextricably linked to rendering accurate interpretations of past human behaviors and activities.

Crabtree (Chap. 9) concludes Part II by taking a resolute stand for large-scale zooarchaeological analysis and the fundamental value and continuing relevance of traditional analytic methods. She deftly illustrates how applications that inform our understanding of the socio-economic and ideological realms of human society—such as documenting taxonomic diversity, constructing dental age profiles, and modelling population demographics to investigate animal husbandry, domestication, expressions of identity, and ritual practice—necessitate the analysis of large faunal assemblages. Crabtree's essential point is that sometimes more *is* more. Accepting this fact requires embracing research designs that make appropriate schedule and budget provisions to recover and analyze large faunal samples and train or retain personnel with the required technical expertise.

Part III explores methodological issues in the isotopic and biomolecular analyses of archaeofaunal remains, serving as a counterpoint to the morphologically-based analytic methods of the previous section. The highly technical, rapidly evolving nature of these fields presents a challenge for non-specialists, who must sort through the significance of analytic procedures and their relevance to the zooarchaeological record. Addressing isotopic (West et al. (Chap. 10)), ancient DNA (aDNA) analysis (Matisoo-Smith (Chap. 11)), and zooarchaeology by mass spectrometry (ZooMS) collagen fingerprinting (Buckley (Chap. 12)), the chapters in this section probe the critical sampling, contextual, and interpretive issues that problematize data and conclusions in these research areas. As the authors reveal, isotopic, aDNA, and ZooMS applications continue to open up exciting new research avenues for zooarchaeology by providing the means to ask new questions at new scales of analysis. These techniques, however, are not without their limitations and potential pitfalls. The chapters in this section offer a welcome framework for non-specialists to help them evaluate the significance and validity of data generated by such methods.

Part IV engages directly with a primary goal of zooarchaeology, the wider understanding of human-animal relationships in the past and its application beyond the sub-discipline. Contributions here explore the methodological considerations posed by comparative and synthetic studies that bring together multiple datasets to understand human behavior and animal interactions more broadly. Through her thoughtful, multi-site investigation of the ecological effects of domestic fauna introduction

by the Spanish in seventeenth century New Mexico, Jones (Chap. 13) explores the interpretive gains and tradeoffs associated with the meta-analysis of zooarchaeological data. She points out that relaxing the scale of analysis, that is, allowing for qualitatively driven conclusions over quantitative ones, is sometimes necessary for the sake of reaching holistic understanding. MacKinnon (Chap. 14) addresses tensions in the integration of ancient textual, historical, artistic, and zooarchaeological information as independent records of human-animal interaction in Classical Rome and Greece. His study highlights how the merger of "evidence" across disciplines may require breaking down boundaries between research cultures as much as it does the integration of disparate datasets and methodologies. Braje et al. (Chap. 15) address the mechanics of reconstructing deep time records of anthropogenic impacts through a case study on archaeological mussel size in the California Channel Islands. Here, focus is shifted forward through time as the authors underscore the contemporary relevance of these records to conservation biology and show how methods used to analyze the past, and the reliability of the data they generate, can critically impact the present. As noted above, the volume concludes with a chapter by Albarella, who draws together the collective contributions and uses this synthesis to explore persistent methodological themes in zooarchaeology and the field's larger contribution to archaeology.

1.3 Looking Ahead

Zooarchaeology in Practice arose from the idea of offering a comparative perspective on methods and methodology through focused case studies across a variety of topics and archaeological contexts. The volume seeks to introduce students to key methodological issues in zooarchaeology while at the same time focus and advance methodological discourse among more senior scholars. By linking methods to interpretive outcomes, the chapters that follow offer a framework for research design and provide practitioners with a set of instructive approaches for addressing methodological challenges encountered in their own research.

Earlier in this introductory chapter we stated that methodological review and revision is an ongoing process. It thus stands to reason that the case studies presented here are just stepping stones along that trajectory. Four or five decades from now, under the aegis of fantastic methodological developments we in the present can barely imagine, future zooarchaeologists may reflect upon the quaintness of the ideas held by this generation of scholars. Rather than be discouraged by this thought, however, we find it inspiring. As archaeologists we know the future is built on the past. Tomorrow's new techniques, break-through methods, and revolutionary understandings rise from the foundations that we lay here in the present; we embrace the promise that this volume might in some way contribute to that advancement of practice.

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Part I
Identification and Quantification

Chapter 2
The History of MNI in North American Zooarchaeology

R. Lee Lyman

2.1 Introduction

Knowledge of a discipline's history provides understanding of why the research questions asked, the analytical techniques used, and the explanatory theories favored today are asked, used, and favored (e.g., Kuhn 1962). Further, knowing our discipline's history facilitates the avoidance of previously identified (but perhaps forgotten) pitfalls and the repetition of errors in technique and logic; a thorough study will highlight historically perceived pitfalls and errors as well as identify perceived avenues to success. Most importantly in the context of this volume, historical knowledge can also serve to remind us of how wise some of our intellectual predecessors were and help us avoid disciplinary amnesia. If we can discern why our predecessors made the analytical choices they did, that may help guide us when we have choices to make during our own research.

The history of North American zooarchaeologists' use of the minimum number of individuals, or MNI, quantitative unit has been commented on by Richard Casteel (1977a), Kent Flannery (1967), Donald Grayson (1979, 1984), Klein and Cruz-Uribe (1984), Elizabeth Reitz (1993), Bruce Smith (1975, 1976), and many others (e.g., Barr 1979; Medlock 1975; O'Connor 2000). These commentators agree on one or both of two things. First, they all state that Theodore E. White "introduced" the MNI quantitative unit to North American zooarchaeology in 1953, and second, some of them indicate that White's (1953a, b) analytical technique of estimating the pounds of meat represented by a collection of zooarchaeological remains popularized MNI among North American zooarchaeologists and prompted its increased use. These two perceptions of the history of North American zooarchaeology are the received wisdom, and they are repeated in our subfield's textbooks (e.g., Reitz and

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Wing 2008, p. 20) and thus the next generation of zooarchaeologists learns this history irrespective of its accuracy.

Those who have commented on the history of North American zooarchaeology have provided no empirical data to substantiate their claims about MNI. This is perplexing because all commentators identified above were trained during the revolution in North American archaeology described as the emergence of the "new" or "processual" archaeology of the 1960s and 1970s (Binford 1968a, b; Deetz 1970; Dunnell 1978; Martin 1971). One of the (alleged) hallmarks of that upheaval was the often made claim that the new archaeology was "scientific" (e.g., Watson et al. 1971), along with the caricature of pre-1960s archaeology as both non-scientific and descriptive (often phrased as "historical"). The sciences rest upon empirical evidence, that is, evidence (or data, if you prefer) that is perceptible to the senses (e.g., Derry 1999; McCain and Segal 1969; Nagel 1961). But so too writing an accurate history of science requires empirical data (e.g., Kuhn 1968) or otherwise the result may be historical fiction or at least be inaccurate.

That none of the zooarchaeologist commentators noted above provided empirical evidence to justify their claims about the history of MNI highlights a lacuna in our historical knowledge. It suggests our knowledge may be incomplete at best and inaccurate at worst. I take steps here to fill this lacuna by presenting and analyzing data regarding the history of MNI. Along the way related historical events are noted. In exploring the history of MNI in North American zooarchaeology, I hope to more thoroughly reveal that history than previously, and to identify the nuanced causes of that history. In short, I intend to demonstrate that the history of the use of MNI was driven by the sincere intentions of early zooarchaeologists to (1) be as logical and scientific as possible; and (2) analytically reveal aspects of human behavior not previously accessed by archaeologists. In particular, I argue that increased use of MNI in the mid-twentieth century resulted from its use as a measured variable intended to monitor three target variables: amount of meat provided by each taxon, taxonomic abundances, and human butchering behaviors.

2.2 Methods and Materials

To determine if the perceptions of zooarchaeological history described above are valid, I acquired copies of as many titles as possible of the North American zooarchaeological literature that appeared between 1900 and 1979, inclusively. I did not consider more recent literature for two reasons: increased use of MNI is said to have occurred well prior to 1979, and the volume of post-1979 literature would have made the task unwieldy. By "North American zooarchaeology" I mean journal articles, book chapters, master's theses, and doctoral dissertations had a North American focus and faunal remains came from archaeological sites located in North America (Panama north to Alaska and Newfoundland), including much of the Caribbean. I excluded titles not written in English, book reviews, titles concerning bone and shell tools, and titles concerning Pleistocene extinctions and domestic dogs. I did not

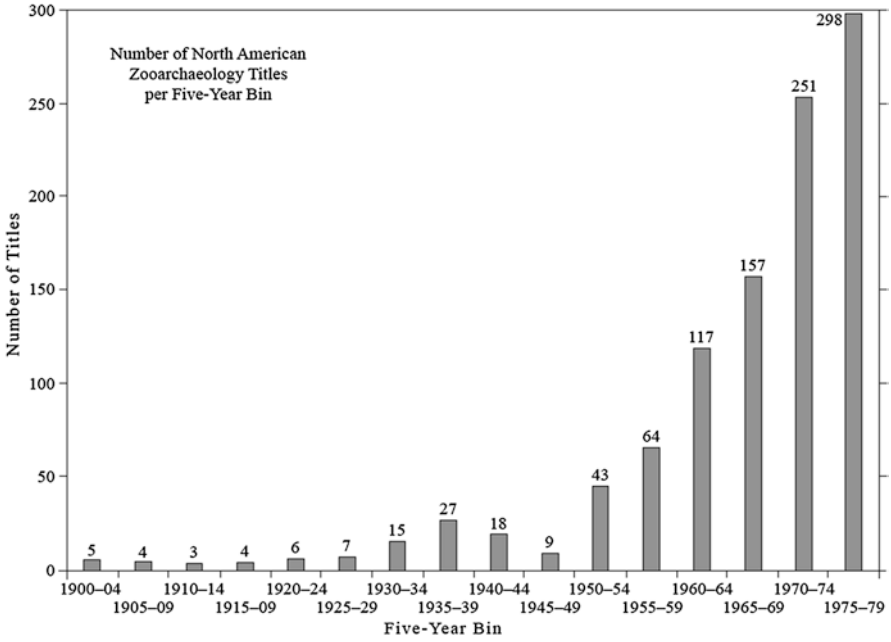

Fig. 2.1 Frequency of titles in North American zooarchaeology per 5-year temporal bin from 1900 to 1979

include zooarchaeological appendices from unpublished site reports, nor did I record published site reports that included a zooarchaeological chapter, section, or appendix authored by the lead archaeologist (e.g., Stanford 1976). To include a representative sample of these would have demanded inspection of all published site reports, an impossible task.

To compile this list of zooarchaeology titles, hereafter referred to as the 1900–1979 bibliography, I first consulted three published zooarchaeology bibliographies (Bogan et al. 1978, 1987; Lyman 1979). I then searched online databases (e.g., Biodiversity Heritage Library) and journals (e.g., *American Antiquity*) for pertinent titles. Next, I examined the references cited in histories of North American zooarchaeology (e.g., Reitz 1993; Robison 1978, 1987; F. L. Stewart 2003; K. M. Stewart 2002). Finally, bibliographies in a sample of titles were inspected. I assume that the known sample (N = 1028 titles) is sufficiently robust that general quantitative trends will be apparent. Indirect evidence that this is the case is found in the fact that the number of titles per 5-year bin increases over the eight decades represented, with a not unexpected decrease during World War II (Fig. 2.1). As also might be expected, the number of master's theses and doctoral dissertations concerning North American zooarchaeology increased considerably after 1969 (Fig. 2.2). While it would be interesting to determine if the proportion of all archaeology titles that comprise zooarchaeology produced between 1900 and 1979 increased or remained static, that

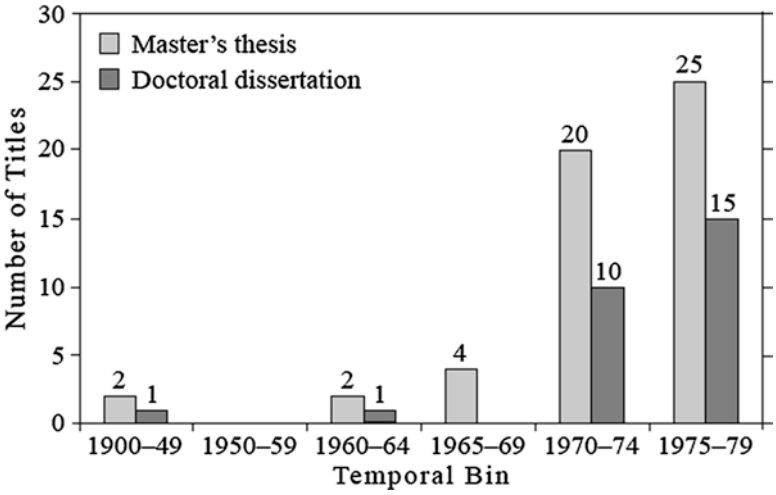

Fig. 2.2 Frequency of master's theses and doctoral dissertations on North American zooarchaeology per temporal bin from 1900 to 1979

is beyond my scope here. The trends shown in Figs. 2.1 and 2.2 are likely at least partially the result of concomitant increases in the number of college students, the number of practicing archaeologists, and the increasing tempo of cultural resource management (e.g., Schiffer 1979) over the time period represented. Such causal variables are, however, irrelevant to my concerns, and thus I focus on the proportion of all zooarchaeological literature that covers a particular topic rather than the absolute frequency of titles.

The frequency of titles provides one kind of data. What the authors of those titles actually did analytically is another kind of data. Thus I acquired and read as many of the titles in the 1900–1979 bibliography as possible. Reading a large portion of that eight-decade sample of zooarchaeological materials was revealing. In short, the lack of adequate comparative collections, the failure of field archaeologists to systematically collect faunal remains prior to about 1970, and the discipline's taphonomic naiveté all, by modern standards, play havoc with many studies. It would be a valuable exercise to revisit some of the old collections and analyze them from today's perspective, assuming those collections still exist (some do not). One historical trend clearly described by the literature concerns when and why the MNI quantitative unit came to be popular.

2.3 Results

2.3.1 Frequency of Use of MNI

Kent Flannery (1967, p. 157) indicated that MNI was "coming to be used increasingly by other faunal analysts" in the 1960s and implied that this was a result of Theodore White "working out the method" of determining the MNI of a taxon.

Donald Grayson (1973, p. 433) reported that "once introduced [by White in 1953a], the minimum number of individuals became the prime unit of manipulation in faunal analysis." Richard Casteel (1977b, p. 141) indicated that MNI was enjoying "growing popularity in faunal studies." And Bruce Smith (1975, p. 3) stated that "although the concept of determining the minimum number of individuals of each animal species represented at archaeological sites was first suggested by Theodore White in 1953, such determinations have not been included in most Middle Mississippi faunal reports." Did the frequency of use of MNI actually increase after 1953 among North American zooarchaeologists? We must answer this question before proceeding to the two more central questions I seek to answer: First, did Theodore White "introduce" MNI to North American archaeologists? And second, was White's meat weight estimation technique the reason that more zooarchaeologists used MNI after 1953 than previously?

To answer the question posed regarding the frequency of use of MNI over time, I compiled evidence from titles in the 1900–1979 bibliography. Some titles did not include quantitative data of any kind, and occasionally, quantitative data were incomplete, such as when an author listed the identified specimens (e.g., humerus, tibia) of a few but not all identified taxa. These observations seem to substantiate Stanley Olsen's (1971, p. 1) assertion that prior to the middle 1960s or so, "it was common practice to place a faunal list at the end of an archaeological site report. Such reports were rarely more than one or two pages long and were in reality 'laundry lists,' tabulating a specified number of animals as being present on the site." This impression was seconded a few years later by Bruce Smith (1976, pp. 278–279) who stated that analytical practice in North American zooarchaeology to that point in time typically involved the construction of a "species list," that is, a list of the species represented in a zooarchaeological collection, perhaps (Smith implied rarely) with NISP, MNI, and estimated amounts of meat per taxon. And, subsequent authors have often characterized pre-1970s North American zooarchaeology as being made up largely of laundry lists. Elsewhere I show that the received wisdom regarding zooarchaeological laundry lists is not entirely accurate (Lyman 2015a).

The bibliography data indicate increased use of MNI after 1953 (Fig. 2.3). The seven articles that appeared in 1950–1954 that report MNI values were all authored by Theodore White, and include two descriptions of his meat weight estimation technique (White 1953a, b). Importantly, the data summarized in Fig. 2.3 indicate that zooarchaeologists in North America were aware of MNI *before* White used it. Given these facts, it is difficult to sustain the notion that Theodore White "introduced" MNI to North American zooarchaeologists. As I have noted elsewhere (Lyman 2008), William Adams (1949a) used MNI in his unpublished M.A. thesis several years before White (1953a, b) published his discussions of the unit. As Grayson (1979, 1984) has pointed out, paleontologists used MNI prior to 1953 (e.g., Stock 1929). Adams was an archaeologist. White was a professional paleontologist who earned his doctorate in 1935 and did paleontological research from 1932 until the late 1940s when he did zooarchaeological research as part of his job as the Smithsonian Institution's River Basin Surveys paleontologist (Lyman 2016). Other paleontologists used MNI prior to White when discussing zooarchaeological collec-

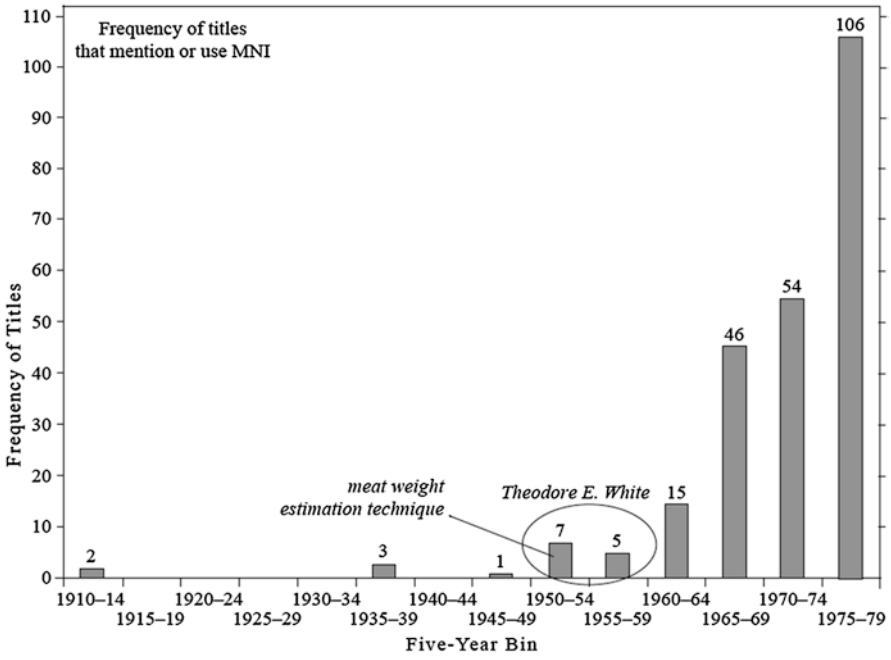

Fig. 2.3 Frequency of titles in North American zooarchaeology in which MNI is mentioned or presented/used

tions, but they published in venues that were unlikely to be read by archaeologists (e.g., Lyon 1937). And Adams did not publish his MNI figures; the published version of his thesis research (Adams 1949b) includes only NISP data. In short, pinning down *who* introduced MNI to archaeology is difficult. Determination of who first used the term might be historically revealing.

2.3.2 The Term "Minimum Number of Individuals"

Theodore White never used the term "minimum number of individuals" in any of his fourteen zooarchaeological publications. Instead he always referred to that value as the "maximum" or "greatest number of individuals" (Lyman 2016). The reason for this is simple: he was referring to the most frequent skeletal part of a taxon as the indicator of the (minimum) number of individuals of a taxon represented in a collection. Referring to what is today known as the *minimum* number of individuals quantitative unit as the *maximum* number of individuals seems an unlikely catalyst for the adoption of this quantitative unit by archaeologists. Only in his unpublished correspondence is it clear that White was aware that the most frequent skeletal part represented a *minimum* of individuals. In an unpublished letter dated November 21, 1952, White urged River Basin Surveys Program

Director for the Missouri Basin Robert L. Stephenson to make sure that a draft report by an archaeologist be modified in order that the RBS program avoid the embarrassment of having to answer queries about why three bones—a mandible, a humerus, and a tibia, all of bison (*Bison bison*)—were thought to represent three individual animals. White was aware of the potential that the skeletal parts could be from the same individual animal. This should come as no surprise because White was, as noted above, trained and worked as a paleontologist (Lyman 2016), and that group of individuals had long used MNI rather than NISP for precisely this reason (e.g., Howard 1930; Stock 1929). They wanted to know whether taxon A was more or less abundant than taxon B; taxonomic abundances were the target variable. If the number of identifiable bones and teeth in a single skeleton differed between taxa, then the NISP per taxon likely would not provide accurate indications of taxonomic abundances. MNI avoided the potential that multiple bones and teeth might derive from the same individual animal (might be interdependent). The fact that they might *not* derive from the same animal is an analytical hurdle zooarchaeologists still have not managed to clear with any reliability (e.g., Lyman 2006).

Given the preceding, it should not be unexpected that the first people in the published North American archaeological literature to indicate the number of individuals in a zooarchaeological collection was a "minimum" were three paleontologists—Wilfred T. Neill, H. James Gut, and Pierce Brodkorb. In their 1956 *American Antiquity* article "Animal Remains from Four Preceramic Sites in Florida", they wrote: "the number of individual animals present could not be determined [because] a femur and an ulna of a given species might or might not represent the same animal. However, a minimum figure could be ascertained." Neill et al. did not use the term "minimum number of individuals" nor did they make it clear why the number was likely a minimum (because, for example, a femur and a humerus representing a taxon might be from the same animal, but they might not be; thus to say a single individual was represented by the two bones was to present the *minimum* number of individuals, even though, potentially, the two bones might actually have belonged to two separate individuals).

In his unpublished M.A. thesis, Adams (1949a, p. 24) wrote "Since any one animal can possess only one of each of these bones [e.g., left humerus, right tibia], then the bone with the highest total will indicate the minimum number of mammals represented by the bone sample." Again, without a bit of thought and knowledge of, for example, a mammal's skeleton (one skull, seven cervical vertebrae, one left and one right radius, etc.), a reader of Adams's sentence might not realize why the *most abundant* skeletal part of a taxon in a collection representing multiple individuals would represent a *minimum* number of individuals. Adams (1949a) does not indicate in his acknowledgments who might have told him about MNI. His advisors were: William J. Wallace (a cultural anthropologist who likely did not know about such things), G. K. Neumann (a physical anthropologist who may have known about MNI or the concept thereof), and William G. Haag, an archaeologist who in his well-known study of prehistoric dogs does not mention MNI (Haag 1948). Thus, where and how Adams learned about MNI cannot be determined.

Pollock and Ray (1957, p. 634) used the term "minimum number of individuals" and defined it as "determined by the count of some recognizably distinctive bone that is found most often in the collection." Again, one has to wonder if a novice would understand why the number of individuals represented a minimum when the most frequently found kind of bone represents that (minimum) value. And if that were not confusing enough, Pollock and Ray (1957) also explicitly describe the major weakness of MNI—that different MNI values will be determined depending on how a collection is sorted into aggregates (stratigraphically, by excavation lot, by archaeological feature, etc.). Although Adams (1949a) had previously identified this problem, his discussion was unpublished. Pollock and Ray's (1957) discussion apparently failed to influence anyone because, as documented below, zooarchaeologists adopted MNI uncritically in the 1960s and 1970s and it was not until the late 1970s that the aggregation problem was identified as significant (Grayson 1979, 1984). Ray was a paleontologist, and he likely used the MNI quantitative unit because that is the unit paleontologists used to determine taxonomic abundances (e.g., Stock 1929).

I. W. Cornwall (1956, p. 241) used the term "minimum number of individuals" when he identified why this quantitative unit would be a better measurement of taxonomic abundances than NISP: "it cannot be assumed that each fragment represents a distinct individual" (recall White's letter to Stephenson mentioned above). It would likely be worth the time to determine how many zooarchaeologists subsequently cited Cornwall's book; finding a trend similar to that shown in Fig. 2.1 could be taken as circumstantial evidence that Cornwall's book influenced North American zooarchaeologists to use MNI. In their otherwise thoughtful review of zooarchaeological techniques, Meighan et al. (1958, p. 8) indicate that to determine taxonomic abundances the "most effective method for determining the number of individuals represented is that described by White (1953a)." Meighan et al. do *not* indicate the estimate is a minimum, and they may have exacerbated confusion by noting, like White, that the skeletal part with the greatest frequency "is used as the unit of calculation in determining the total number of individuals" (Meighan et al. 1958, p. 8).

The next North American archaeologist to use the term "minimum number of individuals" of which I am aware was Charles Cleland in his unpublished 1960 master's thesis (Cleland 1960). Cleland (1960, p. 12) indicated that "the minimum possible number of each species was calculated by taking the greatest number of any single skeletal element of each species." Cleland cited White (1953a) in a subsequent paragraph, but he did not attribute the term or the quantitative unit we now know as MNI to White or anyone else; he does not cite Adams's (1949a) thesis, for example. Reading the pertinent paragraph in Cleland's (1960) thesis without knowledge of the history of MNI would likely give one the distinct impression that Cleland invented this quantitative unit. The historical record is clear, however; Cleland did not design the MNI unit. More pertinent here, his M.A. thesis is not published, so it is unlikely to have influenced anyone to use MNI.

John Guilday, Paul Parmalee, and Elizabeth Wing are often identified as the godparents of modern North American zooarchaeology (e.g., Grayson 1984; Reitz 1993; Reitz and Wing 1999; Robison 1978, 1987). Did they perhaps use the quantitative unit or the term "minimum number of individuals"? Guilday (1963) reports

both "No. Bones" and "No. Ind." for individual taxa, but cites no references and never specifies what the latter quantitative unit is or how it was determined. In his numerous zooarchaeological publications that appeared between 1955 and 1963, with one exception Guilday only reports NISP values. Parmalee (1965) reports "Pieces" and "Minimum No. of Individuals"; I suspect the latter derives directly from White (1953a) because Parmalee calculates meat weight per taxon using White's procedure. Parmalee (1965) does not describe what MNI is or how to determine it; with one exception, he does not determine MNI for any of the numerous zooarchaeological collections he reported between 1956 and 1965.

The one publication in which Guilday presents MNI data prior to 1963 is the same one in which Parmalee first used MNI; they were coauthors. Guilday et al. (1962) present MNI data likely because they estimate meat amounts using White's (1953a) technique. Guilday et al. (1962) do not refer to the values as "minimum number of individuals"; instead, they merely list "individuals" (and also "pieces"). They occasionally qualify the number of individuals with wording such as "at least twenty-one animals" and "a minimum of thirteen beavers" (Guilday et al. 1962, pp. 64, 71), but they do not explain why the number is a minimum nor how the value is determined. Nevertheless, the fact that neither Guilday nor Parmalee determined MNI prior to 1962, and when they do finally present that quantitative unit they do so because they are calculating meat weights using White's technique, suggests Grayson's (1979, 1984) surmise is correct: MNI gained in popularity because archaeologists wanted to determine meat weights to reconstruct prehistoric diet. I examine this notion more thoroughly below, but first a couple other historical tidbits must be explicated.

Wing (1963a, b) presents both the "number of specimens" and the "minimum number of individuals" with no indication as to why the latter is a minimum, how it was determined, or where the quantitative unit might have originated. In her unpublished doctoral dissertation Wing (1962, p. 5) reveals critical details of her understanding of MNI. "In this study the 'minimum number of individuals' is used as an index of the relative abundance of a particular species in a sample of midden remains. For each species this is determined by the count of the most numerous skeletal element in a given lot. In some cases this number may validly be increased by the addition of specimens of an age group not represented in a series of the most frequent element." This echoes White's (1953a) definition of MNI, but Wing cites no one in her discussion of the quantitative unit nor does she cite any of White's papers. The only zooarchaeological study she cites is Burt's (1961), and he presents only NISP data. She acknowledges Clayton E. Ray (see above) who might have told her about the MNI quantitative unit and why it was thought to be a more reasonable quantitative unit with which to measure taxonomic abundances than NISP. In many of her later publications, Wing presents MNI data, often without complementary NISP data. The lesson she learned when writing her dissertation stayed with her, apparently, and she transmitted that knowledge to her students, many of whom still express a preference for MNI as a measure of taxonomic abundances (Emery 2003; Quitmyer 2003; Reitz 2003). Thus another reason MNI gained in popularity after the 1950s was that it provided

what seemed to be, according to paleontological tradition, a more valid measure of taxonomic abundances than NISP. Again, I return to this below.

Finally, Flannery (1967, p. 157) uses the term "minimum number of individuals" and quotes White's (1953a) technique for determination of MNI; he does not indicate the source of the term. Ziegler (1965, p. 52) also uses the term, and cites Heizer (1960) who cites White (1953a). Heizer (1960, p. 97) indicates that to "calculate the meat available from archaeological bones, one must determine the number of individuals by taking the most abundant bone element, must separate these into right or left, and then use the greater number as the unit of calculation." Notice that Heizer does not say *minimum* number of individuals. But Ziegler (1965) also cites Cornwall (1956), whom you will recall used the term "minimum number of individuals." None of the individuals mentioned in this section cite Charles Reed (1963) who cites White's (1953a) meat weight estimation technique. Reed (1963, p. 214) indicates that White's technique "involves identifying all of the bones to species, and, for each species, determining the minimum number of individuals possibly present. This latter count is made by determining the number of animals which must have been involved." The term is here, but I suspect a novice would not know how to determine MNI (it is the most abundant skeletal part) or why it provides a minimum based solely on Reed's terse discussion.

In sum, it is unclear from early use of the term "minimum number of individuals" who might have "introduced" the unit to North American zooarchaeology. Early commentators who bothered to mention how MNI was determined were few in number. These include Wing (1962, p. 68) who, virtually uniquely for the early 1960s, noted that MNI was to be preferred over NISP (without using either acronym) because the former "give[s] equal consideration to each form [taxon] and [does] not favor those with more bones." Thus I suspect that a desire for accurate estimates of taxonomic abundance might account at least in part for the increased use of MNI during the 1960s and 1970s. But Grayson (1979, p. 203; 1984, p. 27) suggests that increased use of MNI was a result of White's (1953a, b) use of it specifically for estimating meat weights. Which reason might be correct? Are perhaps both correct?

2.3.3 Meat Weight Estimation as the Catalyst for Use of MNI

The suggestion that Theodore White's meat weight estimation technique resulted in popularization of the MNI quantitative unit has two test implications. First, there should be an increase in the number of publications that use MNI in favor of NISP, and this should occur after 1953 when White introduced the meat weight estimation technique. The second test implication of the historical notion that White's meat weight estimation technique popularized MNI is that there should be an increase in the number of papers that use White's meat weight estimation method after 1953. The general formula for estimating meat amounts that White (1953a, b) described is:

MNI (% edible of the mean adult live weight of an individual of a taxon) = meat weight.

In short, one must have MNI to operationalize or implement the formula. But tallying per temporal bin the number of titles that use White's formula might be misleading given that there is a general increase over time in the number of zooarchaeological titles produced (Fig. 2.1). Thus the number of titles per temporal bin in which meat weights are estimated could be a function of the number of all titles per temporal bin. To circumvent this problem, I tallied the number of titles that presented NISP data and the number of titles that presented MNI data per temporal bin, and then calculated the percentage of all titles per temporal bin that presented quantitative data of either or both kinds.

Of the 28 titles that presented quantitative data and appeared prior to 1950, 27 (96%) used NISP and five (18%) used MNI (Fig. 2.4); obviously, some authors used both quantitative units. Of the 152 titles that appeared between 1950 and 1969, 105 (69%) used NISP and 67 (44%) used MNI. Finally, of the 187 titles that appeared in the 1970s (1970–1979), 142 (76%) used NISP and 142 (76%) used MNI. These data indicate that the use of MNI picked up sometime during the 1950s or 1960s, confirming the suggestion that the popularity of MNI picked up after 1953. Was the cause for this rise in popularity in fact the use of White's meat weight estimation technique? As noted above, Guilday and Parmalee together first used MNI to estimate meat amounts using White's technique (they were preceded by Cleland (1960) in his unpublished thesis). Cleland (e.g., 1966) also used MNI to estimate meat amounts using White's technique in at least eight publications in the 1960s. Nevertheless, I suggest that this technique was but one of three causes for increased use of MNI.

Figure 2.5 shows the frequencies of publications in which MNI is presented and the frequencies of publications in which White's meat weight estimation technique is used, per temporal bin. There is a positive relationship between estimating MNI and calculating meat weight per taxon, just as one might suspect there would be if White's meat weight estimation technique influenced analysts to determine MNI. Titles in which MNI is used to estimate meat weight increase markedly after 1964. It seems Grayson (1979, 1984) is correct: White's meat weight estimation technique prompted greater use of MNI. But two other facts suggest that use of this analytical technique was not the only catalyst for the increased popularity of MNI.

2.3.4 MNI and Butchering Patterns

White (e.g., 1952a, b, 1953c, 1954, 1955) often presented MNI counts without calculating meat weights, and instead determined the MNI of each skeletal part in order to infer what he referred to as "butchering patterns." Such inferences were later referred to as the schlepp effect (Daly 1969) and the differential transport of skeletal parts (Binford 1978). White's analytical technique was easy to mimic because he used a standard form on which to record frequencies of skeletal parts per taxon. White identified the faunas from more than 130 sites distributed across 10 states, using this form (Fig. 2.6) to summarize his identifications of skeletal parts. Although these quantitative data were (unfortunately) seldom published by the

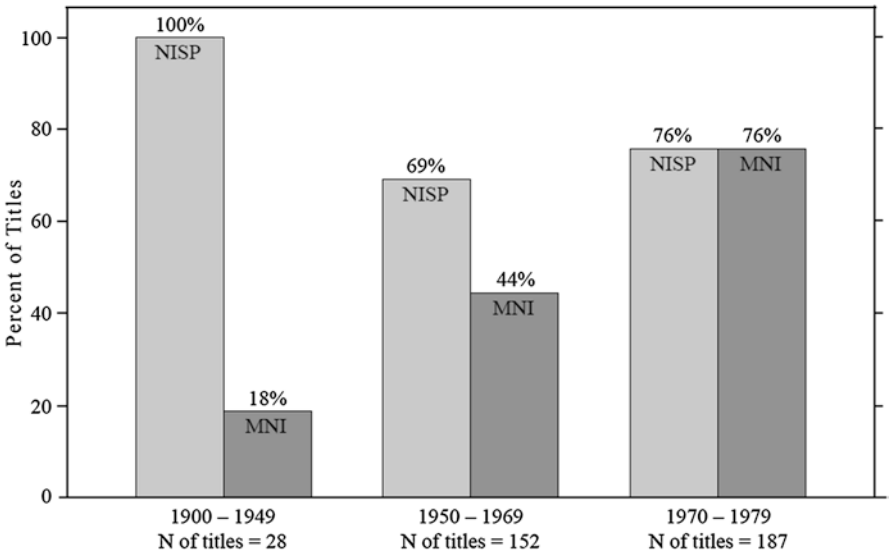

Fig. 2.4 Percentage of titles that used NISP and that used MNI across three temporal bins. Note the overall decrease in use of NISP and the increase in use of MNI over time

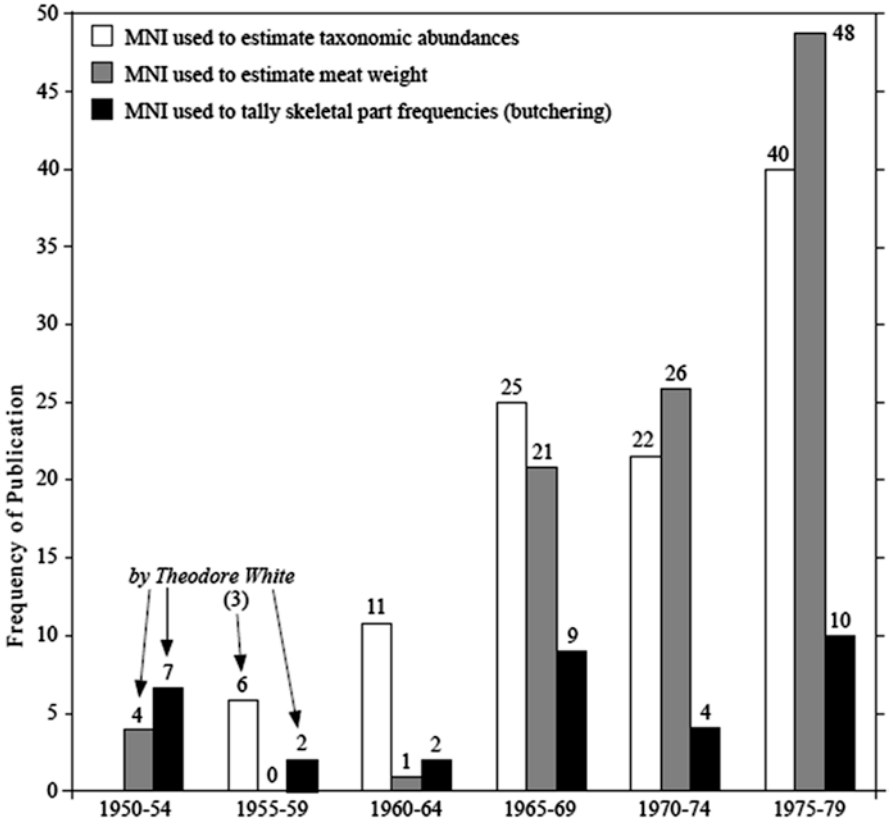

Fig. 2.5 Frequencies of titles in which MNI is used to estimate taxonomic abundances, MNI is used to estimate available meat, and MNI per skeletal part data are presented

SMITHSONIAN INSTITUTION, RIVER BASIN SURVEYS
BONE IDENTIFICATION

Reservoir _____ Site No. _____ Feat. No. _____

Genus _____ Species _____

Common Name Ident. By

	Mature			Immature[1]				
Element	Rt.	Lt.	Ax.	Rt.	Lt.	Ax.	Indivs. Repres.	Remarks[2]
Skull, occiput								
" , horn cores								
" , maxilla								
Mandible								
Hyoid								
Vertebra, atlas								
" , axis								
" , cervical								
" , dorsal								
" , lumbar								
" , sacral								
" , caudal								
Dorsal spines								
Scapula								
Humerus, proximal								
" , distal								
Radius, proximal								
" , distal								
Ulna, proximal								
Carpals								
Metacarpal, proximal								
" , distal								
Pelvis								
Femur, head								
" , proximal								
" , distal								
Tibia, proximal								
" , distal								
Astragalus								
Calcaneum								
Cuboid								
Metatarsal, proximal								
" , distal								
1st phalanx								
2nd phalanx								
3rd phalanx								

[1]This column was often crossed out and the word "Worked" (signifying a bone artifact) was penciled in.

[2]This column was often crossed out and the phrase "% of Greatest No." penciled in. That is, values in the "Indivs. Repres." column were normed to a scale of 1 to 100, to the nearest 0.1 percent.

Fig. 2.6 White's data recording form (retyped)

excavator, White typically provided these data to the archaeologist in charge in precisely this form.

I find it likely that because the quantification technique of determining the MNI per skeletal part (1) was transparent given White's data recording form and (2) provided a common-sensical indication of butchering practices, MNI-per-skeletal-part values were used by many subsequent researchers to infer butchering practices (Flannery 1967; Gilbert 1969; Kehoe 1967, 1973; Kehoe and Kehoe 1960; Lorrain 1967, 1968; Wood 1962, 1968). Employing White's analytical technique of tallying skeletal part frequencies was a second cause of greater use of MNI in the 1960s (Fig. 2.5). If the frequency of papers in which skeletal part frequencies are presented and the frequency of papers in which MNI is used to estimate meat amounts are accurate reflections of cause, then the former was less significant than the latter, but it was an important catalyst nevertheless.

2.3.5 MNI and Taxonomic Abundances

Finally, recall Wing's (1962, p. 68) statement that MNI provided a more accurate estimate of taxonomic abundances than NISP because different taxa have different numbers of bones. As highlighted above, this was why paleontologists used MNI in favor of NISP (e.g., Howard 1930; Shotwell 1955; Stock 1929). Examination of the data in the 1900–1979 bibliography suggests that replacing NISP with MNI to measure taxonomic abundances in zooarchaeological collections was a third cause of the increased popularity of MNI (Fig. 2.5). Did zooarchaeologists actually understand what they were doing? That is, did they know the reason *why* MNI might be better than NISP, at least the reason noted by Wing?

The interdependence problem—a left humerus and a right tibia may have originated in the same individual animal—was the major reason why paleontologists preferred MNI over NISP as a measure of taxonomic abundances. North American zooarchaeologists seem to have adopted this reasoning (largely implicitly) at least initially upon adopting MNI. At about the same time they noted that fragmentation of bones presented exactly the same problem. Cornwall (1956, p. 241), for example, wrote that "it cannot be assumed that each fragment represents a distinct individual." This is the interdependence problem written with respect to fragments rather than anatomically complete skeletal elements. The shift from interdependent bones to interdependent fragments made sense in a way; paleontological remains were seldom broken relative to zooarchaeological remains. MNI quickly became the quantitative unit of choice in zooarchaeology. The adoption process was facilitated by statements such as Chaplin's (1971, p. 70) that the "minimum number of animals that the bones could have come from is an indisputable fact." By the 1970s, it was sufficient to note that zooarchaeologists in general rejected NISP and favored MNI (e.g., Bogan 1976; Medlock 1975; Robison 1977); it was unnecessary to state reasons for the choice of quantitative unit as these were generally understood.

The 1900–1979 bibliography data suggest that the desire for a more accurate measure of taxonomic abundance than NISP provided was less influential on the use of MNI than was the estimation of meat weights. And, the inference of butchering patterns and differential transport of skeletal parts was the least influential cause of the three; that would of course change shortly after Lewis Binford (1978, 1981) published his influential books on just this topic, but that historical episode is beyond my scope here (see Lyman (2012) for an introduction to the significance of those volumes).

2.4 Discussion and Conclusion

Our received wisdom regarding the history of MNI in North American zooarchaeology is inaccurate on several counts. Theodore White, for example, did not introduce this quantitative unit to the discipline; others had used it previously, though the precise source of that unit is unclear. We know it likely came from paleontology, but details other than that are obscure. Use of the term for the unit reveals little. And while the desire to reconstruct prehistoric diet was made possible by White's (1953a, b) meat weight estimation technique, use of that technique was not the only reason MNI came to be used more frequently after 1960 though it seems to have been the main reason. Analysts also sought an accurate estimate of taxonomic abundances, and in the 1960s and 1970s MNI seemed to provide just such an estimate. Finally, as a result of White's quantification of skeletal parts using MNI, subsequent researchers mimicked his analytical protocol in an effort to reveal human behaviors, particularly butchering practices and carcass transport. Both of these latter analytical goals were deemed to be reasonable given the then current state of knowledge about such things as taphonomy, recovery techniques, and statistical properties of NISP and MNI. That would all change in the late 1970s (e.g., Casteel 1977a, b; Grayson 1973, 1978, 1979).

In presenting this history in this volume, one might ask "So what?" There is of course the simple answer that what has been presented in preceding paragraphs is interesting history in its own right, but that likely will not satisfy everyone. I indicated in the introduction that knowing our discipline's history could be beneficial. So what is the benefit here? I think the benefit is not only clear, but significant. Theordore White used MNI per taxon to estimate meat amounts, he used MNI per skeletal part to infer butchering practices, and reflecting paleontological thought of the day, MNI was used (initially by Elizabeth Wing, but after White's pioneering work) as a better measure of taxonomic abundance than NISP. The significant lesson from history is that White and others thought about which quantitative unit best served which analytical function. Our modern failure to recognize this simple fact jeopardizes the zooarchaeological enterprise. As emphasized here and elsewhere, we need a clear conception of a target variable—the variable of interpretive interest—and a clear conception of a measured variable—the variable that is monitored zooarchaeologically (Lyman 2008). And, we need to know how the two are related.

The history of MNI in North American zooarchaeology after 1979 has yet to be written. My impression, and that is all that it is, is that the statistical weaknesses of MNI detected by Casteel (1977a, b) and Grayson (1973, 1978, 1979, 1984) prompted some zooarchaeologists to go back to NISP as the preferred measure of taxonomic abundances during the 1980s and 1990s. About the same time the introduction and use of the minimum number of (skeletal) elements (MNE) quantitative unit (e.g., Binford 1978, 1981, 1984; Binford and Bertram 1977; Brain 1967, 1969, 1976; Bunn 1982, 1986; Bunn and Kroll 1986) reflected an expansion in analytical concerns to taphonomic issues including differential preservation and differential transport of carcass parts. This new quantitative unit quickly permeated North American zooarchaeology (e.g., Lyman 1984, 1985; Todd 1983, 1987). The emergence of new terminology (Lyman 1994a, b) that accompanied these shifts in favored quantitative units makes for a complex history that has been only examined superficially (e.g., Lyman 2008). Despite historical murkiness, what is clear is that MNI is required to calculate the differential survivorship of skeletal parts (Lyman 1994a) and it is also required to estimate meat weight using White's formula. Both kinds of analyses are still undertaken (e.g., Faith and Gordon 2007; Stiner 2005, respectively). What is clear from all of this is that NISP seems appropriate for some analytical tasks, MNE for others, and MNI for still others. Ascertaining when a particular unit is the most appropriate depends on the analytical question of interest, the resolution sought (nominal, ordinal, or interval scale), and the taphonomic history of the collection under scrutiny.

Like Theodore White and subsequent zooarchaeologists, we need to think about the quantitative units we use; in particular, we need to consider if they are the best units for what we hope to measure. Poorly conceived experiments that supposedly test the validity of MNI and NISP as measures of taxonomic abundances (e.g., Dominguez-Rodrigo 2012) will not do the trick. Deeply conceptual studies are few and far between; Badgley's (1986) nearly 30-year-old study is an exemplary one, but it is the only one of which I know. In short, although we might believe that there is little left to learn about zooarchaeological quantification, this is far from true (e.g., Lyman 2015b). As we continue to learn about zooarchaeological quantitative units, new events in our discipline's history will take place. As with our intellectual predecessors, we need to pay attention to that new knowledge.

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Chapter 3
Contemporary Challenges in Zooarchaeological Specimen Identification

Michelle J. LeFebvre and Ashley E. Sharpe

3.1 Introduction

Increasingly, zooarchaeology is practiced in a diversity of academic settings, including universities, museums and forensic laboratories, as well as non-academic settings, such as commercial contracting firms. Likewise, more than ever, zooarchaeology is integrated within transdisciplinary research and applications within and beyond archaeological and anthropological interest, including conservation and applied environmental studies (e.g., environmental reconstruction, assessments of overharvesting/fishing/hunting, analysis of animal behavior change due to human interference, debates of land use and abuse, occurrence of zoonotic diseases, etc.). As such, this chapter focuses on what is perhaps the most fundamental aspect of zooarchaeological research that impacts all types and settings of zooarchaeological practice: the identification of physical specimens (*sensu* O'Connor 2008). We consider how diverse settings of research may impact this fundamental activity of zooarchaeology, how the nature of taxonomic attribution is changing today, and how single identifications compound to affect large compilations of datasets, or "big data."

Of course, archaeological faunal specimens must be identified in order to be of any use and interpretive value in research. Yet, we argue that this primary component of zooarchaeology is sometimes taken for granted or simplified in terms of logistics of analysis, setting(s)/circumstance(s) of analysis, and procedural reporting. That said, we are by no means the first to assert such a critique, nor will we be the last. As argued by Wolverton (2013), across both academic and non-academic

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spheres of study the *de facto* Achilles heel of zooarchaeology has been an overall lack of disciplinary standards for reporting methods of specimen identification and ensuring methodological quality assurance. In the age where data are being shared and compared more than ever before, it is crucial that researchers be cognizant of their own research protocols, why they are chosen, and how they relate to those of others.

In comparison to related fields of study such as paleontology and zoology, zooarchaeology is a relatively late-forming discipline. Derived from these fields, zooarchaeologists have long been aware of some of the methodological pitfalls inherent in these other disciplines. As such, several zooarchaeologists have previously argued for and demonstrated the value of using stringent scientific methodology for recovering (Cannon 1999; Gobalet 2005; James 1997; Payne 1972; Peres 2010; Shaffer 1992; Shaffer and Sanchez 1994; Wing and Quitmyer 1992), quantifying (Cannon 2001, 2013; Claassen 2000; Domínguez-Rodrigo 2012; Gilbert and Singer 1982; Giovas 2009; Glassow 2000; Grayson 1984; Lyman 1994a, 2008; Marshall and Pilgram 1993; Mason et al. 2000; Plug and Plug 1990; Ringrose 1993; Wolverton 2002), and assessing the taphonomic (Bartosiewicz 2008; Gifford 1981; Lyman 1987, 1994b; Orton 2012; Schmitt and Lupo 1995), social (Crabtree 1990; deFrance 2009; Russell 2012), and ecological (Giovas et al. 2017; Lyman and Cannon 2004; Stahl 2008; Wolverton and Lyman 2012) significance of specimens. These arguments are noteworthy for calling attention to issues of analytical and methodological standards, as well as transparency in analytical protocols and decisions in processes of specimen identification and reporting (e.g., Butler and Lyman 1996).

This chapter contributes to this important body of work by offering discussion about some of the inherently epistemological challenges of specimen identification across variable settings of analysis that can impact not only how identifications are made, but also how processes of identification and resulting data are evaluated in terms of quality and validity. In other words, we examine the ever-present dilemma faced by all scientists: how to strike a balance between sound scientific practice and the real-life logistics of such practice. We explore this conundrum and the ways in which zooarchaeologists have sought methodological and conceptual remedies. The discussion, examples, and arguments presented herein are influenced by significant previous assessments of the specimen identification process in zooarchaeology, including key works by Diane Gifford-Gonzalez (1991), Jonathan Driver (1992), and Steve Wolverton (2013).

In a departure from the majority of chapters in this volume, this chapter is not a methodological case study, but rather serves as a reflective essay on the current epistemology and practice of faunal specimen identification. We begin by contextualizing the practice of zooarchaeological specimen identification in terms of analogical inference, highlighting both the strengths and weaknesses inherent to the epistemology of zooarchaeological specimen identifications. Building from this disciplinary background, we review some of the most pervasive methodological challenges contended with by all zooarchaeological practitioners (e.g., sample composition, analytical subjectivity, and quality assessment). From there, we discuss

how the analogical basis of specimen identification and common methodological challenges are impacted by increasingly variable circumstances and settings of zooarchaeological identification and analysis. The examples presented and circumstances described are based on our experiences practicing zooarchaeology under a diversity of situations requiring different approaches to and requirements of archaeological specimen identification. While we readily admit that the examples discussed are not representative of the full range of zooarchaeological research or the perspectives of others, the main goal is to provide points of contemplation and discussion for continued assessment of circumstances of zooarchaeological analysis and potential impacts on disciplinary practice. We believe such a discussion is important to all zooarchaeologists, spanning all levels of experience and expertise.

Ultimately, we argue that logistical, analytical, and methodological variability characteristic of contemporary zooarchaeological research necessitates epistemological flexibility in terms of specimen identification and data evaluation, demonstrating that processes of identification cannot be idealized and will not always fall into tidy methodological categories or standardizations of zooarchaeological practice. We end with a short discussion highlighting how such flexibility is necessary in the age of "big data" research agendas and open access data sharing. As zooarchaeological research continues to be an increasingly significant part of overall archaeological investigation, including applied studies, state and federal cultural mitigation, conservation efforts, and big data agendas, the relationship between the circumstances of analysis and specimen identification will increasingly demand inspection, explanation, reinterpretation, and acceptance.

3.2 Analogy and the Epistemology of Zooarchaeological Identification

At its core, we view the topic of specimen identification as an epistemological issue within zooarchaeology, and zooarchaeology, like all fields seeking to understand and interpret the past, is a historical science that is inherently based on casting projections onto past phenomena and processes through the use of analogy. Regardless of research question, region of study, temporal focus, or interpretive agenda, all zooarchaeological identifications are based on analogical inferences made between archaeological fragments and comparative faunal specimens, as well as learned knowledge of contemporary taxa. The validity and success of zooarchaeological studies are directly dependent on the strength of specimen identification and an analogical relationship to assumed biological behaviors and ecological habitats associated with identified taxa. The use of analogy in zooarchaeology is influenced by and connected to the analogical traditions found in natural and physical sciences such as biology, paleontology, and geology, as well as the greater traditions of anthropology and archaeology. Despite its crucial role in zooarchaeology, the analogical relationship inherent to specimen identifications can easily be taken for

granted in the formulation, execution, and evaluation of zooarchaeological specimen identifications and research design (Atici et al. 2013; Gifford-Gonzalez 1991; Lyman 2010; Wake 2004; Wolverton 2013).

In terms of an archaeological foundation, the epistemology of zooarchaeological identification is perhaps best contextualized within the broader scope of environmental archaeology. Environmental archaeology is a diverse field of archaeology that focuses on the "systemic relationships among people and their environments" (Reitz and Shackley 2012, pp. 1–2; see also Albarella 2001; Branch et al. 2014; Dincauze 2000; Evans 2003; Reitz et al. 1996, 2008). Environmental archaeologists strive to study archaeological traces of human behavior that are indicative of the past environmental conditions people lived in as well as macro-, micro-, and chemical traces of past cultural activities and behaviors directly or indirectly involving and/or impacting the environment. As such, the topics and materials of environmental study are numerous and extremely diverse (Dincauze 2000; Reitz and Shackley 2012). Environmental archaeologists employ several analytical techniques for the analysis of past environmental signatures and material remains (see Dincauze 2000; Evans 2003; Reitz and Shackley 2012; Wilkinson and Stevens 2003). However, regardless of the research question, and the medium and method of study, the common tie in environmental archaeology is the use of environmentally-derived data as a primary point of inquiry and material reference. As such, whether one is working with microscopic starch grains on a sherd of ancient pottery, phytoliths in an anthropogenic soil sample, the chemical composition of a pond sediment core, a human-modified bird femur, a rodent gnawed bone, or artificially perforated bivalve shells, knowledge of the natural history and biological/geochemical character of the specimen under investigation is necessary. An ontological underpinning of environmental archaeology is the understanding that we are working with natural specimens (living, no longer living, or never living) that can be objectively defined and understood within a biological and environmental framework or context of analysis. This understanding means that we accept the tenets and uses of analogy within the biological and physical sciences that we draw on for specimen identification and study, such as the uniformitarian assumptions of biological evolution and geologic stratigraphy.

Animals are the immediate focus of zooarchaeology, and knowledge of their biology and ecology is a cornerstone of zooarchaeology and why we think we can know what we know about the past. Knowledge of an animal's anatomy, morphology, and physiology, as well as where an animal lives, its feeding habits, seasonal migrations, and reproductive habits are important for the ability to assess human exploitation patterns, exploitation technology, anthropogenic impacts, temporal and spatial changes in animal populations, environmental fluctuations, human mobility patterns, seasonal use of taxa, food preferences, cooking techniques, and so on. Zooarchaeologists invariably rely on the contemporary knowledge and research of specialists in biology, zoology, ecology, and paleontology to help inform our understandings of zooarchaeological assemblages, including the particular taxa identified and environmental significance(s) represented—which are key to modeling and interpreting human-animal interactions and relationships (e.g., O'Connor 2008; Olmo 2013).

As a result, zooarchaeologists accept, often inexplicitly, analogical inferences derived from biological sciences about animal biology and ecology through time (Gifford-Gonzalez 1991, p. 234; Lyman 2011), even when the state of knowledge in these other disciplines is in flux or even, as is the case with taxonomic distinctions, in contention. For example, as practitioners of environmental archaeology, zooarchaeologists acknowledge that whatever question(s) we are pursuing, regardless of ontological perspective, the nature of the faunal remains under study is representative of an animal's life history, inclusive of evolutionary, ecological, and biogeographic history. This life history is part and parcel of interpreting how humans interacted with animals, past environmental conditions, and cultural situations. To be sure, archaeologists use analogy in almost all facets of data gathering and interpretation, and it is important to note that the adoption of analogies from other fields is not unique to zooarchaeology (e.g., geologic principles of superimposition in studies of archaeological site formation (Hodder 1982; Wylie 1982, 1985)). As has been thoroughly reviewed and argued by several scholars (e.g., Asher 1961; Binford 1967; Feder 1990; Gifford-Gonzalez 1991; Lyman and O'Brien 2001; Wylie 1982, 2002), analogy is perhaps the most pervasive and enduring epistemological facet of archaeological study (e.g., middle range theory).

Regarding zooarchaeology specifically, Gifford-Gonzalez's 1991 essay in the *Journal of Anthropological Archaeology* provides an intriguing and comprehensive discussion of knowledge production, use of analogy, and interpretation (for a similar discussion, see also Marciniak 1999). Although published more than two decades ago, Gifford-Gonzalez's discussion about the use of relational analogy contextualizes zooarchaeological epistemology, and related challenges, within a larger archaeological framework of analogical inference that remains salient today. Like the whole of archaeology, relational analogies are pervasive in zooarchaeology, where analogical relationships are linked to causal and systematic inferences. The identification of zooarchaeological specimens and implied inferences about animal life history, behavior, and ecology is a relational analogy. This is significant because implicit within zooarchaeological identifications is the acceptance "that bones [and other materials such as shell, exoskeletons, etc.] are produced by a specific biological pathway and exist as living entities in a restricted range of functional contexts… and that these pathways and contexts are the sole necessary and sufficient conditions for the existence of entities we call bones" (Gifford-Gonzalez 1991, p. 225). This use of relational analogy in the identification of zooarchaeological specimens is the foundation from which all other zooarchaeological observations, data, and interpretations are rendered. Furthermore, as described by Gifford-Gonzalez (1991, p. 225), the strength of a relational analogy, or "security", is based on background knowledge of an observed phenomena or material. In the case of zooarchaeological specimen identification, the strength of analogy, and thus taxonomic identification, relies on demonstrative associations between "developmental histories, function, and morphological features of contemporary elements resembling the one under study" (Gifford-Gonzalez 1991, p. 224).

Building on faunal specimen identifications, relational analogies are also key to describing and understanding past cultural and environmental events and contexts represented in zooarchaeological patterning. However, as is the case in

archaeology in general, relational analogies are not a fail-safe against issues of equifinality. Drawing on works and arguments by Binford (1977, 1981), Lyman (1985, 1987), Oliver (1989), Fiorillo (1989), Behrensmeyer et al. (1986), as well as Grayson (1989), Gifford-Gonzalez argues that fleshing out such complexities of equifinality requires the recognition and collection of contextual information that "implicitly or explicitly refers to other bodies of knowledge in which the correlative, if not the causal, relations among the components are well understood" (Gifford-Gonzalez 1991, p. 233). Here, just as in specimen identification, relational analogies are used to provide secure contexts of inference, especially when rendering interpretations of faunal patterning. In sum, neither zooarchaeological specimen identification nor pattern interpretation can be produced in a vacuum. The success of each are dependent upon assumed or accepted analogous relationships drawing on independent sources of knowledge and comparison, such as those provided by comparative skeletal collections, actualistic studies, and ethnoarchaeology. The multiple epistemological traditions of analogy and inference that zooarchaeologists draw on is one of the field's greatest strengths. Yet, as discussed below, zooarchaeological use of analogy in specimen identification is not without challenges and points of potential weakness.

3.3 Factors Influencing and Challenges of Zooarchaeological Identification

The scope and (perceived) success of zooarchaeological research is tied to the recovery, identification, and quantification of archaeological faunal remains. Although this is a seemingly simple and obvious statement (see also Gobalet 2001; Lyman 2002; O'Connor 2008; Wolverton 2013), among these steps the identification of specimens is arguably the most important and significant in terms of data analysis and interpretation of the past (Lyman 2010, 2011). As outlined above, specimen identification is dependent on several analogical factors[1]. Identifying any specimen as a particular element and assigning it to any level of taxonomic classification is an analogical step (Gifford-Gonzalez 1991; Grayson 1984; Lyman 1994a; Reitz and Wing 2008). Several scholars have suggested and demonstrated that the mechanics of this step is worthy of study and scrutiny in and of itself (e.g., Gobalet 2001; Lyman 1986, 2002, 2010, 2011; O'Connor 2008; Rea 1986; Wake 2004; Zeder and Lapham 2010).

Jonathan Driver's seminal 1992 article (reprinted with additional comments in 2011), "Identification, Classification, and Zooarchaeology", is one of the most influential works problematizing the impact and role of zooarchaeological identifi-

[1] In addition to analogical factors, there are also practical issues such as the preservation conditions of a given archaeological context as well as the methods used to recover faunal remains. Although not the focus of this chapter, these are also important factors impacting the efficacy of zooarchaeological research and are implicated in zooarchaeological epistemology.

cation on data generation and interpretation (see also Lyman (1994a, 2010) and Wolverton (2013)). Following Driver (2011a, p. 20), zooarchaeological identifications are based on "previously established classificatory system[s]" used in biology. Such classificatory systems are based on assumptions of uniformitarian and evolutionary concepts of animal biology and development (see also Gifford-Gonzalez 1991). Zooarchaeologists follow biological classificatory systems with the belief that there is "a single appropriate classificatory system" (Driver 2011a, p. 20), using zoological taxonomic nomenclature and anatomical designations to group faunal remains by taxonomic identification and element. Driver explains that the use of previously established binomial nomenclature is a strength of zooarchaeology, in that it readily allows for identifications to be re-organized into additional categories of study for comparison. It also is important to acknowledge that, although Western scientific taxonomy is the most common approach to specimen identification and organization among zooarchaeologists, folk taxonomies also provide structures for identification and the analysis of human-animal relationships (e.g., Marciniak 2011).

Furthermore, as Bovy (2011; see also Bovy 2012) notes, the use of zoological nomenclature should not and cannot be taken as a given because of continuous refinements and re-organization of animal taxonomies and relationships. Biological nomenclature is not static, although it tends to be treated as such in zooarchaeology. In the past, taxonomists would debate species distinctions on the basis of physiology; today, molecular genomics has added a new line of phylogenetic evidence, one that has completely restructured our understanding of taxonomic divisions and evolutionary relationships (e.g., Alström et al. 2006; Bickford et al. 2007; Doolittle 1999; Pyron and Wiens 2011). Some notable recent examples include the restructuring of the Osteichthyes class of fish to that of superclass and ongoing deliberation over the class divisions of ray-finned (Actinopterygii) and lobe-finned (Sarcopterygii) fishes (Betancur-R et al. 2013), as well as the grouping of domestic animals (Gentry et al. 2004) (e.g., the domestic dog (formerly *Canis familiaris*) as a subspecies of the wolf (*Canis lupus*; Larson et al. 2012)). Invertebrate taxa, particularly the mollusks that are the subject of many a zooarchaeologist's purview when working with sites near a marine or freshwater habitat, are being reclassified almost daily (Bucklin et al. 2011; Knowlton 2000; Layton et al. 2014). It is up to the faunal analyst to keep up to date with these rapid and ongoing changes.

Driver (1992) points out there are two important epistemological assumptions that zooarchaeologists must contend with: (1) that single bones will include particular diagnostic features to allow identification of a whole element based on a part to a refined level of taxonomy such as species; and (2) that techniques of identification are so well established that explanation for identification is not frequently necessary. These two assumptions are critical challenges that zooarchaeologists face in routine processes of zooarchaeological identification.

As a result, the use of modern skeletal collections has become a requisite of zooarchaeological identification and analysis (Lyman 2010). The assumption is that the morphology of the archaeological specimen will conform more or less to its modern

counterpart (and vice versa). This, in turn, assumes that the classification of the modern reference specimen is valid based on the strengths of zoological analogical inference, and that the nomenclature is still accurate and has been kept up to date by the curator of the reference collection. Thus, factors impacting this process include access to and quality of a comparative collection, analyst experience, and an implicit understanding of "standard zooarchaeological procedures" (*sensu* Reitz and Wing 1999, 2008).

It is easy to see where this type of reasoning can become circular, whereby zooarchaeologists are forever struggling in an uphill battle against the tumultuous field of taxonomy and are at the beck and call of decisions made by biologists, but we need not give up hope. Rather, faunal analysts should be cognizant of the fact that zooarchaeology, just like any scientific discipline, is dynamic and can only progress through diligent and vigilant assessment and reassessment of identifications and interpretations. The utility of a comparative collection is directly related to the quality of comparative specimens in both number and completeness, as well as geographic, ecological, and biological breadth (e.g., age distribution, size differences, sexual dimorphism, clinal variation, etc.). However, as Driver (2011a) and Wolverton (2013) point out, the most impressive comparative collection alone will not compensate for the use of a classificatory system created for zoology based on complete specimens, which also had soft tissue, pelage, etc. to facilitate identification, and assumed taxonomic relationships. So, how are zooarchaeologists to deal with such epistemological challenges regarding what is perhaps the most fundamental step in zooarchaeological research—the step that is key to us saying we know what we know?

Lyman (2011, p. 34; see also 2010) suggests that zooarchaeologists adopt paleontological protocols of identification because "That protocol addresses every problem Driver identifies." In a more immediate sense, or at least until practitioners collectively follow Lyman's suggestion, the first step is acknowledging the potential weaknesses of the analogical inferences we use to make specimen identifications (Driver 2011). Following this, explicit discussion linking research questions to techniques of analysis and methods of data aggregation and assessment is required (e.g., Driver 2011a; Emery 2010; Giovas 2009; Grouard 2003; Lyman 1994a, 2010, 2012; Mason et al. 1998; Zeder and Lapham 2010). Such a discussion must include descriptions of comparative aids that are used in specimen identification (including modern skeletal collections, photographs, bone cast reproductions, etc.), and explanations of the appropriateness of each aid in relation to addressing the research question.

A second step involves reconciling differences in analyst training, ability, and/or approach to specimen identification. Analyst experience and variability in specimen identification is perhaps the most subjective and difficult methodological challenge in zooarchaeological practice (Wolverton 2013). As Driver (2011a) and others have discussed (e.g., Gobalet 2001; Lyman and VanPool 2009; Vale and Garret 2002; Wake 2004), the only way to address this challenge, in addition to access to a skeletal or invertebrate comparative collection, is through experience, practice, and

mentorship. To this we add that any level of experience can always be improved upon through collaborative efforts with specialists, such as mammalogists, ornithologists, ichthyologists, and paleontologists.

Ideally, replicative studies and comparison are more objective avenues through which to assess the impacts of analyst experience on the creation of zooarchaeological data. However, although the scientific method traditionally encourages repeated testing and verification of results, repeat analysis is often difficult and time-consuming to perform in zooarchaeology, and at times is even impossible if the faunal assemblage is inaccessible (a plight experienced by researchers working in politically hostile regions, such as parts of the Middle East), or entirely lost (as is the case of many collections excavated decades ago, or by archaeologists who were unable to curate or store the assemblage after excavation). Reanalysis can also be seen as a personal affront on the abilities of the original analyst, with social implications for data sharing, big data compilation, and publication. Nonetheless, reassessment of original analyses, especially with new information from other zooarchaeological studies or related fields such as biology, is integral for correcting previous errors and progressing the zooarchaeological field.

A third step, advocated by Wolverton (2013, p. 381), involves the creation of "discipline-wide standards" that will guide laboratory and systematic procedures of faunal analysis. Similar to Lyman's suggestion to follow paleontological protocols, Wolverton argues that efforts towards standardizing procedures of zooarchaeological analysis will allow for quality control and quality assessment of zooarchaeological data and interpretation, thus providing a framework for assessing the validity of identifications. Per Wolverton (2013, pp. 384, 388), quality control in zooarchaeology involves steps or procedures to ensure that laboratory methods of identification are consistent, and quality assessment refers to the ability to verify the use of quality control procedures in order to produce replicable results. In his article, Wolverton offers a thorough review and discussion of Driver's (1992) arguments, and provides a detailed outline of steps zooarchaeologists can take to achieve quality control (for review, see Wolverton 2013, pp. 385–388). He follows with another outline of suggestions for structuring quality assessments. While a full and detailed review of Wolverton's steps is beyond the scope of this chapter, the steps are readily adaptable to different goals of zooarchaeological identification spanning variable research aims across academic and non-academic work agendas.

Echoing Wolverton's (2013, p. 384) statement that Driver's (1992) "paper should be one of the first papers that students of zooarchaeology read", we think that Wolverton's paper should be a close second. The positive disciplinary implications of strengthening processes of specimen identification and data verification through methodological standardization are vast, including the creation of comparative frameworks for assessing and understanding possible methodological, and associated analogical, differences across assemblages. This is key for comparative studies and big data compilations. Most importantly, however, for standardization to be achieved, explicit effort has to be made and publication venues available (e.g., journals, online supplemental data, etc.) to report quality control and quality

assessment procedures guiding identification (Wolverton 2013; see also Butler and Lyman 1996). A notable example of an effort to create procedural standardization in zooarchaeology hails from the Historic England (formerly English Heritage) commission in the United Kingdom. The group has recently established a series of semi-flexible guidelines for researchers to follow (for their zooarchaeological issue, see Baker and Worley (2014)).

In summary, it should come as no surprise that zooarchaeological identification, like every branch of science, should be subject to reanalysis to improve quality and correct errors. Yet zooarchaeology is an interdisciplinary science, meaning that changes and improvements in other disciplines may impact zooarchaeological results, including results of investigations concluded years in the past. Zooarchaeologists must be aware of ongoing scientific debates in related fields, especially those regarding binomial nomenclature, species classification, ecological traits, and geographic ranges. Similarly, they should be aware of the potentials and limitations of their comparative faunal collections, and seek out assistance from others knowledgeable in the field. Finally, they should be open to reanalyzing specimens (or have someone else reanalyze them) as a means of assuring data quality. Incorporating these provisions into a "standard zooarchaeological practice" is integral for maintaining rigorous scientific quality.

3.4 Maintaining Standard Practice in the Face of Adversity: Case Studies

So far, this essay has outlined the analogical foundations of zooarchaeological identifications as a core element in the epistemology of zooarchaeology and reviewed common challenges inherent to specimen identification. Clearly, striving for and maintaining high standards of accuracy and quality directly impacts zooarchaeological practice. Yet, there are also many circumstantial challenges that influence zooarchaeological identification. Here we highlight five specific examples of such challenges, illustrating the diversity of increasingly common settings and analytical parameters in which zooarchaeological identifications take place, including: the inability to transport remains to curatorial facilities with skeletal comparative collections, situations mandating on-site identifications, zooarchaeological analysis within a large-scale commercial contract setting, and inadequate reference collections to distinguish between closely-related species or domesticated breeds.

Before proceeding, we want to point out one problem that zooarchaeologists repeatedly contend with in specimen identification regardless of the setting or circumstance of analysis: the "comprehensiveness" of the zooarchaeological assemblage under study. By "comprehensive", we not only mean the taxonomic make-up of an assemblage, but also the literal size of faunal constituents present in the archaeological record and available for recovery during excavation. A primary example of this is the excavation strategy undertaken to obtain specimens. Ideally,

zooarchaeologists lead or work on projects that prioritize zooarchaeological research and datasets, directing or helping to shape the excavation strategy and scope of faunal sampling (e.g., Keegan 2009; Thornton 2011). In these cases, meticulous excavation and curatorial methods are implemented to obtain and preserve as many specimens as possible, using such techniques as fine-sieve screening, flotation, and curation in a non-humid, climate-controlled location. However, such ideal circumstances are not always possible. Due to time, budget, and logistical (e.g., inability to transport cargo) constraints, zooarchaeologists within academic and commercial professions routinely work with 6.4 mm (1/4 inch) screened (or sometimes entirely unscreened) samples. This is significant because screen size is important for the identification process, not just because it may affect the variety of taxa able to be procured, but because some elements that are most diagnostic on a specimen may be the smallest and easiest to miss without fine-screening (for example, fish otoliths, which may appear as tiny stones to the untrained eye, and are easy to miss without the use of a small-sized mesh). Although, to be sure, fine screening is not always necessary for the recovery of taxonomically or elementally robust samples (e.g., Gobalet 2005; Thornton 2011). While there is not a fail-safe way to ensure the recovery of a totally comprehensive sample, in our collective experience working in Latin America, the Caribbean, and the United States, zooarchaeologists within academic and contract settings are increasingly contributing to the excavation design and overseeing zooarchaeological sampling.

As for circumstantial challenges impacting specimen identification, and as a result the strength of analogical inference, a major issue involves limited physical access to archaeological faunal collections or the inability to transport specimens for off-site analysis in a laboratory setting with curated comparative specimens, microscopes, and other helpful instrumentation (see also Crabtree, Chap. 9). Again, ideally, zooarchaeologists analyze faunal collections in climate-controlled settings with access to an extensive comparative collection that meets their analytical needs, which may include various classes of vertebrates and invertebrates alike as well as particular geographic or ecological representation (Lyman 2010). Yet it is not uncommon for archaeological faunal collections to be located in countries or locations where transfer to a setting with a comparative collection is impossible, often due to legal, political, or cultural reasons.

In truth, a zooarchaeologist's expertise can only go so far in making consistently correct identifications without some type of comparative support, and this is especially the case with assemblages characterized by high taxonomic diversity and/or taxonomically challenging taphonomy. Fortunately, modern technology can improve these circumstances. Photographs, including both 2D and 3D images, are easier to take and store now more than ever before, and a zooarchaeologist can assemble a virtual comparative collection of their own to fall back on when physical references are absent. A number of zooarchaeological (including osteological and malacological) virtual reference collections are now available online, many free of charge (e.g., Betts et al. 2011) (Table 3.1). Crowdsourcing is also a viable option, with experts and amateur analysts willing to offer assistance on forums, blogs, and

Table 3.1 A sample list of virtual reference collections available online (1–5) and zooarchaeology crowdsourcing forums (6, 7)

Organization	Website
1. Florida Museum of Natural History Environmental Archaeology image collection	https://www.floridamuseum.ufl.edu/envarch-gallery/
2. Royal British Colombia Museum Avian Osteology Guide	http://www.royalbcmuseum.bc.ca/NaturalHistory/Bones/homepage.htm
3. University of Nottingham Archaeological Fish Resource	http://fishbone.nottingham.ac.uk/
4. Virtual Zooarchaeology of the Arctic Project	http://vzap.iri.isu.edu/ViewPage.aspx?id=230
5. National Museum of Natural History (France)	http://osteobase.mnhn.fr
6. Bone Commons (International Council for Archaeozoology	http://alexandriaarchive.org/bonecommons/
7. Zooarchaeology Listserve (United Kingdom)	http://www.jiscmail.ac.uk/cgi-bin/webadmin?A0=ZOOARCH

other interactive platforms. Bone Commons, sponsored by the International Council for Archaeozoology (ICAZ) and the related UK-sponsored Zooarch Listserve have become go-to sources for many international experts and newcomers in the field, offering members the chance to share photos of troublesome specimens that others can help identify (Table 3.1). The benefit of such interactive forums is that zooarchaeologists are able to quickly share important additional information that can help make an accurate identification, such as the biology and ecology of the species in question, the locations of similar specimen finds, the nature of any specimen modifications, and whether experts in the same or other disciplines might be interested in seeing the specimen and learning more about the project.

Virtual identifications will never be a replacement for identifying a specimen with an actual collection, and in some cases the analogical inferences guiding identification will be considered weaker by comparison; yet, when combined with other techniques they can prove adequate. For example, one of us (Sharpe) has had difficulty exporting entire zooarchaeological assemblages from sites in Guatemala, where an extensive faunal reference collection is unavailable (partly due to laws prohibiting the capture or collection of endangered taxa), and where current government laws make it difficult to ship large quantities of archaeological material at one time (and if any material is exported, it must be returned before the investigator can export additional material). This has made it impossible to go through a collection and make identifications on a single inspection. Rather, she has travelled between Guatemala and the US multiple times, often within a single year, to compare photos of samples taken from the archaeological collections housed in Guatemala with a reference collection in the United States (often those of the Florida Museum of Natural History). She has also exported subsets of the zooarchaeological material that include key "problem" specimens that can only be identified with a tangible

collection (especially bones of small birds, reptiles, and fish). These methods are not ideal and require considerable planning, cost, time, and effort on the part of the zooarchaeologist.

Similarly, LeFebvre has experience working with culturally sensitive and ritually significant remains in Latin America that required on-site identification due to a strict prohibition on moving the remains beyond the context of recovery and preference for minimal handling of the specimens. This requirement was understood prior to the start of the project, allowing for a zooarchaeological research design tailored to accommodate the prohibition of material transport. In this instance, she was a part of a team of four zooarchaeologists trained to make on-site identifications of anticipated taxa with the aid of a photographic guide compiled prior to the project. Moreover, in an effort to make the most accurate identifications possible, each specimen was discussed and agreed upon by consensus. Although not optimal in terms of comparative collection-based standards or ideals for laboratory-based identifications, the procedures for identification were subject to agreed-upon quality control steps and quality assessment on a specimen-by-specimen basis, providing a shared point of procedural verification and explanation.

On the other end of the spectrum, while identification without the aid of an adequate physical comparative collection is a challenge, it can be just as challenging to identify specimens in labs when using inadequate comparative collections for a given faunal assemblage. Depending on logistical or budget constraints, a zooarchaeologist may be charged with identifying a faunal assemblage that is characterized by taxa not well represented in an available skeletal comparative collection. In our experience, this quandary is quite common and, if funding permits, necessitates travel to seek out and use suitable comparative collections, possibly mailing specimens to colleagues with access to comparative specimens and relying on them to make identifications, or making do with what is readily available regardless of the potential for specimen identification. As is the case for on-site identification, virtual resources are available for help, and 3D scanning and printing technology may prove especially valuable for those cases where only one museum has the specimen necessary to confirm an identification.

An example of this that has plagued many projects in the Indo-Pacific region is the need for comprehensive comparative collections of fish skeletons. Indo-Pacific zooarchaeologists are faced with the greatest diversity of fish in the world, estimated at over 3000 taxa in some areas (Crabtree 2016; Helfman et al. 2009). For many years, zooarchaeologists working with these diverse assemblages had to make do with inadequate reference collections, and many adopted a practice of limiting identifications to a few key cranial elements (the articular, dentary, maxilla, premaxilla, and quadrate), believed to be the most rapid and reliable for distinguishing taxa (Crouch et al. 2007; Leach 1986; Nagaoka 1994; see also Giovas, Chap. 4). Zooarchaeologists working in the Indo-Pacific region have been striving to improve their ability to make more precise identifications with a wider selection of bones, some arguing that it is worth the extra effort so as to examine species-specific fishing trends and resource depletion over time (Campbell 2016; Davidson et al. 1999;

Ono and Clark 2012). Increased communication between collection curators, including the sharing of photos and even 3D scans of specimens, may be the most practical solution for zooarchaeologists to augment their reference materials.

Recently, the authors participated in a large scale, multi-year zooarchaeological identification project in Florida that spanned three laboratories and over 15 different analysts at a given time. The zooarchaeological identifications were a sub-project of a cultural resource management contract. Faunal samples were collected from multiple sites, and at the start of the project an estimate of approximately 500,000 specimen identifications were anticipated over the course of two years budgeted for analysis. Per federal and state mandates, the faunal samples could not leave Florida. In order to accommodate the large scope of required analysis, teams of zooarchaeologists were assembled across three laboratories with variable access to comparative collections of variable taxonomic composition, and were composed of analysts with variable zooarchaeological educational and professional backgrounds, years of experience, and topical interests. We were a part of the team assembled at The Environmental Archaeology (EA) Laboratory at the Florida Museum of Natural History (FLMNH). The FLMNH EA Laboratory provided the most taxonomically, ecologically, and geographically representative comparative skeletal collection available for the analysis.

The analytical parameters of the zooarchaeological analysis mandated identification of specimens to the lowest taxonomic category possible. What this meant in terms of the actual identification processes had to be agreed upon across the labs, tailored to the capability of analysts and available identification resources, and specific to taxa. For instance, analysts developed identification protocols for turtles based on carapace, plastron, cranial, and post-cranial limb morphology regarding which elements could be archaeologically identified beyond the level of Family to Genus (e.g., *Kinosternon* sp.). Similarly, snake vertebrae were not identified beyond the level of Family (e.g., Colubridae, Vipiridae), but cranial elements were identified to at least the level of genus (e.g., *Nerodia* sp., *Agkistrodon*). However, in the cases of identification uncertainty, or "mystery" specimens, these were sent to the FLMNH EA team for identification or verification by analysts with the use of the comparative collection.

The previous examples described instances of zooarchaeologists confronted with mainly "wild" taxa, but distinguishing among domesticated species and breeds can also prove difficult without an adequate comparative collection. The difficulty with domesticated taxa is that their morphology is often dependent on the phenotypic traits for which humans bred them, which can be local to a specific area and time period. A notorious example of this is the ongoing investigation into identifying traits that are most useful for distinguishing sheep and goats (Halstead et al. 2002; Payne 1985; Zeder and Lapham 2010; Zeder and Pilaar 2010). For many years, and even today, zooarchaeologists were unable to identify most caprine bones, relegating them to a general "sheep/goat" (and sometimes antelope) category. In fact, "sheep/goat" has been added to the Encyclopedia of Life (http://eol.org/pages/32609438/overview). Considerable progress has been made to identify particular elements over the decades, but some methods have proven to be successful

only part of the time, especially when regional variations play a role in determining intraspecific morphology. Furthermore, distinguishing between breeds can be integral for tracing exchange and domestication activities in an area. Comparative reference material should ideally include local breeds known to have existed in a region, preferably from several ages; however, this is seldom the case, especially when skeletal material is exported between countries for identification.

The examples described above illustrate some of the ways in which specimen identification can be impacted by circumstances and settings of analysis, and provide points of challenge when considering how to best plan, execute, and evaluate processes of specimen identification. Based on the above examples, we assert that it is not necessarily appropriate to suggest that one approach is more epistemologically or methodologically sound than another, or judge that the bases for specimen identification are more or less accurate among the projects. Rather, as Gifford-Gonzalez (1991), Driver (1992), Wolverton (2013), and Lyman (2010, 2012) all encourage, the basis for the strength of analogical inferences behind zooarchaeological identifications (and resulting data) rests in critical and explicit consideration of how (e.g., laboratory procedures) zooarchaeologists design and carry out identifications in accordance with research goals and interpretive aims.

Zooarchaeologists and archaeologists alike must recognize and plan for the ways in which the logistical, analytical, and methodological variability characteristic of contemporary zooarchaeological practice requires epistemological flexibility in accommodating specimen identification. Driver (1992), Wolverton (2013), and others (e.g., Lyman 2002, 2010; Bochenski 2008; Gobalet 2001) are correct in emphasizing the critical need for detailed reporting of specimen identification procedures. In doing so, zooarchaeologists need to be prepared to be as thorough and transparent as possible when describing specimen identification. We suggest that a willingness to share, describe, critique, and accept approaches to specimen identification that challenge our ideals and/or desires for standard procedures (e.g., the use of virtual aids, blog posts, etc.) will ultimately strengthen the analytical and methodological relationship between zooarchaeology and the disciplines we draw on for analogical inferences, such as biology and paleontology.

3.5 Wider Implications: Specimen Identifications and "Big Data" in Zooarchaeology

Perhaps the best example of the need for epistemological and methodological flexibility in the execution and evaluation of zooarchaeological specimen identification is the growing emphasis on "big data" studies. It is hoped that the data we collect and report in zooarchaeology is read and used by others, be they other zooarchaeologists, scientists in other fields of research, public or private agencies such as environmental engineering or planning firms, and even non-professionals with a fascination of the human past and ancient animals. But the integral first step of

making an identification has lasting implications for anyone reading the zooarchaeological results. The ramifications and analogical basis for making the correct identification are more significant now than ever before, since comparative studies using multiple datasets, as well as combining many studies in electronic databases ("big data") for the purposes of assessing trends, has become increasingly popular in archaeology (Atici et al. 2013; Cooper and Green 2016; Faniel et al. 2013; Gattiglia 2015; Kansa 2005; Kansa and Kansa 2013). But what happens when a zooarchaeologist makes a mistake? What happens when a zooarchaeologist wants to correct or revise one (or several) earlier identifications in a dataset, but that dataset has already been uploaded to a larger collection and has been shared and used in other projects? What happens when a zooarchaeologist spots an error in another researcher's data?

These are the same questions asked by many other scientists in all disciplines today. Biologists, contending with the aforementioned influx of taxonomic changes caused by molecular genetics, have established an online network of linked databases that abide by the Darwin Core standard of biological nomenclature (Table 3.2). Museum collections have also begun to upload data and images for their specimens in these and similar databases, many of which are also linked, so that a change to a species name or related information in one source will simultaneously change for all instances linking to this source. The archaeological community is also beginning to take advantage of the idea behind these "big data" online compilations, such as the increasingly popular open access datasets like the Digital Archaeological Record (tDAR) and Open Context (Table 3.2).

Zooarchaeologists are already beginning to develop their own collaborative databases and are participating with websites such as tDAR and Open Context. Ideally, future online lists containing taxonomic identifications would be linked to the same Darwin Core standards that maintain the most updated accepted taxonomic relationship information and nomenclature. This, then, would solve the problem of invalid synonyms assigned to identifications, although it may raise a number of other dilemmas. For instance, a zooarchaeologist may distinguish between two species at

Table 3.2 1–8: Linked databases following the Darwin Core standard of biological nomenclature. 9–10: Open access online compilations of archaeological data

Organization	Website
1. Darwin Core	http://rs.tdwg.org/dwc/
2. Encyclopedia of Life	http://www.eol.org/
3. Integrated Taxonomic Information System	http://www.itis.gov/
4. Global Diversity Information Facility	http://www.gbif.org/
5. Species 2000	http://www.sp2000.org/
6. World Register of Marine Species	http://marinespecies.org/
7. VertNet	http://www.vertnet.org
8. iDigBio	http://www.idigbio.org/
9. Digital Archaeological Record	http://www.tdar.org
10. Open Context	http://opencontext.org

a site and make interpretations regarding diversity from this data, only to have the molecular phylogenetic research later determine that there is no distinction at all, and the taxa are one and the same. The opposite is also possible, in that zooarchaeologists may be unable to distinguish between two species based on morphological characteristics alone, but the molecular data indicates it is more than one taxon, a phenomena known as "cryptic species" in phylogenomics (Bickford et al. 2007). Molluscan taxonomy is particularly challenging in both these regards; for example, Sharpe has been working with malacological geneticist John Pfeiffer to classify freshwater mussels in Mesoamerica, and has found that several mussel species (family: Unionidae) exhibit remarkable phenotypic plasticity that belies any attempts at identification using physical cues, and negates the previous zooarchaeological identifications (Pfeiffer et al. 2017).

Changes in these large compiled electronic datasets will mean that zooarchaeological identifications can change, even when the designated project zooarchaeologist has retired or is no longer involved with the faunal assemblage and no one else is actively working on the project. Any "big data" projects would need to maintain a record of these changes, including when and how they were made. Zooarchaeologists working with the data should also be vigilant of such changes, as well as the history of nomenclature for a given taxon. Such vigilance is warranted since it may be that secondary interpretations made by an original or subsequent analyst, including quantification, interpretation of local ecology, niche demographics, cultural habits, and so on, are affected by any change made to the initial identification.

3.6 Closing Thoughts

Although it is tempting to perceive zooarchaeological specimen identification as epistemologically straightforward and methodologically simple, as this chapter has discussed, there are inherent complexities in specimen identification common within zooarchaeology. Building off seminal treaties of the topic, we argue that as a community of practitioners, spanning many different settings of practice, we need to be able to accommodate epistemological and methodological flexibility in processes of identification; including where, how, and according to what analogical criteria identifications are made. Zooarchaeological identification and analysis takes place in a variety of settings and under diverse logistical, budgetary, cultural, and political circumstances. Indeed, as zooarchaeology continues to grow and diversify in the types of questions faunal data is used to investigate, in an ideal world, it is no longer advisable to disseminate results without detailed descriptions of the specimen identification processes and techniques. This issue is particularly salient in regards to being able to conduct comparative studies and execute big data research agendas (Driver 2011b; Emery 2004; Wolverton 2013), and for making our data accessible and useful for others outside of the zooarchaeological discipline (e.g., Lyman and Cannon 2004; Rick and Lockwood 2013; Wolverton and Lyman 2012).

Zooarchaeologists must strive to make sure that our foundation for producing data remains as accurate as can be, even if that means correcting obsolete names and incorrect identifications. A willingness to remain flexible and revise earlier data and, by association, interpretations, is what makes our discipline progress.

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Chapter 4
Impact of Analytic Protocols on Archaeofish Abundance, Richness, and Similarity: A Caribbean-Pacific Crossover Study

Christina M. Giovas

4.1 Introduction

In zooarchaeology, taxon identification and quantification are the foundation for subsequent higher-order analysis and interpretation addressing diet, resource exploitation, environmental reconstruction, and animal management strategies in the past. As a consequence, considerable attention has been devoted to issues of data quality in relation to faunal recovery, identification, quantification, modification, taphonomy, terminology, and interpretive constructs (Albarella 2016; Atici and Lev-Tov 2013; Blumenschine et al. 1996; Cannon 1999; Casteel and Grayson 1977; Driver 1992, 2011a, b; Gilbert et al. 1981; Giovas 2009; Giovas et al. 2017; Gobalet 2001, 2005; Lyman 1994, 2008; Lyman and Ames 2004; Nagaoka 1994; Peres 2010; Wolverton 2013). At the same time, competing demands of schedule and budget and the constraints imposed by research questions, field recovery strategies, analytic expertise, the availability of comparative collections, and assemblage preservation influence the choice of methodological approaches and the resulting profile of a zooarchaeological assemblage. For this reason there are few universal methodological rules in zooarchaeology. Instead, factors constraining analytic approaches are tempered by an understanding of context-appropriate methods, relevant archaeological background, and species behavior and ecology (for a recent exploration of these issues see Atici and Lev-Tov 2013).

It is within this context that a method of fish analysis was developed for New Zealand and the (sub)tropical Pacific in the 1970s and 1980s (Anderson 1973; Leach 1976, 1986, 1997; for historical reviews of this method see Lambrides and Weisler 2013 and Vogel 2005). This widely adopted approach (e.g., Dye and Longenecker 2004; Fitzpatrick and Kataoka 2005; Kirch et al. 2010; Masse 1989;

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Morrison and Addison 2008; Vale and Gargett 2002) relies on the identification of five, paired "cranial" bones from a fish's oromandibular skeleton and a set of "special" elements to identify taxa and calculate their abundance. These select cranial elements consist of the quadrate, dentary, maxilla, premaxilla, and articular (sometimes referred to as the angular). Special bones are those which are selectively diagnostic to certain taxa, but are otherwise not used for fish identification. The list of "specials" varies (Dye and Longenecker 2004; Leach 1986, 1997; Ono and Clark 2012; Vogel 2005), but frequently includes: the bones of the pharyngeal mill of parrotfish (Labridae, Scarinae) and wrasses (Labridae); scutes of members of the jack family (Carangidae); the caudal tail spines (bucklers) and first dorsal and anal pterygiophores of surgeonfish (Acanthuridae); burrs (dermal spines) of porcupinefish (Diodontidae); the first and second dorsal spines and associated pterygial carina of triggerfish (Balistidae); the dental plates and teeth of sharks and rays (Elasmobranchii); and in some cases, distinctive vertebrae such as the urostyle of tunas and mackerels (Scombridae) or the centra of sharks and rays. The "five cranials plus specials" method has enjoyed popularity in Oceania, where tremendous diversity exists in tropical Pacific fishes. Its wide use is probably due in part to this diversity; the method streamlines the challenge of identifying unique skeletal characteristics for a given taxon and reduces the required comprehensiveness of reference collections by limiting the number of elements that must be checked against comparative materials (see Lambrides and Weisler 2015 for discussion of regionalization in analytic methods).

One of the original proponents of this method, referred to here as the restricted element approach, was Foss Leach (1986, 1997), who suggested that analysis of this limited set of elements is sufficient to identify the range of fish taxa present in an assemblage (sample richness) and establish the minimum number of individuals (MNI) represented by these. He targeted the articular, dentary, maxilla, premaxilla, and quadrate because he believed these to be identifiable across an array of taxa, circumventing the bias that might arise from including elements that were diagnostic for certain taxa but not others, and allowing for equitable comparison of relative abundances as a result (Leach 1997, pp. 6–8). Leach was rightly concerned with some taxa being underrepresented in analysis due to their possessing fewer elements diagnostic of taxon. However, the relative survivorship of cranial elements, irrespective of their diagnostic potential, was not explicitly considered, perhaps because at the time the method was developed, taphonomic processes affecting fish bone had yet to be systematically investigated (e.g., Butler and Chatters 1994; Butler and Schroeder 1998; Lubinski 1996; Szpak 2011; Zohar et al. 2001; but see Nichol and Wild 1984 for an early discussion on the differential preservation of the "five cranials"). In his manual on archaeological fish analysis for New Zealand, Leach (1997, p. 8) states, "even if further bones were shown to have this property [of being diagnostic to taxon], it is very doubtful whether the extra effort required to identify them would significantly alter the table of relative abundance of fish types established by identifying the five bones already chosen".

In the last 10–20 years, Pacific archaeologists have questioned whether this restricted approach to archaeofish analysis yields a representative picture of taxonomic richness and relative abundance. Several keys studies (Butler 1994; Campbell 2016; Lambrides and Weisler 2013; Ono and Clark 2012; Ono and Intoh 2011; Vogel 2005; Walter 1998; Walter and Anderson 2001; Weisler 1993; see also Whyte et al. 2005 for the Caribbean) have assessed the restricted method against analyses that employ a broader set of elements to determine whether comparable results are achieved. In most cases the restricted approach has been found wanting, with discrepancies between methods ranging from minor to substantial, depending on the study and the nature of the fish assemblage. Identified violations include distortions of taxonomic relative abundance, inversions and/or scrambling of rank order abundance, and undercounting of taxonomic richness, especially for rarer taxa. Because archaeofish analyses in other parts of the world, such as Europe, the Caribbean, and the northeastern Pacific, typically employ a fuller suite of skeletal elements, including vertebrae, these issues are moot in these regions.

The critical studies cited above demonstrate a bias against fish that possess fragile cranial bones readily lost to taphonomic processes, such as tunas and mackerels (Scombridae) and members of Belonoidei (flyingfish, halfbeaks, needlefish, and sauries). They also draw important attention to the complications posed for cross-regional syntheses and comparative assessments of fishing and habitat use when some assemblages, but not others, have been analyzed using the restricted element method. Analyzing a large suite of elements from Rapan fish assemblages, for instance, Vogel and Anderson (2012) point to the abundance of chaetodontids (butterflyfish) and pomacentrids (damselfish) that would have gone unrecorded had the traditional set of cranial and special bones been relied upon. The authors note these two fish families are not widely recorded in Pacific archaeological contexts, despite ethnographic data that suggests they should be found, raising the question of whether their absence reflects actual Polynesian fishing practices or a methodological artifact.

Fraser's (2001) study of prehistoric tuna fishing in the Pacific provokes similar questions. She notes the ethnographic importance of tuna in the region, but attributes the spotty appearance of these fish in archaeological assemblages across the Pacific to cultural choice, including possible social proscriptions. The role that analytic methods may have played in shaping the perceived distribution of tuna abundance is not addressed. Yet, as Ono and Intoh (2011; Ono and Clark 2012; see also O'Connor et al. 2011 on the use of tuna vertebrae to identify pelagic fishing at 42,000 BP) have demonstrated, tuna identification is largely dependent on the analysis of vertebrae, a practice which has was generally uncommon in Pacific archaeology until more recently (see reviews in Lambrides and Weisler 2013, 2016).

Because of these findings, Pacific fish studies in the last decade have increasingly relied on an expanded suite of elements for identification and quantification (e.g., Jones 2009; Lambrides and Weisler 2013; Ono and Clark 2012; Ono and Intoh 2011; Vogel and Anderson 2012; Walter 1998; Weisler 1993; Weisler and Green 2013; Weisler et al. 2010). These studies reflect a concern with accurately capturing

assemblage richness and relative abundance, understanding fish processing activities, and facilitating comparative analyses—concerns which articulate with larger zooarchaeological discussions about data quality (e.g., Driver 1992, 2011a, b; Wolverton 2013). The possible role of statistical effects in generating the discrepancies observed between restricted and expanded analytic methods has yet to be established, however. On one hand, the aforementioned disparities in relative abundance and richness produced by the two approaches could be due to genuine differences in how they perform. On the other hand, because restricted and expanded methods entail pronounced sample size differences as a result of variation in the number of elements that are examined, observed discrepancies may also be due to sample size effects. The omission of rarer taxa by the restricted element approach, for example, is an expected statistical artifact of the sample size reduction inherent to this analytic method. Even the scrambling of taxonomic rank order can be readily achieved by the select addition of just a few NISP or MNI counts to certain taxa, particularly if taxa cluster close together in abundance. Such changes, therefore, may not be meaningful and might be no different than those obtained by resampling from the same context.

Critiques of the restricted element approach have focused on whether this method delivers results that match those obtained by analyzing a wider set of elements. This is not equivalent to establishing that results are representative of the originally deposited zooarchaeological population. The composition of the latter is unknowable since it is usually not possible to excavate an entire site, and even if this could be done, taphonomic processes will have selectively deleted portions of the original record. Because of this fact, analysts in general rely on the working assumption that larger sample sizes better represent the original zooarchaeological population than small ones, all else being equal. Studies finding that expanded element analysis outperforms its restricted counterpart are based on this same assumption. When analytic approaches produce different results, therefore, it is necessary to ask: (1) are observed differences the result of sample size effects; (2) what analytical constructs (e.g., taxonomic richness, quantitative units, screen size fractions) are affected by such differences, if genuine; and (3) can the magnitude of these differences be quantified so they may be comparatively assessed across analytic constructs?

In this investigation, I address these three questions using a previously analyzed tropical fish assemblage from the Caribbean archaeological site of Sabazan on the island of Carriacou (Table 4.1). Because analysis of the Sabazan assemblage followed standard practice in Caribbean zooarchaeology by employing all potentially diagnostic fish elements—that is, every bone fragment was examined for potential identification to taxon—this dataset provides a solid foundation for assessing the representativeness of samples generated using the restricted element approach. The Caribbean and Pacific Oceans share many of the same fish families and genera, and in some cases the same cosmopolitan species (e.g., *Katsuwonis pelamis*, *Auxis rochei*, *Selar crumenophthalmus*, *Sphyraena barracuda*), making the results obtained here informative for Pacific archaeological contexts.

Table 4.1 The original, complete analyzed archaeofish sample from the Sabazan site showing lowest level taxonomic designations. Taxa are listed alphabetically by family. Data from Giovas (2013)

			Site total				
Class	Taxon	Common name	NISP	% NISP	MNI	% MNI	Weight (g)
Chondrichthyes: Elasmobranchii							
	Myliobatidae	Eagle/Cownose ray	1	0.0	1	0.3	2.82
	Total Myliobatidae		1	0.0	1	0.3	2.82
Actinopterygii							
	cf. Acanthuridae		3	0.1	–	–	0.48
	Acanthurus sp.	Surgeonfish	306	9.7	26	6.6	47.26
	Total Acanthuridae		309	9.8	26	6.6	47.74
	Acanthuridae/ Pomacanthidae	Surgeonfish/ Angelfish	1	0.0	–	–	0.05
	Balistidae	Triggerfish	41	1.3	12	3.1	21.66
	Belonidae	Needlefish	6	0.2	3	0.8	0.56
	cf. *Strongylura* sp.	Needlefish	2	0.1	1	0.3	0.01
	Total Belonidae		8	0.3	4	1.0	0.57
	Carangidae	Jack, Pompano, Scad	271	8.6	6	1.5	9.11
	cf. Carangidae		5	0.2	–	–	1.19
	Caranx sp.	Jack	3	0.1	3	0.8	1.37
	cf. *Caranx* sp.		4	0.1	1	0.3	3.70
	cf. *Elagatis bipinnulata*	Rainbow runner	1	0.0	1	0.3	0.34
	Selar crumenophthalmus	Bigeye scad	97	3.1	59	15.1	0.65
	cf. *Selar crumenophthalmus*		55	1.7	2	0.5	0.46
	Trachurus lathami	Rough scad	10	0.3	10	2.6	0.05
	cf. *Trachurus lathami*		17	0.5	12	3.1	0.03
	cf. *Trachurus lathami*/*Selar crumenophthalmus*		75	2.4	1	0.3	0.67
	Total Carangidae		538	17.1	95	24.2	17.57
	Chaetodontidae	Butterflyfish	1	0.0	1	0.3	0.03
	Clupeidae	Herring, Shad	194	6.2	13	3.3	0.44
	Clupeidae/Engraulidae	Herring, Shad/ Anchovy	11	0.3	–	–	0.03
	Diodontidae	Porcupinefish	4	0.1	3	0.8	25.83
	Exocoetidae	Flyingfish	12	0.4	6	1.5	0.36
	cf. Exocoetidae		3	0.1	–	–	0.07
	Total Exocoetidae		15	0.5	6	1.5	0.43
	Exocoetoidea	Flyingfish, Halfbeak	5	0.2	–	–	0.03
	Haemulidae	Grunt	91	2.9	13	3.3	11.92
	cf. Haemulidae		7	0.2	1	0.3	0.15
	Anisotremus sp.	Porkfish, Black margate	1	0.0	1	0.3	0.15
	cf. *Haemulon* sp.	Grunt	24	0.8	6	1.5	6.08

(continued)

Table 4.1 (continued)

			Site total				
Class	Taxon	Common name	NISP	% NISP	MNI	% MNI	Weight (g)
	Total Haemulidae		123	3.9	21	5.4	18.30
	Hemiramphidae	Halfbeak	40	1.3	7	1.8	0.23
	cf. Hemiramphidae		1	0.0	–	–	<0.01
	Total Hemiramphidae		41	1.3	7	1.8	0.23
	Holocentridae	Squirrelfish, Soldierfish	32	1.0	7	1.8	3.47
	cf. Holocentridae		1	0.0	–	–	0.02
	cf. *Holocentrus* sp.	Squirrelfish	2	0.1	1	0.3	0.30
	Total Holocentridae		35	1.1	8	2.0	3.79
	Labridae (excludes Scarinae)	Wrasse, Hogfish	25	0.8	6	1.5	3.14
	cf. Labridae		1	0.0	–	–	0.14
	Bodianus sp.	Hogfish	1	0.0	1	0.3	0.03
	cf. *Bodianus* sp.		3	0.1	1	0.3	1.10
	Halichoeres sp.	Wrasse	4	0.1	3	0.8	1.33
	cf. *Halichoeres* sp.		9	0.3	3	0.8	4.63
	Total Labridae		43	1.4	14	3.6	10.37
	Labridae: Scarinae	Parrotfish	296	9.4	4	1.0	56.03
	cf. Scarinae		2	0.1	1	0.3	0.07
	Cryptotomus roseus	Bluelip parrotfish	1	0.0	1	0.3	<0.01
	Cryptotomus roseus/*Nicholsina usta*	Bluelip/Emerald parrotfish	2	0.1	2	0.5	0.02
	Scarus sp.	Parrotfish	74	2.3	20	5.1	28.17
	cf. *Scarus* sp.		4	0.1	–	–	1.33
	Sparisoma sp.	Parrotfish	284	9.0	50	12.8	135.09
	cf. *Sparisoma* sp.		7	0.2	–	–	1.95
	Total Labridae: Scarinae		670	21.2	78	19.9	222.66
	cf. Labroidei		1	0.0	–	–	0.09
	Total Labroidei		6	0.2	–	–	1.08
	Lutjanidae	Snapper	27	0.9	9	2.3	4.99
	cf. Lutjanidae		4	0.1	2	0.5	0.82
	cf. *Ocyurus chrysurus*	Yellowtail snapper	1	0.0	1	0.3	0.12
	Total Lutjanidae		32	1.0	12	3.1	5.93
	Lutjanidae/Serranidae	Snapper/Grouper, Sea bass	11	0.3	–	–	5.08
	cf. Lutjanidae/ Serranidae		2	0.1	–	–	0.17
	Total Lutjanidae/ Serranidae		13	0.4	–	–	5.25
	Malacanthidae	Tilefish	1	0.0	1	0.3	0.02
	cf. *Mugil* sp.	Mullet	1	0.0	1	0.3	0.06

(continued)

Table 4.1 (continued)

			Site total				
Class	Taxon	Common name	NISP	% NISP	MNI	% MNI	Weight (g)
	Total Mugilidae		1	0.0	1	0.3	0.06
	Mullidae	Goatfish	6	0.2	2	0.5	0.08
	cf. Mullidae		27	0.9	5	1.3	0.06
	Total Mullidae		33	1.0	7	1.8	0.14
	Ostraciidae	Trunkfish, Cowfish	4	0.1	3	0.8	0.02
	Pomacentridae	Damselfish	44	1.4	9	2.3	0.09
	cf. Pomacentridae		7	0.2	1	0.3	<0.01
	Total Pomacentridae		51	1.6	10	2.6	0.09
	Cynoscion sp.	Weakfish	1	0.0	1	0.3	0.06
	cf. *Cynoscion* sp.		1	0.0	1	0.3	0.27
	Total Sciaenidae		2	0.1	2	0.5	0.33
	Scombridae	Tuna, Mackerel	8	0.3	–	–	1.44
	cf. Scombridae		1	0.0	–	–	0.07
	Auxis sp.	Bullet/Frigate tuna	180	5.7	10	2.6	39.91
	cf. *Auxis* sp.		3	0.1	–	–	1.85
	Euthynnus alletteratus	Little tunny	2	0.1	1	0.3	0.34
	Katsuwonus pelamis	Skipjack	79	2.5	13	3.3	40.64
	cf. *Katsuwonus pelamis*		8	0.3	–	–	6.22
	Thunnus sp.	Tuna	51	1.6	9	2.3	18.48
	cf. *Thunnus* sp.		3	0.1	–	–	2.19
	Auxis sp./ *Katsuwonus pelamis*	Bullet/Frigate tuna/ Skipjack	14	0.4	–	–	8.55
	Katsuwonus pelamis/Euthynnus alletteratus	Skipjack/Little tunny	79	2.5	–	–	31.25
	Thunnus sp./ *Katsuwonus pelamis*	Tuna/Skipjack	24	0.8	–	–	11.48
	Thunnini	Tuna	292	9.3	2	0.5	95.76
	cf. Thunnini		1	0.0	–	–	0.03
	Total Scombridae		745	23.6	35	8.9	258.21
	Serranidae	Grouper, Sea bass	150	4.8	10	2.6	60.88
	cf. Serranidae		8	0.3	–	–	1.34
	cf. *Cephalopholis fulva*	Coney	1	0.0	1	0.3	0.11
	Epinephelus sp.	Grouper	5	0.2	3	0.8	5.18
	cf. *Epinephelus* sp.		2	0.1	1	0.3	0.49
	Mycteroperca sp.	Grouper	1	0.0	1	0.3	0.27
	Epinephelinae	Coney/Grouper	12	0.4	5	1.3	1.58
	cf. Epinephelinae		1	0.0	–	–	<0.01
	Total Serranidae		180	5.7	21	5.4	69.85
	Sphyraena sp.	Barracuda	1	0.0	1	0.3	0.29

(continued)

Table 4.1 (continued)

			Site total				
Class	Taxon	Common name	NISP	% NISP	MNI	% MNI	Weight (g)
	Total Sphyraenidae		1	0.0	1	0.3	0.29
	Tetraodontiformes	Triggerfish, Filefish, Puffer, Porcupinefish	1	0.0	–	–	0.33
	cf. Tetraodontiformes		1	0.0	–	–	0.58
	Total Tetraodontiformes		2	0.1	–	–	0.91
	Taxon B (comparative material unavailable)		17	0.5	3	0.8	0.01
	Taxon C (comparative material unavailable)		25	0.8	7	1.8	0.03
	Total Identified Actinopterygii and Chondrichthyes		3153	100.0	392	100.0	714.77
	Indeterminate Actinopterygii (1.6 mm excluded)		1890	–	–	–	281.15

4.2 Study Assemblage and Archaeological Background

The fish assemblage employed in this study comes from the Ceramic Age (ca. 500 BC–AD 1500) archaeological site of Sabazan on the island of Carriacou, which belongs to the tri-island nation of Grenada. Carriacou is a small island, ca. 34 km^2, located in the Grenadines group of the southern Lesser Antilles (Fig. 4.1). Island-wide survey and excavation of archaeological sites indicate Carriacou was first inhabited around AD 400 by Amerindians engaged in a mixed farming, fishing, and foraging economy (Fitzpatrick et al. 2009, 2014; Fitzpatrick and Giovas 2011; Kaye 2003; Kaye et al. 2011). Based on a suite of 26 radiometric assays, the site of Sabazan dates from this early period and was continuously occupied until ca. AD 1400 (Bullen and Bullen 1972; Fitzpatrick and Giovas 2011; Giovas 2016a). The island was apparently abandoned some time after this date and prior to arrival of European settlers in the eighteenth century.

The Sabazan site lies on along an embayment of the Atlantic Ocean (Fig. 4.2), and extends up to 65 m inland from the coast. The site's eastern section is exposed along a ca. 110 m wave-cut profile that reveals rich midden deposits capped by sterile sediments. Present site area is approximately 3000–4000 m^2, but Sabazan has been undergoing progressive erosion from wave action and rising sea level and may have been at least twice as large in the past (Giovas 2016b). Archaeological deposits are over 1 m thick in some areas and contain abundant ceramic sherds, shell and bone artifacts, and well-preserved faunal remains, especially those of fish and shellfish. Excavation conducted by the author in 2005, 2007, and 2008 consists of a series of test pits, a 2 × 1 m block (Trench 1), two 1 × 1 m units (Trenches 2 and 3),

Fig. 4.1 Map of the Caribbean with inset showing the location of Carriacou in the Grenadines

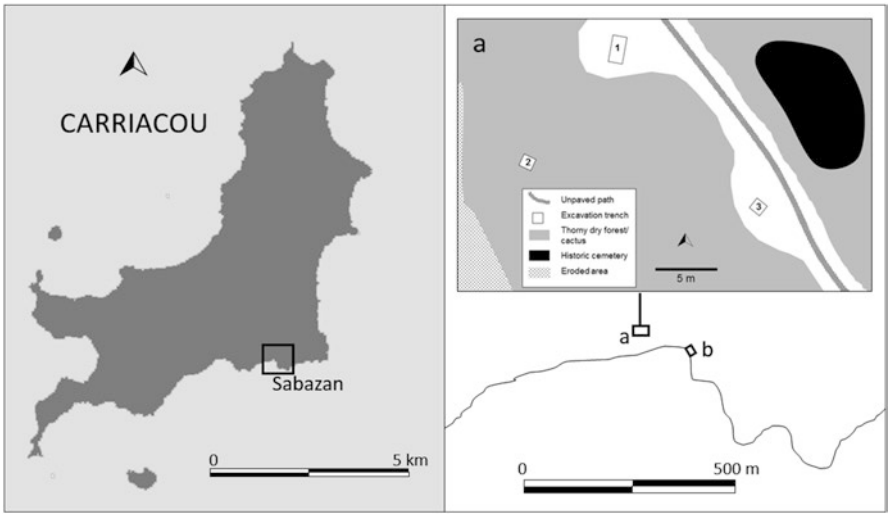

Fig. 4.2 Map of Carriacou showing the location of the Sabazan site and the placement of (**a**) three excavation trenches and (**b**) the coastal profile column sample

and a 50 × 50 cm column sample. The earliest dated basal deposits indicate initial settlement of the site at AD 400–560 (AA-67535, AA67536). Details of excavation and faunal analysis are reported in Giovas (2013, 2016a, b).

Zooarchaeological and human bone isotopic investigations indicate Carriacou's inhabitants relied heavily on marine resources (Fitzpatrick et al. 2009; Giovas 2009, 2013, 2016a, b; Krigbaum et al. 2013), commensurate with evidence from elsewhere in the Lesser Antilles highlighting the importance of fisheries to residents of small islands (e.g., Carder et al. 2007; Grouard 2013; Keegan et al. 2008; LeFebvre 2007; Newsom and Wing 2004; Wing and Wing 2001). The name Carriacou is said to be an

indigenous term meaning “land of many reefs”. This is reflected in the presence of shallow-water fringing and barrier reefs just a few hundred meters off Sabazan’s shoreline that give easy access to open pelagic waters beyond (Tupper et al. 2013, ReefGIS map data). Sabazan’s zooarchaeological record suggests this environmental configuration strongly influenced the nature of resource exploitation at the site, where a significant degree of fishing beyond the outer reef occurred (Giovas 2013, 2016a, b).

4.3 Methods

Fish remains in this study come from Square 1 of Trenches 1 and 2 and the coastal profile column sample located ca. 110 m southeast of the main excavation area (Fig. 4.2). Analyzed deposits span ca. AD 600–1400. All archaeological sediments were hand-troweled following natural stratigraphy, subdivided into 10 cm arbitrary levels, and wet-screened through nested 6.4 mm (1/4 inch) and 1.6 mm (1/16 inch) mesh. Use of 3.2 mm (1/8 inch) sieves is standard practice for the Pacific (Nagaoka 1994, 2005; see Lambrides and Weisler 2016 for a review of screen use in the Pacific), but this screen gauge was not employed at Sabazan. The 1.6 mm fraction from the site, therefore, captures specimens that would otherwise be caught in a 3.2 mm sieve.

Faunal material was returned to the field lab for cleaning, drying, and processing and transported back to the United States and Canada for analysis comprising element and taxon identification, quantification, and description of modifications (e.g., cut marks, burning, pathology). In addition, the differential distribution of elements and taxa across screen-size fractions was recorded. Taxonomic identifications were made employing comparative collections of the Vertebrate Paleontology section of the Royal Ontario Museum (Toronto, Canada), the Fisheries Archaeological Research Centre at McMaster University (Hamilton, Canada) and the Environmental Archaeology Lab of the Florida Museum of Natural History, University of Florida (Gainesville, USA). Specimens were identified to the lowest taxonomic level possible, with some specimens identified to the species level, but most assigned to genus or family (Table 4.1). Small specimens were placed under magnification at 10×–64× to facilitate identification. In the original analysis, parrotfish were assigned to the family Scaridae. Recent revision of parrotfish systematics now places this group as a subfamily (Scarinae) within the wrasse family (Labridae) (Page et al. 2013; Westneat and Alfaro 2005; Westneat et al. 2005). I follow this new nomenclature here, but to preserve analytic resolution I treat parrotfish as distinct from other labrids since their skeletal elements can be easily distinguished from those of other Caribbean wrasses.

The full suite of identified elements includes 55 distinct bones (Table 4.2), although not all of these are diagnostic for all taxa recorded (a list of lowest-level taxonomic identifications achieved for each element appears in Appendix B of Giovas 2013). Following the terminology designated by Wheeler and Jones (2009, pp. 122–124), elements identified come from the neurocranial, branchiocranial, appendicular (pectoral and pelvic girdles), vertebral, and caudal skeleton, with certain scale and fin elements included. Only otoliths were specifically excluded from

Table 4.2 Full list of fish skeletal elements identified to taxon in this study. Fish skeletal areas and regions after Wheeler and Jones (2009). Note that the ultimate vertebra is assigned by some to the caudal skeleton

Skeletal area	Skeletal region	Element
Neurocranium		
	Olfactory	Ethmoid
		Prefontal
		Vomer
	Orbital	Frontal
	Otic	Epiotic
		Exoccipital
		Post-temporal
	Basicranial	Basiocciput
		Parasphenoid
Branchiocranium		
	Oromandibular	Articluar (angular)
		Dentary
		Entopterygoid (mesopterygoid)
		Maxilla
		Palatine
		Premaxilla
		Quadrate
	Hyoid	Basihyal
		Ceratohyal
		Dorsal hypohyal
		Epihyal
		Hyomandibular
		Opercle
		Preopercle
		Ventral hypohyal
	Branchial	Ceratobranchial 5
		Dental plate
		Epibranchial 4
		Hypobranchial 3
		Lower pharyngeal grinder
		Pharyngobranchial 2
		Upper pharyngeal grinder
Appendicular		
		Basipterygium
		Cleithrum
		Coracoid
		Radial
		Scapula
		Supracleithrum

(continued)

Table 4.2 (continued)

Skeletal area	Skeletal region	Element
Vertebral column		
		Anterior vertebra
		1st Anterior vertebra (Atlas)
		2nd Anterior vertebra
		3rd Anterior vertebra
		Posterior vertebra
		Antepenultimate vertebra
		Penultimate vertebra
		Ultimate vertebra (urostyle)
Caudal		
		Hypural
Fins and others		
		1st dorsal spine
		2nd dorsal spine
		Dorsal 1st pterygiophore
		Ventral 1st pterygiophore
		1st pectoral ray
		Buckler
		Burr
		Scale, scute
		Tooth

the analysis due to the fact that these were relatively few (n ≈ 80), and suitable comparative Caribbean specimens to facilitate identification were lacking (most otoliths of museum reference specimens remained trapped within the neurocranium). Subsequent inspection indicates the presence of parrotfish and grunt ototliths among these fishes, which are relatively common in the analyzed assemblage (Giovas 2016a) (Table 4.1).

Several systems for the naming and classification of vertebral elements are employed within zooarchaeological fish analyses (e.g., Cannon 1987; Casteel 1976; Gabriel et al. 2012; Lepiskaar 1983; Wheeler and Jones 2009). These systems are based on an ichthyological understanding of fish anatomy, with reference to both hard and soft tissue characteristics, and can be problematic in zooarchaeological applications due to fragmentation and erosion of the vertebral features required to facilitate classification. Because of this, I employed a modified version of these systems specifically designed to facilitate zooarchaeological identification of vertebrae. In this system, the vertebral column is divided into anterior and posterior portions based on its position with reference to the first vertebra with a fused haemal arch, that is, where the haemapophyses first unite. This specific vertebra is designated as the first posterior vertebra, with all vertebrae preceding it designated as anterior and all vertebrae following it as posterior. The advantage of using this protocol is that even in cases where the parapophyses, haemapophyses, or haemal

spines are broken away from the vertebral centrum—as is frequently the case in archaeofish assemblages—it is usually possible to tell by the morphology of the remaining portion whether vertebrae are anterior or posterior.

This identification method essentially collapses precaudal and caudal vertebrae into one "posterior" category and eliminates the difficulty associated with differentiating late precaudal from early caudal vertebrae when spines and processes are missing. In this study, this approach was easily applied from one fish family to the next without requiring taxon-specific adjustments. Wherever possible, further identifications were made within these anterior and posterior categories to specifically identify vertebral position, e.g., first anterior (atlas), second anterior, third anterior, first posterior, antepenultimate, penultimate, ultimate (urostyle) vertebra, etc. The proatlas was treated as part of the basiocciput, and hypurals were designated separately from vertebrae. As an aside, I note that fish size and biomass reconstructions should ideally employ vertebrae identified to a specific position on the vertebral column, so basic anterior/posterior designations require further refinement (e.g., Lambrides and Weisler 2015) if they are to be used for such applications.

Both NISP and MNI (Grayson 1984; Reitz and Wing 2008) were employed to quantify fish remains. The results reported in this study take into account the differential impact of restricted and expanded analytic element methods on each quantifier. MNI was calculated based on the most abundant element per stratum and trench (arbitrary 10 cm levels within strata were analytically aggregated), taking into account mutually exclusive taxonomic identifications and element portion (e.g., landmarks), side, and size. Using these criteria, MNI was tallied first for the 6.4 mm fraction. The MNI for the 1.6 mm fraction was then assessed based on (1) the repetition of elements used to establish MNI in the 6.4 mm fraction; (2) the presence of elements whose count exceeded the MNI recorded for the 6.4 mm fraction; and (3) the presence of elements belonging to fish whose small size precluded capture in the larger screen (Table 4.3). This strategy eliminated the issue of specimen interdependence across screen size fractions. A hypothetical example illustrates the method: seven, morphologically redundant *Acanthurus* sp. hyomandibulars occur in the 6.4 mm fraction of a context. These are the most frequently occurring element and yield a MNI of seven for the 6.4 mm fraction. If two additional, redundant *Acanthurus* sp. hyomandibulars occur in the 1.6 mm fraction of the same context, these contribute an additional two MNI, with a total MNI of nine for the context. However, if 10 *Acanthurus* sp. atli occur in the 1.6 mm fraction and, based on size, these could reasonably belong to the seven individuals in the 6.4 mm fraction, then the MNI for the 6.4 mm component remains seven and for the 1.6 mm it becomes three, for a total MNI of 10. The MNI tallies recorded in 1.6 mm line items in Table 4.3, therefore, represent individuals not accounted for by material from the 6.4 mm fraction and may be treated independently (i.e., they are additive to the 6.4 mm MNI counts). While this method is not without potential issues, it does segregate quantification of the 6.4 mm sieved component from that of the fine fraction, permitting comparison with assemblages where fine screening was not used. The importance of this will become evident later. Only specimens securely identified to the family level or below are included in this study; fish identified to family with a *confer* designation are excluded.

Table 4.3 Sabazan archaeofish abundance by family and screen size fraction

			Restricted set of elements		Expanded set of elements	
Class	Fish family	Common name	NISP	MNI	NISP	MNI
Elasmobranchii						
	Myliobatidae—6.4 mm	Eagle/Cownose ray	1	1	1	1
	Myliobatidae—1.6 mm		0	0	0	0
	Total Myliobatidae		1	1	1	1
Actinopterygii						
	Acanthuridae—6.4 mm	Surgeonfish	22	13	235	20
	Acanthuridae—1.6 mm		11	3	71	6
	Total Acanthuridae		33	16	306	26
	Balistidae—6.4 mm	Triggerfish	15	5	38	10
	Balistidae—1.6 mm		2	1	3	2
	Total Balistidae		17	6	41	12
	Belonidae—6.4 mm	Needlefish	0	0	3	2
	Belonidae—1.6 mm		0	0	5	2
	Total Belonidae		0	0	8	4
	Carangidae—6.4 mm	Jack, Scad	13	6	60	10
	Carangidae—1.6 mm		10	5	473	85
	Total Carangidae		23	11	533	95
	Chaetodontidae—6.4 mm	Butterflyfish	0	0	0	0
	Chaetodontidae—1.6 mm		0	0	1	1
	Total Chaetodontidae		0	0	1	1
	Clupeidae—6.4 mm	Herring	0	0	0	0
	Clupeidae—1.6 mm		0	0	194	13
	Total Clupeidae		0	0	194	13
	Diodontidae—6.4 mm	Porcupinefish	4	3	4	3
	Diodontidae—1.6 mm		0	0	0	0
	Total Diodontidae		4	3	4	3
	Exocoetidae—6.4 mm	Flyingfish	0	0	2	1
	Exocoetidae—1.6 mm		0	0	10	5
	Total Exocoetidae		0	0	12	6
	Haemulidae—6.4 mm	Grunt	30	11	82	13
	Haemulidae—1.6 mm		8	1	34	7
	Total Haemulidae		38	12	116	20
	Hemiramphidae—6.4 mm	Halfbeak	0	0	0	0
	Hemiramphidae—1.6 mm		0	0	40	7
	Total Hemiramphidae		0	0	40	7
	Holocentridae—6.4 mm	Squirrelfish	3	2	19	5
	Holocentridae—1.6 mm		0	0	15	3
	Total Holocentridae		3	2	34	8
	Labridae (excludes Scarinae)—6.4 mm	Wrasse	14	4	27	8
	Labridae (excludes Scarinae)—1.6 mm		5	2	15	6

(continued)

Table 4.3 (continued)

			Restricted set of elements		Expanded set of elements	
Class	Fish family	Common name	NISP	MNI	NISP	MNI
	Total Labridae (excludes Scarinae)		19	6	42	14
	Labridae: Scarinae—6.4 mm	Parrotfish	307	66	537	68
	Labridae: Scarinae—1.6 mm		51	9	131	9
	Total Labridae, Scarinae		358	75	668	77
	Lutjanidae—6.4 mm	Snapper	8	5	17	8
	Lutjanidae—1.6 mm		3	2	11	2
	Total Lutjanidae		11	7	28	10
	Malacanthidae—6.4 mm	Tilefish	0	0	0	0
	Malacanthidae—1.6 mm		0	0	1	1
	Total Malacanthidae		0	0	1	1
	Mugilidae—6.4 mm	Mullet	0	0	1	1
	Mugilidae—1.6 mm		0	0	0	0
	Total Mugilidae		0	0	1	1
	Mullidae—6.4 mm	Goatfish	0	0	0	0
	Mullidae—1.6 mm		1	1	6	2
	Total Mullidae		1	1	6	2
	Ostraciidae—6.4 mm	Boxfish	0	0	0	0
	Ostraciidae—1.6 mm		4	3	4	3
	Total Ostraciidae		4	3	4	3
	Pomacentridae—6.4 mm	Damselfish	0	0	1	1
	Pomacentridae—1.6 mm		0	0	43	8
	Total Pomacentridae		0	0	44	9
	Sciaenidae—6.4 mm	Weakfish, Croaker	0	0	2	2
	Sciaenidae—1.6 mm		0	0	0	0
	Total Sciaenidae		0	0	2	2
	Scombridae—6.4 mm	Tuna	42	20	730	35
	Scombridae—1.6 mm		1	0	14	0
	Total Scombridae		43	20	744	35
	Serranidae—6.4 mm	Grouper, Seabass	43	14	132	14
	Serranidae—1.6 mm		14	3	40	7
	Total Serranidae		57	17	172	21
	Sphyraenidae—6.4 mm	Barracuda	0	0	1	1
	Sphyraenidae—1.6 mm		0	0	0	0
	Total Sphyraenidae		0	0	1	1
Total all families—6.4 mm			502	150	1892	203
Total all families—1.6 mm			110	30	1111	169
Total all families combined			612	180	3003	372
Richness (n families)			14		24	

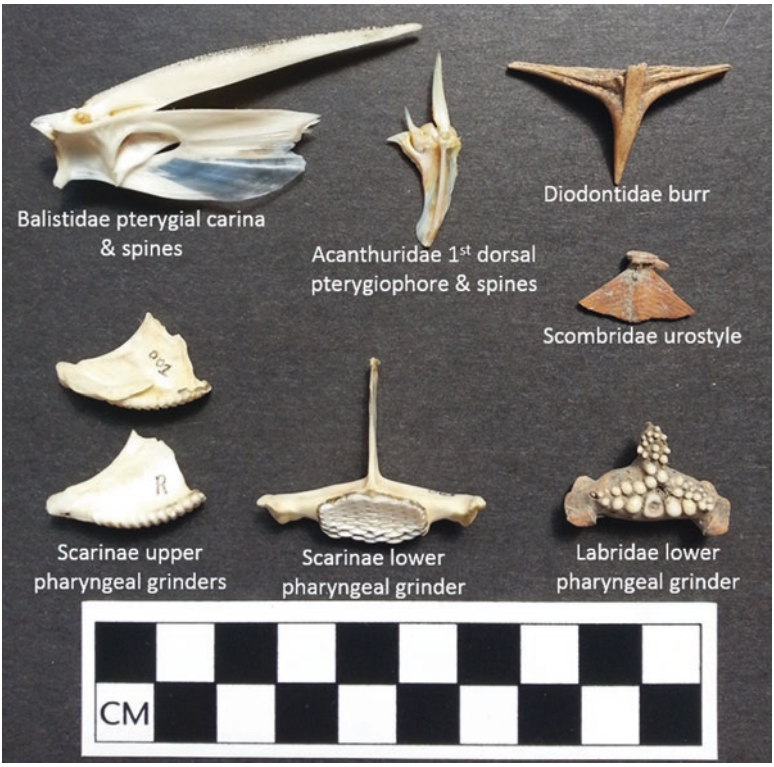

Fig. 4.3 Some designated special elements used in this study. The diodontid, scombrid, and labrid specimens are archaeological

Using these identifications, the fish dataset was then culled to remove all elements except those falling into the restricted set of cranial elements: dentary, maxilla, premaxilla, articular, and quadrate; and those designated as specials: burrs (Diodontidae), scales (Ostraciidae), scutes (bony scales along the lateral line; Carangidae), bucklers (Acanthuridae), dorsal and anal first pterygiophores/interhaemals (Acanthuridae), first and second dorsal spines (Balistidae), upper and lower pharyngeal grinders (Labridae and Scarinae), dental plates and teeth (Elasmobranchii), and ultimate vertebrae (Scombridae) (Fig. 4.3). This last element was included even though Pacific fish studies often exclude vertebrae (see discussions in Lambrides and Weisler 2013, 2015; Ono and Clark 2012; Ono and Intoh 2011; Walter 1998) because Leach (1986) specifically notes the diagnostic nature of the ultimate vertebra (urostyle) of tunas and mackerels. NISP and MNI were then recalculated for this restricted set following the procedure outlined above. Although open for inclusion in the analysis, no elasmobranch vertebral centra were identified. The restricted and expanded assemblages are presented in Table 4.3. For both approaches, NISP and MNI counts have been aggregated at the family level to facilitate comparison and statistical analysis. A detailed discussion of Sabazan's fish assemblage at the lower taxonomic level of analysis is given by Giovas (2013, 2016a, b).

4.4 Results

4.4.1 Richness, Abundance, and Rank

Comparison of the results provided by the restricted and expanded approaches indicates several discrepancies between the two methods. First, the identified assemblage for the expanded analysis is substantially larger than that of the restricted approach, where reliance on just a handful of elements reduces NISP by 80% (NISP = 612 vs. NISP = 3003) and MNI by 52% (MNI = 180 vs. MNI = 372) (Table 4.2). Commensurate with previous findings (e.g., Butler 1994; Lambrides and Weisler 2013; Campbell 2016; Vogel 2005; Weisler 1993), the expanded approach adds to assemblage richness, increasing the number of identified families from 14 to 24. Although not explored here, this increase in taxonomic richness carries implications for assemblage evenness and diversity. Notably, most of the additional taxa are uncommon and many—herrings and sardines (Clupeidae), halfbeaks (Hemiramphidae), needlefish (Belonidae), and flyingfish (Exocoetidae)—share the characteristic of being identified largely on the basis of vertebrae, especially vertebrae captured by finer-gauge mesh (<6.4 mm) (Table 4.4).

Second, there are significant changes in the relative abundance of taxa and substantial alterations in MNI-based rank order abundance (Table 4.5). Scarines and scombrids rank first and second using the restricted approach, accounting for more than half the assemblage as measured by both NISP and MNI. When the full set of identifiable elements is relied upon, these taxa still rank highly—second and third—but the relative abundance of scarines based on NISP falls from 58.5 to 22.2%, and based on MNI falls from 41.7 to 20.7%. The decline in parrotfish MNI-based relative abundance follows from the fact that expanding the set of elements analyzed for this taxon increases MNI by only two individuals. Scombrid MNI declines by less than two percent, but NISP increases dramatically from 7.0 to 24.8%.

The increase in tuna NISP (virtually all of the identified scombrid specimens fall within the tuna tribe, Thunnini) reflects the incorporation of elements such as the basipterygium, hyomandibular, coracoid, ventral hypohyal, opercle, and anterior and posterior vertebrae. These bones are fairly robust and distinctive to tribe, if not genus and species, and tend to be more common in the assemblage than either the articular, dentary, maxilla, premaxilla, or quadrate. The greater abundance of the former elements compared to these five cranials is not unexpected given the relative fragility of these latter elements. In the restricted element approach, scombrid MNI was largely determined by counts of the ultimate vertebra. Using the expanded approach, however, the above-listed elements also contribute to establishing the minimum number of tuna individuals in a given context.

Particularly noteworthy in the disparities between the two methods is the relative rank of Carangidae, the family comprising jacks, scads, pompanos, and runners. Using the restricted element approach, this taxon is low ranking and uncommon (3.8% NISP, 6.1% MNI). The expanded approach elevates these fish to the first rank based on MNI (25.5%) or third rank based on NISP (17.7%). This is primarily due

Table 4.4 The distribution of identified elements across eight taxa possessing small body size and fragile cranial elements in the Sabazan archaeofish assemblage

	6.4 mm fraction identified elements (NISP)		1.6 mm fraction identified elements (NISP)						
Taxon	Opercle	Vertebra	Premaxilla	Maxilla	Hyomandibular	Dorsal hypohyal	Ventral hypohyal	Vertebra	Total NISP
Belonidae	–	3	–	–	–	–	–	5	8
Chaetodontidae	–	–	–	–	–	–	–	1	1
Clupeidae	–	–	–	–	–	–	–	194	194
Exocoetidae	–	2	–	–	–	–	–	10	12
Hemiramphidae	–	–	–	–	–	–	–	40	40
Selar crumenphthalmus	–	2	1	2	1	5	1	85	97
cf. *Selar crumenophthalmus*	–	1	2	1	–	–	–	51	55
Trachurus lathami	–	–	–	–	–	–	–	10	10
cf. *Trachurus lathami*	–	–	–	–	–	–	–	17	17
cf. *Trachurus lathami* or *Selar crumenophthalmus*	–	6	–	–	–	–	–	55	61
Pomacentridae	1	–	–	–	–	–	–	43	44
Total	1	14	3	3	1	5	1	511	539

Table 4.5 Taxon relative abundance and rank based on analysis of restricted and expanded sets of fish skeletal elements

Restricted set of elements						Expanded set of elements					
Family	NISP	% NISP	MNI	% MNI	Rank (MNI)	Family	NISP	% NISP	MNI	% MNI	Rank (MNI)
Labridae: Scarinae	358	58.5	75	41.7	1	Carangidae	533	17.7	95	25.5	1
Scombridae	43	7.0	20	11.1	2	Labridae: Scarinae	668	22.2	77	20.7	2
Serranidae	57	9.3	17	9.4	3	Scombridae	744	24.8	35	9.4	3
Acanthuridae	33	5.4	16	8.9	4	Acanthuridae	306	10.2	26	7.0	4
Haemulidae	38	6.2	12	6.7	5	Serranidae	172	5.7	21	5.6	5
Carangidae	23	3.8	11	6.1	6	Haemulidae	116	3.9	20	5.4	6
Lutjanidae	11	1.8	7	3.9	7	Labridae (excludes Scarinae)	42	1.4	14	3.8	7
Balistidae	17	2.8	6	3.3	8.5	Clupeidae	194	6.5	13	3.5	8
Labridae (excludes Scarinae)	19	3.1	6	3.3	8.5	Balistidae	41	1.4	12	3.2	9
Diodontidae	4	0.7	3	1.7	10.5	Lutjanidae	28	0.9	10	2.7	10
Ostraciidae	4	0.7	3	1.7	10.5	Pomacentridae	44	1.5	9	2.4	11
Holocentridae	3	0.5	2	1.1	12	Holocentridae	34	1.1	8	2.2	12
Mullidae	1	0.2	1	0.6	13.5	Hemiramphidae	40	1.3	7	1.9	13
Myliobatidae	1	0.2	1	0.6	13.5	Exocoetidae	12	0.4	6	1.6	14
Belonidae	–	–	–	–	–	Belonidae	8	0.3	4	1.1	15
Chaetodontidae	–	–	–	–	–	Diodontidae	4	0.1	3	0.8	16.5
Clupeidae	–	–	–	–	–	Ostraciidae	4	0.1	3	0.8	16.5
Exocoetidae	–	–	–	–	–	Mullidae	6	0.2	2	0.5	18.5
Hemiramphidae	–	–	–	–	–	Sciaenidae	2	0.1	2	0.5	18.5
Malacanthidae	–	–	–	–	–	Chaetodontidae	1	0.0	1	0.3	22
Mugilidae	–	–	–	–	–	Malacanthidae	1	0.0	1	0.3	22
Pomacentridae	–	–	–	–	–	Mugilidae	1	0.0	1	0.3	22
Sciaenidae	–	–	–	–	–	Myliobatidae	1	0.0	1	0.3	22
Sphyraenidae	–	–	–	–	–	Sphyraenidae	1	0.0	1	0.3	22
Total	612		180			Total	3003		372		

to the inclusion of vertebrae belonging to two small carangid species, the bigeye scad (*Selar crumenophthalmus*) and the rough scad (*Trachurus lathami*) (Table 4.1). When analysis is restricted to the five cranial and special bones, the presence of these species barely registers. Since the consistently small size of the vertebrae (most derive from the 1.6 mm screen fraction and are <3–4 mm in centrum width) indicates these schooling taxa were likely caught with nets, their omission has significant implications for reconstructing fishing strategies used by pre-Columbian people at Sabazan. I return to this issue in the following section.

Finally, as noted above, changes in taxonomic richness, relative abundance, and rank order are to be expected in comparative assessments of restricted and expanded analytic techniques. It is also clear that some families in this study, such as Acanthuridae, are relatively unaffected by differences in approach (Tables 4.4 and 4.5). In other cases, the differences are not drastic and are not unlike those which might be observed due to a reduction in sample size—where random chance plays a greater role in structuring sample composition, disproportionately impacting relative abundance—or resampling of the same population. In light of this, we should consider whether the restricted and expanded methods produce statistically different quantitative data and if so, whether these differences can be measured to pinpoint the areas of greatest analytic bias.

4.4.2 Chi-Square Tests and Similarity Indices

To address these questions I employed two procedures: (1) chi-square testing using a Monte Carlo approximation of the true significance (*p*-value) based on 200,000 replicates (this mitigates any issue of small sample size and low expected frequencies); and (2) calculation of assemblage similarity using the Morista-Horn similarity index. The Morisita-Horn index is employed in ecological applications to assess the degree of taxonomic overlap between species groups or habitats, taking into account both the taxa present and their abundance (Magurran 1988, pp. 95–96, 2004, pp. 174–175). It is particularly sensitive to the abundances of the most prevalent taxa and is scaled so that sites of absolute similarity return an index value of 1.0. Statistical procedures employed R software, a chi-square Excel macro created by Cannon (n.d.), and a Morisita-Horn similarity index calculator developed by the author.

Chi-square tests were applied to the full, family-level assemblages as quantified by both NISP and MNI using expanded and restricted element sets. Test results indicate that the restricted and expanded analyses differ statistically from each other in their taxonomic composition and abundance data, whether this is quantified by NISP or MNI (Table 4.6). The two methods do not produce the same zooarchaeological information. To quantify the degree to which one measure of abundance might be disproportionately impacted over the other, I used the Morista-Horn index to compare assemblage similarity as quantified by NISP and by MNI. Results reveal that the MNI-based assemblages are more similar to each other than the NISP-based

Table 4.6 Chi-square tests and Morista-Horn similarity indices for restricted and expanded element analyses based on NISP and MNI by screen size fraction

	Combined 6.4 and 1.6 mm fractions		6.4 mm fraction		1.6 mm fraction	
	NISP	MNI	NISP	MNI	NISP	MNI
x^2:	499.70	72.09	277.48	12.06	196.65	46.45
df:	23	23	17	17	18	17
(Monte Carlo) *p*:	<0.001	<0.001	<0.001	0.865	<0.001	<0.001
Morisita-Horn index:	0.637	0.751	0.683	0.965	0.436	0.528

assemblages (Table 4.6). This outcome indicates that analytic reliance on a restricted set of five cranial bones plus special elements tends to bias NISP information more than it does MNI, although both are clearly affected.

The earlier findings for carangids suggest taxonomic quantifications are affected by an interplay between identified elements, particularly vertebrae, and the size of the screen mesh capturing these elements. In the expanded assemblage, 88.7% of carangid NISP and 89.5% of carangid MNI is determined by elements caught in the 1.6 mm fine-gauge screen, whereas in the restricted sample, only 43.5% NISP and 45.5% MNI derives from fine fraction material (Table 4.3). In this study, fish possessing comparatively delicate oromandibular bones tend to be relatively small-bodied. They include the chaetodontids and pomacentrids, which have highly compressed forms and small mouths, as well as the hemiramphids, exocoetids, belonids, clupeids, *S. crumenophthalmus*, and *T. lathami.* While some of these fishes may grow to larger sizes—ca. 30–150 cm total length, depending on species (Carpenter 2002; Smith 1997)—those present in the Sabazan assemblage for the most part come from smaller species or younger individuals. The distribution of elements across screen size shows that the remains of these eight taxa are largely concentrated in the 1.6 mm screen fraction (97.2% of NISP) and primarily identified on the basis of vertebrae (97.4% of NISP) (Table 4.4). Again, this suggests that the independent variables of fish size, bone density, and recovery methods are interacting with the analytic selection of elements to determine the rates of specimen identification and taxon relative abundance. The lower density bones of fish crania have been shown to survive less readily in archaeological contexts than denser post-cranial elements like vertebrae (Butler and Chatters 1994). The eight taxa listed here have characteristically gracile, thin, and even paper-like articulars, dentaries, maxillae, premaxillae, and quadrates that are not expected to survive well in archaeological contexts. Small size may exacerbate density-mediated attrition because, compared to large elements, small ones possess a greater surface area relative to volume for decay processes to act upon. Given that clupeid remains, including oromandibular elements, are highly abundant at northwest North American coastal sites despite their fragility (McKechnie et al. 2014), however, effects of environmental pH, thermal alteration (Lubinski 1996), or butchery methods (Butler 1993; Hoffman et al. 2000) could also explain the paucity of cranial elements for these taxa at Sabazan.

To test whether the restricted method disproportionately excludes elements more likely to be caught in the fine-gauge screen, the restricted-element and expanded-element assemblages were split into 6.4 and 1.6 mm subassemblages. Chi-square tests were then conducted on each of the subassemblages, as quantified by NISP and by MNI. Results confirm the differential impact of methodologies across screen size and quantifier (Table 4.6). The 1.6 mm subassemblages are statistically different, whether quantified by NISP or MNI. The 6.4 mm subassemblages also differ significantly from each other based on NISP, but interestingly not as measured by MNI. In other words, an analyst employing the restricted element approach, looking at only the 6.4 mm fraction and concerned with only MNI, can expect to obtain the same results as she/he would by relying on all identifiable elements, at least for assemblages with a taxonomic composition similar to this study. The sample size in such a case would be smaller, with implications for further quantitative applications, but both approaches would provide comparable information on richness and relative abundance.

The Morisita-Horn index quantifies the similarity between subassemblages (Table 4.6). Index values of 0.683 and 0.436 for the NISP-based 6.4 mm and 1.6 mm subassemblage, respectively, indicate the two identification methods produce different results. The lower index value for the 1.6 mm fraction supports the interpretation that these disparities have a greater impact on NISP in the finer-gauge screen. Chi-square adjusted residuals reveal statistically significant increases in the abundance of clupeids, hemiramphids, pomacentrids, and small carangids, as anticipated above. Belonids, chaetodontids, and exocoetids all increase as well, but sample sizes for these families were too small to yield statistically significant findings (Table 4.7).

Morisita-Horn values for the MNI-based subassemblages tell a different story. The high index value for the 6.4 mm subassemblage (0.965) reveals that here the restricted and expanded methodologies produce virtually identical results in terms of taxonomic composition and abundance, corroborating the insignificant chi-square statistic. The low index value for the 1.6 mm subassemblages (0.528), on the other hand, highlights how the restricted element approach biases against the identification and quantification of fish elements that tend to be captured by fine-gauge screens. The restricted method preforms only marginally better here than for NISP quantifications of the 1.6 mm subassemblage.

One final important observation is warranted with respect to economically important taxa, that is, those contributing more than 5% to relative abundance (Carangidae, Scarinae, Scombridae, Acanthuridae, Serranidae, and Haemulidae). Standardized adjusted residuals for the six chi-square tests were calculated to determine which taxa exhibited significant changes in relative abundance when additional elements were analyzed. Table 4.7 lists each chi-square test as a column. Taxa with statistically significant adjusted residuals appear in bold font, indicating where significant changes in relative abundance were detected (adjusted residuals $\geq +1.96$ or ≤ -1.96, corresponding to a p-value of ≤ 0.05). The sign preceding the taxon name indicates whether a significant increase (+) or decrease (−) in abundance was recorded when an expanded set of elements was used in analysis. Results reveal that

Table 4.7 Taxa that experience statistically significant changes in relative abundance when an expanded set of elements is analyzed, based on adjusted residuals for the chi-square tests in Table 4.6 (adjusted residuals ≥1.96 or ≤−1.96, corresponding to a *p*-value of ≤0.05). Each column represents a designated chi-square test between datasets produced by the restricted and expanded analytic methods. All chi-square tests are significant ($p < 0.05$), except that for the 6.4 mm fraction with quantification based on MNI. Taxa with statistically significant alterations in abundance appear in bold font. The + or − sign indicates the direction of the change in abundance with the expansion of elements analyzed. Labridae excludes the subfamily Scarinae, which was tested separately

6.4 and 1.6 mm fractions	6.4 and 1.6 mm fractions	6.4 mm fraction	6.4 mm fraction	1.6 mm fraction	1.6 mm fraction
NISP	MNI	NISP	MNI	NISP	MNI
Acanthuridae (+3.711)	Acanthuridae (−0.789)	**Acanthuridae (+5.172)**	Acanthuridae (+0.378)	Acanthuridae (−1.443)	Acanthuridae (−1.567)
Balistidae (−2.535)	Balistidae (−0.067)	Balistidae (−1.326)	Balistidae (+0.733)	**Balistidae (−2.425)**	Balistidae (−0.891)
Belonidae (+1.278)	Belonidae (+1.396)	Belonidae (+0.893)	Belonidae (+1.219)	Belonidae (+0.705)	Belonidae (+0.599)
Carangidae (+8.744)	**Carangidae (+5.432)**	Carangidae (+0.674)	Carangidae (+0.413)	**Carangidae (+6.851)**	**Carangidae (+3.410)**
Chaetodontidae (0.452)	Chaetodontidae (+0.696)	–	–	Chaetodontidae (+0.315)	Chaetodontidae (0.422)
Clupeidae (+6.464)	**Clupeidae (+2.538)**	–	–	**Clupeidae (+4.779)**	Clupeidae (+1.571)
Diodontidae (−2.497)	Diodontidae (−0.914)	**Diodontidae (−2.020)**	Diodontidae (−0.375)	–	–
Exocoetidae (+1.566)	Exocoetidae (+1.713)	Exocoetidae (+0.729)	Exocoetidae (+0.861)	Exocoetidae (+0.999)	Exocoetidae (+0.954)
Haemulidae (−2.620)	Haemulidae (−0.608)	Haemulidae (−1.549)	Haemulidae (−0.343)	**Haemulidae (−2.312)**	Haemulidae (+0.208)
Hemiramphidae (+2.871)	Hemiramphidae (+1.852)	–	–	**Hemiramphidae (+2.023)**	Hemiramphidae (+1.135)
Holocentridae (+1.438)	Holocentridae (+0.858)	Holocentridae (+0.849)	Holocentridae (+0.753)	Holocentridae (+1.226)	Holocentridae (+0.735)
Labridae (−2.986)	Labridae (+0.254)	**Labridae (−2.091)**	Labridae (+0.653)	**Labridae (−2.518)**	Labridae (−0.801)
Labridae: Scarinae (−18.130)	**Labridae: Scarinae (−5.170)**	**Labridae: Scarinae (−13.663)**	Labridae: Scarinae (−2.010)	**Labridae: Scarinae (−9.712)**	**Labridae: Scarinae (−4.342)**
Lutjanidae (−1.888)	Lutjanidae (−0.765)	Lutjanidae (−1.362)	Lutjanidae (+0.300)	Lutjanidae (−1.632)	**Lutjanidae (−1.972)**
Malacanthidae (+0.452)	Malacanthidae (+0.696)	–	–	Malacanthidae (+0.315)	Malacanthidae (0.422)
Mugilidae (+0.452)	Mugilidae (+0.696)	Mugilidae (+0.515)	Mugilidae (+0.861)	–	–
Mullidae (+0.187)	Mullidae (−0.027)	–	–	Mullidae (−0.489)	Mullidae (−0.891)
Myliobatidae (−1.247)	Myliobatidae (−0.526)	Myliobatidae (−1.009)	Myliobatidae (−0.215)	–	–
Ostraciidae (−2.497)	Ostraciidae (−0.914)	–	–	**Ostraciidae (−4.063)**	**Ostraciidae (−2.428)**
Pomacentridae (+3.013)	**Pomacentridae (+2.104)**	Pomacentridae (+0.515)	Pomacentridae (+0.861)	**Pomacentridae (+2.101)**	Pomacentridae (−1.216)
Sciaenidae (+06.39)	Sciaenidae (+0.986)	Sciaenidae (0.729)	Sciaenidae (+1.219)	–	–
Scombridae (+9.697)	Scombridae (−0.626)	**Scombridae (+12.876)**	Scombridae (+1.001)	Scombridae (+0.319)	–
Serranidae (−3.319)	Serranidae (−1.653)	Serranidae (−1.216)	Serranidae (−0.837)	**Serranidae (−4.441)**	Serranidae (−1.353)
Sphyraenidae (+0.452)	Sphyraenidae (+0.696)	Sphyraenidae (+0.515)	Sphyraenidae (+0.861)	–	–

the restricted element method consistently fails to represent economically important taxa in a similar manner as an expanded analytic approach, irrespective of whether these are quantified by NISP or MNI. Ten taxa show no significant changes with expanded analysis: Belonidae, Chaetodontidae, Exocoetidae, Holocentridae, Malacanthidae, Mugilidae, Mullidae, Myliobatidae, Sciaenidae, and Sphyraenidae; but all of these are comparatively rare, suggesting these results may be due in part to sample size effects. I discuss the implications of the collective results below.

4.5 Discussion

The intellectual context in which the restricted approach to fish analysis developed is important to bear in mind. As discussed previously, the method was pursued in the belief that it standardized analytic units (i.e., skeletal elements examined) across fish taxa, allowing for equitable comparison of relative abundances. In the context in which this method was initially implemented, using New Zealand fish assemblages during an era when fine-screening was not regularly employed, the restricted element method may have come close to doing this in some cases. But the approach has been widely applied beyond this context, sometimes uncritically so, and as previous critiques (Butler 1994; Campbell 2016; Lambrides and Weisler 2013; Ono and Clark 2012; Ono and Intoh 2011; Vogel 2005; Whyte et al. 2005) have suggested, the method does not perform as originally intended.

This investigation confirms that the use of a restricted set of elements in archaeofish analysis generates taxonomic information that differs from analysis employing all available diagnostic bones. Importantly, it builds on the studies cited above by demonstrating that these differences are statistically significant and do not occur as a consequence of sample size effects created by increasing NISP and MNI with expanded analysis. Results presented here, moreover, show that the discrepancies produced by the restricted element method do not occur uniformly across taxa or screen size. Some taxa, like acanthurids, are appropriately quantified by a restricted approach (in absolute, but not relative abundance), while others, such as small carangids, are not. Overall bias is greatest for that component of the fish assemblage captured by the fine mesh (1.6 mm) screen and greater when abundances are measured by NISP compared to MNI.

There are two underlying effects driving these results. The fact that bias is consistently greater for NISP than MNI is a predictable outcome for comparisons that involve a derived measurement. MNI is calculated from identified specimens and thus will always be equal to or less than NISP. Because of this, the degree of difference between the two analytic approaches will always be less when using MNI as a quantifier than when using NISP (except when there is a one to one relationship between NISP and MNI). There is an additional layer of complexity to this effect. The restricted element method essentially alters the relationship between NISP and MNI by changing the rate at which MNI is added for a given increment of NISP. The magnitude of this effect varies among taxa, which is what causes the observed changes in relative abundance when the two analytic methods are contrasted.

Clearly the restricted element method has a differential impact across fish families. Disparities are driven by the particular skeletal characteristics of the taxa in the assemblage, the size of specimens, and whether a given element belongs to the restricted set of cranial and special bones. Due to this, even in cases where the restricted method provides NISP or MNI values for a taxon that are identical to those of an expanded approach, *relative* abundance for that taxon may still be skewed because other taxa may have been differentially quantified. As a result, economic importance will be overemphasized for some taxa and diminished for others. This is precisely the scenario Leach (1986, 1997) was attempting to avoid by restricting analysis to a few, select elements, and it carries implications for reconstructions of fishing strategies and habitat exploitation, as well as broader, comparative syntheses.

Much of the bias observed in this study is against small fish identified by vertebrae caught in the 1.6 mm screen, i.e., hemiramphids, *T. lathami*, *S. crumenophthalmus*, clupeids, and possibly exocoetids. In addition, while the majority of identified elements for tuna derive from the 6.4 mm component, undercounting of this fish family is also evident. In this case, however, it is not screen size, but the inclusion of ultimate vertebrae among the set of special elements that leads to the degree of positive identification of tuna specimens when the restricted method is used. Undercounting of tuna would have been more pronounced in this study if ultimate vertebrae not been taken into account—tuna would have all but disappeared from the assemblage. Scombridae, Exocoetidae*, T. lathami* and certain hemiramphid and clupeid taxa are coastal pelagic and/or offshore pelagic fishes. Had a restricted method been relied upon in the original archaeofish analysis, the strong emphasis on pelagic fishing evident at the Sabazan site would have been lessened. For the Caribbean, this would be a significant loss to our understanding of marine exploitation by pre-Columbian peoples. Sites exhibiting high levels of tuna exploitation are relatively uncommon (e.g., Carder et al. 2007; Giovas 2016a, b; Newsom and Wing 2004; Steadman and Jones 2006). The instances where they do occur may have to do with conditions of coastal bathymetry that allowed pre-Columbian peoples to easily access migrating tuna stocks when they come closer to shore at certain times of the year (Collette 2002; Taquet et al. 2002).

A similar bias is seen in the reconstruction of fishing strategies. Smaller, schooling taxa, such as clupeids, *T. lathami*, and *S. crumenophthalmus,* were undoubtedly caught using nets, as indicated by the small size and relatively standard width of anterior vertebrae and atli (LeFebvre 2007). The limited ability of the restricted element method to detect these taxa means that inferences about prehistoric Caribbean fishing would have instead been based on the remaining fishes in the assemblage. These are ones which ethnohistorically were taken through a combination of traps, hook-and-line techniques, and fish poison, among other methods (Keegan 1986; Newsom and Wing 2004). Reliance on a restricted set of elements in this case would have diminished the prehistoric importance of net fishing, at least for the Caribbean, and insight into a key maritime adaption would be have been lost.

One final concern raised by archaeologists such as Vogel (2005) and Lambrides and Weisler (2013) is that heavy reliance on the restricted approach in earlier decades problematizes wider syntheses examining regional variation in fishing strategies, the socio-economic importance of fishing activities, and anthropogenic

environmental impacts. This study offers some hope on that front. The findings suggest that at the 6.4 mm analytic level, a restricted approach based on MNI can provide results that are representative of those which would have been obtained by analyzing a wider set of elements (assuming taxonomic composition similar to that recorded here). For the many older studies based on faunal material that was not fine screened, it is possible to compare data from different contexts at this analytic level (assuming all material from coarse screening was retained for analysis). This comparison should be accompanied by the understanding that while the samples involved may be analytically comparable, they may still not be representative of the overall zooarchaeological population since the lack of fine screening has likely resulted in lower taxonomic richness (Cannon 1999; Gobalet 2005; Gordon 1993; James 1997; Nagaoka 1994, 2005; Zohar and Belmaker 2005).

4.6 Conclusion

Employing zooarchaeological data from the Caribbean site of Sabazan, this chapter has used a quantitative approach to comparatively evaluate a method of restricted archaeofish analysis against the practice of analyzing most or all possible diagnostic elements. Results indicate analysis that is restricted to the five cranial and "special" bones yields taxonomic and abundance information inherently different from that produced when using all identifiable fish elements. This study confirms previous research showing discrepancies in rank order abundance, relative abundance, and taxonomic richness when limiting analysis to a small set of elements. Beyond this, it demonstrates that these discrepancies are statistically significant and cannot be explained by sample size effects alone.

Similarity indices and chi-square testing used to localize biases by taxon, quantifier, and screen fraction, demonstrate that the greatest disparities between approaches are associated with NISP-based assemblages and small taxa whose elements are caught in fine-gauge screen. Overall, the tests conducted here suggest the restricted element approach does not yield results comparable to the zooarchaeological information provided by an expanded method, except under very special circumstances. In the context of the Caribbean study site, Sabazan, the restricted method leads to mistaken interpretations of marine habitat exploitation and incomplete reconstructions of fishing technology and diet of pre-Columbian peoples. In light of these findings, I recommend that zooarchaeologists analyze all potentially diagnostic skeletal elements, given the resources on hand and study-specific constraints, as has been practiced by some Pacific analysts for a number of years (e.g., Campbell 2016, Lambrides and Weisler 2013, 2015; Ono and Clark 2012; Ono and Intoh 2011; Vogel 2005; Vogel and Anderson 2012; Weisler 1993; Weisler and Green 2013; Weisler et al. 2010). Archaeofish studies, especially comparative investigations, might also benefit from researchers stating explicitly which elements were used to identify each taxon (e.g., Giovas 2013, Appendix B; Walter 1998, Tables 6.2 and 6.3; Weisler and Green 2013, Table 1). Although the lists generated by this undertaking may be extensive, the ability to publish this information as online supplements

makes the practice feasible. These data may help to advance archaeofish methodology not only by documenting which elements are diagnostic to which fish at which taxonomic level, but also by clarifying whether variation observed among assemblages is truly due to differences in fish representation or simply differences in analytic protocols.

A final note is warranted with regard to such constraints. This chapter began by considering the competing demands zooarchaeologists face when conducting analyses. Faunal analysis is often time-consuming, and the challenges zooarchaeologists encounter in this context, particularly those of schedule and budget, are very real. These frequently manifest as a trade-off between analyzing a large volume of faunal material in a less comprehensive manner or analyzing fewer specimens more comprehensively. The latter scenario may also impose requirements for additional analytic expertise. Professionals working in the cultural resource management sector, in particular, may be constrained by legislative standards and the willingness of the client to fund extended analysis. While it might be tempting to label expedient methodologies as slap-dash shortcuts and dismiss these outright, we should resist the urge to do so. Methodological advancement in zooarchaeology should be inclusive of more efficient methods that allow practitioners to tackle additional assemblages, ask more questions, and explore bigger ideas. At the same time, however, it is incumbent upon zooarchaeologists to weigh these approaches critically and ensure that such methods produce reliable, sound results before embracing them.

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Part II
Beyond Quantification: Taphonomy, Fragmentation, and Assemblage Size

Chapter 5
Bone Taphonomy in Deep Urban Stratigraphy: Case Studies from York, United Kingdom

Clare Rainsford and Terry O'Connor

5.1 Background

One of the many practical challenges that zooarchaeology has to face is understanding the taphonomy of excavated assemblages. It is quite obvious that the circumstances of formation of the excavated assemblage, and the range of processes that have acted between the death of the animals concerned and the point of analysis, will have amended the characteristics of the assemblage, possibly to the point of occluding any trace of the original human activities (Lyman 1994; Stahl 2014). This is a challenge for any research in zooarchaeology or Quaternary paleontology. In this paper, we explore a particular set of circumstances: the taphonomy of bone assemblages from deep stratigraphy associated with past habitation at urban densities.

Urbanization has come to most parts of the world, though in many it is a comparatively recent adaptation. Southwest Asia has early towns and just a few, most obviously Jericho, show prolonged continuity of occupation. More often, as at Çatalhöyük or Tel-e Malyan, urban density of occupation has long since ceased. Compared to Southwest Asia, urbanization came late to northern Europe, though many towns have a long record of continuous occupation (Barley 1977; Hodges and Hobley 1988; Holt and Rosser 2014). In some, such as Köln or London, the modern city has its origins in a town established during the period of Roman urbanization of Europe, and that center has continued to be the focus of settlement. In others such as Warsaw and Aarhus, the origins are of early medieval date, usually from the eighth to tenth centuries CE (Callmer 2007). Whatever the origin, these sites tend to have in common high densities of structures and people, with areas of open ground

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being localized and often short-lived (Magnusson 2013; Święta-Musznicka et al. 2013). As a consequence, each generation lived and worked on the debris of its predecessors, much as in the familiar Middle Eastern *tel* mounds, though European towns generally lack the high input of degraded mudbrick that constitutes such a high proportion of *tel* stratigraphy. More commonly, the stratigraphy combines building debris, ranging from timber and thatch to stone and plaster, with occupation debris, including food and other animal-processing wastes, residue from craft and industrial processes, and human and other animal feces. The fine matrix, though seldom investigated, typically combines components of the local subsurface geology (often alluvial or glaciofluvial in origin) with weathering products of inorganic structures (Lehmann and Stahr 2007). In sedimentary terms, urban archaeological stratigraphy in northern Europe ranges from porous, clast-supported rubble to dense, matrix-supported and highly-organic muds. As the lithology tends towards the latter, the generally temperate and humid climate of the region leads to low rates of organic decay, and organic-rich sediments will tend to hold a high proportion of stagnant pore-water, thus further reducing the rate and extent of decay in a fascinating positive feedback loop (e.g., Kenward and Hall 1995).

The geochemistry of these urban sediments, and thus their potential for bone degradation, is highly variable and generalizations are hazardous. That said, the conditions most inimical to bone preservation, i.e., low pH combined with rapid or 'flushing' drainage of pore-water, are rarely encountered (Hedges 2002; Hollund et al. 2013). Low pH is most likely to occur through circumstances of formation that are unlikely in an urban context, such as the accumulation of *Sphagnum* peats, or through prolonged decalcification of a porous sediment by the through-flow of mildly acidic meteoric water. This, too, is unlikely in urban deposition simply because the density and dynamism of urban living prevents the stability that *in situ* decalcification requires. Furthermore, people contribute materials such as plaster, mortar and ash, which are likely to raise the local pH. Given the tendency for urban settlement in Europe to be in river valleys, the inorganic matrix is likely to be fine-grained. Coupled with low topographical relief and, often, enhanced organic content, most urban sediments are unlikely to drain rapidly. In short, urban sediments often predispose good preservation of buried bones. Add to that a high density of population utilizing animal carcasses in many ways, and it is little surprise that the historic towns of northern Europe have yielded considerable quantities of excavated animal bones (e.g., O'Connor 2010; Rainsford et al. 2014).

These large assemblages obviously have great potential in terms of inferring past human activities. At a broad scale, they offer large samples of livestock, reflecting decision-making in the surrounding pastoral hinterland and the marketing processes by which animals entered the urban system. At a finer scale, the assemblages have the potential to reflect very local activities; the debris from a single meal, debitage from bone-working, the burial of a companion animal. However, that level of detail will only persist in the archaeological record if pre- and post-depositional impacts on the original assemblage have been minimal. Here we consider the three main stages of the taphonomic trajectory faced by bones in urban deposits: pre-deposition, in-ground diagenesis, and post-deposition. For each stage, examples are used to

show important aspects of bone taphonomy that can contribute to zooarchaeological interpretation. Obviously, many of these factors are shared by bone assemblages in any archaeological sediment, and we have focused on those that are particularly characteristic of urban depositional and diagenetic environments. Examples are mostly from our first-hand experience in York, UK, particularly at the recent Hungate excavation (Rainsford et al. 2014). At the time of writing, results from Hungate are in the process of preparation for publication. This, and most other sites mentioned here, were excavated by York Archaeological Trust.

5.2 Pre-Deposition

By the time that an animal is slaughtered, decisions will already have been made regarding the disposition of its remains. In the urban context, with close co-location of butchers and craftworkers in various carcass products, those decisions are likely to have been a mutually-contingent web of needs and compromises (Smith 2010; Yeomans 2007). The consequence will have been a sequence of processes, beginning with the slaughter and primary butchering (i.e., skinning and gutting, removing lowest-value parts) of the beast, and ending when the last traces have been deposited as refuse or have reached their functional end-point. Each process has three nodes: an input, a product, and a waste. Either the product or the waste may become the input of another process (O'Connor 1993). For example, suppose that a sheep is slaughtered and skinned. The feet are initially left on the hide to serve as useful 'handles' during the early stages of processing. After the initial shaving and defatting, the feet are not necessary and are cut off—they become waste, and may be deposited at that point. Several sites in York have yielded deposits of sheep feet, i.e., of phalanges and metapodials found together (O'Connor 1984a), which are likely to represent the results of this process. However, the metapodials are also useful material for small artifacts, such as knife and other handles, and so may have become input to a craft process. Bearing in mind that we are dealing with fresh bone, including marrow and fat, it is not unlikely that stock-piled material became putrefying and unusable at times, leading to deposition of metapodial assemblages *without* phalanges. All of these different deposited assemblages have been recognized in medieval and later deposits in York, including the 'dressed' lamb carcasses that were the product of the original primary butchering process. (Bond and O'Connor 1999, pp. 368–369; O'Connor 1984b) The point is that intensive utilization of animal carcasses by different workers in close juxtaposition within the town will lead to the deposition of a number of different and highly characteristic assemblages from different stages in the unmaking of carcasses (Fig. 5.1).

Some deposition will have been local to the point of its generation, so a horners' quarter within the town may show a concentration of deposits with the characteristic waste of horncores and frontalia. Just such a quarter exists in York for the late twelfth to thirteenth century, located 100 m or so north of the Hungate site (Bond and O'Connor 1999, pp. 380, 410). The exciting possibility of locating specific

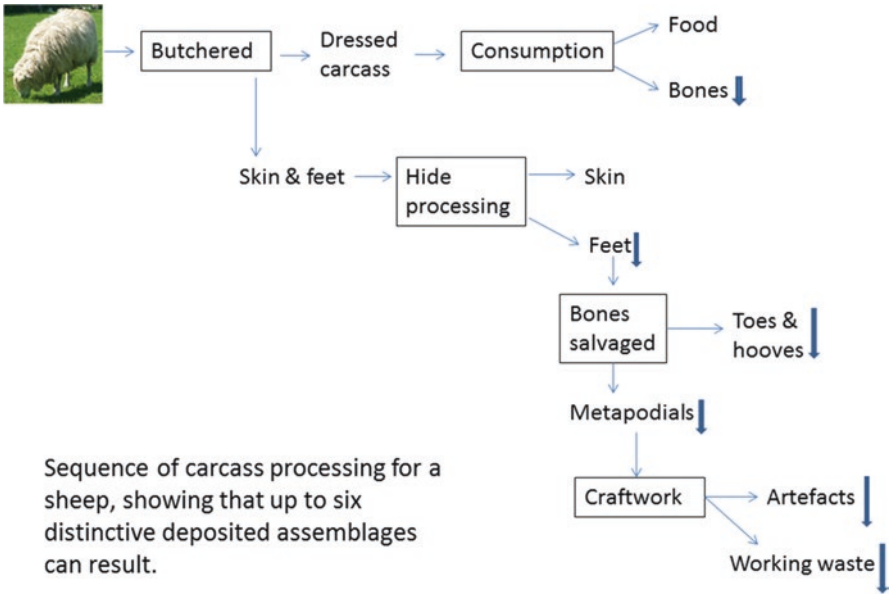

Fig. 5.1 Postulated sequence of carcass processing for a sheep, showing that up to six distinctive deposited assemblages can result

activity areas is complicated by the need for an urban community to manage their refuse deposition. Urban histories in England and elsewhere in Europe are rife with ordnances and appeals to butchers' better natures, all attempting to limit noxious wastes to specific areas, often a riverside or convenient brownland (Evans 2010; Sabine 1937). It is no surprise, therefore, that the Hungate site produced a number of assemblages with abundant cattle and goat horncores, contemporary with the nearby horners' quarter. Detailed measurement of the goat horncores shows that they are indistinguishable from those found nearby, and they are butchered off the skulls in the same way, confirming that at least some of the horners' waste was removed from the immediate vicinity of workshops and deposited on nearby land in which numerous refuse pits were being dug and filled.

On occasion, deposits can be identified as consisting of waste deriving from household or consumer sources which has been disposed of locally, either within the property bounds or on waste ground in the vicinity. One example of this is a currently unpublished assemblage from make-up and construction levels under a late nineteenth/early twentieth century yard from a wealthy household close to York Minster (7 Minster Yard). The bones from this assemblage were taxonomically diverse, representing ribs and vertebrae from sheep and pig (i.e., chops and chine), chicken (*Gallus gallus*), rabbit (*Oryctolagus cuniculus*), turkey (*Meleagris gallopavo*), and a substantial assemblage of game birds, including swan (*Cygnus* sp.), tufted duck (*Aythya fuligula*), teal duck (*Anas crecca*), partridge (*Perdix perdix*), red grouse (*Lagopus lagopus*), sandpiper (small Scolopacidae), and woodcock (*Scolopax rusticola*). This is consistent with

a high-status late eighteenth/nineteenth century diet, and if it is impossible to be certain that the material came from 7 Minster Yard itself, it is highly likely to derive from the area. Assemblages like this, which are both temporally and spatially precise, have immense potential to provide information regarding diet across time and how known variations in wealth affect consumption practices in different areas of the city. Assemblages with such a particular catchment are rare in any archaeological context, but most especially in urban settings where the need for organized refuse disposal is likely to accentuate spatial-averaging, and intensive occupation over many generations increases the probability of resedimentation. Equally, it is rare that an assemblage which appears to be precise both temporally and spatially represents the results of only one depositional process. Open areas where rubbish can be deposited are restricted in urban settings, particularly so following urban expansion with increasing industrialization in the eighteenth century, so potential deposition sites are typically used for multiple waste products. One instance is from late nineteenth century Hungate, where a large pit created by robbing of a wall contained consumption waste (hare, chicken, rabbit), companion animals (adult and juvenile dogs), and the trimmings of sea fish (heads and tail), which may derive from a local fried fish shop recorded in the area. These are all consistent with activities in the local area, conceivably within the same household, but clearly show several different *processes* contributing to a single archaeological deposit.

Urban areas were not only inhabited by humans, and urban bone assemblages can sometimes demonstrate the pre-depositional activities of scavengers. Cats, dogs, and various species of rodent (rat (black, and latterly brown), mouse, vole) were all common sights within the medieval urban environment, and modification of bone by gnawing is frequently recognizable within assemblages. On rare occasions, bone may be accumulated almost entirely by non-human agency. A section of a nineteenth century gasworks excavated at Hungate yielded a very small faunal assemblage compared to elsewhere on the site. A number of the elements recovered were from small taxa (chicken and rabbit) and displayed evidence of rat gnawing and, in one instance, cat toothmarks. It appears probable that this area was predominantly kept free of refuse but, as a relatively secluded area at night, would have been an attractive refuge for rats and nocturnal predators.

It is clear from the above that urban bone assemblages are formed and affected by a myriad of pre- depositional processes, and disentangling these is an essential step to recognizing the information potential of an assemblage. However, this is further complicated for the simple reason that each generation lives on the same small patch of land on which the predominant land surface deposits are the refuse and ejectamenta of previous generations. Whenever people dug new refuse or latrine pits, old refuse was recycled to the surface, some of it to be buried again as residual or redeposited material within a new context. This perthotaxic recycling is likely to have been unfavorable to the long-term survival of organic materials, as it represents a repeated disruption of the equilibriation process, challenging the material with a new geochemical environment, one that would at least initially have been subaerial (Rosell et al. 2014; Sorg et al. 2012). Bone is amongst the most robust of organic debris, so is likely to have survived cycles of exposure and reburial, although it is

also likely that these processes would rapidly have depleted the amount of old bone undergoing recycling. Assemblages containing residual material are frequently recognizable owing to their diverse diagenetic condition, which is visible as variation in coloration, mineral deposition, or surface condition (see below). Having made due allowance for inherent susceptibilities of, for example, immature versus mature or cortical versus cancellous bone, that diversity will be a consequence not only of the differing post-mortem intervals involved, but also because an old and partially-degraded bone redeposited into a new context is likely to respond differently to that geochemical environment than a freshly-deposited bone.

5.3 In-Ground Diagenesis

We have already mentioned some of the factors in urban archaeological lithology: highly variable clast size and sorting, highly variable organic content, and only early-stage pedogenesis. It is rare to encounter soils *sensu stricto* in urban archaeology, though some slightly weathered deposits could be classed as entisols. Urban refuse deposits were often high in nitrogen and phosphates, in particular derived from body wastes, and more likely to be of high, rather than low, pH. The principal factor driving bone degradation, therefore, will be the movement of pore-water and its consequent inhibition of equilibriation between buried bones and their matrix.

At one extreme, we see open-textured and clast-supported deposits, for example of brick, tile, and other mineral building debris, with rapid flow-through of water and ample oxygen both dissolved in pore-water and as gas within pore spaces. In these circumstances, it is commonly the case that the organic phase of bones has preferentially degraded, the collagen being more susceptible to degradation than bioapatite. In fact, the mineral and organic phases convey a degree of mutual protection, and bone degradation will always involve both phases, even if to differing degrees (Collins et al. 2002; Smith et al. 2007). In the conditions considered here, although the collagen is preferentially destroyed, the surviving mineral phase is often also heavily altered, with recrystallization of bioapatite (Trueman et al. 2008) and secondary formation of brushite, calcite, aragonite, and other phosphate and carbonate minerals (Natali et al. 2014). The outcome on excavation is bone that retains much of its surface integrity and overall morphology, and which may appear to be well preserved. It is typically yellow to pale brown in color, indicating only minor surface deposition of iron minerals. On closer examination, the bone tissue is friable, often distinctly white rather than cream or brown, and it can be crumbled by use of the thumbnail. This diagenetic end-point is often described as 'chalky', a term that describes it well. Chalky bone stores well if allowed to air-dry slowly then packed to minimize abrasion and direct impact. In the absence of careful handling and packing, it readily becomes a mass of brittle fragments.

At the other extreme lie the distinctive organic deposits, usually based on a silt- to clay-grade mineral matrix, with a very high humic content, indicated by weight-loss-on-ignition in the range 20–40%, and a correspondingly high water content (for

example, Kenward and Hall 1995, pp. 634–635, 717–721). Water flow-through has been negligible through the life of these deposits, and they have rapidly become deoxygenated. Bone in such a matrix has the potential to reach a stable equilibrium quite rapidly, especially if, as is often the case, bones are the predominant or only large clast in the sediment. In these circumstances, the mineral-organic composite of bone is highly stable. Porosity tests of bone buried for many centuries indicate minimal disruption of the nano-structure, and collagen fibrils are readily recovered in excellent condition (Nielsen-Marsh and Hedges 1999). On excavation, the bone is hard and resilient and often dark brown in color. The characteristic coloring derives from deposition of predominantly iron compounds in the surface millimeter or so of bone, at least some of it probably in humin complexes (high molecular weight components of soil humus that are insoluble and often complexed with metal ions) (Dupras and Schultz 2013, pp. 323–325). Depending on the specific geochemistry of the deposit, there may be secondary crystallization of iron pyrite (FeS_2) or vivianite ($Fe.Fe_2(PO_4)_2.8H_2O$) (McGowan and Prangnell 2006). The possibility that burial in a high-iron environment inhibits microbial damage to the bones deserves further investigation (Müller et al. 2011). Bone in this condition, hereafter 'dark' bone for descriptive convenience, is very robust and will store well following air-drying. That does not mean it is stable in perpetuity, however. Observation of dark bones in store in York over a 30-year period, although anecdotal not systematic, show some lightening of color, suggesting that humins may be degrading in dry, oxygen-rich conditions. To date, this has not been further investigated, though it would be anticipated that color change indicative of superficial oxidation would indicate degradation of biomolecular content.

Those are the extremes, and most urban sediments lie somewhere between. It is no surprise, then, that many excavated assemblages tend towards one or other of those end-points. The informative cases are those that do not. Locally exceptional conditions may arise, for example, where bones have been deposited into a structure or feature previously used for some distinctive purpose. At Hungate, several groups of bones were recovered from a sixteenth century brick structure used to mix lime mortar. Bone recovered from within or adjacent to "use" deposits, containing substantial amounts of mortar, was in good, if mortar-encrusted, condition. In several cases, mortar appeared to have permeated at least the macro-scale porosity of the bone fragments. Preservation conditions were exceptionally good in the backfilling layers above the mortar deposits, with bone appearing fresh, and large and fragile elements (e.g., half a sheep cranium; goose tracheal rings) being preserved complete. The unusual composition of these backfilling deposits, with one containing several elements of a single butchered sheep and another containing a small collection of bird bones, indicates that these were rapid events where a discrete collection of fresh rubbish was included with the backfilling soil.

Where bones have been deposited into wet sediments rich in phosphates, such as an active latrine pit, mineralisation of the adjacent sediment may occur through calcium phosphate deposition, preserving evidence of the sediment matrix as a crust on the surface of the bone (Fig. 5.2). Unusual states of bone preservation may also show circumstances where changes in local or regional drainage have substantially altered

Fig. 5.2 Cattle rib fragment from Hungate, York, showing phosphate mineralization of adjacent sediment, probably of fecal origin

the burial environment. A human skull of Early Iron Age date from the Heslington East site on the outskirts of York very clearly showed the consequences of a lowered water table. On excavation, the skull was almost black in color, resembling 'dark bone', leading us to expect very good preservation. In retrospect, the predominance of mid-brown iron colors, rather than the greeny-gray colors typical of anoxic gleyed sediments, in the surrounding sediment should have modified that expectation. The mandible was conventionally sampled for radiocarbon dating, but had to be resampled when it became clear that the collagen yield was much lower than expected. The skull contained preserved brain tissue (O'Connor et al. 2011), yet the organic phase of the bone was poorly preserved. The burial environment was initially conducive to bone preservation, and those conditions allowed the rapid stabilization of the brain tissue. Subsequently, and perhaps quite recently, changes in local hydrology allowed oxygenation of the deposits, leading to degradation of the collagen. The substantially-altered brain tissue, meanwhile, had stabilized in a condition that was less susceptible to degradation by oxidation or hydrolysis. Some confirmation can be seen in bones from the same site that show distinctive oxidized-iron colors and are in a poor state, yet retain pseudomorphs of pyrite, now completely oxidized but indicative of a very different previous burial environment (Fig. 5.3).

One particular point that needs to be borne in mind is that most animal bone in urban settlements went into the ground separated from the rest of the animal, in particular from the major organs and vascular system. An animal that is slaughtered and butchered will not undergo the same putrefactive stages as a complete animal, in which the gut microbiota can invade the rest of the body, initiating degradation in

Fig. 5.3 Sheep metatarsal from Heslington East site, York. The poor state of preservation is consistent with an aggressive, oxidizing burial environment, but the presence of oxidized former pyrite nodules within the bone (below) indicates an earlier phase of anoxic conditions

many tissues, including bone (Jans et al. 2004; Jans 2008; White and Booth 2014). Furthermore, many bones will have been cooked to some extent. Although the consequences of cooking for the integrity of bone collagen are not insignificant (Koon et al. 2010), cooking has the advantage of sterilizing the bones, of removing the endogenous biota as a factor in diagenesis. Cooked bone may therefore either be more vulnerable to destruction in the ground, if cooking caused appreciable collagen damage thus facilitating breakdown of the mineral-organic complex, or less vulnerable if the collagen damage was less intensive and the biotically-mediated putrefaction was effectively halted (Fig. 5.4).

The diagenesis of buried bone is complex and not fully understood, despite considerable progress in recent years. In urban archaeological contexts in particular, the greater diversity of initial geochemistry and the greater probability of redeposition

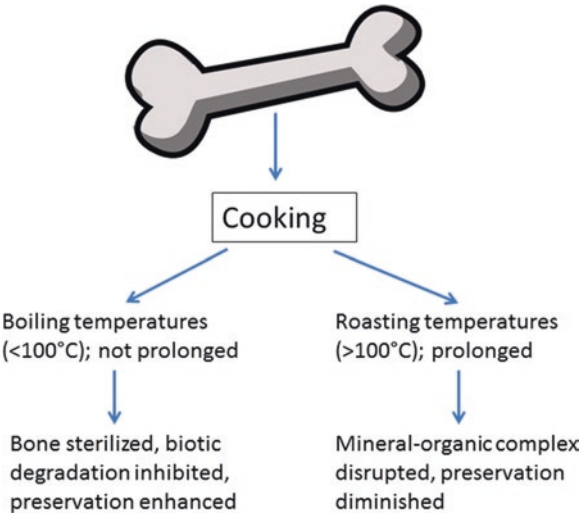

Fig. 5.4 The effects of cooking on bone survival depend on the form and duration of cooking, and may not be simple to predict

add further levels of complexity. That said, the condition of bone on excavation may be a useful reflection of the past geochemical environment in which it has lain, showing, for example, when recent groundwater changes have amended the sediments from their original condition. There may be other indications of land-use changes too: bones from some Roman period contexts at the 5–7 Blake Street site in York still smell strongly of mineral oil and diesel, reflecting the location of the vehicle inspection pit in the garage that occupied the site in the mid-twentieth century.

5.4 Excavation and After

Here we are primarily concerned with excavation choices and constraints, and post-excavation research design: the sullegic processes of archaeological investigation. Again, some of these questions are generic to archaeology as a whole, but particular characteristics of the urban archaeological context require consideration. To a large extent these are issues of sampling and of the contrary pressures inherent in ancient and modern towns. What is the relationship between the excavated area, the 'site' in any meaningful sense, and the urban settlement in any given phase? And how can a coherent sampling policy be implemented when, as is often the case, the ancient town under investigation underlies a modern urban settlement?

Urban settings necessitate a clear differentiation of 'the site,' in the sense of a particular excavation, from 'the site' in the sense of the whole settlement that we are trying to investigate. Each intervention is only a sampling exercise. Within a modern urban context, the placement and extent of excavation trenches is very highly constrained by extant buildings and transport infrastructure. Neighborhood redevel-

opments may occasionally allow extensive areas to be investigated, as at Hungate, but more often the excavation sample is a small patch, such as a strip delimited by the foundations of adjacent buildings. Those physical limits often extend below ground, isolating islands of stratigraphy. Of course, a modern town built over an extensive prehistoric site will have similar consequences. However, in the context of urban archaeology, this pattern of isolation and patchy accumulation has been going on for centuries: the occupation activity of each phase affecting the survival of earlier evidence as well as constraining the ongoing deposition of evidence. This becomes an issue for zooarchaeology when, for example, a narrow trench samples parts of a group of near-contemporary refuse pits. We see some of the pits in plan and some in section, and may recover an appreciable assemblage of bones from them. However, we have little idea of any associated structures (or none), or of whether those few pits represent the whole of a patch of deposition or just a small fraction of a 'swarm' of pits on a large area of waste ground. Such 'keyhole' archaeology obviously limits our understanding of the circumstances of deposition, hence limiting our interpretation of those assemblages (see Crabtree, Chap. 9), with little likelihood that contemporary occupation would allow the strategic placement of further keyholes by way of elucidation.

Another challenge of these "keyhole" sites is the small size of the assemblages that they produce. Assemblages totaling less than 500 fragments are typical, with many single-trench excavations yielding less than this. To take one example, the excavation of the footings for a lift-shaft within York Minster yielded 454 fragments of animal bone, while the assemblage from 7 Minster Yard (mentioned above) totaled only 258 fragments. Clearly, the identified fraction of these assemblages is even less. Urban excavation is typically multi-period, and this can mean attempting to elucidate temporal change on a site using "phases" which can consist of fewer than 20 fragments. Unsurprisingly, most assemblages from small interventions are never published or made use of in further research. However, small as these samples are, they are often the only information available from many areas within the historic city center. One way forward is to view these, rather than as sites in their own right, as interventions within a larger site (i.e., the city), which have the possibility to yield detailed spatial information (see, for example, Maltby 2010). The assemblage of high-status consumption waste from 7 Minster Yard, discussed above, is similar to an assemblage excavated of the same date from the courtyard of York Guildhall and Mansion House, representing a range of game birds and high-quality cuts of meat. These form an illuminating comparison to assemblages of the same date from poor housing at Hungate, which show a similar preponderance of chicken and rabbit (which can be raised locally), but an absence of game birds (which require access to land or estates and the resources to hunt them).

Combining information from various assemblages has also provided information on the presence of rats within the city. From Hungate, it is clear that the post-medieval rat population was largely sparse and controlled, but congregated within abandoned buildings such as 7 Haver Lane (Rainsford 2013). The co-occurrence in samples from 7 Haver Lane of *Rattus rattus* and *Rattus norvegicus* indicated co-existence within the unoccupied building, though the two species are likely to

have occupied different parts of the structure. Evidence from Coffee Yard showed rats using abandoned spaces within buildings within the city center, their bones being associated with rat-gnawed bones of larger species, and often in sediments derived from structural dereliction. York Guildhall, which as a high-status building might be expected to be pest-free, actually showed substantial evidence of rat activity, thanks to its location by the River Ouse. This is a useful reminder that interpretation sometimes has to regard the town and its opportunities as they might have been perceived by another species.

The problems of gray literature sites are not restricted to zooarchaeology, and have been rehearsed extensively elsewhere (e.g., Aitchison 2010). The current practice of tendering excavation contracts within a city to any of various competing companies means that it is almost impossible for any zooarchaeologist to develop a comprehensive knowledge of all assemblages excavated within a city (Broderick 2014). The record from any one city becomes poorly-integrated and dispersed, and small excavations that are not considered worthy of publication in their own right can easily become 'lost'. Additionally, the pace of commercial archaeology means that any written synthesis will quickly become out of date. This challenge is not amenable to a simple solution, nor to one that will 'fit' all circumstances. Extensive on-line databases are a possible way forward, having proved both feasible and useful in specific research contexts (Buckland et al. 2011; Williams and Smith 2013). Any such database needs, for practical reasons, to be a rich source of metadata, directing the user to any published or 'gray literature' sources, to any available original records of the bones, and to the last recorded location of the material. In addition, content or links would have to give access to the stratigraphical context and other 'finds' if the animal bones are not to lose their essential context. In the UK, Museum of London Archaeology (MOLA) has a particularly rich and detailed database, though even this is difficult to use effectively without support from MOLA personnel. Unpublished, 'gray literature' sources continue to be under-used, perhaps because of a perception that they lack the peer-review and editorial control of fully-published work. Nonetheless, the gray literature is where a lot of research resides, and techniques that would allow automatic trawling and indexing of gray literature sources promise to make this source far more available and of greater utility (Vlachidis et al. 2013). Key to any improvements in accessibility will be better incorporation of metadata relating to the animal bones within any database entries for the excavation as a whole.

5.5 Summing Up

Taphonomic issues are inescapable in zooarchaeology, especially so in urban zooarchaeology. The complexity of human settlement at urban densities, with multiple activities closely co-located in space and over short periods of time, generates a deposited assemblage that is rich in potential information if we can discern the

original 'low entropy' system as first deposited. Those same busy urban activities complicate matters through re-use of the same crowded patches of land, resedimenting material that may have been originally deposited weeks or centuries previously. The diagenetic environment of urban sediments is highly diverse and distinctive, greatly increasing the range of possible end-members to be encountered in the excavated assemblage. The factors that we can directly control, those of sampling and research design, are subject to constraints such as urban planning and commercial tendering that are not driven by archaeological concerns. Finally, our own research design and publication decisions (do we publish results from this town site-by-site, or thematically, or in one huge monograph?) complicate the need to take an overview of past and recent results. In urban zooarchaeology, perhaps more than in other zooarchaeological specialisms, the taphonomic record and its interpretation may constitute the most valuable information to be derived from excavated animal bones, more so than the species composition of assemblages or husbandry decisions inferred from the urban refuse. That observation may come to inform curatorial decisions, according research value to assemblages more for what they indicate about site formation and geochemical processes than for their composition of cows and goats (Rainsford et al. 2014). The taphonomic information is valuable in itself, not simply as a "filter" applied to other evidence, and it makes a significant contribution to our understanding of past practices and activities in urban settlements.

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Chapter 6
Low-Survival Skeletal Elements Track Attrition, Not Carcass Transport Behavior in Quaternary Large Mammal Assemblages

J. Tyler Faith and Jessica C. Thompson

6.1 Introduction

Anthropologists have long observed that when hunter-gatherers acquire large vertebrate prey they are faced with decisions about which body parts to transport for later processing and consumption and which to leave behind at the kill site (Abe 2005; Bartram 1993; Bunn et al. 1988; O'Connell et al. 1988, 1990; White 1952; Yellen 1977). These decisions are routinely evaluated in archaeological contexts through analysis of skeletal part frequencies (Faith and Gordon 2007; Lyman 1994, 2008). However, it is widely recognized that due to destructive taphonomic processes (e.g., carnivore destruction, trampling, sediment compaction, and leaching), the skeletal parts recovered by archaeologists frequently do not reflect what was originally discarded by human foragers (Cleghorn and Marean 2004, 2007; Lupo 1995, 2001; Lyman 1984, 1985, 1993, 1994; Marean and Cleghorn 2003; Marean and Frey 1997; Marean and Spencer 1991). In many cases, the survival potential of a skeletal element or element portion is mediated by its structural density (Lam and Pearson 2005; Lam et al. 2003; Lyman 1994).

Given the importance of skeletal part data to inferring carcass transport decisions, it is imperative that zooarchaeological methodology controls for destructive processes. Several methods have been developed to extract meaningful behavioral signals from bone assemblages subject to attrition (reviewed in Cleghorn and Marean 2004). These include Stiner's (2002) anatomical region profile (but see Pickering et al. 2003), Rogers' (2000) analysis of bone counts by maximum

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likelihood, and the high- and low-survival model of skeletal element survivorship developed by Marean and Frey (1997) and Marean and Cleghorn 2003; see also Cleghorn and Marean 2004, 2007). The latter proposes that skeletal parts can be divided into a high-survival subset that accurately reflects what was originally deposited and a low-survival subset that does not. This taphonomic model is increasingly implemented by zooarchaeologists, particularly in the context of Paleolithic faunal assemblages (e.g., Faith 2007a; Faith et al. 2009; Marean and Kim 1998; Saladié et al. 2011; Schoville and Otárola-Castillo 2014; Thompson 2010; Thompson and Henshilwood 2011; Yeshurun et al. 2007; Yravedra and Domínguez-Rodrigo 2009). This study tests the applicability of the high- and low-survival model of skeletal element survivorship through examination of large mammal skeletal part data across 33 African faunal assemblages and 10 Eurasian assemblages (Table 6.1, Fig. 6.1), emphasizing how low-survival element abundances vary as a function of attrition. The broad applicability of this taphonomic model is illustrated by drawing from assemblages accumulated by both humans and non-human bone collectors (e.g., carnivores, raptors) and subject to varied taphonomic histories.

6.2 Density-Mediated Attrition

Parts of a complete carcass may be removed or destroyed via a number of taphonomic pathways (Lyman 1994). Density-mediated attrition refers to those processes that result in differential survivorship patterned according to bone density (Lyman 1993). For both large and small-bodied mammals, known or suspected density-mediated processes include carnivore attrition, human consumption of low-density parts, post-depositional crushing, fluvial winnowing, and diagenetic processes, among others (Lyman 1994). Bone densities vary between elements and also between portions of the same element, with some of the most dramatic intra-element differences found in the long-bones (Lam and Pearson 2005; Lam et al. 2003). For large mammals, long-bone density typically patterns according to five major regions. The least dense are the two epiphyseal ends, which are largely composed of cancellous bone overlain by a thin wall of cortical bone. The exterior cortical bone thickens as it approaches the middle shaft of the long bone, creating portions of intermediate density at the near-epiphyses and highest density at the mid-shaft. Because skeletal elements have different shapes and structural functions, the precise location of these density transitions differ by element and taxon, as do their absolute densities (Carlson and Pickering 2004; Lam et al. 1999; Lyman 1994; Stahl 1999).

For long-bones of large mammals, and especially ungulates, there is also a strong relationship between bone density and the distribution of within-bone nutrients. The dense long-bone shafts contain marrow, which is a concentrated source of fat of high nutritive value to humans and carnivores (Blumenschine and Madrigal 1993). Fat is also present within the cancellous portions, but in the form of bone grease that must be extracted either through comminution and cooking (Lupo and Schmitt 1997) or through direct consumption and digestion within the gut (Marean 1991). It

Table 6.1 Skeletal part frequencies across assemblages (in MNE). *KC* Kobeh Cave, *MZ* Mezmaiskaya Cave, *DK1* Die Kelders Cave 1, *PEC* Porc-Epic Cave, *BPA* Boomplaas Cave, *AAD* Amboseli Airstrip Den, *BBC* Blombos Cave, *PP13B* Pinnacle Point 13B

Assemblage	Cranium	Mandible	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal	Astragalus	Calcaneus	Ulna	Carpals	Ribs	Atlas	Axis	Cervical	Thoracic	Lumbar	Sacral	Pelvis	Tarsals	Scapulae	Phalanges
KC: Size 2	30	22	64	48	38	63	96	36	3	5	26	12	31	1	1	9	12	9	2	12	8	4	25
MZ: Level 1C Size 1/2	4	6	5	5	6	6	8	5	1	1	5	1	11	0	0	4	10	5	3	3	1	2	9
MZ: Level 2 Size 1/2	6	9	6	4	4	7	8	8	3	2	4	0	10	1	1	4	8	3	1	4	0	3	2
MZ: Level 2A Size 1/2	7	3	6	6	4	8	12	4	0	2	4	0	16	0	1	3	6	5	1	3	0	3	3
MZ: Level 2B2 Size 1/2	7	7	8	10	2	5	4	3	0	0	7	0	18	0	0	2	4	2	0	6	0	2	6
MZ: Level 2B3 Size 1/2	7	9	6	5	1	6	3	1	5	3	4	0	10	0	1	1	5	3	0	2	0	2	4
MZ: Level 2B4 Size 1/2	8	10	6	5	4	5	10	3	1	1	5	2	13	1	0	2	7	2	0	3	2	3	7
MZ: Level 2B4 Size 3/4	5	6	6	3	3	4	9	3	0	0	5	0	2	0	0	2	1	1	0	2	0	2	5
MZ: Level 3: Size 1/2	12	18	8	9	12	7	6	8	5	6	5	5	16	0	1	6	7	8	1	4	1	4	2
MZ: Level 3: Size 3/4	12	20	7	5	4	8	14	5	0	3	4	0	14	0	0	3	4	2	1	4	0	1	6
DK1: Layer 10 Size 1/2	7	4	7	4	5	10	9	5	1	6	4	5	18	1	1	8	10	12	5	4	2	3	25
DK1: Layer 10 Size 3/4	4	5	12	8	5	9	13	11	1	3	5	0	20	0	0	6	4	6	1	3	1	5	5
DK1: Layer 11 Size 1/2	7	6	3	2	4	4	5	4	2	0	4	2	18	1	2	5	6	7	1	4	1	3	11
DK1: Layer 11 Size 3/4	2	3	3	2	1	1	3	3	0	0	1	1	20	1	0	2	2	1	1	1	0	1	7
PEC: Size 1/2	14	32	59	109	35	316	98	45	9	12	84	7	62	7	3	12	4	10	4	164	2	43	60
PEC: Size 3/4	10	20	12	10	3	35	16	18	4	2	2	1	11	1	1	2	3	4	3	11	4	1	3
BPA: BLD Size 1/2	17	28	39	35	31	18	30	40	37	19	24	33	150	8	13	34	100	63	5	18	10	27	252
BPA: BLD Size 3/4	4	5	2	2	3	1	3	2	0	2	1	3	5	0	1	3	3	3	1	1	2	0	28
BPA: BLA Size 1/2	6	10	14	12	6	7	11	12	8	3	10	6	14	3	1	7	21	16	0	3	3	5	56
BPA: CL Size 1/2	7	17	14	8	13	11	16	8	3	7	6	10	28	1	1	9	15	17	0	2	3	3	75
BPA: CL Size 3/4	30	70	20	17	9	17	23	10	1	1	3	7	26	0	0	8	5	15	0	1	10	1	112

(continued)

Table 6.1 (continued)

Assemblage	Cranium	Mandible	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal	Astragalus	Calcaneus	Ulna	Carpals	Ribs	Atlas	Axis	Cervical	Thoracic	Lumbar	Sacral	Pelvis	Tarsals	Scapulae	Phalanges
BPA: BP Size 1/2	4	12	5	5	1	6	11	3	3	1	2	4	18	0	0	4	5	4	0	3	1	2	16
BPA: BP Size 3/4	9	15	5	4	3	5	10	5	0	1	1	1	3	0	1	2	3	3	0	1	6	1	21
BPA: OLP Size 1/2	5	15	6	6	1	11	12	1	2	4	2	5	19	1	1	5	7	11	1	3	3	1	39
BPA: OCH Size 1/2	22	38	15	22	11	33	28	17	13	20	5	44	56	3	10	2	15	27	2	11	19	11	146
BPA: LOH Size1/2	5	8	5	5	1	5	4	3	1	5	2	3	7	1	1	4	6	11	3	4	2	3	45
AAD: Size 2 mammals	2	6	5	12	9	5	9	9	0	0	0	0	11	1	2	4	6	1	2	2	0	2	0
AAD: Size 3 mammals	9	8	26	18	14	6	12	4	12	12	16	0	8	8	2	6	9	5	5	2	0	12	17
BBC: M1 Size 1/2	–	–	12	8	6	10	11	15	1	8	5	11	25	2	3	11	19	7	4	12	11	15	54
BBC: M1 Size 3/4	–	–	12	7	8	13	14	10	3	2	5	3	15	3	0	13	15	6	0	4	5	1	20
BBC: M2 upper Size 1/2	–	–	11	10	8	9	5	9	0	1	5	15	16	1	1	6	14	9	3	9	7	4	23
BBC: M2 upper Size 3/4	–	–	5	4	5	3	4	3	0	0	0	2	5	0	1	3	6	4	0	1	3	0	5
BBC: M2 lower Size 1/2	–	–	2	3	4	2	2	5	3	2	2	5	4	1	0	2	2	3	0	2	3	1	15
BBC: M3 Size 1/2	–	–	6	3	2	3	7	5	2	3	0	11	9	3	0	3	8	5	1	8	8	3	30
PP13B: Disturbed/surface Size 1/2	1	7	11	12	3	5	5	5	1	3	4	16	21	1	1	20	13	11	0	6	7	4	25
PP13B: Disturbed/surface Size 3/4	1	1	6	6	5	4	7	4	0	1	2	4	6	1	1	5	5	5	0	2	5	0	7
PP13B: Upper Sands Size 1/2	5	10	9	10	4	7	7	4	3	4	8	7	28	1	1	9	10	12	4	9	5	6	18
PP13B: Upper Sands Size 3/4	1	2	6	6	5	4	11	7	1	2	1	4	10	0	1	4	9	8	0	3	2	5	12
PP13B: SBS/upper RS Size 1/2	2	11	13	14	5	7	11	5	1	4	6	13	26	2	1	15	22	14	1	10	6	7	27
PP13B: SBS/upper RS Size 3/4	2	1	7	6	4	4	9	7	0	1	3	2	6	0	1	5	8	7	1	2	4	1	11

Assemblage	Cranium	Mandible	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal	Astragalus	Calcaneus	Ulna	Carpals	Ribs	Atlas	Axis	Cervical	Thoracic	Lumbar	Sacral	Pelvis	Tarsals	Scapulae	Phalanges
PP13B: Lower RS Size 1/2	2	3	5	6	2	6	4	0	0	3	6	4	7	1	0	4	9	7	1	8	5	0	6
PP13B: Lower sands Size 1/2	1	2	5	5	1	4	2	3	0	0	3	4	2	1	0	1	5	2	0	2	2	1	2
PP13B: LC-MSA lower Size 1/2	0	4	5	3	2	5	5	4	4	1	1	0	7	1	0	3	4	5	0	2	1	4	8

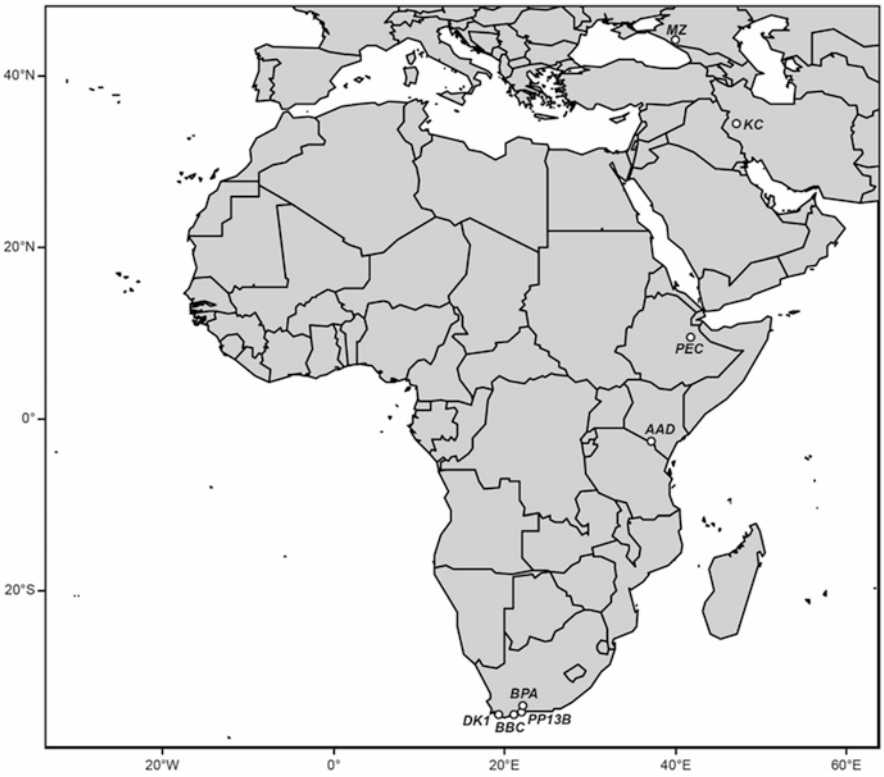

Fig. 6.1 Location of sites included in the analysis. *KC* Kobeh Cave, *MZ* Mezmaiskaya Cave, *PEC* Porc-Epic Cave, *AAD* Amboseli Airstrip Den, *DK1* Die Kelders Cave 1, *BPA* Boomplaas Cave, *BBC* Blombos Cave, *PP13B* Pinnacle Point 13B

has been shown in experimental, naturalistic, and ethnoarchaeological settings that carnivores will consume long-bone ends and other low-density elements in order to access the bone grease, and that the higher-density shafts are therefore more likely to survive (Bartram and Marean 1999; Faith et al. 2007; Gidna et al. 2015; Marean and Spencer 1991; Marean et al. 1992). This actualistic work provides a point of departure for understanding the processes that may lead to the differential representation of skeletal elements and element portions in the zooarchaeological record (Marean et al. 2004; Pickering et al. 2003; Yravedra and Domínguez-Rodrigo 2009).

Variation in exactly how often denser elements survive may arise from human treatment of long bones prior to deposition, for example, if bones have been cooked and the grease extracted, low-density trabecular bone may be less attractive to carnivore scavengers (Lupo 1995; Thompson and Lee-Gorishti 2007). Depositional environment also plays a role; where bones are exposed to episodic wetting and drying or heating and cooling, dense long-bone shafts may fragment

more readily than cancellous bone, particularly when the bones are already highly mineralized (Conard et al. 2008). This can create a situation in which spongy elements or element portions may preserve in a more identifiable state, but only after already being depleted through density-mediated processes prior to mineralization. Thus, survivorship may be best compared between sites within similar depositional settings.

6.3 Large Mammal Skeletal Element Survivorship

Building on observations from experimental, ethnographic, and archaeological bone assemblages (Bartram and Marean 1999; Binford et al. 1988; Blumenschine 1988; Blumenschine and Marean 1993; Brain 1981; Lupo 1995; Marean and Frey 1997; Pickering et al. 2003), Marean and Cleghorn 2003 propose that skeletal parts of large-bodied mammals can be divided into a high-survival and low-survival subset on the basis of their physical properties (Fig. 6.2). The high-survival subset includes elements with portions that are high in density and with thick cortical walls lacking cancellous bone. These include long-bones (for ungulates: femur, tibia, metatarsal, humerus, radius, metacarpal), the cranium, and the mandible. Although carcass transport decisions are structured by a range of variables that may be difficult to discern from large bone accumulations (Binford 1978; Lupo 2001; O'Connell et al. 1988, 1990; Schoville and Otárola-Castillo 2014), the abundances of high-survival

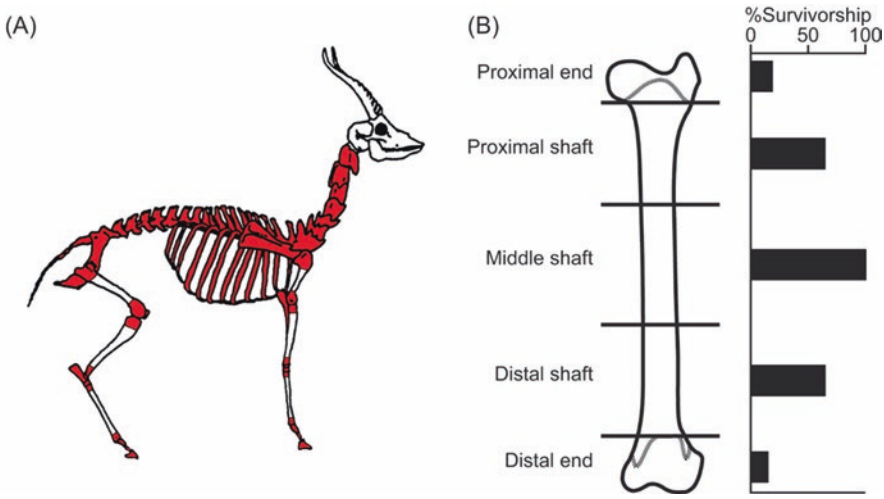

Fig. 6.2 (**a**) Size 2 bovid skeleton illustrating low-survival elements and portions (in *red*) and high-survival elements (in *white*) (skeleton modified from Bunn and Kroll 1986). (**b**) Survivorship of various portions of the femur, based on 50 femora fed to captive hyenas (Marean and Spencer 1991)

elements in archaeological assemblages are thought to be a reasonably accurate portrayal of what was originally discarded by human foragers. Thus, they offer the best option for analysis of carcass transport decisions. In contrast, the low-survival subset—including vertebrae, ribs, pelves, scapulae, and ulnae—is characterized by bones with thin cortical walls and low-density, grease-rich cancellous portions. Small compact bones (e.g., carpals and tarsals) and phalanges are considered low-survival elements given that these tend to be readily swallowed by carnivores, particularly in the case of smaller ungulates (Marean 1991). The sensitivity of low-survival elements to density-mediated taphonomic processes, including carnivore destruction, means that these bones may not accurately reflect what was originally discarded at a site, rendering them inappropriate for analyses of carcass transport behavior.

If the distinction between high- and low-survival elements is robust and broadly applicable, this places a considerable limitation on our ability to infer carcass transport behaviors from skeletal element data by limiting faunal analysts to a relatively small number of primarily appendicular elements (Fig. 6.2). Of perhaps greater importance, it also implies that zooarchaeological analyses that incorporate low-survival elements in behavioral interpretations are methodologically problematic. Given the significance of understanding this methodological issue, our aim here is to assess the following question: how sensitive are low-survival elements to attrition?

6.4 Methods

Zooarchaeological measures of skeletal element abundances must be designed to quantify those elements or element portions least affected by density-mediated attrition, bearing in mind that any individual fragment will only be included in such counts if it is identifiable at minimum to skeletal part. Methods for quantifying skeletal parts vary between researchers and have different potentials for capturing the densest parts, such as long bone shafts (Marean et al. 2001; Thompson and Marean 2009).

The following analyses make use of skeletal element data compiled from 33 African Quaternary faunal assemblages from six sites: Porc-Epic Cave in Ethiopia (Assefa 2006), the Amboseli Airstrip Hyena Den in Kenya (Faith 2007b; Hill 1989), and Die Kelders Cave 1 (Marean et al. 2000), Blombos Cave (Thompson and Henshilwood 2011), Pinnacle Point Cave 13B (Thompson 2010), and Boomplaas Cave (Faith 2013) in South Africa. We also consider ten Eurasian Quaternary assemblages from two sites: Kobeh Cave in Iran (Marean and Kim 1998) and Mezmaiskaya Cave in Russia (Cleghorn 2006) (Table 6.1, Fig. 6.1). These sites were selected because they fall within similar time ranges (Late Pleistocene through the Holocene: 126,000 years ago to present), are all from cave settings (except the Amboseli Airstrip Hyena Den), and had minimum number of element (MNE) values calculated by researchers using similar methods (see below). Skeletal part data are combined for both Body Size 1–2 (0–84 kg) and 3–4 (84–900 kg) mammals (Brain

1981) to improve sample sizes; all reported assemblages from these sites with a total MNE (minimum number of elements) less than 45 are excluded from this study.

Our emphasis on Africa and Eurasia does not reflect an underlying expectation that the taphonomic model of skeletal element survivorship is only applicable in these regions, but rather the importance of ensuring analytical comparability across samples. Our analyses require that (1) *all* identifiable ungulate long-bone shaft fragments are included in MNE calculations; (2) MNE counts are aggregated by body size class (after Brain 1981); and (3) MNE counts for long-bones are provided for different portions (ends and shafts). These criteria, particularly points one and two, are most commonly met for African assemblages, where the exceptional diversity of Bovidae (>80 extant African species), which are the dominant large mammal in nearly all African Quaternary sites, means that zooarchaeologists working on these faunas assign all ungulate long-bone shaft fragments to one of several standard body size classes rather than attempting identifications at lower taxonomic resolution. This contrasts with the situation in many other contexts, where, even when shaft fragments are considered, there is often a greater focus on assigning them to genus or species (e.g., Grayson and Delpech 2003; Morin 2004), in which case smaller and more fragmentary specimens may not be included in published skeletal inventories. All of the MNE counts used here are derived using the fraction summation approach or by counting overlaps on fragments traced into standardized bone templates (Marean et al. 2001). Long-bones are divided into five portions: proximal and distal ends, proximal and distal shafts, and a midshaft (Fig. 6.2).

To evaluate the sensitivity of low-survival elements to destructive processes, it is necessary to provide an index of attrition for each assemblage. We use the percentage of long-bone end destruction as a proxy for attrition here. Following the taphonomic model of bone survivorship, long-bones are classified as high-survival elements because their mid-shafts are dense and lack cancellous bone; to reiterate, this is only applicable if all long bone portions are incorporated into the MNE counts, including the shaft portions. In contrast, long-bone ends, defined by Marean and Spencer (1991) as the most proximal and distal portions that include the epiphyses and metaphyses (Fig. 6.2), are preferentially destroyed by attritional processes and can be considered low-survival portions of the long-bones (e.g., Binford et al. 1988; Blumenschine and Marean 1993; Marean and Spencer 1991; Marean et al. 1992; Pickering et al. 2003; Yravedra and Domínguez-Rodrigo 2009). Because long-bones include both low- and high-survival portions, the loss of long-bone ends provides a reasonable measure of attrition. Assuming that long-bones are transported intact, one can expect to recover two ends for every long-bone in the absence of attrition; the loss of proximal and distal ends reflects destructive taphonomic processes. For example, consider a hypothetical bone assemblage with a total MNE of 50 femora and a MNE of 25 ends. Given that 50 femora are present, in the absence of attrition one would expect 100 ends (50 proximal and 50 distal) to have initially been present. The recovery of only 25 implies that 75% have been destroyed. This simple relationship requires that shafts consistently preserve in an identifiable state, although extreme fragmentation may render them less identifiable or pose challenges when factoring identifiable shaft fragments into MNE calculations

(e.g., if the exact position of fragment on a standardized bone template cannot be determined or if no quantifiable landmarks are preserved). The percentage of long-bone end attrition is calculated here as:

$$\frac{\sum(\text{long bone MNE}\times 2)-\sum(\text{long bone end MNE})}{\sum(\text{long bone MNE}\times 2)}\times 100$$

To the extent that destruction of long-bone ends provides a reliable measure of attrition in a given assemblage, we predict that higher attrition should be reflected by decreasing abundances of low-survival elements. We examine these relationships for all low-survival elements combined and for individual elements, the abundances of which are quantified using various derivatives of the MNE. These include MAU (minimal animal units: MNE normalized by the number of times the element occurs in the skeleton) and %MAU (MAU of an element divided by maximum MAU value observed in an assemblage and scaled to 100), as described further in Lyman (2008).

6.5 Results

Skeletal part data for the 43 assemblages examined here are reported in Table 6.1. For all long-bones, the highest MNE counts are derived from shafts (mid-shafts or near-epiphyses), which are consistently greater than those potentially derived from ends; levels of long-bone end destruction range from 34 to 89% (Table 6.2). Relative abundances of low-survival elements (MAU) range from 14 to 52%, consistently less than the 65% (15 low-survival elements divided by 23 elements total) that would be expected of a case in which all high- and low-survival elements are evenly represented.

Excluding the Blombos Cave assemblages, for which crania and mandibles were not quantified, we observe significant inverse correlations between long-bone end destruction and the abundance of low-survival elements relative to the total for all elements (MAU) for Size 1–2 (Spearman's rho: $r_s = -0.655$, $p < 0.001$, df = 23) and Size 3–4 mammals ($r_s = -0.650$, $p = 0.022$, df = 10) (Fig. 6.3). Removing the DK1 Size 1–2 (Fig. 6.3) outlier, high coefficients of determination (Pearson's r^2: Size 1–2 = 0.445, Size 3–4 = 0.610) imply that a substantial amount of variance (44.5–61.0%) in the abundance of low-survival elements can be explained by attrition of long-bone ends; when attrition is high, low-survival elements are rare.

To explore the effects of attrition on individual elements, Table 6.3 reports correlation coefficients between %end destruction and the abundance of individual elements (%MAU). For 12 of the 15 low-survival elements, we observe significant negative relationships, meaning that these elements consistently decline in abundance as long-bone end destruction increases. The exceptions include the astragalus, small tarsals, and carpals. Among the high-survival elements, only the humerus ($r_s = -0.404$, $p = 0.013$) exhibits a significant correlation.

Table 6.2 The number (MNE) of long-bone epiphyses ends relative to the total long-bone MNE. *KC* Kobeh Cave, *MZ* Mezmaiskaya Cave, *DK1* Die Kelders Cave 1, *PEC* Porc-Epic Cave, *BPA* Boomplaas Cave, *AAD* Amboseli Airstrip Den, *BBC* Blombos Cave, *PP13B* Pinnacle Point 13B

Assemblage	Long-bone ends	Total long-bone	%End destruction
KC: Size 2	88	345	87.2
MZ: Level 1C Size 1/2	27	35	61.4
MZ: Level 2 Size 1/2	26	37	64.9
MZ: Level 2A Size 1/2	35	40	56.3
MZ: Level 2B2 Size 1/2	16	32	75.0
MZ: Level 2B3 Size 1/2	15	22	65.9
MZ: Level 2B4 Size 1/2	17	33	74.2
MZ: Level 2B4 Size 3/4	13	28	76.8
MZ: Level 3: Size 1/2	38	50	62.0
MZ: Level 3: Size 3/4	28	43	67.4
DK1: Layer 10 Size 1/2	37	40	53.8
DK1: Layer 10 Size 3/4	35	58	69.8
DK1: Layer 11 Size 1/2	29	22	34.1
DK1: Layer 11 Size 3/4	13	13	50.0
PEC: Size 1/2	274	662	79.3
PEC: Size 3/4	24	94	87.2
BPA: BLD Size 1/2	176	193	54.4
BPA: BLD Size 3/4	7	13	73.1
BPA: BLA Size 1/2	36	62	71.0
BPA: CL Size 1/2	40	70	71.4
BPA: CL Size3/4	22	96	88.5
BPA: BP Size 1/2	18	31	71.0
BPA: BP Size 3/4	7	32	89.1
BPA: OLP Size 1/2	24	37	67.6
BPA: OCH Size 1/2	87	126	65.5
BPA: LOH Size1/2	18	23	60.9
AAD: Size 2 mammals	19	49	80.6
AAD: Size 3 mammals	78	80	51.3
BBC: M1 Size 1/2	42	62	66.1
BBC: M1 Size 3/4	30	64	76.6
BBC: M2 upper Size 1/2	34	52	67.3
BBC: M2 upper Size 3/4	10	24	79.2
BBC: M2 lower Size 1/2	12	18	66.7
BBC: M3 Size 1/2	16	26	69.2
PP13B: Disturbed/surface Size 1/2	34	41	58.5
PP13B: Disturbed/surface Size 3/4	26	32	59.4
PP13B: Upper Sands Size 1/2	24	41	70.7
PP13B: Upper Sands Size 3/4	23	39	70.5
PP13B: SBS/upper RS Size 1/2	39	55	64.5
PP13B: SBS/upper RS Size 3/4	22	37	70.3
PP13B: Lower RS Size 1/2	17	23	63.0
PP13B: Lower sands Size 1/2	11	20	72.5
PP13B: LC-MSA lower Size 1/2	14	24	70.8

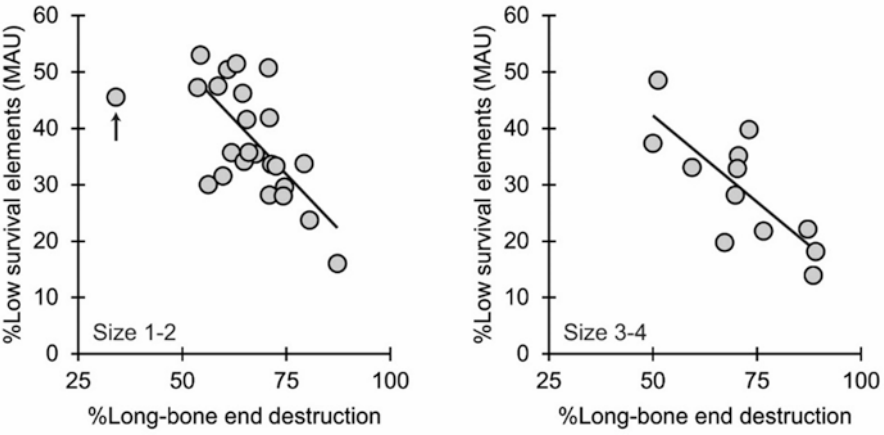

Fig. 6.3 Bivariate scatter plots illustrating the relationship between %Long-bone end destruction and the %abundance of low survival elements (in MAU) for Size 1–2 (*left*) and Size 3–4 (*right*) mammals. Solid lines indicate ordinary least squares regression, with the Die Kelders Cave Layer 11 Size 1–2 outlier (marked by an *arrow*) excluded from calculation

Table 6.3 The correlation (Spearman's rho) between element abundances (%MAU) and epiphyseal destruction. Significant values in bold

Element		r_s	p
High-survival	Cranium	−0.179	0.288
	Mandible	0.039	0.821
	Humerus	**−0.404**	**0.013**
	Radius	−0.305	0.066
	Metacarpal	−0.212	0.208
	Femur	−0.028	0.870
	Tibia	−0.037	0.828
	Metatarsal	−0.231	0.169
Low-survival	Astragalus	−0.208	0.216
	Calcaneus	**−0.413**	**0.011**
	Ulna	**−0.500**	**0.002**
	Carpals	−0.283	0.090
	Ribs	**−0.514**	**0.001**
	Atlas	**−0.525**	**0.001**
	Axis	**−0.339**	**0.040**
	Cervical	**−0.560**	**<0.001**
	Thoracic	**−0.372**	**0.023**
	Lumbar	**−0.444**	**0.006**
	Sacral	**−0.368**	**0.025**
	Pelvis	**−0.447**	**0.005**
	Tarsals	−0.135	0.426
	Scapulae	**−0.480**	**0.003**
	Phalanges	**−0.306**	**0.066**

6.6 Discussion

Our analyses demonstrate that the destruction of long-bone ends predicts the relative abundance of low-survival elements. When all low-survival elements are considered together (Fig. 6.3), the strong correlations suggest that attritional processes severely overprint any potential signature of differential bone transport. Similar negative relationships are observed for nearly all low-survival elements considered individually (Table 6.3). Together, these results provide archaeological support for the high- and low-survival model of skeletal element survivorship (see also Bartram and Marean 1999; Marean and Frey 1997; Marean and Kim 1998; Marean et al. 2000). Based on experimental, naturalistic, and ethnoarchaeological observations (Blumenschine and Marean 1993; Lupo 1995, 2001; Marean and Spencer 1991; Marean et al. 1992; see also the reviews in Cleghorn and Marean 2007; Pickering et al. 2003), we are confident that the relationship between the destruction of long-bone ends and low-survival element abundance observed here is due to density-mediated attritional processes. Carnivore destruction is a likely candidate, as it is well-known to produce similar patterns (Blumenschine and Marean 1993; Cleghorn and Marean 2007; Lupo 1995; Marean and Spencer 1991; Marean et al. 1992), and carnivore toothmarks are observed across most of the archaeological assemblages (Assefa 2006; Cleghorn 2006; Faith 2007b, 2013; Marean et al. 2000; Marean and Kim 1998; Thompson 2010; Thompson and Henshilwood 2011). Other density-mediated process (e.g., sediment compaction, chemical leaching) are likely to have also contributed.

Our analysis of the relationship between long-bone end destruction and the abundance of individual elements reveals several exceptions that do not fit the expected pattern (Table 6.3). Among low-survival elements, these are the astragalus, carpals, and smaller tarsals. These are considered low-survival elements (Cleghorn and Marean 2004, 2007; Marean and Cleghorn 2003) because they can be swallowed whole by carnivores following human discard (Marean 1991), although their abundances are not predicted by long-bone end destruction (Table 6.3). This may imply that this taphonomic process was not universal across assemblages, or that these elements remain identifiable even after post-depositional attrition. Unexpected results are provided by the significant correlation between epiphyseal destruction and %MAU for the humerus (Table 6.3). Due to the presence of a high-density portion that resists attritional processes (the mid-shaft), we would have expected its abundance to vary independent of attrition. One potential explanation is that high attrition renders this element less identifiable or less quantifiable (in MNE) than other high-survival counterparts. At Die Kelders Cave 1 and Boomplaas Cave, data are available on the frequency of long-bone shaft fragments with right angle breaks, an indicator of post-depositional fragmentation (Marean et al. 2000; Villa and Mahieu 1991). Across assemblages from these two sites, there is a strong correlation between epiphyseal destruction and the frequency of long-bones with right-angle breaks (r_s = 0.722, p = 0.004). This implies that assemblages with high attrition, and therefore fewer identified humeri, are also subject to more intense

post-depositional fragmentation. In turn, this might pose analytical challenges with respect to identifying fragments of this element or recognizing landmarks needed to facilitate MNE calculations (using the fraction summation approach) or confidently establish the position of a fragment on a standard bone template.

These exceptions to the high- and low-survival model of bone survivorship, although few, suggest that there may be cases in which some high-survival elements do not accurately reflect what was originally discarded by human foragers and some low-survival elements do. The approach developed here—examining the association between epiphyseal deletion and bone survivorship—offers one means of identifying and controlling for these potential exceptions in other faunal assemblages.

On the whole, our results support the view, based on actualistic work, that low-survival elements are not suitable for interpretations of carcass transport behavior by past human foragers. Exceptions may be made for assemblages subject to exceptionally low attrition, in which case all elements deposited by human foragers are likely to survive. Provided that long-bones are transported intact and that shaft fragments are quantified, such a case is easily recognized by the absence of long-bone end destruction. However, we expect this taphonomic scenario to be exceptionally rare in the archaeological record. It is certainly not evident across any of the assemblages examined here, where the lowest level of long-bone end deletion is still a substantial 34.1% (Table 6.2). Even for cases where long-bone end attrition is modest, we cannot reliably determine which low-survival elements disappeared (see Rogers 2000 for a maximum likelihood approach for tackling this issue). Because of this, we recommend that whenever an assemblage has been subject to attrition, analyses of carcass transport strategies focus on the high-survival subset.

How applicable are our results? While the focus of our analysis is on African and Eurasian late Quaternary faunal assemblages, there is ample reason to believe that the patterns documented here would be evident in zooarchaeological assemblages from other time periods and regions (Marean et al. 2004). Large-bodied bone crunching taxa (e.g., hyaenids, canids, ursids, and some felids) capable of producing similar patterns are found throughout the continents. In addition, while carnivore bone destruction may be the most well-studied density-mediated taphonomic processes (Cleghorn and Marean 2007), it is hardly the only one (Lyman 1994). For example, taphonomic evidence from Boomplaas Cave, which provides 10 of the 34 assemblages examined here, indicates a complex history of human, carnivore, and raptor accumulation throughout its >65 ky sequence (Faith 2013), with some assemblages showing abundant evidence for carnivore bone destruction in the form of toothmarks (e.g., OCH Size 1–2: 55% of long-bone mid-shaft fragments lacking dry-bone breaks) and others showing none (e.g., BLD Size 3–4). Despite this taphonomic variability, we observe a highly significant relationship between long-bone end destruction and the abundance of low-survival elements across the 10 Boomplaas Cave assemblages ($r_s = -0.827$, $p = 0.003$), but no relationship between long-bone end destruction and toothmark abundances (% of fragments with a toothmark: $r_s = -0.383$, $p = 0.275$; data from Faith 2013). This implies that low-survival elements track attrition caused by a range of taphonomic processes, not just carnivore activity, though it would be worthwhile to explore similar patterns in contexts lack-

ing bone-crunching carnivores. At Boomplaas Cave, the high frequency of right-angle fractures on long-bone shaft fragments (from 19.7 to 61.9%) implies substantial post-depositional fragmentation, perhaps due to a combination sediment compaction, leaching, and burning, which may also account for the attrition of low-survival elements and long-bone ends at this site. It follows that because a range of taphonomic processes contribute to preferential destruction of low-survival elements, we can expect the patterns documented here to be evident in other contexts.

6.7 Conclusions

This chapter adds to the existing body of archaeological, ethnoarchaeological, and actualistic data supporting a distinction between a subset of high-survival elements that resists destructive processes and a low-survival subset that does not (Cleghorn and Marean 2004, 2007; Marean and Cleghorn 2003; Marean and Frey 1997; Marean and Spencer 1991). Just how sensitive are low survival elements to attrition? At least based on the assemblages examined here, the answer is unequivocal: *very sensitive*. Attrition explains much of the variation in low-survival element abundances, with nearly all low-survival elements affected. We strongly recommend that unless evidence to the contrary can be provided—requiring evaluation on a case-by-case basis—low-survival elements should be excluded from zooarchaeological analyses of carcass transport behavior; due to destructive processes, their abundances in archaeological sites are a poor reflection of carcass transport behavior by people.

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Chapter 7
Influence of Bone Survivorship on Taxonomic Abundance Measures

Jacob L. Fisher

7.1 Introduction

The prey choice model (also known as the diet breadth model) grounded in optimal foraging theory has proven to be a valuable tool for formulating predictions regarding animal exploitation across space and time, especially among small scale societies. The underlying logic of the model is quite simple: individual hunters make decisions when foraging that favor resources that provide the highest net return based on a currency. Such high ranked resources should always be pursued when encountered by the hunter, while the inclusion of lower ranked resources into the diet is dependent on the encounter rates of higher net return resources. Since high ranked prey are typically large bodied animals with low recruitment rates (Broughton et al. 2011), the long-term effect is resource depression when predation exceeds reproduction and in-migration. As encounter rates for higher ranked resources decline, foragers are expected to incorporate greater numbers of lower ranked prey items into their diet.

The artiodactyl index (AI) is commonly used for testing the predictions of the prey choice model in western North America due to its simple computation and intuitive meaning. As originally conceived (Bayham 1979), the AI is a ratio-based measure that compares the relative abundance of artiodactyls (e.g., deer, bighorn sheep, pronghorn) to leporids (e.g., jackrabbits, cottontail rabbits) to measure the trade-offs predicted by the prey choice model within a typical terrestrial patch. AI values are expected to decline over time if large game populations were depressed, and such changes may be tested using chi-square analysis and similar operations (Cannon 2001). The measure has since been modified into a variety of abundance indices that compare any set of high ranked and low ranked resources within a patch (e.g., Broughton 1994).

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While abundance indices are simple to use, researchers must carefully review the data being inputted in such measures. For example, the practice of aggregating faunal data from multiple assemblages masks fundamental differences among the assemblages related to variation in habitats, seasonality, site function, settlement patterns, recovery strategies, and analytical decisions (e.g., Fisher 2015; Lyman 2003). Here, I focus on one particular kind of variation: differing taphonomic trajectories that may impact the relative taxonomic abundances. Researchers most commonly use the total number of identified specimens (NISP) of each set of taxa when calculating the abundance index, but NISP values may be affected by differences in selective transportation, butchering and processing methods, and post-depositional attrition (Lyman 2008, pp. 29–30).

Taphonomic forces begin with an animal's death and include decisions made by the hunter about which portions of the carcass to transport. Transportation decisions depend on a wide range of situational variables, such as the size of the animal, the number of individuals in a hunting party, and the distance to the residential base (e.g., Bartram 1993; Lupo 2006; Metcalfe and Jones 1988; O'Connell et al. 1990). As such, a single artiodactyl that has undergone some field processing will be represented by fewer skeletal parts than smaller game at the residential site. All else being equal, the AI is expected to decrease as large game are transported from greater distances even if the actual number of individual animals captured has remained the same. Subsequently, skeletal parts are fragmented through cultural and natural processes that affect the NISP and abundance measures (Cannon 2013), adding a second layer of complexity. Moderate fragmentation rates may result in an increase in NISP if each resulting portion can still be identified to taxon and element, while heavier fragmentation will lead to a decrease in NISP as fragments can no longer be identified (Grayson and Delpech 1998). For example, fracturing long bones to access marrow from the medullary cavity may increase the NISP, while heavy grease extraction activities that require pot-sized portions may result in a decrease in NISP.

Further fragmentation and deletion of skeletal parts may occur after discard through a number of post-depositional processes. Bone waste that is left on the surface is more likely to suffer from weathering (Behrensmeyer 1978; Phoca-Cosmetatou 2005), trampling (Behrensmeyer et al. 1986; Olsen and Shipman 1988), and scavenging (e.g., Marean and Spencer 1991; Marean et al. 1992; Munson and Garniewicz 2003) processes that systematically damage bone. Bone survivorship may be reviewed by comparing volume density values for specific skeletal portions against the frequency in which these portions are present in an archaeological assemblage (see Lam et al. 2003; Lyman 1994 for review). Density-mediated destruction studies have largely centered on disentangling the equifinality between bone survivorship and cultural practices, such as selective transportation and access to animal resources (Grayson 1989; Lam and Pearson 2005; Lyman 1985, 1994; Marean et al. 1992; see also Faith and Thompson, Chap. 6). This is reflected by the greater number of studies on bone density of large bodied mammals (Brain 1981; Elkin 1995; Kreutzer 1992; Lam et al. 1998; Lyman 1984, 1985; Stahl 1999; Symmons 2005) compared to those on small mammals (Lyman et al. 1992; Pavao and Stahl 1999).

Importantly, cultural practices of converting raw animal resources into consumable products may have direct consequences on the subsequent preservation of skeletal parts and thus NISP values. Scavengers systematically damage and delete skeletal parts from the assemblage in ways that correspond to the nutrition value and bone densities of the portion (e.g., Marean and Spencer 1991; Marean et al. 1992; Munson and Garniewicz 2003). Bone grease is frequently located in the portions of bone that are the least dense (e.g., cancellous bone of long bone epiphyses and the axial skeleton), and scavengers are more likely to destroy these parts in proportion of their fat content if it was not extracted prior to discard (Hudson 1993; Kent 1993; Lupo 1995; Lupo and Schmitt 1997; Speth 2000; Ugan 2005, 2010). As such, the attractiveness of discarded bone debris to scavengers is partly dependent on how animal resources were processed, which in turn is expected to vary according to the nutritional content of meat and skeletal components of the animal resource, the degree of nutritional stress for both the prey and consumer, and other factors (Church and Lyman 2003; Fisher and Johnson 2014; Outram 2002; Ugan 2005; Wandsnider 1997). For example, Speth (2000) applies this logic, comparing skeletal part representation with bone density, marrow index, and grease index values, to argue that jackrabbit and cottontail rabbits at the Henderson Site in New Mexico were mostly likely stewed, while prairie dogs (*Cynomys ludovicianus*) were roasted.

Notably, processing methods for a single resource may vary across time according to the overall foraging efficiency of the consumer. The marrow and grease component of the skeleton is a critical resource to foragers during times of resource stress (Speth and Spielmann 1983), and the extent of fragmentation and bone survivorship may be a function of dietary stress (Outram 2002). Marrow may be accessed with relative ease by breaking open bones to access the medullary cavity, but foragers may ignore low yielding parts (e.g., phalanges) during more plentiful times. Grease rendering has comparatively high extractive costs (Binford 1978, Lupo and Schmitt 1997, Outram 2002), although less intensive processes such as stewing may sufficiently extract grease as well. Outram (2002) uses the marginal value theorem to show that foragers should continue to process a carcass despite declining marginal net returns when the costs of finding, killing, and transporting a second resource are high. Intensified processing is expected when encounter rates with high ranking resources are low due to resource depression caused by overpredation or less favorable climatic conditions. Thus, the NISP of the high ranked resource may *increase* due to greater processing when in fact hunting efficiency has actually *decreased* and greater numbers of lower ranked resources are being acquired.

Ugan (2005, 2010) previously evaluated the relationship between culinary processing, density-mediated destruction, and taxonomic abundances using Parowan Valley assemblages from the eastern Great Basin. He found that density-mediated destruction varied among the artiodactyl assemblages from occupational units; when artiodactyl remains were abundant, there was lower skeletal part diversity and a strong statistical relationship between bone density and skeletal part representation (2005, p. 238). Just as Outram (2002) predicts using the marginal value theorem, Ugan hypothesized that during drier climatic periods, lower overall return rates for artiodactyls would have led to more intensive grease processing, which in turn would have promoted higher bone survivorship as such discarded remains are less attractive

to carnivores. During more favorable climatic conditions, hunting success of such large game would have increased due to an increase in encounter rates corresponding with higher game population densities; consequently, less intensive processing during plentiful times would have resulted in a decreased representation of artiodactyl remains as scavengers ravage discarded remains with nutritional content. Thus, the abundance index values were ultimately a reflection of climate rather than encounter rates with high ranking taxa, the decline of which is frequently taken to reflect resource intensification related to increases in human population densities. Fisher and Johnson (2014) similarly found high preservation levels for leporids remains at Antelope Cave, a Virgin Ancestral Pueblo site, despite evidence that domesticate dogs were present. They attribute the high level of preservation to intensive processing and limited access to higher ranked prey in a marginal arid environment.

Bone survivorship is expected to vary across contemporaneous deposits within a site due to variation in foraging efficiency differences among households, as well as differences in disposal. Bone that is rapidly buried is less likely to be ravaged by scavengers or exposed to weathering and other destructive forces. These forces may result in certain site contexts having strongly positive relationships between volume density and element representation, such as abandoned use surfaces that are left exposed, compared to contexts formed through the rapid accumulation of bone waste, such as in designated trash disposal area. Similarly, rapid accumulation of faunal remains due to feasting or hunting strategies (e.g., large communal hunts of pronghorn or jackrabbits) may result in greater survivorship but are not a reflection of day-to-day foraging activities.

In summary, the rate of bone attrition is expected to vary among taxa and assemblages in ways that influence our ability to evaluate the predictions of the prey choice model. If large game become less abundant on the landscape due to overhunting or less favorable environmental conditions, the prey choice model predicts that diet breadth should incorporate greater quantities of higher cost and typically smaller game resources. Yet, large game that are successfully captured are expected to be processed to a greater extent, which may counterintuitively lead to increased fragmentation and increased survivorship, both of which may result in an increase in NISP for large game when in fact fewer individuals were captured. The effects of differential survivorship may be investigated by identifying the variance in attrition among different animal resources and correlating this with an abundance index. Here, I draw upon data from a single archaeological site to illustrate such variation in density-mediated destruction among artiodactyl and leporid taxa across various contexts.

7.2 Five Finger Ridge Site Background

Five Finger Ridge is a large Fremont Period village site located in Clear Creek Canyon of central Utah (Fig. 7.1). The site was occupied at the end of the Fremont Period (ca. AD 400–1300), an archaeological culture of the eastern Great Basin

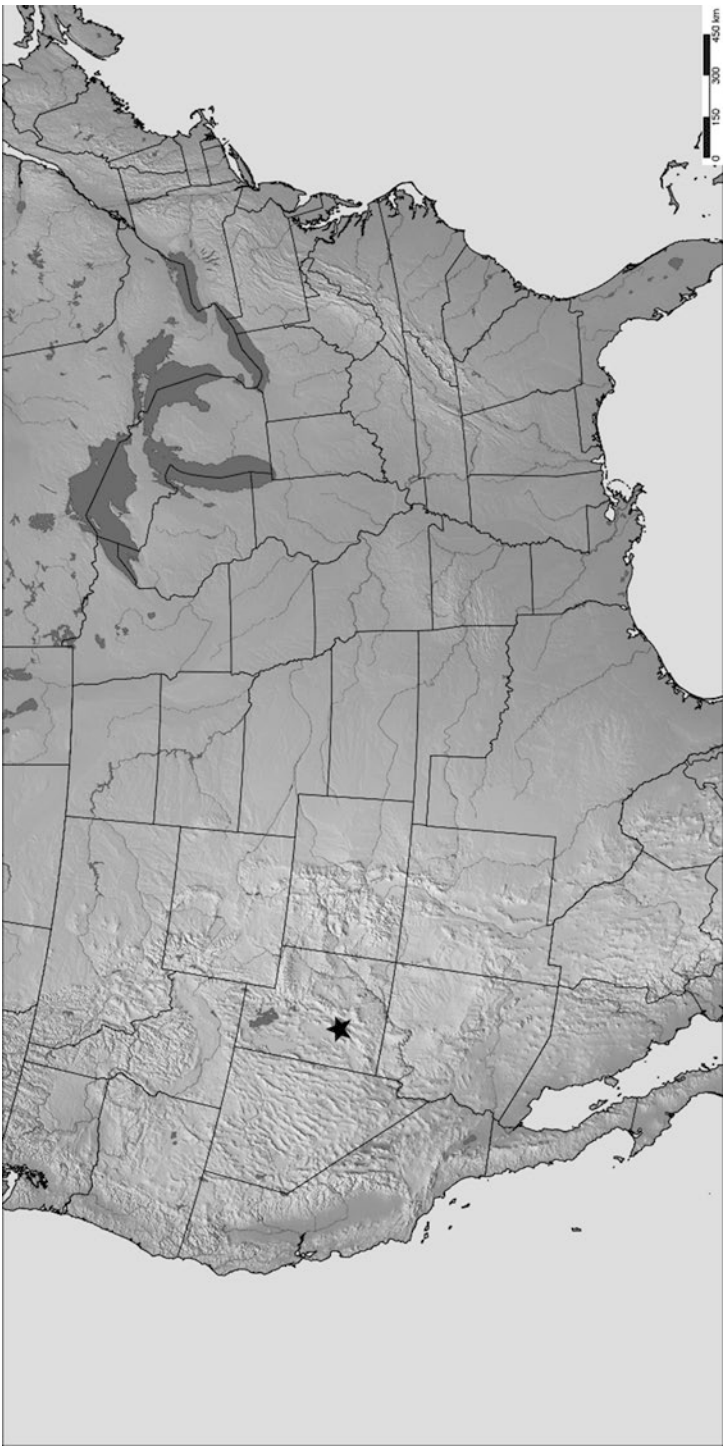

Fig. 7.1 Map of United States with location of Five Finger Ridge site (*star*) in the state of Utah

and northern Colorado Plateau. This period correlates with increased summer temperatures and moisture that allowed for maize horticulture and the appearance of bison (*Bison bison*) in the region (Grayson 2006; Madsen 1989; Madsen and Simms 1998; Rhode 2000; Talbot and Wilde 1989; Wigand and Rhode 2002). When summer monsoonal precipitation weakened ca. AD 1300 archaeological traces of bison, maize, and the Fremont disappear.

The site was excavated in 1984 by the Office of Public Archaeology at Brigham Young University in preparation for the construction of an interstate highway (Janetski et al. 2000; Talbot et al. 1998). Backhoes were initially used to define features, followed by hand excavations using a 1 × 1 m grid. Structure fill was excavated to within 20 cm of the floor as a single unit. The upper 10 cm of the lower fill was sifted through 1/4 inch (6.4 mm) screens, switching to 1/8 inch (3.2 mm) screens for the lower 10 cm of fill immediately above floor. All floor sediments, subfloor pits, hearths, and other features were screened using 1/8 inch sieves.

Excavated structures consist of subterranean, subrectangular pithouses (n = 37), circular to oval subterranean secondary pit structures (n = 23), rectangular surface structures (n = 19), a single square surface structure, and a single jacal (thatched wattle-and-daub) surface structure. Activity areas include use surfaces (n = 21), borrow areas where earth has been moved to construct other features (n = 7), and open features (n = 6). Pithouse structures vary in size from 5.5 to 31.6 m^2 with a mean of 12.9 m^2; however, the largest structure is an outlier and may be associated with village leaders. Secondary pit structures vary from 1.2 to 9.9 m^2 with a mean of 3.9 m^2, and rectangular storage structures range from 3.6 to 11.5 m^2 with a mean of 6.8 m^2 (Talbot et al. 2000). Feature floor deposits were assigned to temporal period based on a battery of dating methods, including radiocarbon, dendrochronology, archaeomagnetic dates, and obsidian hydration (Talbot et al. 2000). Three temporal periods were established: Period 1 (dates older than AD 1200), Period 2 (AD 1200–1300), and Period 3 (younger than AD 1300). Five Finger Ridge was most intensively occupied during Period 2, which is further subdivided into Period 2A (AD 1200–1250) and Period 2B (AD 1250–1300).

A greater abundance of faunal remains from pithouse floors compared to the other structures reflects heavier consumption and food preparation within these areas (Talbot et al. 2000). Variation in the quantity of bone on structure floors may represent differences in floor maintenance or seasonality of abandonment (Talbot and Janetski 2000). Food preparation appears to have been focused in the front of the pithouse and the area surrounding a central hearth (Talbot and Janetski 2000). Further, the distribution of faunal remains differs significantly between the floor and lower fill contexts, indicating that they were deposited as separate events (Talbot and Janetski 2000). As seen in Table 7.1, approximately 90% of the total NISP consists of unassigned medium-bodied artiodactyls, deer (*Odocoileus hemionus*), bighorn sheep (*Ovis canadensis*), unassigned leporids, jackrabbits (*Lepus* sp.), and two species of cottontail rabbits (*Sylvilagus audubonii* and *S. nuttallii*). Also noteworthy is the presence of canid remains, as domestic dogs and coyotes likely would have been attracted to disposed animal remains.

Table 7.1 Mammalian fauna identified at Five Finger Ridge

Taxon	NISP	%
Chiroptera/Eulipotyphyla	3	0.02
Leporidae	238	1.4
Lepus sp.	1729	10.3
Sylvilagus spp.	8732	52.0
Rodentia	248	1.5
Sciuridae	79	0.5
Ammospermophilus leucurus	3	<0.1
Cynomys sp.	2	<0.1
Marmota flaviventris	16	0.1
Spermophilus sp.	232	1.4
Tamia sp.	4	<0.1
Thomomys sp.	834	5.0
Dipodomys spp.	4	<0.1
Perognathus sp.	19	0.1
Castor canadensis	47	0.3
Crecetinae	1	0.1
Neotoma spp.	85	0.5
Microtus sp.	27	0.2
Ondatra zibethicus	50	0.3
Erethizon dorsatum	34	0.2
Carnivora	14	0.1
Canis spp.	28	0.2
Ursus americanus	11	0.1
Mustela frenata	14	0.1
Spilogale gracilis	1	<0.1
Lynx canadensis	1	<0.1
Lynx rufus	7	<0.1
Artiodactyla	2520	15.0
Odocoileus hemionus	838	5.0
Antilocapra americana	40	0.2
Bison bison	32	0.2
Ovis canadensis	917	5.5
Total NISP	16,793	

7.3 Methods

Measures of density-mediated destruction, abundance indices, and related analyses were computed among structural and activity area contexts, as well as across temporal units. Density-mediated destruction was evaluated for the artiodactyl taxa and cottontail rabbits. These taxa were chosen based on their relatively high abundances at the site, the availability of bone density data, and their frequent use in constructing abundance indices for evaluating resource intensification in western North

America (e.g., Broughton 1994; Janetski 1997; Szuter and Bayham 1989; Ugan 2005). Medium-bodied artiodactyls (deer, sheep, and pronghorn) were aggregated into a single category since some elements cannot be identified to species and inter-taxonomic variability in density values between artiodactyl taxa appear to be relatively minimal (Lam et al. 1999).

The density values for sheep provided by Lyman (1984) are used for all artiodactyl skeletal parts with the exception of selected long bone scan sites; I use the corrected values for limb bones provided by Lam et al. (1998). Since some skeletal parts of sheep were not included in these two analyses, values for deer (Lyman 1984) are used to supplement the missing values. Bone tool fragments, tool manufacturing debris, and neonatal specimens were removed from analysis. Neonatal (late fetal or newborn individuals less than a few weeks of age) artiodactyl remains were recovered frequently (NISP = 437). Juvenile skeletal parts have bone density values that are typically lower than adults, and high density portions are not distributed across the skeleton in the same rank order (Symmons 2005). Values for *Sylvilagus floridanus* (Pavao and Stahl 1999) are used as a proxy for *S. audubonii* and *S. nuttallii*. The caudal vertebrae, sternebrae, ribs, astragalus, metapodials, and phalanges of *Sylvilagus* were removed from this analysis to control for potential screening biases resulting from the use of 1/4 inch screens (Shaffer 1992; Shaffer and Sanchez 1994). Recovery of adult artiodactyls is not expected to be significantly impacted by screen-size recovery biases since small fragments (<1/4 inch) of large mammal bone cannot generally be identified to taxon and skeletal part.

Standardized number of identified specimens (NNISP) is used as the measure of skeletal abundance for comparison against density values. This measure is computed by dividing the number of identified specimens (NISP) containing a particular scan site on a skeletal part by the number of times the element is represented in a body (e.g., the NISP of paired appendicular elements and the mandible are divided by two; proximal, middle, and distal phalanges by eight, lumbar vertebrae by seven, etc.). NNISP has been shown to be a strong predictor of the minimum number of elements (MNE) measure due to statistical sampling (Grayson and Frey 2004). This relationship is present for both *Sylvilagus* and the artiodactyl taxa from the Five Finger Ridge assemblage (*Odocoileus* $r^2 = 0.79$, $p < 0.001$; *Ovis* $r^2 = 0.88$, $p < 0.001$; *Sylvilagus* $r^2 = 0.95$, $p < 0.001$). With the significantly positive relationship between MNE and NNISP, density-mediated destruction is evaluated using NNISP values instead of the derived MNE measure.

Null NNISP values are removed from analysis as it is unknown whether they represent real absences in the original population or are the result of destructive forces (Lam and Pearson 2004). Including the null values assumes that the faunal assemblage originally contained the complete skeleton, which is especially unlikely to be the case for large game that was selectively transported to reduce travel costs from the kill locality. The absence of high density skeletal parts would be suggestive of selective transportation, especially when such parts have low economic utility (e.g., tarsals and carpals). However, the absence of low density skeletal parts, such as much of the axial skeleton, could be due to subtraction associated with post-depositional forces or disposal at a primary processing site to reduce travel costs. It is noted that density-

mediated destruction analyses were conducted with the null values, but the more conservative approach of removing the null values is presented here since the results are not substantially different. When evaluating variability in attrition among site contexts, I restricted the analysis to proveniences with artiodactyl sample sizes (NISP) of greater than 30.

In evaluating the impact of differential survivorship on relative taxonomic abundances, I use an abundance index (AI) formed by dividing the frequency of artiodactyls with the total frequency of artiodactyls and *Sylvilagus*:

$$AI = \frac{\Sigma NISP_{Artiodactyl}}{\Sigma NISP_{Artiodactyl} + \Sigma NISP_{Sylvilagus}}$$

I select this measure because it has become standard in addressing issues related to resource depression and diet breadth (e.g., Bird and O'Connell 2006; Broughton 2002; Lupo 2007), including those in the Fremont area (e.g., Janetski 1997; Janetski et al. 2000; Ugan 2005). Neonatal specimens are not calculated into this measure since such young individuals represent sessile resources with low pursuit costs and lower caloric returns. As discussed above, NISP may be impacted by a number of factors, such as differential survivorship, selective transportation, the number of skeletal parts among species (Lyman 2008), and there are reasons to believe that these influences are not equally distributed across taxa. Using the minimum number of individuals (MNI) when computing the abundance index may circumvent these issues since each individual should be represented by dense skeletal portions. MNI was computed based on the most redundant skeletal part within each context for spatial comparisons and the aggregated dated contexts for temporal periods.

7.4 Results

7.4.1 Site Wide Evaluation

The relationship between artiodactyl NNISP for the site-wide assemblage and volume density is significantly positive for artiodactyls ($r^2 = 0.42$, $p < 0.001$; Fig. 7.2). The relationship for *Sylvilagus* is marginally insignificant ($r^2 = 0.08$, $p = 0.07$; Fig. 7.3). These data suggest that bone density partly explains the skeletal part representation for artiodactyls, but not for cottontail rabbits, although some other factors are likely influencing skeletal representation as well (e.g., variation in food processing, use of high density parts for bone tools, etc.).

Much of the attrition at Five Finger Ridge is best explained by carnivore ravaging based on the relative abundance of carnivore markers (e.g., digestive polishing, gnaw marks, punctures, etc.) across the site and among skeletal parts of varying nutritional quality. Carnivore marks on artiodactyl bones were not uncommon (9.6% of total NISP) and mostly consist of flaking (1%), pits (18%), punctures

(3%), scores (13%), digestive polishing (16%), or a combination of these traits (46%). These markers are non-randomly distributed among artiodactyl skeletal parts ($\chi^2 = 92.03$, $p < 0.001$). When the chi-square adjusted residuals for the presence of carnivore markers are compared with Binford's (1978) logged-transformed grease index values to correct for a curvilinear relationship, there is a significant relationship ($r^2 = 0.29$, $p = 0.004$; Fig. 7.4). Carnivore markers, primarily in the form of digestive polishing (95% of markers), were found on approximately 10.2% of the identified *Sylvilagus* specimens. These markers are non-randomly distributed among *Sylvilagus* skeletal parts ($\chi^2 = 231.24$, $p < 0.001$). Following Speth (2000),

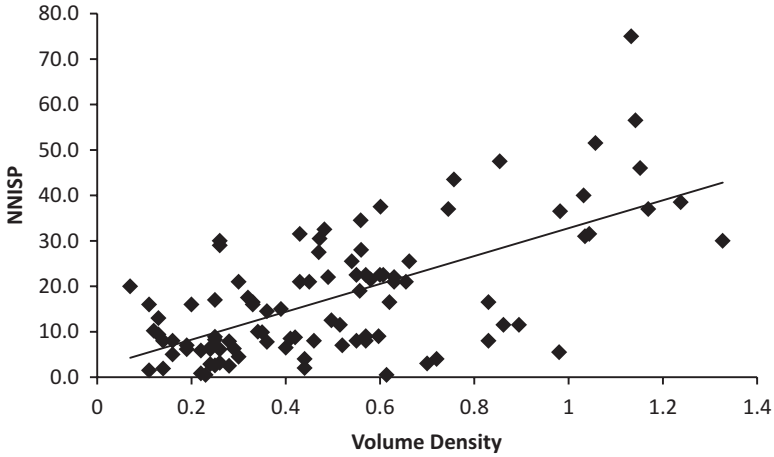

Fig. 7.2 Relationship between bone density values and normed number of identified artiodactyl specimens (NNISP) for the complete Five Finger Ridge assemblage ($r^2 = 0.42$, $p < 0.001$)

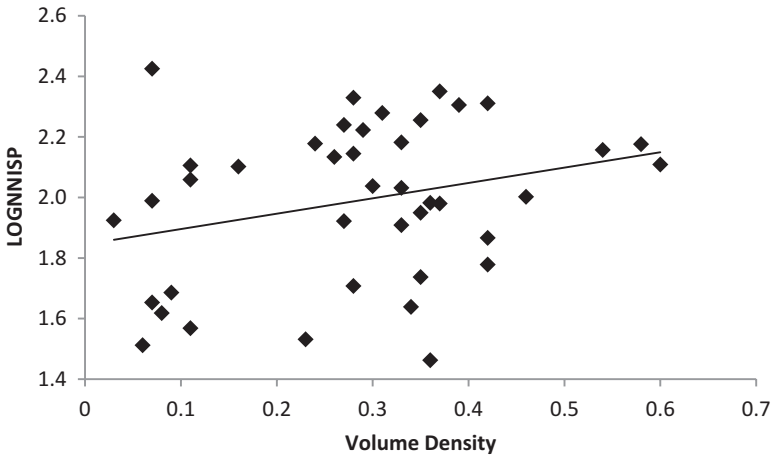

Fig. 7.3 Relationship between bone density values and normed number of identified *Sylvilagus* specimens (NNISP) for the complete Five Finger Ridge assemblage ($r^2 = 0.08$, $p = 0.07$)

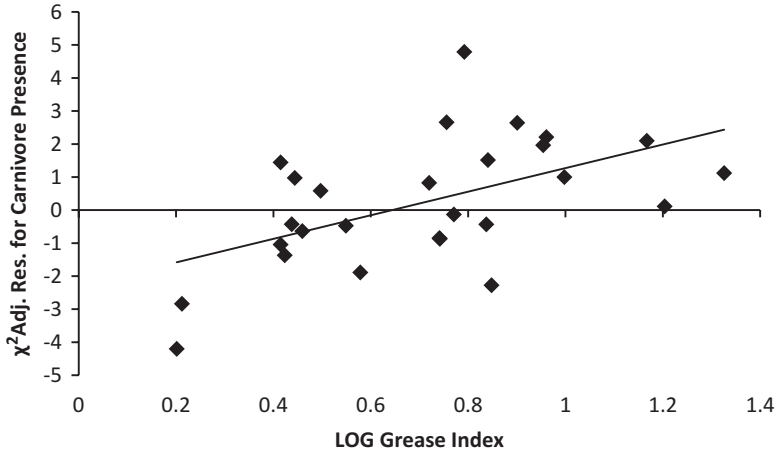

Fig. 7.4 Relationship between the chi-square adjusted residuals for the presence of carnivore marks and the grease index for each artiodactyl skeletal part ($r^2 = 0.29$, $p = 0.004$)

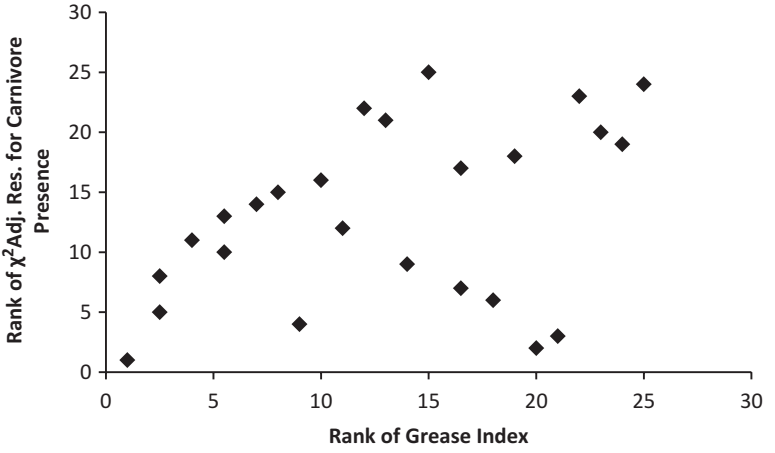

Fig. 7.5 Rank-ordered relationship between the chi-square adjusted residuals for the presence of carnivore marks and the grease index for each *Sylvilagus* skeletal part (Spearman's rho: $r_s = 0.41$, $p = 0.04$)

the adjusted residuals for carnivore markers on leporids are compared against Binford's utility index values for caribou since comparable data on grease content that takes into account bone density and volume is not available for the former; as there is no reason to believe that the absolute values for caribou correspond tightly with those for *Sylvilagus*, the relationship is examined using Spearman's rho. As with the artiodactyl remains, there is a significant relationship between the frequency of carnivore markers and fat volume among *Sylvilagus* remains (Spearman's rho: $r_s = 0.41$, $p = 0.04$; Fig. 7.5).

Burned artiodactyl specimens are rare (2.5% of NISP). Burning is randomly distributed across the artiodactyl skeleton ($\chi^2 = 7.30$, $p = 0.40$). As such, heat-altered surfaces cannot be conclusively related to roasting activities and may have resulted from being exposed to fire after disposal. Filleting cutmarks (Binford 1981) are common in the artiodactyl assemblage (41% of total cutmarks), and it may be that meat was deboned prior to cooking. The presence of impact marks on 10.5% of the artiodactyl specimens indicates that marrow was accessed from bone cavities. Intensive grease extraction would have occurred after the meat and marrow were removed, consisting of boiling bone parts that have been reduced in size for long durations of time. The reduction of bone portions may be identified by the presence of chop marks, which are rare in the Five Finger Ridge assemblage (n = 12) and likely represent disarticulation of the carcass as they are generally located near joints. "Pot polish" on the edges of bone surfaces may occur after boiling bones for long durations in ceramic pots, but polishing may also result from trampling, alluvial actions, and other post-depositional forces (e.g., Hurlbut 2000; Turner and Turner 1999; White 1992). Pot polishing was not noted in the assemblage. While grease may still have been extracted less intensively via wet cooking, the relationship between carnivore marks and bone grease values suggests that secondary consumers were attracted to discarded bones with remaining nutritional value.

Evidence of culinary processing is limited to burning for the *Sylvilagus* assemblage. While the distribution of burning is more strongly patterned among the *Sylvilagus* remains compared to the artiodactyls ($\chi^2 = 27.16$, $p = 0.007$), it is so infrequent that roasting does not appear to have been a common preparation method at the site. Although it cannot be conclusively identified, it is likely that leporids were stewed but for a relatively brief duration since it is clear that carnivores were still scavenging skeletal parts with the highest grease content.

7.4.2 Spatial Comparisons

There is considerable variability in the degree to which density-mediated destruction explains skeletal part frequencies for both artiodactyls and *Sylvilagus* within individual contexts (Table 7.2). Some contexts follow the site-wide pattern where attrition is relatively high for artiodactyls but not *Sylvilagus*, such as Structures 30 and 38; comparatively low AI values from these contexts may be due to relatively lower rates of survivorship for artiodactyl remains. In contrast, bone density values from Structure 29 and Activity Area 9 are a stronger predictor for *Sylvilagus* skeletal part representation compared to artiodactyls, and these two contexts have relatively high AI values. This suggests that the varying degrees of bone attrition has an impact on this measure used to evaluate the prey choice model.

AI values calculated using NISP and MNI values vary considerably among proveniences, ranging from 0.10 (high *Sylvilagus* abundance) to 0.73 (high artiodactyl abundance). This variation is not dependent on sample size ($r^2 = 0.04$, $p = 0.23$).

Table 7.2 Artiodactyl and *Sylvilagus* skeletal part attrition, number of identified specimens (NISP), minimum number of individuals (MNI), and abundance indices (AI) in Five Finger Ridge structure and activity area fill contexts

	Artiodactyl				*Sylvilagus*					
			NNISP:VD				LOGNNISP:VD		AI	AI
Provenience	NISP	MNI	r^2	p	NISP	MNI	r^2	p	(NISP)	(MNI)
Activity area 09	274	7	0.06	0.03	393	17	0.33	0	0.41	0.29
Activity area 24	94	4	0.04	0.16	190	7	0.10	0.05	0.33	0.36
Activity area 28	156	5	0.09	0.01	219	13	0.14	0.02	0.42	0.28
Structure 03	158	3	0.02	0.29	548	15	0.06	0.12	0.22	0.17
Structure 04	26	2	0.18	0.05	67	2	0.06	0.18	0.28	0.50
Structure 09	30	2	0.01	0.59	27	2	0.05	0.15	0.67	0.50
Structure 14	32	2	0.30	0.01	16	2	0.01	0.8	0.24	0.50
Structure 17	39	2	0.01	0.55	121	5	0.13	0.05	0.27	0.29
Structure 20	32	2	0.01	0.71	85	6	0.03	0.34	0.50	0.25
Structure 21	61	3	0.17	<0.01	62	5	0.01	0.65	0.26	0.38
Structure 22	115	3	0.10	0.01	323	14	0.05	0.17	0.33	0.18
Structure 26	171	1	0.03	0.22	340	13	0.09	0.07	0.46	0.07
Structure 28	176	5	0.00	0.91	204	8	0.06	0.16	0.40	0.38
Structure 29	101	4	0.12	0.02	154	5	0.41	<0.01	0.45	0.44
Structure 30	104	2	0.29	<0.01	125	7	0.02	0.5	0.20	0.22
Structure 33	46	3	0.06	0.17	188	6	0.09	0.07	0.18	0.33
Structure 36	53	2	0.31	<0.01	236	12	0.05	0.15	0.15	0.14
Structure 38	45	2	0.55	<0.01	246	8	0.12	0.03	0.18	0.20
Structure 48	50	2	0.17	0.24	80	3	0.12	0.07	0.19	0.40
Structure 56	98	4	0.18	<0.01	414	20	0.09	0.07	0.22	0.17
Structure 57	83	4	0.07	0.04	292	11	0.15	0.02	0.71	0.27
Structure 60	79	3	0.13	0.04	33	1	0.01	0.64	0.36	0.75
Structure 61	239	4	0.02	0.21	419	18	0.33	<0.01	0.28	0.18
Structure 70	46	4	0.12	0.04	69	5	0.05	0.19	0.40	0.44
Structure 75	66	2	0.18	<0.01	99	5	0.07	0.19	0.29	0.29
Structure 79	66	2	0.01	0.52	160	7	0.03	0.3	0.53	0.22

To evaluate the relationship between attrition and the abundance index, the log-transformed abundance index values were compared against significant ($p < 0.05$) coefficient of determination (r^2) values for artiodactyl attrition. There is a significant negative relationship ($r^2 = 0.47$, $p = 0.004$; Fig. 7.6) that demonstrates that as density-mediated destruction increases, artiodactyl relative abundance decreases. Since this comparison does not take into account the rate of attrition for *Sylvilagus*, a similar comparison was made using coefficient of determination values for *Sylvilagus*; there is no significant relationship ($r^2 = 0.04$, $p = 0.62$). It appears that

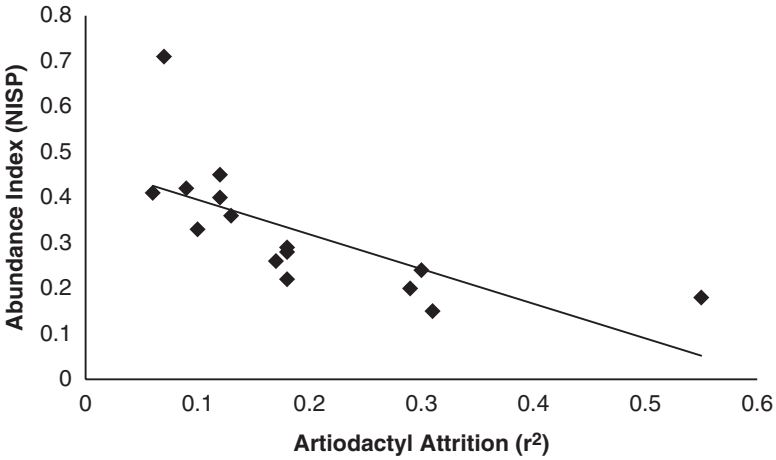

Fig. 7.6 Relationship between the abundance index based on NISP values and significant coefficient of determination values for artiodactyl density-mediated destruction ($r^2 = 0.47$, $p = 0.004$)

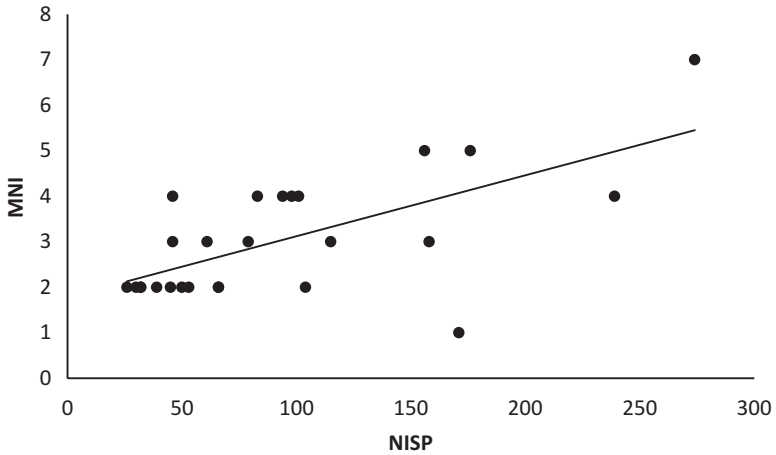

Fig. 7.7 Relationship between artiodactyl MNI and NISP values for individual site contexts ($r^2 = 0.43$, $p < 0.001$)

the relative survivorship of artiodactyl remains is a strong predictor for the abundance index.[1]

The relationship between MNI and NISP among site contexts is significant for both artiodactyls ($r^2 = 0.43$, $p < 0.001$; Fig. 7.7) and *Sylvilagus* ($r^2 = 0.85$,

[1] Simpson's 1/D values were also computed for each site context as this diversity measure incorporates a wider range of taxa than the abundance index. When 1/D values are compared against the difference in attrition among site contexts, the relationship is similarly significant ($r^2 = 0.35$, $p = 0.04$). This is likely due to the fact that artiodactyl and leporid remains are by far the most common taxa and thus are driving the relationship.

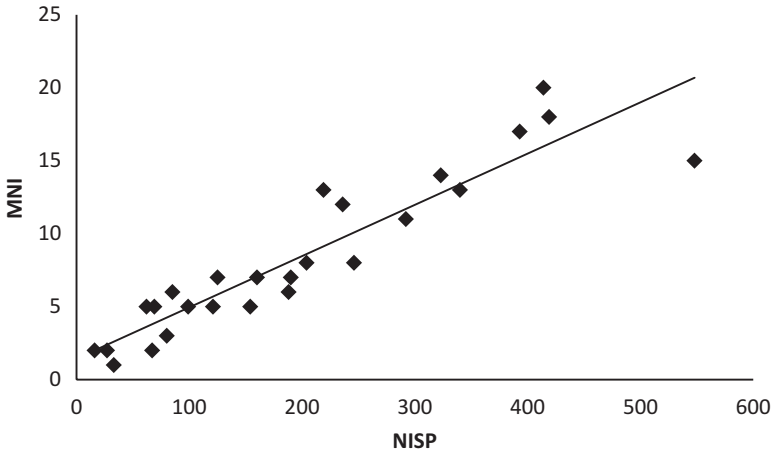

Fig. 7.8 Relationship between *Sylvilagus* MNI and NISP values for individual site contexts ($r^2 = 0.85$, $p < 0.001$)

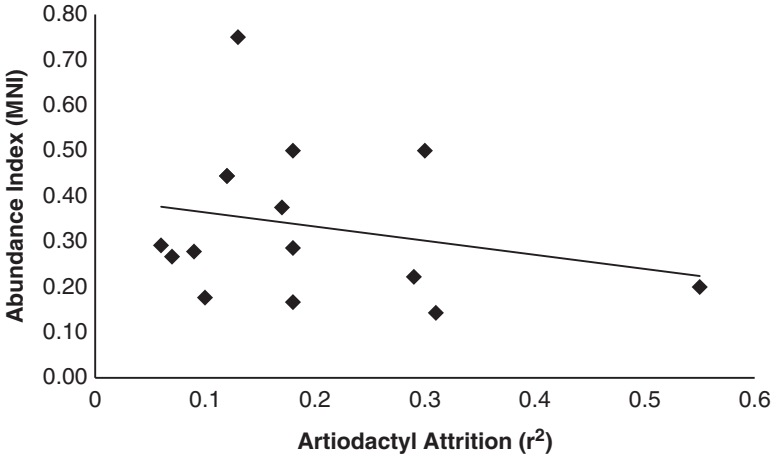

Fig. 7.9 Relationship between the abundance index based on MNI values and significant coefficient of determination values for artiodactyl density-mediated destruction

$p < 0.001$; Fig. 7.8). It is noteworthy that NISP is a much weaker predictor of MNI for artiodactyls, possibly reflecting issues associated with density-mediated destruction that results in the survivorship of fewer but denser specimens per individual. When the abundance index is computed using MNI values and compared against the coefficient of determination for artiodactyl attrition, there is no relationship ($r^2 = 0.06$, $p = 0.39$; Fig. 7.9). However, this does not necessarily mean that the abundance index based on MNI values is a stronger reflection of foraging behaviors across site contexts, as it is highly probable that large game were shared broadly across the site and secondary consumers were an active depositional

agent. For both taxa, there is significantly higher frequency of carnivore markers in structural fill than floor surfaces (artiodactyl $\chi^2 = 6.89$, $p = 0.009$; *Sylvilagus* $\chi^2 = 47.87$, $p < 0.001$), indicating that secondary consumers were likely depositing bones in abandoned site contexts.

7.4.3 Temporal Comparisons

Density-mediated destruction was also evaluated across temporal units and compared against the abundance index values. As seen in Table 7.3, there is no significant relationship between volume density and skeletal part representation for *Sylvilagus* for all four temporal periods. In contrast, the relationship for artiodactyl remains is significant for three of the four temporal periods; the marginally insignificant relationship for Period 3 is likely a reflection of the small sample size. The abundance index values show relatively little variation among temporal units regardless of whether NISP or MNI values are used (Fig. 7.10); the relative abundance of artiodactyls to cottontail rabbits does not significantly differ among temporal units (NISP: $\chi^2 = 4.15$, $p = 0.25$; MNI: $\chi^2 = 0.80$, $p = 0.85$).

7.5 Discussion

Since measures of relative taxonomic abundances are ultimately based on the number of identified specimens, it is critical that we evaluate the influence of selective transportation, survivorship, fragmentation and similar factors vary across taxa and time prior to testing hypotheses regarding human behavior and exploitation of faunal resources. It is expected that the rate at which secondary consumers ravage discarded bone will correspond with the methods used to transform raw animal products into consumables; methods that effectively remove lipid content from bone are likely to result in greater survivorship of the discarded remains, and such processing

Table 7.3 Artiodactyl and *Sylvilagus* skeletal part attrition, number of identified specimens (NISP), minimum number of individuals (MNI), and abundance indices (AI) among Five Finger Ridge temporal periods

	Artiodactyl				*Sylvilagus*					
			NNISP:VD				LOGNNISP:VD			AI
Period	NISP	MNI	r^2	p	NISP	MNI	r^2	p	AI (NISP)	(MNI)
1	298	7	0.08	0.01	767	24	0.04	0.24	0.28	0.23
2A	188	5	0.32	0.001	427	12	0.04	0.23	0.31	0.29
2B	301	8	0.32	0.001	699	23	0.00	0.74	0.30	0.26
3	15	2	0.22	0.07	57	3	0.00	0.91	0.21	0.40

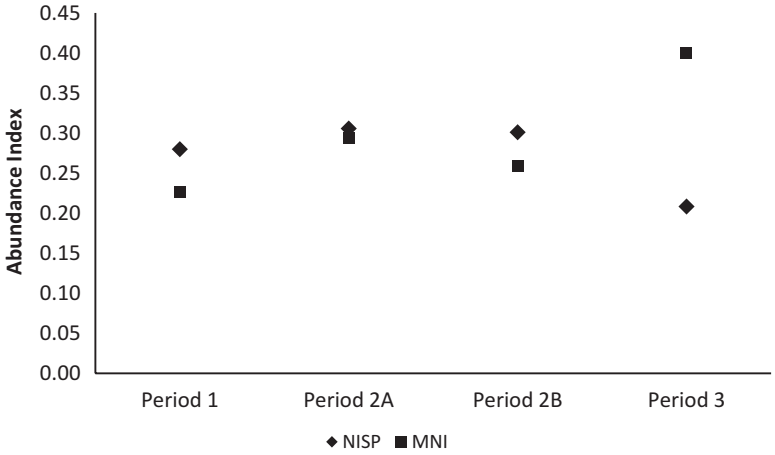

Fig. 7.10 Relationship between abundance index values based on NISP and MNI, and temporal designations

methods are expected to correspond with individual animal, the degree of resource stress experienced by the foragers, and other factors.

Corroborating previous investigations (e.g., Ugan 2005), this case study demonstrates that the number of identified specimens in an assemblage is ultimately influenced by complex taphonomic histories that may increase or decrease the rate of identification for one taxon over another. The relationship between attrition and taxonomic abundances from Five Finger Ridge is different from that detected by Ugan (2005), who found that density-mediated destruction for artiodactyls and lagomorphs were strongly correlated. At Five Finger Ridge, density-mediated destruction of artiodactyls and *Sylvilagus* do not correspond with one another. Nonetheless, the fact that both studies have demonstrated relationships between attrition and relative taxonomic abundances is the critical lesson here.

Regardless of how the differences in density-mediated destruction patterns are explained, differing rates of survivorship can have an impact on relative taxonomic abundances. This finding demonstrates the importance of accounting for variation in density-mediated destruction among multiple species before any human behavioral inferences are formed from taxonomic diversity measures. My original research goals at Five Finger Ridge (Fisher 2010) were to identify real spatial differences in taxonomic representation that represent differences in individual foraging decisions and spatial organization. Spatial differences are expected to vary between the sexes (e.g., Bird 1999; Hawkes 1996), between individuals within a sex (e.g., Lupo and Schmitt 2004; Smith et al. 2003), and within a single individual's life-history (e.g., Bird and Bliege Bird 2000; Kaplan et al. 2000). However, relative skeletal part abundances and taxonomic abundances within each context at Five Finger Ridge are not an accurate reflection of real spatial differences in taxonomic representation, but are instead the product of varying taphonomic processes.

The intertaxonomic and intrasite variation in skeletal part attrition may relate to depositional processes. Carnivores frequently remove faunal remains from their original context and redeposit them elsewhere (e.g., Kent 1981; Marean et al. 1992; Ugan 2010), and this may alter the distribution of skeletal parts in a way that corresponds with their nutritional utility and density values. Skeletal remains with high grease content are expected to be removed by scavengers from their original location of discard and deposited elsewhere (within or outside the archaeological site), leaving skeletal parts with low nutritional value behind. Based on ethnoarchaeological work in the American Southwest, Kent (1981) found that that the spatial distribution of faunal remains is determined primarily by domestic dogs that frequently take bones to specific locations to avoid competition with other dogs. However, identifying secondary deposition by carnivores may be difficult, as Kent also found an absence of carnivore markers on bones that were broiled or boiled. As such, cultural or behavioral interpretations based on spatial distribution of faunal remains must be demonstrated rather than assumed in regions where secondary consumers such as coyotes and domestic dogs are present.

The lack of demonstrable temporal change in the abundance index regardless of whether NISP or MNI measures are used is in contrast to other data from Five Finger Ridge that show changes in taxonomic exploitation when analyses are restricted to animals of similar body size. Fisher (2012) argues that there was an expansion of pinyon-juniper woodlands in the vicinity of Five Finger Ridge based on an increase in the relative abundances of *Sylvilagus nuttallii* over *S. audubonii*, as well as a decrease in the relative abundance of jackrabbits to cottontails. There is also a significant decrease in the relative abundance of bighorn sheep to deer in Period 2A, corresponding with significantly different carbon and strontium isotope values that collectively suggest that fewer sheep were acquired from higher, more distant elevations at this time (Fisher and Valentine 2013). Further, when relative body part representation is evaluated using Stiner's (2002) anatomical units that contain an even distribution of high density parts to control for density-mediated attrition, the mean food utility index values (Broughton 1994; Metcalfe and Jones 1988) increases incrementally through time. This indicates that low utility parts were increasingly discarded prior to transportation to Five Finger Ridge, most likely to reduce travel costs as local abundances of artiodactyls decreased (Broughton 1994; Nagaoka 2005). Collectively, these data demonstrate that real temporal trends associated with foraging efficiency and local environmental changes can be identified even when the abundance index measure does not demonstrate such a trend.

7.6 Conclusion

Abundance indices are frequently used to evaluate the diet breadth model based on optimal foraging theory (for examples, see Bird and O'Connell 2006; Lupo 2007; Morgan 2015). This research area has significantly contributed to our understanding of the relationship between humans and their surrounding environments, such as the

impact of climate-induced resource fluctuations and overhunting by prehistoric peoples. The potential relationship between conversion of raw animal resources into food products and bone attrition rates demand the evaluation of density-mediated destruction. Variation in differential survivorship among taxa across sites and time should be expected by researchers. Since these influences cannot easily be controlled, caution must be exercised prior to testing hypotheses derived from optimal foraging theory, especially when multiple assemblages are combined into a spatial or temporally averaged dataset (Lyman 2003). One cannot simply remove from analysis assemblages that demonstrate high levels of attrition as it is also critical to understand why some assemblages appear to be unaffected by density-mediated destruction. The relative survivorship of zooarchaeological remains captured in these variable assemblages may actually be a product of behaviors related to foraging efficiency. While using derived measures (e.g., MNI) may bypass some of the issues with differential transportation, survivorship, and fragmentation, these introduce a range of additional problems (see Lyman 2008 for review). Instead, researchers must rely on a number of independent measures in conjunction with relative taxonomic abundances for testing foraging theory predictions.

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Chapter 8
Shell Fragmentation Beyond Screen-Size and the Reconstruction of Intra-Site Settlement Patterns: A Case Study from the West Coast of South Africa

Antonieta Jerardino

8.1 Introduction

Studies on shell taphonomy and shell fragmentation are useful for increasing the accuracy and thus reliability of behavioral and environmental inferences supported by shell analysis (Claassen 1998; Muckle 1985; Waselkov 1987). More specifically, these studies allow a better understanding of depositional sequences and site stratigraphy by facilitating the separation of cultural and natural processes; the assessment of post-depositional disturbance in shell deposits; identification of activity areas; the evaluation of retrieval method (screen sizes) effectiveness; as well as the estimation of shell weight loss and biases in prey selection and shell size (e.g., Claassen 1998; Faulkner 2010, 2011; Ford 1989; Jenkins 2006; Jerardino and Navarro 2008; Muckle 1985, 1994; Peacock 2000; Shiner et al. 2013; Stein 1992). In general, this body of work has shown that the archaeological record is likely to be biased in one or more ways, and while cogent explanations regarding shell fragmentation are formulated, most of them exist in the realm of postscripts rather than testable scenarios. Few archaeological studies, however, have been designed explicitly to assess quantitatively the relationship between shell fragmentation and the factors responsible for them (for instance, Muckle 1985, and references therein; Stein 1992).

Shell fragmentation in archaeological assemblages is the result of a combination of factors such as exoskeletal shell traits and taphonomic factors that act mostly after deposition. Other than the negative effects of industrialization and natural catastrophic

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episodes (Claassen 1998; Waselkov 1987), the following is a summary and by no means comprehensive review of the main factors affecting shell fragmentation.

As is obvious and shown by studies, taxa with more robust or heavily ribbed shells will break up less easily than fragile ones lacking these traits (Ford 1992; Gutiérrez-Zugastí 2011; Mowat 1994; Muckle 1985; Waselkov 1987). Resistance to breakage seems to depend to a large extent on shell thickness, but also on the internal shell architecture, its structure (presence of nacre, crossed-lamellar, foliated … etc.), mineralogy (calcite and/or aragonite) and quantities of organic fraction in the shell matrix. The latter is susceptible to chemical oxidation and/or organic decomposition which can accelerate with warm temperatures (Claassen 1998; Driscoll and Weltin 1973; Faulkner 2011; Zuschin et al. 2003). Shell size, which is related to shell robustness, has also been argued as a factor in shell fragmentation in surface midden deposits, (Ford 1989; Jerardino and Navarro 2008), although inter-site variability has been observed for same-size valves and explained as a result of differences in animal through-fare (Mowat 1994).

Taphonomic factors that act upon shells before human collection and deposition include physical abrasion and rolling in intertidal zone as well as encrustation, abrasion, and perforation from various aquatic animals, resulting in shell pitting and thus greater vulnerability to breakage (Claassen 1998; Muckle 1985). After collection and deposition, water can negatively impact shells easily as a result of direct immersion (i.e., flooding), ground water saturation (fluctuating water tables), or atmospheric humidity (rain, dew or fog). All of these variables can bring about the decomposition of organic shell content, dissolution (depending on the acidity of burial environments), weathering, and chemical conversion (Claassen 1998; Faulkner 2011; Ford 1989; Stein 1992; Waselkov 1987; Zuschin and Stanton 2001). Root growth (aided by water) enhances shell fragmentation and weight loss through slow shoving and crushing and by increasing levels of acidity, which further contributes to this process (Claassen 1998; Faulkner 2011; Waselkov 1987). Heating, particularly above 200 °C, is especially conducive to shell fragmentation, weight loss and, when shell is turned into lime, complete obliteration (Claassen 1998). Burnt shell fractures more easily because the organic fraction that provides shells with elasticity and cohesion is combusted and the crystallinity of the calcium carbonate is severely altered, resulting in the breakdown of the internal shell structure (Claassen 1998). Wind action can also abrade shell, particularly when transporting sand (Muckle 1985; Rick 2002).

Compaction due to overburden and contact between shells has been shown to induce breakage in paleontological and modern assemblages (Zuschin et al. 2003; Zuschin and Stanton 2001), but this is yet to be properly tested in archaeological contexts as argued by Muckle (1985). Low shell densities, on the other hand, may translate into less shell breakage as shell can get cushioned by finer and softer sediments (i.e., fine sands and loam) and thus minimize physical and possibly other types of damage (Gutiérrez-Zugastí 2011; Muckle 1985). Other depositional processes can aid in the preservation of shell. For instance, it has been suggested that

rapid burial (high sedimentation or accumulation rates due to human or natural agency) is conducive to better preservation of shell material and stratigraphic context (Claassen 1998; Faulkner 2011; Muckle 1985; Stein et al. 2003; Waselkov 1987). However, this relationship remains to be explored explicitly and quantitatively. Processing for consumption, intense occupation events, human trampling, dumping and excavations of semi-subterranean features, such as roasting pits and post holes, can also contribute substantially to shell fragmentation (Balbo et al. 2010; Cannon 2013; Faulkner 2011; Ford 1989; Maggs and Speed 1967; Muckle 1985; Waselkov 1987). Shellfish foraging choices might add further to the complex interplay of variables affecting shell preservation. For instance, the influence of species richness and diversity on the degree of fragmentation of a single taxon has hardly been considered (but see brief reference in Mowat 1994, pp. 208–209 and in Maggs and Speed 1967, p. 87). In other words, would a species of shell (whatever the vulnerability to fracturing) break up more easily when present in greater or lower relative abundances? Or, would the inclusion of different numbers of shell taxa in different proportions affect shell fragmentation of each of these species?

Thus, many are the causes that drive shell fragmentation in archaeological contexts, and these need to be addressed on a case-by-case basis given the variable contexts within which sites have formed. Ideally, as many of these variables as possible ought to be examined at single sites to understand shell taphonomy (i.e., Stein 1992), although often this is not possible. Moreover, some of the analytical steps involved in quantifying shell fragmentation, such as screening through stacked meshes of different sizes and weighing the retained contents (Muckle 1985; Stein 1992), can be time consuming and pose challenges in finding additional space for processing and storing adequate numbers of shell samples. Shell fragmentation is also quantified by means of counting shell fragments and establishing ratios such as NISP/MNI (or its inverse), (NISP/weight) × 100 or Diagnostic Fragments/NISP (Faulkner 2011; Gutiérrez-Zugastí 2011; Jenkins 2006) which adds a further step when quantifying shell assemblages. There would be obvious advantages to devising a way in which standard data is habitually collected when quantifying archaeomalacological assemblages in order to reliably quantify shell fragmentation.

In this chapter, a new method for quantifying shell fragmentation is thus presented with data from a shell midden from the West Coast of South Africa. The causal link between shell fragmentation and intensity of site-usage, shell species composition, and original shell size is explored through the use of several quantifiable proxies (i.e., fragmentation index, deposition rate, shell density, residential permanence index). Undeniably, the available radiocarbon data is somewhat limited, which translates into a low-resolution chronology and rather coarse-grained proxies for intensity of site occupation. However, this case study is of an exploratory nature and its methodological lessons can be tested in the future. Once the observed consistency and predictability of the relationship between shell fragmentation and site-usage is verified at other sites, then this method can be used as a tool for reconstructing settlement patterns locally and elsewhere.

8.2 Case Study

A large and diverse set of observations on shellfish assemblages from the West Coast of South Africa has been generated over the last 50 years, but studies specifically on shell taphonomy have been extremely limited. While Maggs and Speed (1967) examined shell fragmentation as a way to characterize site formation processes, Jerardino and Navarro (2008) and Noah (2007) looked at the effect of shell fragmentation on the differential preservation of limpet shells along their size range. However, neither of these studies were designed to identify the factors behind shell fragmentation. Doing so is thus now necessary if we are to improve our understanding of site formation and variability in mollusc assemblages along the South African West Coast.

Among the many sampled shell middens in this region, Pancho's Kitchen Midden is one of the best suited for studying shell fragmentation explicitly. This site was excavated systematically and with great detail following the natural stratigraphy and much effort was made to isolate as many individual depositional events as possible. Its abundant shell contents allowed sampling of large shell bulks along contiguous squares (1 × 1 m) and establishing a detailed quantitative assessment of mollusc taxa as well as associated sediments and artifacts (Jerardino 1997, 1998). Shell fragmentation of a single taxon and under different species composition can be also studied because its faunal sequence changes from a nearly mono-specific to one with a mix of species. Moreover, as the surface extent of this site (~113 m^2) is modest when compared to others in the area, there is a better control on the spatial variability of strata, and thus a good degree of confidence can be placed on the assumptions that support the quantification of proxies (see Sect. 8.3 below). Lastly, the study area is part of a dryland-dominated landscape that extends through much of central and northern parts of the South African West Coast (Chase and Meadows 2007). This means limited precipitation and low water tables which reduce the incidence of additional taphonomic factors affecting shell preservation.

8.2.1 Pancho's Kitchen Midden: Location, Stratigraphy and Dating

Pancho's Kitchen Midden is a small rocky overhang with a low-sloping talus situated about 1.7 km from the coast and at an altitude of 45 m above present sea level (32° 20′20.58″ S, 18° 19′57.66″ E) (Fig. 8.1). The shelter faces south-west and, being relatively small, it must have offered only marginal protection from the elements. It is located on the south-facing foothills of Waterkloof. Nearby, a streamlet that becomes active during the winter rains runs about 8 m below the site's talus slope and mostly below ground. The deposit extends for about 12 m from the highest point of the site to the visible edge of the midden (Fig. 8.2).

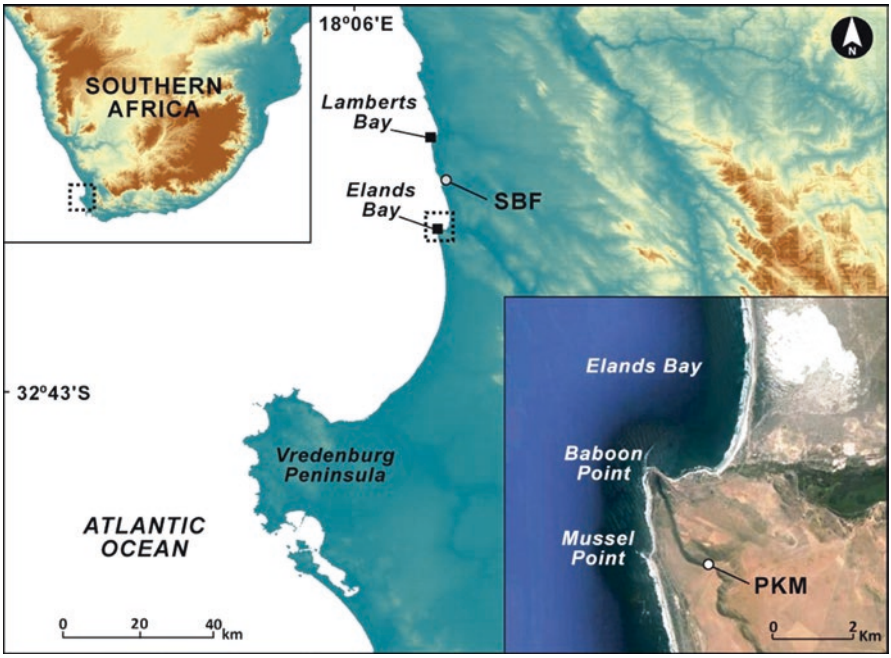

Fig. 8.1 Geographic location of Pancho's Kitchen Midden (PKM) and Steenbokfontein Cave (SBF)

The main matrix component of Pancho's Kitchen Midden is marine shell collected by people and lesser additions of aeolian sand, decomposed organic matter, and relatively small quantities of bones mainly from small bovids and tortoises (Jerardino 1997, 1998). The site's stratigraphy consists of an alternating series of dense shell middens characterized by varying textures, shell condition, and subtle color differences (Fig. 8.3). Some small rodent borrowing and root infested areas were noted and isolated during field excavations, but no pits or other features caused by human agency were identified within the extent of the excavation. Rocks of various sizes, the larger ones most likely brought in by people, were encountered throughout the stratigraphic sequence (Fig. 8.3). None of them are likely to be roof fall material as no scars of such process are evident on the overhang wall. Individual discrete dumping events and/or removal of shell deposit are not evident and were probably minor. Hence, shell heaps possibly forming after meals would have leveled off as human activity continued at the site, thus leading to the formation of shell lenses. These stratigraphic units were grouped into seven main layers. Six radiocarbon dates are available for this sequence (Table 8.1). Initial occupation of this site started ca. 3800 cal BP, followed by successive visits between ca. 3200 cal BP and ca. 540 cal BP. Based on the available dates and the stratigraphic overlay, an occupational hiatus is evident between Layers 3 and 2 which date to ca. 2670 cal BP and ca. 755 cal BP, respectively (Table 8.1).

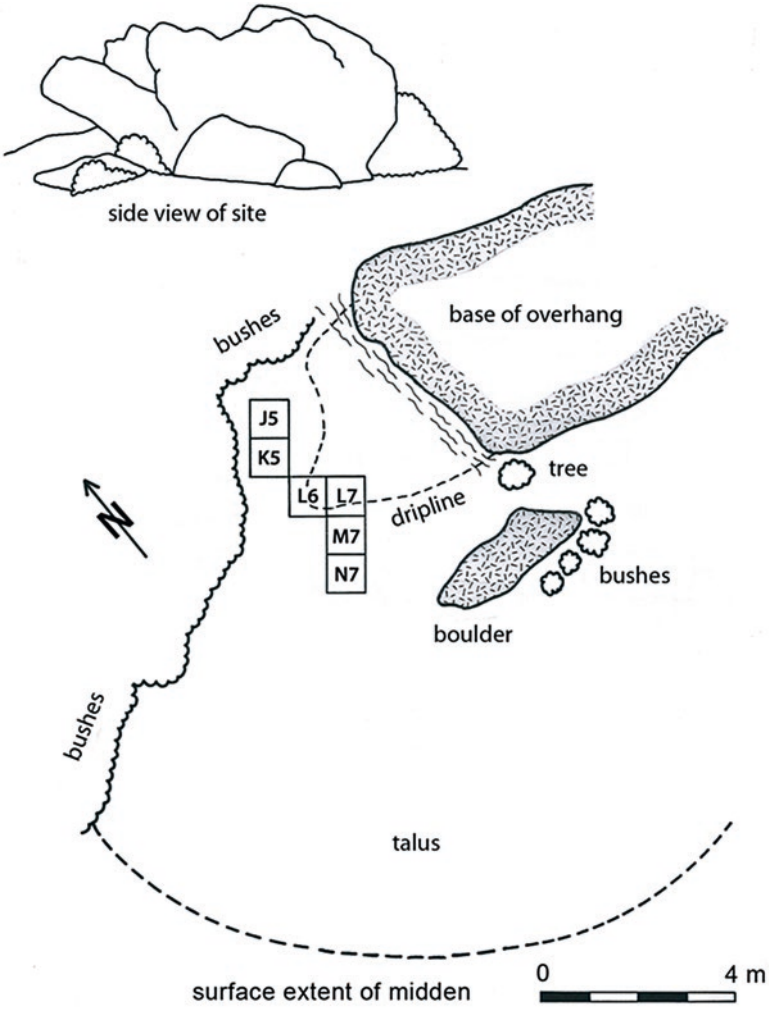

Fig. 8.2 Site plan of Pancho's Kitchen Midden showing the location of excavated squares

All recovered black mussel (*Choromytilus meridionalis*) shells were fragmented throughout the sequence, although close to forty whole limpet shells from different species were found among samples from the topmost stratigraphic layer. Differences in mussel shell preservation among layers were observed during excavations, although little evident burning (i.e., calcined or blackened shell) was noted. The most noticeable aspect of shell preservation was observed in Layer 3, dating to immediately before the occupational hiatus (Table 8.1), where shell is visibly chalkier and more fragmented than in the rest of occupational episodes. Black mussels dominate throughout the site sequence, but the diversity of mollusc species is higher

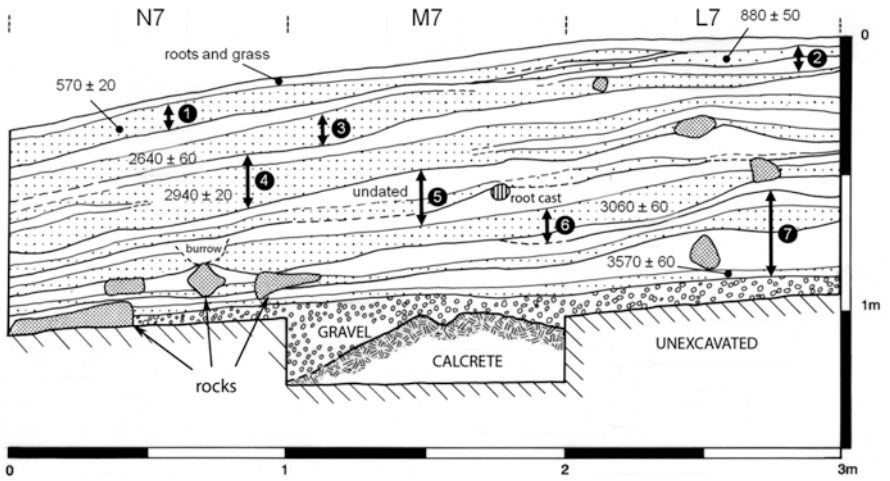

Fig. 8.3 Stratigraphy at Pancho's Kitchen Midden and associated radiocarbon dates (uncalibrated): west facing section of squares N6/N7, M6/M7 and L6/L7 (see Fig. 8.2 for site plan). *Arrows* indicate stratigraphic extent of shell lenses grouped into seven main layers, each of which are indicated by numbers on *black circles*. Shell lenses that showed higher concentrations of shell during excavations are indicated with stippled shading, while those that had somewhat less quantities of shell have no shading

Table 8.1 List of radiocarbon dates obtained from Pancho's Kitchen Midden. All dates are on charcoal. Uncalibrated values are corrected for $\delta^{13}C$, and calibrated dates were calculated with OxCal program (https://c14.arch.ox.ac.uk/) using ShCal13 calibration curve for the Southern Hemisphere (Hogg et al. 2013). For undated Layer 5, it was assumed that it dated to a time chronologically equidistant between the layers above and below (see text)

Layer	C^{14} (corrected for $\delta^{13}C$)	$\delta^{13}C$	Cal BP (μ)	Cal BP range (1σ)	Cal BP range (2σ)	Lab no.
1	570 ± 20	−24.2	535	547–527	554–515	Pta-5605
2	880 ± 50	−23.8	755	790–686	904–668	Pta-5921
3	2640 ± 60	−23.0	2670	2784–2514	2850–2488	Pta-5602
4	2940 ± 20	−23.7	3030	3070–2970	3156–2949	Pta-5990
5	Not dated	–	(3115)	–	–	–
6	3060 ± 60	−24.2	3200	3336–3080	3366–3005	Pta-5923
7	3570 ± 60	−24.1	3800	3888–3716	3976–3641	Pta-5743

in the two topmost layers. Mollusc species composition changes from one where black mussel is the overwhelmingly dominant species (96.5–98.9%) in Layers 3–7, to an assemblage where limpets, whelks, and barnacles make a modest but noticeable contribution in Layers 1 and 2, although black mussels continue to be the dominant species (Table 8.2: 73.8–94.7%).

Table 8.2 Observations on average percentage of black mussels, shell density of all species and average black mussel prismatic band widths (mm) and their respective standard deviation for left and right valves in each stratigraphic layer at Pancho's Kitchen Midden

Layer	% Black mussels	Average shell density (kg/m^3)	Average black mussel prismatic band width, left valves (mm) ± standard deviation	Average black mussel prismatic band width, right valves (mm) ± standard deviation
1	73.8	605.1	9.6 ± 1.3	9.5 ± 1.3
2	94.7	451.3	8.2 ± 1.2	8.1 ± 1.1
3	98.9	451.2	8.7 ± 1.4	8.6 ± 1.4
4	98.2	494.6	8.1 ± 1.1	8.1 ± 1.2
5	97.2	508.2	7.8 ± 1.4	7.8 ± 1.4
6	98.5	508.3	8.4 ± 1.5	8.4 ± 1.4
7	96.5	342.7	9.0 ± 1.5	9.0 ± 1.4

8.3 Methods

All shell samples used in this study were screened on site through a 1.5 mm (1/16 inch) mesh and were recovered from several squares and different stratigraphic units. Layer 1 samples originate from four stratigraphic units sampled from squares K5, L6, M7, N7; Layer 2 is made of samples from three stratigraphic units from squares K5, L6, L7; and Layer 3 is represented by shell from two stratigraphic units sampled over squares K5, L6, L7, M7, N7. Layers 4–7 were sampled only from squares L7, M7, N7, but with varying numbers of stratigraphic units represented in them, namely: four each in Layers 4 and 6, and three in Layers 5 and 7, respectively. The decision to sample some stratigraphic units and not others depended mainly on their integrity (lack of disturbance) and quantity of material. For the purpose of this study, shell density was quantified as mass of shell per unit volume (kg/m^3). A comprehensive report on the mollusc assemblage has been published before which showed that samples sizes of metrical data are adequate (Jerardino 1997).

Minimum number of individuals (MNI) of black mussels in South African West Coast sites are routinely established through the highest number of either left or right hinges. Size observations, on the other hand, are obtained by measuring the maximum width of the dark prismatic band (Fig. 8.4) of both left and right valves and by applying a reconstructive morphometric equation (Buchanan 1985). Preservation of the widest point along this prismatic band renders a black mussel shell as measurable, and if the hinge is attached to a measurable band, then such a shell fragment is classified as countable and measurable (c & m). Hinges not attached to a measurable prismatic band (or to none at all) are classified as countable-only shells (c) (Fig. 8.4).

Bivalves tend to break more easily than many species of gastropods due to their large surface area to mass ratio (Waselkov 1987), but the shell of black mussels is considerably thicker than that of *Mytilus edulis* which is known to fragment into very small pieces (Ford 1992; Muckle 1985, 1994). Prismatic bands are the thickest

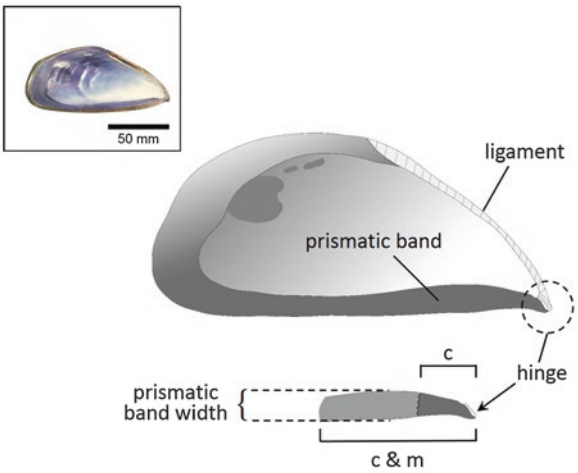

Fig. 8.4 Diagram of a black mussel (*Choromytilus meridionalis*) shell (interior of a left valve) and schematic detail showing metric observation derived from the prismatic band and an example of a countable and measurable fragment (c & m) and countable fragment only (c). Inset shows picture of the interior of a black mussel shell (photograph by George Branch). Note that the dark thin band around the lower edge is the periostracum (the outer proteinaceous layer) which forms a flap that covers the outer edge of the prismatic layer

part of black mussel shells and considerable force is needed to break it across. Whole fresh black mussels can easily be opened by placing them on hot coals or ashes for a short while, and the repeated presence of charcoal, and sometimes also hearths, at several local sites (Jerardino 1997, 2007, 2010, 2012) suggests that this method was commonly used. It thus seems likely that detachment of hinges from prismatic bands is unlikely to be the direct result of food processing before consumption, but rather of site usage. Although it is reasonable to conclude so, it should to be verified by quantified means. All things being equal, if trampling is a major factor in black mussel fragmentation, then fast deposition and burial of shell material should be conducive to less shell fragmentation due to less exposure to the natural elements and their related weathering processes. Furthermore, since shell size might also be a factor in how well shell preserves, possible correlation between black mussel metric observations (Table 8.2; Jerardino 1997, Table 4) and changes in shell fragmentation will be explored. In this chapter, I investigate the effect of site use (residential permanence), deposition rate, and shell size on shell fragmentation.

8.3.1 Quantifying Black Mussel Fragmentation

A proxy for black mussel shell fragmentation (fragmentation index, or FI) is established through quantifying the percentage of countable-only hinges (c) from among all countable hinges that include both countable-only (c) and countable hinges with

measurable parts (c & m) attached to them (Fig. 8.4). In other words, FI = (Σ c/(Σ c + c & m)) × 100. The smaller the percentage, the smaller the proportion of countable-only shells among all countable black mussels and, therefore, the higher proportion of prismatic bands attached to hinges and, consequently, the less fragmented black mussel shells there are. Conversely, higher FI values reflect relatively greater fragmentation levels among black mussel shells. Given the presence of left and right hinges, FI can be calculated with quantified observations for both mussel valves.

8.3.2 Quantifying Deposition Rates

Deposition rates are quantified as numbers of cubic meters of archaeological debris accumulated over a 100 years (m^3/100 years). The total amount of volume accumulated during each episode of occupation (identified as "layers") and the time span that elapsed during their accumulation are estimated. The shape of the surface extent of the site closely resembles the quarter of a full circle. Based on a site plan drawn during fieldwork (Fig. 8.2), a radius of 12 m was used to calculate the surface area of a circle, and the resulting number was divided by four (113 m^2). Based on available stratigraphic observations (Fig. 8.3, and additional section drawings), it is safe to assume that Layers 3–7 have the same surface extent as calculated for the entire site (113 m^2), while Layer 1 covers an area of 100 m^2 and Layer 2 extends over a much reduced area, namely 45 m^2. Conservative estimates of their spatial extent were made by observing the reduction in the depth of layers away from the apex of the site as recorded in section drawings (Fig. 8.3, and additional section drawings). Average thickness of each layer was determined through the same means, and the total volume for each layer was estimated through multiplying corresponding average thickness by the estimated surface areas.

Only one radiocarbon date is available for each layer, hence occupational episodes are not bracketed by age determinations that would allow some measure of passing of time. But radiocarbon dates were obtained from the base of each occupational episode. Thus, in order to simplify calculations, it is assumed that occupation was nearly continuous unless there is evidence to the contrary; the time that elapsed during the accumulation of each layer started at the mid-point calibrated date (μ) of a layer and ended with the mid-point calibrated date of the following one. Since Layer 5 is not dated, it was assumed that it dated to a time chronologically equidistant between the layers above and below. Because of the evident occupational hiatus above Layer 3, and given the absence of any faunal or artifactual content related to the southern Neolithic (ceramics and domestic fauna dating to the last 2000 years; see Jerardino et al. 2014), it was assumed that occupation of Layer 3 ended by 2000 ca. cal BP at the latest. As for the time span associated with the last occupational episode (Layer 1), it was assumed that it lasted between its calibrated mid-point date until immediately before the earliest and more permanent European presence at the Cape (AD 1652; Malan et al. 2013) as no early colonial artifacts of any kind

were identified during fieldwork. All radiocarbon dates were calibrated using OxCal program and the latest updated ShCal calibration curve (Hogg et al. 2013). Occupation time span values were rounded to the nearest half decade.

8.3.3 Proxy Measure for Residential Permanence

The rate of deposition of unfinished ostrich eggshell (OES) beads and finished beads and pendants made of any material has been used as an appropriate index of the relative length (residential permanence) of visits at South African stratified sites (Jerardino 1995). The manufacture of OES beads among southern African Khoisan foragers is a very time consuming task (Marshall 1976; Silberbauer 1965), and it is likely that such an activity was undertaken in the past during longer occupations of a camp site. Likewise, under circumstances of multi-task activity which characterize longer periods of residence in a camp (Yellen 1977), there is a higher risk of losing a piece of personal ornamentation due to wear and accident. Consequently, an increase in residential permanence at a given site should be identifiable by relatively high deposition rates of unfinished OES beads and finished beads and pendants of a variety of materials. But the relatively small size of Pancho's Kitchen Midden excavation and small number of unfinished OES beads and finished beads and pendants are not sufficiently adequate to estimate their rates of accumulation with confidence. Instead, density values (n/m^3) for these artifacts are used as a proxy measures for residential permanence, although it has to be born in mind that density values in general can vary due to changes in the rates of shell discard rather than the rate at which these quantified items were incorporated into the deposit (see Jerardino 1995, 2016).

Spearman's rank correlation tests were used for exploring possible statistical correlation between shell fragmentation and other variables. This non-parametric statistical test was deemed appropriate because assumptions of normality of data could not be taken for granted and also because of the coarse-grained, ordinal nature of the data. These statistical analyses were undertaken with Free Statistics Software (v1.1.23-r7) (Wessa 2015).

8.4 Results

Black mussel fragmentation indices (FI) for left and right valves are very similar and follow the same trend throughout the stratigraphic sequence (Fig. 8.5a). Highest values, indicating greatest shell fragmentation, occur in Layer 1 (76.3–78.3%), Layer 3 (79.2–84.4%) and Layer 4 (76.9–81.9%), whereas lowest FI values reflecting less fragmentation are recorded in Layer 5 (55.3–63.3%), Layer 6 (55.5–58.9%) and Layer 7 (62.7–63.1%) (Table 8.3, Fig. 8.5a). The results also show that FI values vary notably in the absence of changes in species composition and average prismatic band width (Table 8.2, Fig. 8.5: Layers 3–7). Deposition rates varied

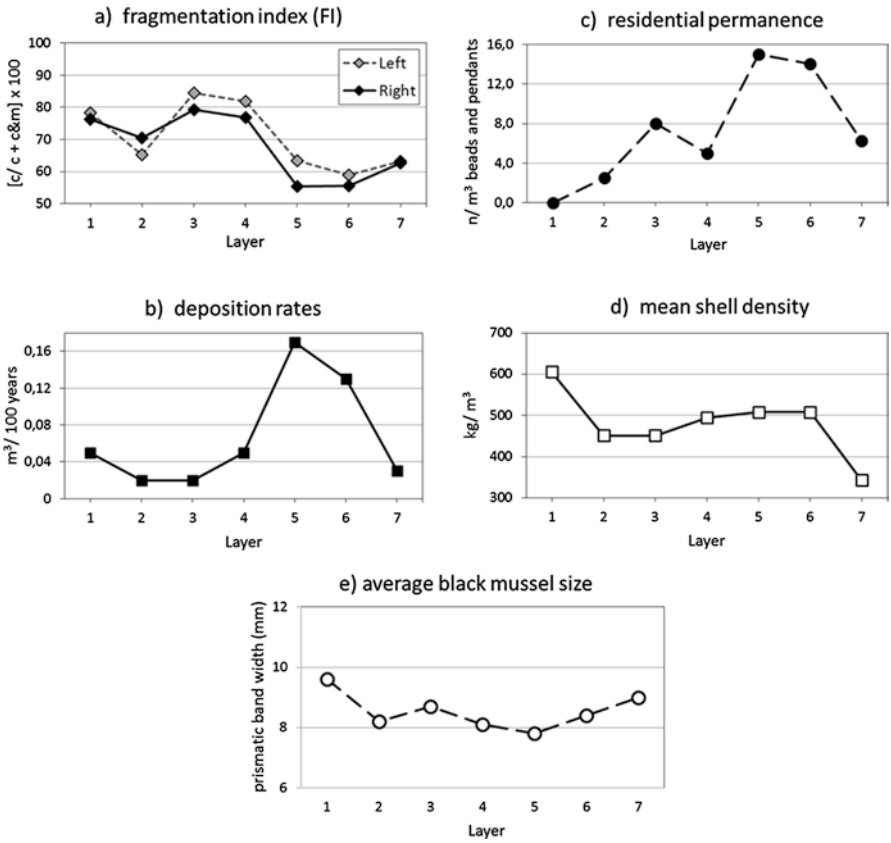

Fig. 8.5 Summary diagram showing trends in (**a**) black mussel fragmentation index; (**b**) deposition rates; (**c**) residential permanence index: densities of beads and pendants (finished and unfinished); (**d**) average shell densities; (**e**) average prismatic band widths (*left* valves, Jerardino 1997)

noticeably throughout the occupation of Pancho's Kitchen Midden, with deposits piling up most rapidly during the accumulation of Layers 5 and 6 (0.13–0.17 m^3/100 years) (Table 8.4, Fig. 8.5b). Residential permanence fluctuated markedly through time. Longer visits were probably more common during the accumulation of Layers 5 and 6, while shorter visits are associated with the formation of Layers 1 and 2 (Table 8.5, Fig. 8.5c). Average shell densities (kg/m^3) also show marked trends through time, with highest densities registered in Layers 1, and Layers 4–6 (Table 8.2, Fig. 8.5d). As reported earlier, changes in prismatic band widths (proxy measure of black mussel shell size) are statistically significant from one layer to the next (Jerardino 1997), with smallest average values for Layers 2, 4 and 5 (Table 8.2).

The correlation between FI and rate of deposition was investigated with the application of Spearman's rank correlation tests. The results show that FI and rates of deposition are inversely related in general, but surprisingly this relationship is not

Table 8.3 Observations on average fragmentation indices ((Σ c/ (Σ c + c & m)) × 100) and standard deviation of black mussels (*Choromytilus meridionalis*), numbers and size range by way of MNI (c + (c & m)) of studied black mussel samples for left (L) and right (R) valves and from each stratigraphic layer at Pancho's Kitchen Midden

Layer	Average fragmentation index (FI)	Std	Number of analyzed samples	Sample size range (MNI)
1 (L)	78.3	4.0	6	155–411
1 (R)	76.3	6.5		166–352
2 (L)	65.3	4.4	3	187–267
2 (R)	70.4	11.8		189–262
3 (L)	84.4	5.6	5	175–389
3 (R)	79.2	6.8		179–399
4 (L)	81.9	10.7	5	239–453
4 (R)	76.9	11.2		209–392
5 (L)	63.3	7.3	3	204–364
5 (R)	55.3	4.1		209–347
6 (L)	58.9	11.9	6	194–410
6 (R)	55.5	14.1		205–380
7 (L)	63.1	11.0	5	100–213
7 (R)	62.7	16.5		104–172

Table 8.4 Observations on average depth, estimated total volume, time elapsed during deposition (rounded to the nearest half decade), and deposition rates for each stratigraphic layer at Pancho's Kitchen Midden

Layer	Depth (m)	Volume (m^3)	Time (Cal years)	Rate of deposition (m^3/100 years)
1	0.12	12.0	240	0.05
2	0.08	3.6	220	0.02
3	0.09	10.2	670	0.02
4	0.18	20.3	360	0.05
5	0.13	14.7	85	0.17
6	0.10	11.3	85	0.13
7	0.15	16.9	600	0.03

statistically significant (left valves: r_s (rho) = −0.472, p = 0.283; right valves: r_s (rho) = −0.654, p = 0.110), even when applying a logarithmic transformation to deposition rates (same output for left and right valves). When values for Layers 1 and 2 are excluded to eliminate the possible influence of a different species composition (or even possible inaccuracies in the calculation of deposition rates for these layers), the relationship between these two variables is also inverse but still not statistically significant. However, results for right valves approaches the level of significance at the α = 0.05 level (left valves: r_s (rho) = −0.500, p = 0.450; right valves: r_s (rho) = −0.900, p = 0.083).

Possible correlation between FI values and shell density was investigated also by means of Spearman rank correlation tests (left valves: r_s (rho) = −0.142, p = 0.782;

Table 8.5 Observations on numbers of finished and unfinished beads and pendants, volume of material from which they were excavated, and their densities at Pancho's Kitchen Midden

Layer	Finished + unfinished beads and pendants (n)	Excavated volume (m^3)	Beads and pendants density (n/m^3)
1	0	0.6	0.0
2	1	0.4	2.5
3	4	0.5	8.0
4	4	0.8	5.0
5	6	0.4	15.0
6	7	0.5	14.0
7	5	0.8	6.3

right valves: r_s (rho) = −0.250, p = 0.594). Same tests of probability show that FI and average black mussel band width are not statistically associated (left valves: r_s (rho) = −0.035, p = 0.963; right valves: r_s (rho) = −0.360, p = 0.427).

8.5 Discussion

An alternative method for quantifying shell fragmentation of the South African black mussel (*C. meridionalis*) is presented here through the calculation of a fragmentation index (FI) based on the frequency of preserved mussel hinges that are joined, and not joined, to their contiguous prismatic band (Fig. 8.4). Similarity in the distinct trends in FIs through time displayed by left and right valves suggests that the same set of factors behind their patterning are at work throughout the occupational sequence and underlines the suitability of this method for quantifying shell fragmentation. Isolating and counting mussel hinges from shell samples consumes much less time and demands less laboratory space and equipment than passing the same samples through a series of sieves with different mesh sizes and subsequent weighing of the retained fractions. Moreover, weights of retained shell fragments may be biased due to differential chemical dissolution along stratigraphic profiles. Counting mussel hinges is also quicker than counting all mussel fragments for establishing NISP/MNI ratios. Hence, the advantages of this alternative method are evident and bid for its use in future.

The small differences between FI values calculated for left and right valves (2–5%) and near identical chronological patterns strongly suggest that the sample size of black mussels in each layer is robust (MNI ≥ 100) and that the factors behind this pattern are not shaped by random variation associated with sampling (Fig. 8.4a). Qualitative assessment of the patterning in the data indicates that shell fragmentation is low in layers where deposition rates were fastest and visits longest, while greater shell fragmentation is registered where deposition rates were slowest and visits were shortest (Fig. 8.4). Evidently, longer visits result in fast deposition rates and less fragmented, or better preserved, marine shell. From this it follows that higher rates of shell discard in Layer 5 and 6 have resulted from more extended

visits rather than from an increase in the frequency of visits (see Jerardino 1995). This is so because the frequency of unfinished OES beads and finished beads and pendants, both of which are made and lost during longer visits (see Sect. 8.3 above), are on the rise in these very same stratigraphic units. The possibility that, instead, larger groups would have contributed with proportionately more of these artifacts in Layers 5 and 6 would not explain the trends seen here because more people would have probably resulted in more shell collected and discarded on site (main matrix component) thus levelling off artifact densities. Moreover, the rise in densities of unfinished OES beads and finished beads and pendants in Layers 5 and 6 happens despite a concomitant rise in shell densities, meaning that the increase in artifact densities is not the result of dwindling matrix content (shell). Artifact densities and the interplay of their behavioral causes is a matter beyond the concern of this chapter (see Jerardino 1995, 2016).

Although trends in shell fragmentation and deposition rates are inversely related, this correlation is not significant according to statistical tests. A larger pool of observations could show otherwise, but these are limited by the number of stratigraphic layers (n = 7). Increasing the pool of observations would necessitate using data from shell lenses within the stratigraphic layers, but doing so would be complicated by the lack of chronometric resolution and the spatial and stratigraphic control needed for estimating lengths of visits and volume of deposit. It is also worth noting that the quantified deposition rates may not be precise since the scale of excavation might be too small for estimating volumes accurately. Deposition rates were calculated conservatively based on a limited number of radiocarbon dates. If these could be more accurately quantified in the future, the relationship between FI and deposition rates might turn out to be significant. Although it is impossible to say at this stage that deposition rates may have been under- or overestimated for some or all layers, the values here presented are meaningful (at least proportionally among layers) as trends in residential permanence closely follow those of deposition rates. This pattern makes common sense as longer visits over a certain period would lead to more shell accumulated than visits of shorter duration over the same time span (see Cannon 2013). Hence, it is hard not to consider the inverse relationship between shell fragmentation and deposition rates as obvious and convincing. Black mussel fragmentation in the context of Pancho's Kitchen Midden seems to be directly related to intra-site settlement patterns, where shell is better preserved as a result of longer visits that bring about faster burial rates and protection from trampling. Shells preserve more poorly on account of shorter visits and thus greater impact of trampling. The latter is known from experimental studies to be an important agent in bivalve shell fragmentation (Muckle 1985). The studies based on mollusc assemblages from other local sites and beyond will put this reconstruction to the test or qualify it within particular settings and combination of variables.

Site abandonment and significant hiatuses in site occupation appear to have also contributed to shell fragmentation. FI values for Layers 1 and 3 are some of the highest in the sequence, not only because deposition rates were low at that time, but possibly also because shell deposits lay unprotected and exposed to the action of natural weathering processes (UV rays, thermal fluctuations, wind, rain, bioturba-

tion, plus animal and human thoroughfare) for about a 1000 years before more material was discarded on top or shell was removed by archaeologists. The fact that shell was visibly chalkier in Layer 3 than in other stratigraphic units strongly suggests substantial decay of the organic fraction and the dissolution of calcium carbonate from shells as a result of protracted exposure to physical and chemical weathering. This would partly explain the high FI values in this stratigraphic unit. Similar conclusions were arrived by Ash et al. (2013), in the context of low sedimentation rates and high shell fragmentation, and by Shiner et al. (2013), where alternation in the distribution of shell fragment size and shell dissolution data at four sites is best accounted for by repeated mound use and periods of abandonment. Long-term and repeated exposure to the natural elements as a result of site abandonment has been shown to reduce the survival of even dense bone (Conard et al. 2008).

Shell compaction, as reflected in shell density, is not statistically correlated with shell fragmentation, at least for black mussels and within the range considered in this case study. Except for Layer 1, shell densities follow somewhat the general trends in residential permanence and related deposition rates. This pattern makes intuitive sense because more shell and added faunal remains relative to other components of the site matrix (i.e., wind-blown sand and matter derived from organic decay) would be incorporated and packed down into the deposit as visits become longer and deposition rates increase as a result. The reason why Layer 1 has the highest average shell density for the entire sequence (18–56% more than the rest of layers) might have to do with site abandonment. As the remains of the last occupation lay unprotected on the surface of the site for centuries, wind and rain may have removed a great deal of sand and organic fractions from its matrix, and more shell relatively to these other components would have been preserved. Moreover, the distinctive species composition of Layer 1, which includes robust limpets and barnacles, might also explain highest shell densities. Shell from the mussel-dominated Layer 3 probably also lay at the mercy of the elements and animal traffic for centuries before being buried by Layer 2 material, but its average density is relatively low (Table 8.2; Fig. 8.5d).

On the other hand, species composition does not seem to have a clear influence in black mussel shell fragmentation. Substantial differences in FI values (30–40% change) take place in Layers 3–7 in the absence of a change in species composition (black mussels are overwhelmingly dominant in both layers with ≥96.5%). However, it is possible that changes in species composition might influence FI values somewhat in assemblages where shifts in the dominant species are more pronounced than the ones observed here (Table 8.2). The inverse relationship between FI and deposition rates in Layers 3–7 is not reflected in Layers 1 and 2 (Fig. 8.5a, b), where the percentages of black mussels drop somewhat (73.8–94.7%) (Table 8.2). It is possible that the addition of large and robust shells of limpets and barnacles to the shell assemblage could have been a minor but contributing factor in the attrition of mussel shells, but this is yet to be tested with further case studies.

A comparison of average prismatic band widths in the absence of changes in species composition (Layers 3–7) shows that mussels do not seem to break more or less easily when they are smaller or larger, at least within the range of average values considered (7.8–9.0 mm) (Table 8.2). Average prismatic band widths for Layer

3 (left: 8.7 mm, s.d. = 1.4 mm, right: 8.6 mm, s.d. = 1.4 mm) and Layer 6 (left: 8.4 mm, s.d. = 1.5 mm, right: 8.4 mm, s.d. = 1.4 mm) are the most comparable, but exhibit very different FI values for left and right valves (Layer 3: 84.4, 79.2, Layer 6: 58.9, 55.5). Overall, larger black mussels are represented at Pancho's Kitchen Midden when compared to natural assemblages, as nearly half of the latter consist of shells with narrow prismatic band widths (2.2–6.1 mm) (see Jerardino (2014) for full shell lengths).

FI observations thus allow the study of shell fragmentation by moving away from screen-based quantification and from NISP/MNI ratios and closer to shell part representation (see Lyman 2008, pp. 250–254; Giovas 2009; Gutiérrez-Zugastí 2011; Harris et al. 2015). Other than the purpose for which it was devised in this study, this measure of shell fragmentation may also allow better inter-taxonomic comparisons than NISP:MNI ratios as the shell of some species are more vulnerable to breakage than others. Further studies will test the utility of FIs, as defined here in terms of shell part representation, when comparing the extent to which different species are fragmented within and between assemblages.

The interpretations offered here on shell fragmentation as a result of site usage ought to apply not only to assemblages of similar species composition, but also taphonomic history, that is, same post-depositional processes overall. An alternation of shell lenses exposed to low and high burning or the inclusion of highly variable quantities of sand and rocks would introduce additional variables other than trampling when explaining shell fragmentation. This is evidently reflected in the variable preservation of black mussel shells from Steenbokfontein Cave (Fig. 8.1) (Jerardino and Swanepoel 1999; Jerardino and Yates 1996). Preliminary and unpublished observations show that FI values for stratigraphic layers subjected to substantial burning (Layers 3b, 4a, and 4b) have, respectively, higher average FI values (left valves: 66.9, 83.0, 64.2; right valves: 61.6, 81.5, 64.9) than those calculated for stratigraphic units with much less burning (Layers 1, 2, 3a, and 5) (left valves: 31.7, 44.2, 15.8, 48.1; right valves: 29.6, 44.0, 14.3, 47.0). Further studies ought to explore the above issues through controlled experimental work and analyses of mollusc assemblages recovered from multicomponent sites with marked changes in original shell sizes, species composition, and chemical alteration (and, hopefully, with minimal gaps in their occupational sequences).

The approach for quantifying shell fragmentation used here can be applied to other mollusc species from different geographic and cultural contexts within South Africa and elsewhere in the world. This is to be desired due to differential shell preservation depending on the species studied and the need to verify inferences derived from one taxon alone. The choice of shell parts will necessarily have to include those which preserve well in archaeological contexts, are diagnostic of species and can be useful for deriving minimum number of individuals, and do not break easily as a result of food processing. For bivalves that live either in soft-bottom or hard substrate, the hinge and area surrounding it (i.e., umbo) will probably remain central for FI calculations, although some species would lend themselves less useful than others because their shells are thinner, more brittle, and/or their hinge geometry could be such that would easily lead to shell breakage (e.g., certain

small oysters, mussels from the genera *Aulacomya* and *Perna,* and the families Pinnidae and Solenidae). For gastropods, the apex seems an obvious shell part to use when studying shell fragmentation the way presented here. For instance, the percentage of apices from broken shells among all limpet shells from the same species (which include the sum of countable only and whole shells) could be used for establishing measures of shell fragmentation. For whelks or snails, the relative proportion of apices with their central columella attached or not attached to them could also be useful. Among chitons (class Polyplacophora), the intact survival of the sturdiest of the eight plates in an individual (usually the front or back plate) could also provide a quantitative measure of shell fragmentation. Obviously, some choices of species and shell parts would be more sensitive to breakage than others and thus amenable to the methodology presented here. Focusing on those species and shell parts that break readily, but not too easily either, would give best results, as a range of FI values would be most useful for evaluating variability in shell fragmentation.

8.6 Conclusions

A great number of factors can affect shell preservation. Some are intrinsic to each species (robustness), and many others relate to taphonomic process before and after deposition. Among the latter, chemical weathering from exposure to the elements and life forms, burning, and intensity of site usage are the most important. The method for quantifying shell fragmentation presented here is probably less influenced by chemical weathering than the methods relying on sieving through stacked meshes because weight can be lost due to a number of taphonomic processes. Black mussel hinges remain attached to prismatic bands even when the shell is very chalky, although the extent of this remains to be quantified. This method is also less time consuming as indices can be calculated with data that is routinely gathered for MNI calculations, and counting or weighing shell fragments is not necessary.

When levels of burning, matrix constitution, and species composition do not vary significantly between stratigraphic units, shell fragmentation appears to be affected mainly by intra-site settlement patterns. Black mussel shells preserve better when deposition rates are faster as a result of longer occupation, and suffer greater fragmentation when deposition rates are slower resulting from shorter visits. When visits decline to such an extent that a significant gap in site occupation (several centuries) is obvious, then shell fragmentation is exacerbated as a result of the protracted exposure of shell remains to the weathering action of the natural elements. Following the methodology outlined here, additional studies on black mussel shell fragmentation at other sites might well show the same causative association. If so, then fragmentation indices as calculated here could then be used as effective tools in reconstructing patterns of site usage. Hence, this method not only would save time and resources for quantifying shell fragmentation, but would also contribute towards a better understanding of intra-site settlement patterns and, by extension, of those at a regional scale.

The basic rationale that sustains this alternative method can be applied to other South African species and to those common in shell middens elsewhere in the world. The success of this exercise would depend on the choice of the species to study as obtaining a continuous, rather than discrete, range of FI values would be best for evaluating shell preservation on a quantitative basis. Most importantly, shell robustness and architecture of the diagnostic and countable elements and their contiguous shell material would need to be taken into account when applying this method to other species.

Comparability of methods is always desirable in archaeology as this allows for making stronger cases and for assessing assemblages against others with potentially different faunal composition and depositional histories. Consequently, future work on shell taphonomy would certainly benefit from experimental studies and from laboratory analyses where different methods for evaluating shell fragmentation are applied jointly to a number of assemblages and results compared.

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Chapter 9
The Value in Studying Large Faunal Collections Using Traditional Zooarchaeological Methods: A Case Study from Anglo-Saxon England

Pam J. Crabtree

9.1 Introduction

In the past 10–15 years there have been a number of important methodological developments in zooarchaeology. They include improved methods for the study of ancient DNA (Campana et al. 2013; Larson et al. 2012; see also Matisoo-Smith, Chap. 11), isotopic studies of both human and animal remains (Pilaar Birch 2013; Makarewicz and Sealy 2015), analyses of phytoliths on animal teeth (Piperno 2006; Gobetz and Bozart 2001), and geometric morphometric studies (Outram et al. 2009; Cucchi et al. 2011), among others. However, to be effective these new technologies should be applied to well-collected and well-analyzed assemblages of animal bone remains. The case study presented in this chapter will illustrate the value of traditional methods of faunal analysis, most of which were developed and standardized in the 1970s and 1980s, based on a series of large Romano-British and Anglo-Saxon faunal collections from East Anglia, Britain. In addition to basic identifications and measures of taxonomic abundance (Lyman 2008; Lyman, Chap. 2), traditional methods include the analysis of age and sex profiles, basic measurement studies, and studies of butchery patterns and practices.

While these methods have been standard practices in zooarchaeology since the 1980s (e.g., Grigson 1981), the importance of the study of large faunal collections has taken on an increasing urgency in the twenty-first century. Many large-scale excavations, especially in areas outside Northwest Europe and North America, are generating large faunal collections, and many of these projects need zooarchaeologists. Ph.D. students who want to study these collections face two hurdles. First, Ph.D. programs in continental Europe, the British Isles, and North America are encouraging students to complete their degrees more quickly than in the past. A 2011

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United States National Academy of Sciences survey of 82 Ph.D.-granting anthropology departments indicated that the mean time-to-degree in the majority of the departments in 8 years or more (Ostriker et al. 2011; see also Rocks-Macqueen 2011). My own department averages 8 years to degree, and the administration would like us to reduce this to seven. The analysis of large animal bone collections takes time, and, as we try to reduce time to degree, fewer and fewer students are developing the skills needed to work with large collections in a timely manner, such as a broad knowledge of comparative skeletal morphology that includes experience with human osteology. In addition, carrying out field and lab work abroad requires external funding. Grant applications also take time, and research funding has been increasingly difficult to obtain, especially since the economic crash of 2008.

Against the backdrop of these challenges, field archaeologists continue to excavate these large faunal collections. Further change to the research landscape arises from modern information technologies—including database managers for zooarchaeology, GIS (geographical information systems) technologies, and online data publication—that have provided new opportunities for data analysis and sharing that were unavailable in the 1970s and 1980s. This case study will illustrate the value of the "traditional" zooarchaeological techniques that were used in the analysis of a series of Romano-British and Anglo-Saxon sites that were studied between 1977 and 2009 by showing that more extensive analysis can reveal patterns of animal husbandry and the use of secondary products, economic intensification, and changes in animal sizes, hunting, and butchery patterns that might otherwise not be apparent.

9.2 Archaeological Background

9.2.1 West Stow

West Stow is an early Anglo-Saxon (ca. 450–700 CE) site that was excavated by Stanley West between 1965 and 1972 (West 1985). The site is located in the Lark River valley near the modern town of Bury St. Edmunds in Suffolk, England (Fig. 9.1). Excavations at the site revealed 69 small sunken-featured buildings (known as SFBs or grubenhaüser) clustered around seven small timber buildings. Excavations at the site also uncovered a pre-Roman Iron Age farmstead and a series of first and second century Romano-British pottery kilns (West 1989). The 176,338 animal bones and fragments recovered from these excavations were identified by the author between 1977 and 1979 at the Faunal Remains Unit of the Department of Archaeology, University of Southampton (Crabtree 1990a, b). A total of 66,017 of these mammal, bird, and fish fragments could be identified to species; an additional 36,925 specimens were identified to higher order categories such as small artiodactyl ("sheep-sized"). The remainder were unidentified fragments. Four additional sunken-featured buildings were discovered during rescue excavations carried out in

Fig. 9.1 Map of England showing the locations of West Stow, Brandon, and Icklingham

advance of a new Visitors' Centre at the site. The 8722 animal bones from these new excavations, known as West Stow West, were identified during 2009 and are currently being prepared for publication (see also Crabtree and Campana 2015). They include 3318 animal bones and fragments that could be identified to species. These data have been published online at http://opencontext.org/projects/59E7BFBC-2557-4FE4-FC14-284ED10D903D. The original West Stow faunal assemblage was carefully hand-collected, a practice that was common in Britain in the 1960s and 70s, with the exception of the material that was subjected to flotation in 1972. In the more recent excavations, one-quarter of the fill of each SFB was sieved through 6 mm mesh, and all material that was recovered through fine screening was examined by the author.

9.2.2 Icklingham

Icklingham is a late Romano-British (third and fourth century CE) town located about 5 km from West Stow (Fig. 9.1). Initial excavations were carried out at the site under the direction of Stanley West and Jude Plouviez (1976). A second program of excavation was carried out by Catherine Hills of Cambridge University between 1997 and 2000. The 26,221 animal bones and fragments from both excavations were identified in three stages between 1989 and 2008 (Crabtree 2010a). Of these

8129 bones and fragments could be identified to species and an additional 3290 could be identified to higher order taxa. While the material from the original West/Plouviez excavations was carefully hand collected, the material from the subsequent 1997–2000 excavations was sieved.

9.2.3 Brandon

Finally, Brandon (Carr et al. 1988; Tester et al. 2014) is a Middle Saxon (ca. 700–850) estate center located on the Little Ouse River in northern Suffolk, about 18 km north of West Stow (Fig. 9.1). Open-area excavations that were carried out at the site during the 1980s revealed the remains of 35 houses and two churches. Recent research indicates that this estate center may have served as a monastic foundation for at least part of its existence (Tester et al. 2014). The 154,616 mammal bones included 48,310 that could be identified to species and an additional 19,647 that could be identified to higher order categories. The 4096 bird bones included 3168 specimens that could be identified to genus or species. The mammal and bird bones were initially identified and analyzed at the Cambridge University faunal remains unit in 1990 and 1991 (Crabtree and Campana 2014, 2015). The fish bones were identified by Humphrey and Jones (2014). At Brandon, 63 archaeological contexts were sieved through 10 mm mesh, and the author examined all the mammal and bird remains that were recovered from the sieved samples.

9.3 Goals, Materials, and Methods

The long-term goals of the Icklingham, West Stow, and Brandon faunal research were twofold: (1) to understand changing animal husbandry patterns and hunting practices between the late Roman Period and the Viking Age; and (2) to examine the relationship between these faunal changes and the social and political transformations that took place in eastern England between the fourth and the ninth centuries CE (Crabtree 2014). Systematic and consistent recording of information presents a major challenge for analysts who are working with large faunal assemblages. When I began this research in 1977, the Windows operating system was still a figment of Bill Gates' imagination. Roger Jones (n.d.) of the Ancient Monuments Laboratory (now part of English Heritage) had developed a computer system that used 8-line punch tape, magnetic tapes, and minicomputers to record basic zooarchaeological data for large British faunal collections. Working with my colleagues at the Faunal Remains Unit in Southampton, we expanded the system so that we could record a wider range of basic zooarchaeological data. The new and expanded system allowed us to record the following information for each bone or bone fragment: archaeological context, species (or higher-order taxon), anatomical element, portion, handedness, degree of fragmentation, as well as sex when known. We developed a series of

mnemonic codes that allowed us to record the nature, location, and direction of any butchery traces or evidence of pathology. We also recorded all bone measurements following the recommendations of von den Driesch (1976). Information on aging was recorded based on both epiphyseal fusion of the long bones (Silver 1969) and dental eruption and wear (Grant 1975, 1982). This system was used to record the data from the original West Stow excavations.

While this system allowed analysts to record a lot of standard zooarchaeological data, the use of 8-line punch tape was cumbersome and error-prone. With the explosion of personal computing in the 1980s, my colleague, Douglas Campana, developed a database manager called ANIMALS that allowed us to record the same basic zooarchaeological data on the PC (Crabtree and Campana 1987). The system, now known as FAUNA (Campana 2010) has been updated to run on Windows 7.0. The Brandon, Icklingham, and West Stow West data were recorded using ANIMALS/FAUNA, and ANIMALS was also used to re-analyze the original West Stow faunal data from the sunken-featured buildings prior to publication (Crabtree 1990a).

Given the labor involved to record identifications and associated data, why then did we analyze these big faunal assemblages? Why not select a sub-sample of some sort for more detailed analysis? The short answer is that we did not know which archaeological contexts would be most interesting and valuable when we started this research in 1977. West Stow was the first early Anglo-Saxon rural settlement to be extensively excavated using relatively modern methods, so we had no prior research to guide us. However, the decision to completely analyze these large samples paid off in a number of different ways. We were able to examine the spatial distributional of the faunal remains across the sites and the patterns of species and body-part distributions in different types of features (Crabtree 1990a, pp. 18–25). The large assemblages also allowed us to examine possible changes in size for individual bone measurements, rather than having to use the log ratio method to combine measurements from different bones (Meadow 1999; see also Holmes 2014). Our data also allowed us to identify statistically significant differences in age profiles through time that have important implications for animal husbandry practices.

9.4 Results

At the most basic level, the analysis of these large assemblages has allowed us to identify some important but rare species that probably would have been missed if we had only identified part of these faunal collections. For example, at West Stow we identified a single metacarpus of a brown bear (*Ursus arctos*). The find is interesting because bears had disappeared from Southeast England in later prehistoric times. The bear must have been obtained from elsewhere in Britain or from the European continent, possibly as part of a bear skin. Although most of the fish bones recovered from West Stow were locally available species like pike (*Esox lucius*) and perch (*Perca fluviatilis*), a single bone of a marine flatfish may point to some limited trade or exchange with the coastal regions. These data are significant because they

are evidence for trade and exchange in animal products. They stand in contrast to the data for the large domestic mammals, which point to a greater degree of self-sufficiency in animal use.

Our most unusual find at Brandon was the nearly complete skeleton of a peregrine falcon (*Falco peregrinus*). Measurements indicate that the bird was a female (Crabtree 2012, p. 23), and female birds were often preferred for hawking because of their larger size (Prummel 1997, p. 336). The Brandon falcon represents the earliest direct evidence for falconry in Anglo-Saxon England. The Brandon assemblage also produced a small number of bones of marine mammals, including a gray seal (*Halichoerus grypus*) and a vertebra of a dolphin or small whale. The presence of marine mammals in medieval sites is often an indication of high status (Gardiner 1997) and, along with the evidence for falconry, supports the inference that Brandon was a high-status site.

Why are these rare species important? In the 1970s and 1980s, many zooarchaeologists were focused primarily on the reconstruction of paleoeconomy (e.g., Higgs 1975; Higgs and Jarman 1972), including questions of hunting practices and animal domestication. Over the past 30 years it has become increasingly clear that zooarchaeological studies can also play an important role in our understanding of past social organization and ideology (e.g., Crabtree 1990b; deFrance 2009; Kirch and O'Day 2003; Sykes 2006). One way of examining the social context of food is through the identification of luxury food items. As Ervynck et al. (2003, p. 431) note, "…rarities often represent the best examples of luxury foods, simply because they are fairly expensive." They further note that imported goods that are common in their place of origin may be considered luxuries if they are rare in their place of consumption. The marine mammals from Brandon are likely to represent luxury foods since they would have been uncommon at this inland site. By way of contrast, substantial numbers of bottlenose dolphins (*Tursiops truncatus*) were recovered from the contemporary Anglo-Saxon site of Flixborough. However, this site is located on the Humber estuary, and Dobney et al. (2007, p. 207) have suggested that there may have been a well-organized bottlenose dolphin fishery in the estuary from the ninth century onward. The Brandon falcon and the bear bone from West Stow (which may have been part of a bear skin) appear to be luxury items as there is no evidence to suggest that these rare specimens were part of the diet.

It has long been recognized that relatively small faunal assemblages can provide basic data on the relative importance of the major vertebrate taxa (Gamble 1978). If the primary goal of a faunal study is simply to identify the relative importance of the major mammalian species in an assemblage, a NISP of as few as few hundred identified specimens may suffice. At the Late Iron Age *oppidum* of Manching in Bavaria, Germany, the animal bones were identified by the year in which they were excavated, rather than by feature or stratigraphic unit (Boessneck et al. 1971, p. 145; see also Gamble 1978). The species ratios based on NISP are not substantially different between the 1959 season (NISP = 96) and the 1957 season (NISP = 123,118) (Table 9.1). Moreover, the rank order of importance for the main domestic mammal species remains the same despite the dramatic difference in sample size. However, the 1959 assemblage was limited to the remains of domestic mammals, with only

Table 9.1 Species ratios based on NISP for the main domestic mammal species recovered from the 1957 and 1959 excavations at Manching

	1957 NISP	%	1959 NISP	%
Horse	6606	5.4	10	10.4
Cattle	48,572	39.5	42	43.8
Sheep/goat	27,629	22.4	13	13.5
Pig	40,311	32.7	31	32.3

the bones of horses, cattle, caprines, pigs, and dogs identified. The trade-off for relying on such a small sample is that the 1959 assemblage provided no information on domestic poultry-keeping or hunting, fishing, and fowling of wild animals. In contrast, a wide range of domestic birds, wild birds, wild mammals, and fish remains was recovered from the much larger 1957 assemblage. In short, increasing the sample size increased taxonomic richness at the site. Hambledon (1999, p. 39) has suggested researchers use of faunal assemblages with a NISP of greater than 300 for comparative studies on the relative importance of the Eurasian domesticates (cattle, caprines, and pigs). In a similar vein, Lyublyanovics (2015, p. 50) has suggested that small faunal assemblages should be used in non-quantitative arguments and that the species ratios calculated for these small assemblages should be viewed as tendencies rather than being taken at face value.

Most archaeologists, however, want more information from faunal assemblages than simple species ratios based on NISP. Studies of age and sex profiles require much larger faunal samples. The recovery of large numbers of ageable mandibles can reveal significant changes in animal husbandry practices through time. For example, the initial excavations at West Stow revealed evidence for a loom emplacement and substantial numbers of loom weights in some of the sunken-featured buildings (West 1969). These finds raised the questions of whether the inhabitants of West Stow were engaged in specialized wool and textile production. We tried to answer this question using age profiles based on dental eruption and wear for the sheep mandibles. As noted above, the state of eruption or wear on each mandibular tooth was recorded following Grant (1975, 1982). The complete and nearly complete mandibles were grouped into age classes following Payne (1973). Detailed analyses of the age profiles from both West Stow and West Stow West showed that sheep husbandry at the site was focused on meat-production, milk-production, and herd security (Redding 1984). A majority of the sheep were culled during the first 2 years of life (Payne's Stages A-D), and relatively few were kept to older ages, suggesting that, in contrast to the inference from the loom weights, wool production played a relatively minor role on the West Stow economy (Fig. 9.2). These older animals probably produced wool for local use rather than wool for trade or exchange. Comparisons of the age profiles for the fifth century, sixth century, and late sixth to seventh century sheep suggest no real changes in sheep husbandry through time at West Stow Crabtree (1990a, pp. 83–94).

Age profiles from the nearby Middle Saxon site of Brandon revealed a significant difference in sheep management strategies. The Brandon sheep are generally

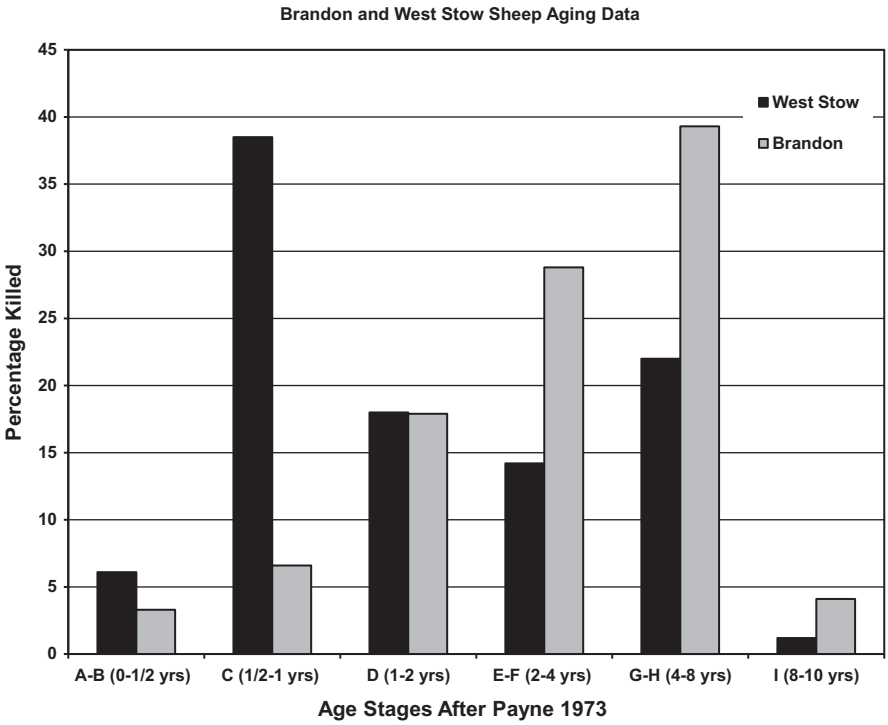

Fig. 9.2 Age profiles based on mandibles for sheep from Brandon and the original West Stow excavations

older than the West Stow sheep, and the age profile includes many more sheep culled between four and 8 years of age (Paynes's Stages G and H) (Fig. 9.2). A chi-square test comparing the Brandon and West Stow age profiles produces significant results (χ^2 = 222.13, p = 0.0001, df = 5). Non-parametric testing based on a Kolmogorov-Smirnov test supports the same conclusion that the differences between the two age profiles are significant ($p < 0.001$, D–stat = 0.348672) (Crabtree 2007, p. 167). Although young sheep produce high quality wool, wool production reaches its peak between 5 and 7 years of age (O'Connor 2010, p. 12). In addition, data from pelves and horn cores indicate that a majority of the Brandon sheep were male, and males, especially castrated males, are excellent wool producers. While Brandon was a high-status site that was ecclesiastical at least for part of its history and West Stow was an earlier rural settlement site, the changes observed here are part of a broader pattern of intensification and specialization that is seen in Anglo-Saxon animal husbandry at this time (Crabtree 2010b; see also Crabtree 1996, 2015). For example, intensified pork production appears to have begun at the site of Wicken Bonhunt in Essex as early as the late sixth to seventh century and was clearly present in the Middle Saxon faunal assemblage from that site (Crabtree 2012, p. 57). Detailed studies of field systems point to the beginnings of agricultural intensification at this time as well (Oosthuizen 2013).

The aging data from West Stow and Brandon provide a much more detailed picture of the changes that took place in animal husbandry during the Early and Middle Saxon periods than do the data from sites with much smaller faunal collections, such as the Early and Middle Saxon site of Quarrington in Lincolnshire (Rackham 2003). The Quarrington excavations yielded just over 3200 animal bones and fragments, of which 1075 could be definitively assigned to the Early Saxon period and an additional 1013 could be assigned to the Middle Saxon period. The species ratios based on several different methods of quantification suggested that sheep increased in importance during the Middle Saxon period (Rackham 2003, p. 260 and Table 8). However, there are simply too few sheep bones from the Early and Middle Saxon assemblages to allow for the construction of more detailed age profiles based on either epiphyseal fusion of the long bones or dental eruption and wear. The author concludes that the Early Saxon kill pattern "may reflect a non-focused management of a largely subsistence character", while the Middle Saxon cull patterns "indicates that mutton and wool were probably important products and suggests a more strongly controlled or directed cull" (Rackham 2003, pp. 271–272). While these data are certainly suggestive, they lack the statistical rigor that larger faunal samples, like those from West Stow and Brandon provide. Rackham (2003, p. 273) notes in conclusion that "larger samples would be needed to confirm the interpretations outlined above." A review of the faunal remains from Early and Middle Saxon rural sites in eastern England (Crabtree 2010b, p. 127) shows a "general, although not universal, increase in the relative importance of sheep between the Early Saxon and the Middle Saxon periods." Age profiles that may be indicative of increasing wool production are also seen at the Middle Saxon rural site of Yarnton in Oxfordshire (Mulville and Ayres 2004) and at the late sixth to eighth century site of Bloodmoor Hill in Suffolk (Higbee 2009).

How large a faunal assemblage is needed to construct a detailed age profile based on dental eruption and wear? Payne (1973) suggested that age profiles should be based on at least 30 ageable mandibles. The overall size of a faunal assemblage needed to yield 30 or more ageable mandibles will depend on a number of factors including the evenness of the assemblage itself. An assemblage that is dominated by a single mammalian species will require fewer specimens than an assemblage that yields roughly equal numbers of three or four different mammal species. In addition, Payne (1973) and Grant (1982) published their dental aging methods at a time when the distinctions between sheep and goats based on mandibles and mandibular teeth were poorly developed (see Payne 1985; Halstead et al. 2002; Zeder and Pilaar 2010). If an analyst working with caprine remains wants to construct separate aging profiles for sheep and goats, larger faunal assemblages (at least 30 sheep mandibles and 30 goat mandibles) will obviously be needed. In her comprehensive study of faunal assemblages recovered from Iron Age sites in Britain, Hambleton (1999, p. 19) notes that Shennan (1988) has recommended a minimum sample of 40 mandibles in order to compare age profiles using a Kolmogorov-Smirnov test. Hambledon (1999, p. 19) further notes that only about 40% of the cattle, sheep, and pig assemblages that she surveyed met this criterion.

Other factors that can affect an analyst's ability to construct a dental age profile include the degree of fragmentation of the animal bones themselves and the nature of the archaeological site from which the bones were recovered. Faunal assemblages associated with urban consumers who purchase joints of meat from markets may include fewer ageable mandibles, since they are often removed during primary butchery. Our research suggests that a faunal assemblage of 5000 to 10,000 animal bones and fragments may be needed in order to construct detailed age profiles for the main domestic mammal species (cattle, sheep, goats, and pigs) based on dental eruption and wear. The actual NISP needed will depend on factors such as the evenness of the species distribution and the degree of fragmentation seen in the bones themselves. Gamble (1978, p. 344), however, has suggested that faunal assemblages of 10,000 to 50,000 total fragments may be necessary in order to reconstruct the age profiles of the main domestic mammals.

Age profiles can be constructed from much smaller assemblages if they are based on epiphyseal fusion of the long bones. However, epiphyseal fusion ceases when an animal reaches bodily maturity (about three to three and half years for sheep). If, for example, we want to identify more specialized wool production in the zooarchaeological record, we need to be able to distinguish mature (3 year old) sheep from the older 5 to 7 year-old animals that are peak wool producers. This is not possible using epiphyseal fusion data alone. In general, age profiles based on epiphyseal fusion are less useful for exploring questions related to secondary products use than are age profiles based on dental eruption and wear because variation in the former may arise due to nutritional status or breed (e.g., Popkin et al. 2012).

Another advantage of the analysis of large faunal assemblages is that these studies allow researchers to explore spatial relationships in the distributions animal bone remains across a site. Although GIS technologies have revolutionized archaeological spatial studies in the past 15 years, these programs were not available when we initially identified the fauna from Brandon in 1990–1991. Animal bones from Brandon that were not associated with a specific feature were recorded by grid square. When spatial analysis programs became widely available in the early twenty-first century we were able to examine the distribution of the large domestic mammal species by grid square. Even though the overall Brandon assemblage is dominated by the remains of sheep (Crabtree 2012, p. 14), this very simple spatial analysis revealed a high concentration of cattle bones surrounding a late Middle Saxon high status dwelling (Fig. 9.3).

Studies of butchery traces can reveal the presence of specialist butchers (e.g., Seetah 2005). These studies can also help us distinguish farmers who are producing meat primarily for home consumption and specialist producers who are supplying meat to local urban markets. At the time I began the West Stow project in 1977, I was interested in the possibility of continuities in animal production between Late Roman Britain and Early Anglo-Saxon England, especially in those areas outside the major Roman urban centers. Analysis of the faunal remains from Icklingham, a small Late Roman crossroads town, and West Stow, a nearby large Anglo-Saxon settlement, was one obvious way to test possible continuities in animal production and consumption. Even though Icklingham was a very small Romano-British town, the animals were butchered in very standardized ways, indicating that these animals

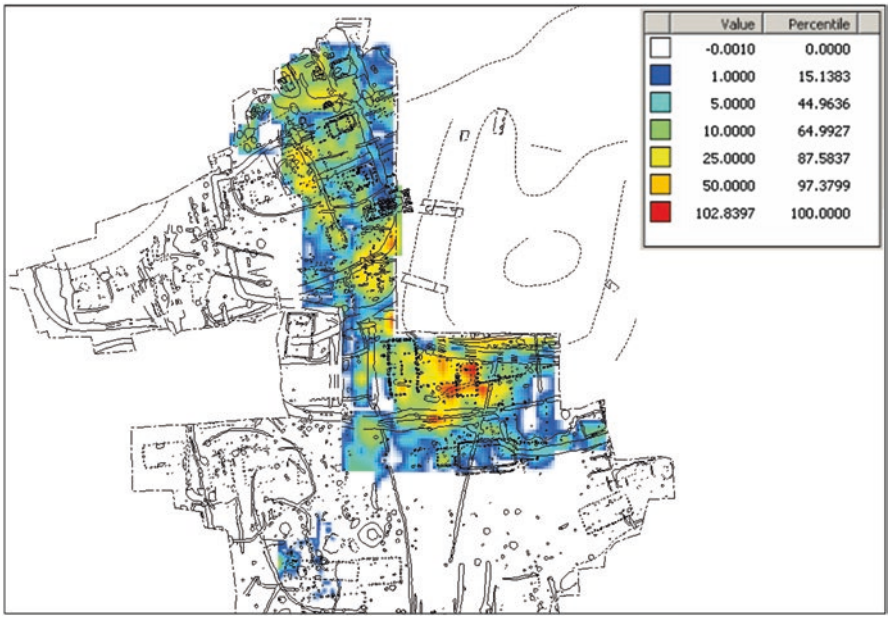

Fig. 9.3 Plan of the Brandon excavations showing the distribution of the cattle remains by fragment count (Tester et al. 2014, p. 109, Fig. 4.56), reproduced with permission of the Suffolk County Council which holds the copyright to the image

were probably broken down by specialists (Crabtree 1991, 2010a). Recently, Hammon (2011) has shown that standardized butchery practices continued into the fifth and sixth centuries at the Romano-British city of Wroxeter, which was the fourth largest city in Roman Britain. In the Lark Valley region of East Anglia, no such continuity is evident. The standardized patterns of butchery that are seen at Icklingham are not seen at the fifth to seventh century site of West Stow. Instead, the West Stow animal bones appear to have been butchered on a more *ad hoc* basis for home or local consumption (Crabtree 1991).

While traces of butchery can be observed in many small animal bone assemblages, studies of butchery *patterns* require large samples with multiple examples of butchery on each skeletal element. Our own research suggests that faunal assemblages of at least 5000 to 10,000 fragments may be necessary for detailed studies of butchery patterns and practices. Again, Gamble (1978, p. 344) suggests that even larger faunal assemblages, on the order to 10,000 and 50,000 fragments, may be necessary to reconstruct butchery patterns and practices.

A major advantage of large faunal samples is that they provide large numbers of measureable bones and consequently more detailed information on animal sizes and size changes through time. While many studies of long-term changes in animal size in Britain and elsewhere have relied on log-scaling of several different measurements against a standard (e.g., Holmes 2014), the large numbers of measurements taken on the animal bones from West Stow and Brandon allowed us to compare

individual measurements. While the sheep from West Stow showed no clear size changes between the fifth and the seventh centuries CE (Crabtree 1990a, pp. 49–50), the eighth to ninth century Brandon sheep were significantly smaller than their West Stow counterparts (Crabtree and Campana 2014, pp. 300–301). In a comprehensive study of size changes in cattle, sheep, and pigs in Anglo-Saxon England, Holmes (2014, p. 79) notes that the major limitations of her study are "poor sample sizes." Of the 42 sites included in her survey, the largest sets of measurements came from Brandon and West Stow.

Finally, conventional studies of large faunal collections can provide a basis for more detailed analyses of these animal bones using modern methods. For example, the large late medieval faunal assemblage from Dudley Castle (West Midlands, United Kingdom) served as the basis for subsequent ancient DNA studies (Campana 2008). While conventional osteometric analyses indicated that the largest of the late Roman cattle from Icklingham were larger than any cattle recovered from West Stow (Crabtree 2010a), more detailed osteometric studies point to a clear decrease in the size of cattle between the Late Roman and the earliest Saxon periods (Rizzetto 2014; see also Rizzetto et al. 2017).

9.5 Conclusions

The analysis of large faunal collections is time-consuming and occasionally frustrating. However, I have hoped to show that the results of these studies can justify the effort. An important point is that while these large-scale studies are time-consuming, they are relatively inexpensive. Most of the work can be done with an osteometric board, a couple of pairs of calipers, and access to reference material and, under optimal circumstances, a good comparative collection. The only other instrumentation needed is a hand lens, a camera and camera stand, and a personal computer with a good database management program. While equipment costs may be low, the actual funding needed to support such research may be significant, as this can require travel to field sites and collections repositories, associated living expenses, etc. External funding has become much more difficult to obtain, especially since the Great Recession. Even students who want to carry out large scale faunal research may not be able to do so for a lack of long-term funding to support their research goals.

As I noted at the outset, studies of large faunal assemblages take time, and today's master's and Ph.D. students are under great pressure to finish their degrees as quickly as possible. However, students who work on large faunal assemblages develop the skills necessary to analyze faunal collections quickly and accurately. These skills are in great demand. Changing antiquities laws in countries such as Turkey and Egypt mean that many faunal collections must be analyzed in the field, often using a small or incomplete comparative collection. Master's and Ph.D. research projects based on large faunal collections allow students to develop the skills needed to take on these challenging field projects. Not only are the assemblages likely to yield evidence for

rare species, they also yield animal bones from a wide range of archaeological contexts with a great variety of taphonomic histories. Moreover, Icklingham, West Stow West, and Brandon are mainly single-period sites. Many archaeological projects involve multi-period excavations, and adequately large assemblages are needed from each chronological phase in order to assess possible changes through time. These basic faunal studies form a critical part of the archaeological record, and they need to be completed before high-tech studies like aDNA analyses and stable isotope assays can be carried out.

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Part III
Isotopic and Biomolecular Techniques

Chapter 10
Molluscs and Paleoenvironmental Reconstruction in Island and Coastal Settings: Variability, Seasonality, and Sampling

Catherine F. West, Meghan Burchell, and C. Fred T. Andrus

10.1 Introduction

Archaeologists commonly rely on broad-scale paleoenvironmental and climate proxies to address past human-environmental interactions and the role of environmental parameters in shaping cultural practices, driving social change and decision-making, and human responses to fluctuations in local environmental conditions. However, environmental data derived from broad-scale proxies that are external to the archaeological record, such as marine or ice cores, may be geographically distant and are of limited use for understanding the subtle nuances of human-environmental interactions (e.g., Pringle 2009). Instead, paleoenvironmental proxies derived from the archaeological record are preferable because these data provide immediate temporal and spatial details of environmental change. Such environmental records are necessary for understanding the local effects of broad-scale climate or environmental change, as well as geographic and spatial variability. In addition to considering the importance of geographic scale, archaeologists must consider the temporal scale of paleoenvironmental proxies. Because humans experience environmental change at a short-term scale (such as seasonal or annual change), high-resolution paleoenvironmental datasets are useful for studying the short-term climate or environmental variability that influences people, rather than proxies that may provide centennial or millennial-scale data. This kind of detail is essential

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when interpreting human-environmental interactions to make meaningful connections between human behavior and environmental or climate change.

Local and high-resolution environmental proxies are available in the calcium carbonate accretionary structures commonly recovered from archaeological sites, including molluscs (Andrus 2011; Leng and Lewis 2014; Prendergast and Stevens 2006; Twaddle et al. 2015; West 2013). The growth history (sclerochronology) and geochemical composition of molluscs (ratios of oxygen isotopes ^{18}O and ^{16}O, expressed as $\delta^{18}O$), particularly bivalves, provide detailed data on local environmental conditions (Gröcke and Gillikin 2008; Schöne and Surge 2005; Thomas 2015a, b). In archaeology, molluscs are well-preserved in middens worldwide, and a combination of sclerochronology and oxygen isotope analysis has been applied to understand the season of mollusc collection, to source their provenience, and to reconstruct environmental parameters and climate patterns (Andrus 2011). However, while these methods have been well tested and broadly published in the earth sciences, archaeological studies have been limited by uncritical applications of these methods, sample size restrictions, and the time and money necessary to produce detailed datasets. These limitations and poor sampling strategies can lead to erroneous interpretations of both environmental conditions and human behavior.

Despite these limitations, in recent years archaeologists have adopted methodological advances from the earth sciences for sampling and interpreting stable isotope data from mollusc shells recovered at archaeological sites. Most significant among these are high-resolution sampling strategies that employ growth and age studies, or sclerochronology, in combination with oxygen isotope records in mollusc shells derived from island and coastal sites (e.g., Burchell et al. 2013a, b, c; Hallmann et al. 2013; Mannino et al. 2003; Thompson and Andrus 2013). Studies employing this methodology focus on two major lines of inquiry: (1) determining the season of collection, which reveals trends in mollusc collection seasonality; and (2) generating paleoenvironmental data that can be used to reconstruct both local and broader patterns in past local climates. High-resolution sampling strategies and resulting data add new dimensions for interpreting human-environmental interactions, including long-term changes in seasonal variability (Hallmann et al. 2013) and increasingly detailed understandings of marine landscape use (Burchell et al. 2013a; Thompson and Andrus 2013).

In this chapter, we argue that sampling methods that consider (1) the growth rate of the species in question, and (2) the research objectives are essential for accurately generating and interpreting oxygen isotope results. We review current techniques in the oxygen isotope analysis of molluscs and address future directions for this method, focusing on several issues. We outline the fundamental principles of oxygen isotope analysis and relate this to the target questions pursued by archaeologists in their analysis of mollusc shell oxygen isotope ratios. Within this context, we present what we consider effective sampling strategies for mollusc oxygen isotope analysis and examine the limitations of this kind of work. In particular, we argue that improved, high-resolution sampling methods provide more useful results than low-resolution methods, in both seasonality studies and paleoenvironmental reconstruction. Low-resolution methods, which have been widely used in archaeology, may produce inaccurate results that lead to flawed interpretations of human behavior.

10.2 Background

The process of sampling stable isotopes in accretionary tissues in archaeological contexts, such as molluscs or fish otoliths, was introduced in the 1970s (Shackleton 1973). This methodology is based on Urey's (1947) study, which established the principle that calcium carbonate in such structures is precipitated in, or uniformly offset from, isotopic equilibrium with surrounding water and can be used to interpret paleotemperature. Because we lack data concerning past $\delta^{18}O$ of the water (which co-varies with salinity), and the molluscs were likely derived from coastal habitats affected by variable tides and freshwater runoff, the interpretation of absolute temperatures based on shell $\delta^{18}O$ is limited. Modern specimens are used to establish the relationship among the oxygen isotope ratio of shell carbonate ($\delta^{18}O_{shell}$) and ambient water ($\delta^{18}O_{water}$), temperature, and individual species (e.g., Böhm et al. 2000; Epstein et al. 1953; Grossman and Ku 1986; McCrea 1950), which can be used to estimate or calculate past environmental conditions.

As marine molluscs grow submerged in ocean water, they incorporate oxygen from the surrounding water into the calcium carbonate of their shells (Rhoads and Pannella 1970). The variation of $\delta^{18}O_{shell}$ values is influenced by local environmental variables, such as water temperature and the $\delta^{18}O_{water}$. The oxygen isotope ratio of water is controlled by evaporation and mixing of fresh and saltwater, thus $\delta^{18}O_{water}$ values in coastal regions typically vary with salinity. Other factors, such as biomineralogical processes, can influence isotope fractionation in shells, but typically $\delta^{18}O_{shell}$ values can be analyzed throughout the growth of the shell to produce a record of environmental conditions over the lifetime of the animal, including seasonal changes in water temperature, patterns of freshwater input, geographic variability, and season of harvest. Such reconstructions require that either water temperature or the $\delta^{18}O_{water}$ value can be constrained. Constraining one of these variables can be difficult in estuarine settings where both temperature and $\delta^{18}O_{water}$ vary throughout the year.

10.3 Research Objectives

One of the most common applications of shell growth line analysis and stable isotope analysis is to determine the season of mollusc harvest by past peoples (e.g., Andrus and Crowe 2000; Andrus 2012; Bailey et al. 1983; Bar-Yosef Mayer et al. 2012; Burchell et al. 2013a, b; Claassen 1983; Coupland et al. 1993; Coutts 1970; Culleton et al. 2009; Deith 1986; Eerkens et al. 2013; Godfrey 1988; Ham and Irvine 1975; Hallmann et al. 2013; Jew et al. 2013; Jones and Quitmyer 1996; Kennett and Voorhies 1996; Killingley 1981; Mannino et al. 2003, 2007; Maxwell 2003; Milner 2001; Rick et al. 2006; Stephens et al. 2008; Thompson and Andrus 2013). Seasonal data have a long history in archaeology (Binford 1980; Cannon 2002; Coutts and Highham 1971; Monks and Johnston 1981; Price and Brown

1985; Rowley-Conwy 1993; Willey 1953), which has emphasized settlement patterns and foraging activity based on the seasonal acquisition of resources. Seasonal data can inform questions about hunter-gatherer decision-making and adaptation to resource availability, landscape variability, and potential food scarcity, dynamic patterns of landscape use, and the social rituals and economic activities that may be tied to resource locations and availability. However, such data tend to be low resolution and it may be difficult to pinpoint a precise season of occupation or animal harvest. For example, the remains of migratory animals (mammals, fish, or birds) may be used to estimate season of occupation at an archaeological site. However, these migrations may happen during multiple seasons and the timing is likely influenced by long-term changes in environmental or climate conditions. Using the high-resolution and precise seasonal data available in molluscs, archaeologists can test broader ideas about landscape use and provide direct evidence for the timing of site occupation, how people moved around and foraged across a landscape, and resource harvesting intensity.

In addition to extracting seasonality information, there is significant interest in understanding change in environmental conditions through time and across space using oxygen isotope ratios in mollusc shells, particularly bivalves (Hallmann et al. 2011, 2013; Jones et al. 2005; Kennett and Voorhies 1996; Rollins et al. 1987; Wang et al. 2013). Change in environmental conditions through time are presumed to be based on changes in climate, while those changes seen across space are presumed to be based on regional variability in island and coastal environments. The kinds of environmental changes that may be reconstructed from shell oxygen isotope records include water temperature, salinity, storminess, and precipitation. While climate records are certainly available from other proxies (tree rings, marine and ice cores, pollen records, glacial chronologies, etc.), shells from archaeological deposits are advantageous for two reasons: (1) they provide a direct connection between the archaeological record and climate conditions on a fine-grained, seasonal scale; and (2) shells derive from a largely sessile animal, so the oxygen isotope record in a shell reflects the conditions at a single location. Therefore, environmental data produced from shell oxygen isotope ratios have the potential to provide detailed information that can explain human behavior and decision-making in a proximal environmental context.

If the environmental changes reconstructed from shell oxygen isotope records occur over a long time scale or appear to vary in tandem with more distant proxies, we may ask if they are related to broader regional or global climate change. Andrus (2011, p. 2897) argues that "perhaps the greatest potential impact of midden sclerochronology to broader science will be in paleoclimatic and environmental studies." In particular, as described above, shell oxygen isotope records have great potential for identifying and characterizing short-term changes in climate. For instance, archaeologists working in northern latitudes have revealed the seasonal effects of Late Holocene abrupt climate changes, such as the Medieval Warm Period or the Little Ice Age, from shell isotope analysis (Hallmann et al. 2011, 2013; Surge and Barrett 2012; Wang et al. 2013). More specifically, the seasonal data available in shells have demonstrated changes in seasonal duration and intensity during these periods in a variety of geographic and cultural contexts across the northern

hemisphere. Similarly, archaeologists working on the coast of Peru are assembling a history of El Niño-related climate change spanning the terminal Pleistocene to the present from the ancient mollusc record (e.g., Andrus et al. 2008; Etayo-Cadavid et al. 2013; Jones et al., 2010b; Rollins et al. 1987). In both regions, such data have been used to illuminate the climatic and environmental contexts in which social or cultural change occurred.

10.4 Limitations

While the use of high-resolution sclerochronology and stable isotope analysis does not have a long history in archaeology, it is increasingly applied in an archaeological context (Andrus 2011). Traditionally, macrostructures, such as lines produced during periods of growth cessation, have been used in archaeological studies to determine age and season of harvest (i.e., Claassen 1983; Clark and Clarke 1980; Coupland et al. 1993; Coutts 1970; Crockford and Wigen 1991; Ham and Irvine 1975; Keen 1979; Maxwell 2003; Milner 2001). Only in the past few years have archaeologists acknowledged the utility of a fine-grained approach to shell sampling and begun looking within the growth lines at the microstructures or lunar daily growth increments (LDGI)–the micro-lines formed by tidal action (e.g., Burchell et al. 2013a, b, c). Given the potential of this approach to refine seasonality estimates and the accuracy of seasonality interpretation in freshwater influenced coastal environments, it is important to acknowledge both the advantages and the limitations of this methodology. Here, we address the four areas of limitation we feel are common methodological problems in studies of stable isotopes in archaeological shell: (1) shell context; (2) mollusc biology; (3) water conditions; and (4) cost.

10.4.1 Shell Context

In archaeological contexts, shells are commonly found in middens, which constitute a collection of proxy environmental data that can be used to understand prehistoric environmental, climate, and behavioral dynamics. Middens may record these variables on short (annual) or very long (millennial) time scales, depending on the nature of human habitation. However, middens are also the result of human harvesting, human decision-making, individual and amassed dumping events, and taphonomic processes (Stein 1992; Stein et al. 2003). Each of these factors needs to be understood to select the appropriate shells for later analysis and to better interpret stable oxygen isotope data. This complexity is particularly important if shell stable isotope data are used for paleoclimate or paleoenvironmental reconstruction, which requires high-resolution temporal control. Such detailed control is best obtained by taking radiocarbon dates directly from the shells analyzed for oxygen isotopes, assuming adequate correction for the radiocarbon reservoir effect is possible (Jones

et al. 2010a; Kennett et al. 2002). Alternatively, the carbonized remains of short-lived terrestrial plant species excavated in closed context or close association with shells may be used (e.g., Etayo-Cadavid et al. 2013).

10.4.2 Shell Biology

While shells have great potential as paleoenvironmental proxies, a range of intrinsic factors—those inherent to the molluscan species, such as life history and habitat requirements—can influence $\delta^{18}O$, complicating interpretation. Calibrations performed on modern shells are used to inform and offset these effects, but even then, discerning among these influences may be quite difficult (Andrus 2011; Hallmann et al. 2009). The stable isotope record sampled from a shell will be influenced by ontogenetic processes and environmental variability. Ontogeny refers to mollusc shell growth and how this changes through the life of the animal. For example, as molluscs age, their extension rate typically slows and they deposit thinner calcium carbonate increments in their shells (Andrus 2011; Claassen 1998; Schöne 2008) (Fig. 10.1a). In addition, they may experience growth cessation at various periods due to stress, spawning, or other factors (Andrus 2011; Claassen 1998) (Fig. 10.1e). Environmental variability influences $\delta^{18}O_{shell}$ as a function of broader temporal or spatial changes in environmental conditions (discussed below) and as a function of species-specific habitat needs and tolerances. As noted above, to the extent that it is possible, these variables must be calibrated using modern shells and modern environmental data to make accurate interpretations of archaeological isotope data.

10.4.3 Water Conditions

While chemical measurements, particularly oxygen isotope ratios, are commonly used to estimate past marine conditions, the precipitation of oxygen isotope ratios in shell calcium carbonate is dependent on both water temperature and oxygen isotope content of water ($\delta^{18}O_{water}$), which typically co-varies with salinity. The oxygen isotope ratio of water may be influenced by environmental variables, such as evaporation, freshwater runoff, precipitation, and tidal mixing in estuaries (Tan 1989). Some shells will grow in seawater where temperature is the dominant influence on oxygen isotope ratios (e.g., the desert coasts of Peru, which are influenced by upwelling of cold water; Carré et al. 2005), while others will grow in mixed water where $\delta^{18}O_{water}$ and temperature have varying temporal and spatial influences (e.g., rainy versus dry seasons in Pacific Mexico; Kennett and Voorhies 1996). Recognition of these phenomena and their differential effects is absolutely vital to interpreting stable isotope data, as a reliable, independent temperature proxy has not yet been found that could be used to verify $\delta^{18}O_{shell}$ (but see Eiler 2011 and Henkes et al. (2013) on clumped isotopes, and Schöne and Surge (2012) for a discussion of metals).

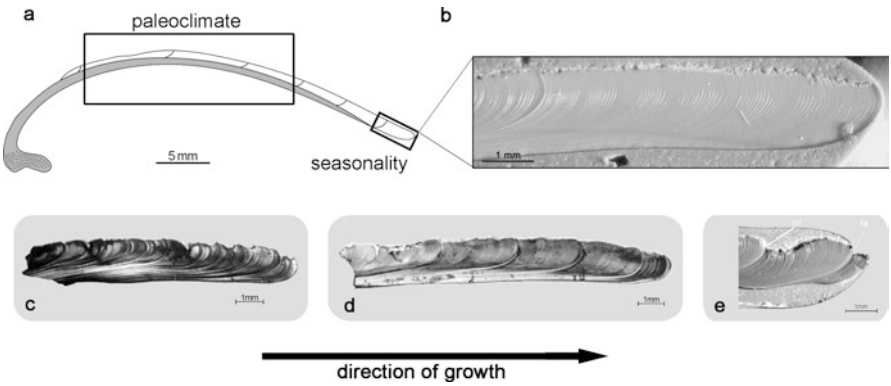

Fig. 10.1 Cross section of a *Saxidomus gigantea* shell showing different portions of growth and different kinds of growth patterns. (**a**) The location on the shell that is best suited for paleoclimate and seasonality studies; (**b**) shell stained with Mutvei's solution showing the contrast of lunar daily growth increments (LDGI) and bundles of neap and spring tides over a 7-week period in the terminal growth of the shell. The difference in growth rates between (**a**) and (**b**) has implications for the sampling resolution; (**c**) senile growth in the ventral margin of an older (>8 years) specimen; (**d**) mature growth in the ventral margin of younger (<8 years) specimen; (**e**) example of a "false annuli" (fa) in a summer-collected shell resulting from a growth disturbance from a storm on June 7, 2007 and a winter line (wl), or growth annuli formed between November–March (modified from Burchell 2013; Burchell et al. 2013b, 2014; Cannon and Burchell 2009)

10.4.4 Cost

Collectively, the considerations discussed above affect sampling strategy. Analysts must choose an adequate sampling resolution within each shell and determine the overall number of shells needed for analysis from a given site. Ideally, the highest-resolution sampling strategy possible is desirable (i.e., sub-monthly resolution), as this reduces time averaging and will likely yield the most accurate and precise environmental reconstruction or season of capture estimate. Similarly, a larger number of shells from each stratum, feature, and site will improve statistical confidence in reconstructions of past environment or behavior. However, practical concerns of cost and time investment will limit the number of samples that can be analyzed in a given project. Here again, modern calibration studies can be a useful tool as they may be employed to identify a practical, cost-effective sampling strategy that also adequately address the research question at hand (e.g., Burchell et al. 2013a).

10.5 Effective Sampling

Acknowledging both the utility and limitations of stable isotope analysis in archaeological shells, we now turn to a discussion of sampling strategies to emphasize the important relationship between chemical analysis and sclerochronology for both seasonality and paleoclimate reconstruction.

10.5.1 Sclerochronology

Sclerochronology is the analysis of growth bands (through lines and increments) in accretionary structures. To reiterate, archaeologists have looked at macrostructures for decades to differentiate between presumed "winter" and "summer" growth, but looking within these lines at the microstructures with a combination of sclerochronology and oxygen isotope analysis reveals growth details previously unavailable (Fig. 10.1b).

Most species grow very quickly in the first years of life, and extension rates slow as they age, which, if not considered, may lead to increased sample time averaging across growth lines and increments in isotopic studies (e.g., Eerkens et al. 2013) (Fig. 10.2c). These growth patterns can also vary in width and seasonal timing due to environmental changes, and pairing growth analysis with oxygen isotope analysis can be used to reveal variation in environmental conditions that cause variation in growth patterns (e.g., Jones et al. 2012). Finally, this combination of methods can be used to determine season of death (or harvest) with more precision than simply counting growth increments (Schöne and Surge 2012; Surge and Schöne 2015) (Fig. 10.2).

10.5.2 Resolution for Seasonality

Seasonality of mollusc collection has been estimated using growth lines and increments with relatively low-resolution results that simply distinguish "warm" from "cold" periods. Further, complicating seasonal assessment, growth line analysis cannot distinguish between "cold" period growth lines and the similar-looking disturbance lines caused by spawning, stress, or other external influences. For example, a spawning line that is produced in the spring is likely to be mistaken for a winter line in a visual analysis, while older mollusc shells form lines aperiodically, regardless of seasonality, which leads to incorrect age and season of death estimates (Fig. 10.1c–e). Given these limitations, the addition of oxygen isotope analysis to seasonality studies provides accuracy when identifying the season of shellfish collection. As seen in Fig. 10.2b, throughout one year, a shell will record isotopic cycles that reflect seasonal cycles, whether driven by temperature, salinity, or a combination of the two. Live-collected shells and water samples are used to illuminate and calibrate this seasonal cycle for specific locations.

As mentioned, low-resolution methods, such as visual assessments or sampling for oxygen isotope analysis from the shell edge alone, are insufficient to determine a precise season of collection. To demonstrate this, Burchell et al. (2013a) assessed the effects of low vs. high-resolution sampling strategies for establishing the season of harvest in butter clam (*Saxidomus gigantea*) shells that were live-collected in British Columbia in summer. As illustrated in Fig. 10.2a, for the low-resolution sampling strategy, Burchell et al. (2013a) employed a hand-held drill with a 1 mm drill bit, beginning ~0.5 mm from the ventral margin of the shell, following methods outlined by Kingston (2007) and Mannino et al. (2007). For the high-resolution

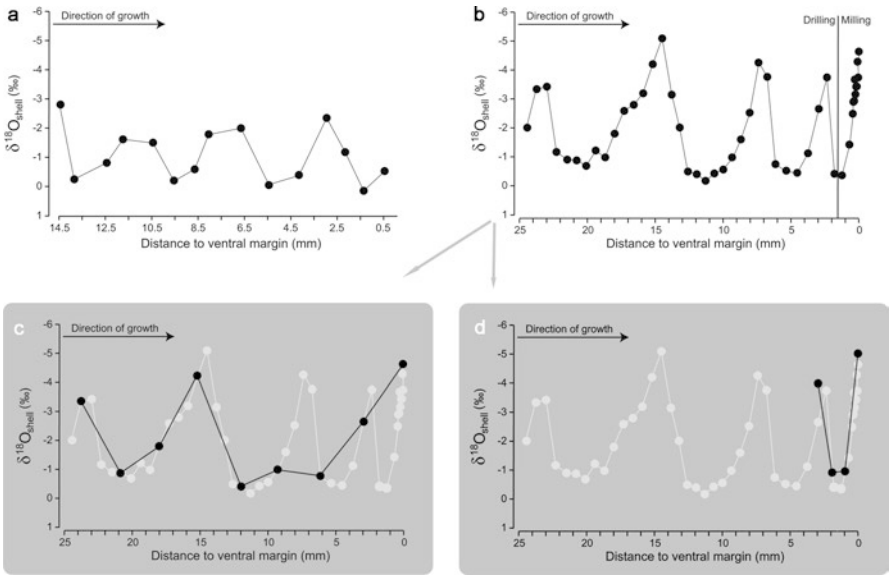

Fig. 10.2 A comparison of high and low-resolution sampling methods from Burchell et al. (2013b), Jew et al. (2013), and Eerkens et al. (2013). The data presented in plots a and b are measured stable oxygen isotope data from a live-collected *Saxidomus gigantea* from Kakushdish Harbour, British Columbia, which was sampled in two ways by Burchell et al. (2013b): (**a**) illustrates low-resolution sampling of the live-collected shell using 1 mm spatial increments, commonly applied in archaeological studies of shell seasonality; (**b**) illustrates continuous, high-resolution micromilling in the same shell using 100-μm steps directly from the ventral margin followed by micro-drilling at 0.5 mm increments. The data presented in plots c and d compare the high-resolution data from plot b to modeled low-resolution sampling strategies seen in the literature: (**c**) modeled low-resolution sampling with samples spaced 3 mm apart (based on method presented by Jew et al. 2013); (**d**) modeled sampling resolution with samples spaced 1 mm apart (based on method presented by Eerkens et al. 2013)

strategy, illustrated in Fig. 10.2b, they used a micromill mounted to a stereomicroscope with a 0.5 mm cylindrical drill bit to sample directly from the ventral margin to mill material off of the growing edge in the upper shell layer. The more coarsely sampled shell showed less seasonal amplitude that did not capture the full range of annual temperature and salinity changes. More significantly, this low-resolution sampling strategy suggested the shell was harvested in winter (Fig. 10.2a), though the shell tested was actually collected in the summer. Summer collection was detected by the fine-grained sampling strategy (Fig. 10.2b).

10.5.3 Resolution for Paleoclimate

Because a principle goal of paleoclimate studies is to calculate an absolute value for various environmental variables, such as temperature, fresh water input, or storminess (i.e., "wet" and "dry"), we argue that the sampling strategy must be even more

rigorous than the more commonly applied low-resolution shell seasonality studies. This kind of measure is extremely sensitive and can be altered dramatically by a low sampling resolution (e.g., Goodwin et al. 2003) and time averaging from ontogeny (Fig. 10.1), in contrast to a season of capture study, where a more qualitative assessment of seasonality is required.

Early studies that relied on low-resolution sampling strategies—for instance, one sample per month of growth—will reveal only broad differences in seasonality or even annual conditions (e.g., Kennett and Voorhies 1996), and will also be subject to time averaging. Hallmann et al. (2009, 2013), Schöne (2008), and Goodwin et al. (2003) have argued that increasing the sampling resolution allows for detailed examination of local changes in climate that may influence environmental variables over several seasons of a mollusc's life. For example, Hallmann et al. (2013) employ a 1 mm cylindrical mill bit and contiguous micromilling to create an uninterrupted isotope record over several years of shell growth. This approach produces a sub-daily record of climate information that can be used to address seasonal variability and changes in seasonal extremes through time. Such information is important because it reveals the full range of seasonality and local effects of broad-scale climate change. Understanding seasonality in these terms allows broad-scale climate change to be related to the scale of human perception and experience. Unfortunately, the approach is limited by expense because of the number of samples required. Therefore, the challenge for archaeologists is to connect these very detailed (both temporally and spatially) data with both archaeological time scales and broad-scale atmospheric and oceanic climate data to understand the human response. We also argue that there should be tight temporal control to determine patterns of environmental and climate change, which may be best achieved by radiocarbon dating each sampled shell.

To illustrate the importance of a high-resolution sampling strategy for paleoenvironmental reconstruction, specifically paleo-sea surface temperature (PSST), we compare the high-resolution *S. gigantea* data presented in Fig. 10.2b (Burchell et al. 2013b) to the results of low-resolution sampling strategies proposed in recent studies. We use methods presented by Jew et al. (2013), who reconstruct seasonality and PSST using California mussels (*Mytilus californianus*), and Eerkens et al. (2013), who make the same estimates using clam (*Macoma* sp.) and mussel (*Mytilus* sp.). As seen in Fig. 10.2, the comparison of high and low-resolution methods demonstrate that meaningful seasonal data are missing from the plotted isotope profiles when low-resolution methods are applied to *S. gigantea*. When modeled for the *S. gigantea* record, Jew et al.'s (2013) method (Fig. 10.2c) produces samples at 3 mm increments and shows the same season of death as the fine-grained method; however, the full amplitude of $\delta^{18}O$ values that account for seasonal changes in both temperature and salinity are lost. Also, this low-resolution method creates aliasing of the seasonal signal by recording fewer oscillations, which greatly changes the apparent longevity and growth rate of the clam. When modeled for *S. gigantea*, the method presented by Eerkens et al. (2013) uses a finer sampling resolution (samples spaced 0.5 mm apart), as seen in Fig. 10.2d. When compared to the high-resolution sampling strategy shown in Fig. 10.2b, this method shows the same season of death and is very close to the milled sample over one year of growth (within analytical preci-

sion, 2-sigma). However, when reconstructing paleoclimate conditions it is important to capture more than one year of growth. This not only reveals the full amplitude of seasonal change, but also variations in marine climate over the lifetime of a shell (Bailey et al. 1983).

Techniques exist to at least partially address the impact of lowered sampling resolution, variable growth rate, and missing data (e.g., Beelaerts et al. 2010; De Ridder et al. 2007; Wang et al. 2015; Wilkinson and Ivany 2002), assuming the presence of a regular underlying sinusoidal signal driving the isotope data. However, these methods cannot fully address the shortcomings of extremely discontinuous low resolution sampling as seen in Fig. 10.2c. Based on these comparisons, therefore, studies that use low-resolution sampling strategies to maximize the number of samples risk inaccurate measures of past environmental conditions, which has implications for the interpretation of human-environmental interaction in the context of environment and climate change.

10.5.4 Sample Size: Number of Shells and Sites?

Finally, we address the question that all archaeologists ask: how many archaeological sites and shells should we be analyzing? Certainly the answer to this question will be driven by the project's research questions and budget, but we argue that very small sample sizes will likely not reflect the broader environmental and climatic trends we are trying to identify. Studies that sample very few shells from one site to determine the season of occupation or changes in environmental conditions will likely not capture the potential range of variability or the patterns in human behavior, environmental conditions, and climate. For example, in paleoenvironmental reconstruction, more shells sampled per time period will improve confidence in the reconstruction and the more time span covered by sampling will create a more comprehensive profile of change. Additionally, the duration of occupation of a site and shell accumulation rate will influence the number of samples necessary to accurately characterize the local environment and/or season of capture patterns. In their study of the Gulf of Florida coast, for example, Thompson et al. (2015) use high-resolution sampling of 52 shells excavated from multiple midden and mound sites. With this sampling strategy, they are able to demonstrate the season of shell deposition between site types (midden vs. mound) and to establish the sites' accumulation rates, both of which may have been missed with a smaller sample size.

10.6 Conclusions and Future Directions

The final question we pose here is: how collaborative should this research be? We argue that shell biologists, geochemists, paleoclimatologists, and archaeologists will find collaboration mutually beneficial. While some scientists successfully

bridge the gap between archaeology and other disciplines, for most, collaboration will be imperative. The archaeological record contains longitudinal data that are increasingly relevant to contemporary understandings of climate change and marine dynamics, and archaeologists can contribute to the marine sciences with these records. On the other hand, archaeologists must look beyond their own science to understand the advanced sampling and calibration methodologies that are developed and applied in the biological and geochemical disciplines if their data are to be accurate and relevant. Archaeologists and their collaborators have made great progress in the sampling strategy and interpretation of seasonality data. However, reconstruction of paleoclimate data from shell isotopes is still in its early stages and will benefit from further refinement of the methods.

The future of this work lies in this refinement and in the development of new methods that will illuminate environmental variables. Sclerochronology is not infallible, and "blind" studies may be one approach to refining current approaches to seasonality. For example, modern shells of known collection conditions may be sent to labs that are kept ignorant of these conditions. The resulting reconstructions are compared to these known conditions, and the results will increase estimates of precision that could be applied to the same species in similar environments. Given the potential lack of precision, archaeologists must acknowledge that season of harvest estimates are imperfect, and results should be interpreted in the appropriate archaeological, environmental, and research context.

Increased confidence in season of capture estimates coupled to the extremely fine-scaled growth analysis (e.g., Burchell et al. 2013b; Hallman et al. 2009) opens the possibility that sclerochronology can be used to identify short-term events (days to weeks). Potential evidence of brief feasting or processing episodes has been identified using mollusc oxygen isotope records (e.g., Blitz et al. 2014; Thompson and Andrus 2011), but as of yet the techniques employed are too low resolution to confidently define these practices. However, continued improvement in defining the periodicities of fine-scale growth increments, in conjunction with ultra high resolution stable isotope analysis for corroboration, could make this possible soon. Along with detailed excavation data, this technique could provide a new window into ancient human activity.

In addition, three analytical methods show potential for illuminating the influence of various environmental and physiological variables on shell chemistry. These include: (1) elemental analyses, primarily the ratio of metals to calcium; (2) analysis of the shell's organic fraction; and (3) clumped isotope paleothermometry.

In many organisms, the ratios of barium (Ba), magnesium (Mg), and strontium (Sr) to calcium (Ca) are a useful past water temperature proxy. However, this method has shown mixed results in many biogenic carbonates, including bivalves (Gillikin et al. 2005; Schöne et al. 2011, 2013; Surge and Lohmann 2008; Surge and Walker 2006). As this method develops, details emerge about the effects of mineralization, age, ontogeny, environmental conditions, and changing metabolism on these ratios (e.g., Pérez-Huerta et al. 2013; Surge and Walker 2006), as well as the potential for clumped isotope analysis to resolve confounding environmental factors (Henkes et al. 2013, see below).

Analysis of a shell's organic fraction has been applied to modern shells to address pollution using nitrogen isotopes ($\delta^{15}N$; Carmichael et al. 2008; Fertig et al. 2010), and this approach will have wide application in archaeology to address marine productivity, nutrient cycling, and hydrology over the long-term. However, before this method can be applied to understand the past, there must be a clearer understanding of shell organic matter diagenesis—the effects of both cooking and burial—and an improved understanding of the environmental processes that control the chemical composition of organic matrices.

Clumped isotope analysis may provide a useful method for assessing past temperature that does not require independent knowledge of $\delta^{18}O_{water}$ (see Passey 2015 for a simple description of the rationale). Clumped isotope paleothermometry hinges on the temperature-dependent likelihood that ^{13}C and ^{18}O bond together—or "clump"—in calcium carbonate minerals. As temperature increases, there is decreasing affinity for ^{13}C and ^{18}O to bond to one another. Therefore, knowledge of the $\delta^{18}O$ of water is not needed to calculate paleotemperature using this method. To date, the method does not yet yield the precision necessary for most paleoclimate applications, and its comparatively large sample size requirements and higher cost both limit its utility for season of capture estimates. However, as improved calibration, better understanding of confounding variables, and refined analytical techniques are developed, this technique may become a powerful tool for widespread assessment of ancient coastal climate using archaeological shells that cannot currently be used to assess past water temperature because of unknown $\delta^{18}O_{water}$ variation. This technique may also refine season of capture estimates by helping to distinguish seasonal temperature variation from $\delta^{18}O_{water}$ variation.

A combination of the sampling strategies and methodological innovations described here, as well as an understanding of the limitations of these methods, will add new and significant dimensions to interpreting human-environmental interactions through time and across space.

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Chapter 11
Ancient DNA in Zooarchaeology: New Methods, New Questions and Settling Old Debates in Pacific Commensal Studies

Elizabeth Matisoo-Smith

11.1 Introduction

Recent developments in DNA technology have revolutionized evolutionary biology and opened up new opportunities particularly for ancient DNA studies. The application of these new methods will no doubt be valuable for zooarchaeological research generally, but they will be particularly useful in the study of human transported species introduced to island environments, where the phylogeography of such species can reveal key information about human population origins and migration and interaction histories. Here, I will briefly review the history of the commensal approach for tracking Pacific migration. I will then introduce the basic methodology and advantages of Next Generation Sequencing, particularly focusing on its application in ancient DNA studies, and then I will discuss how these new approaches can both allow us to address new questions about human-animal interactions and settle old debates about the origins and introduction histories of the commensal animals in the Pacific and more widely.

11.2 The Commensal Approach

Part of the colonization strategy of early Pacific communities was the transportation of their important plants and animals and the introduction of these species to the new island environments being settled. It is generally accepted that the initial settlement of Remote Oceania (see Fig. 11.1) was associated with the expansion of the Lapita culture, and that Lapita peoples introduced domesticated dogs, pigs, chickens, and the Pacific rat (*Rattus exulans*) to the islands they settled (Kirch 2000)

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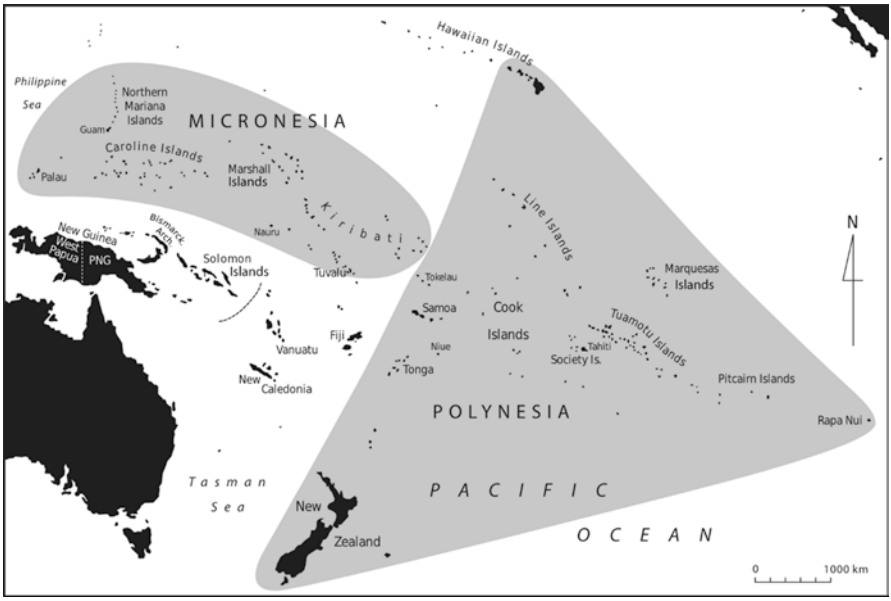

Fig. 11.1 Map of the Pacific showing the Polynesian Triangle and the islands of Micronesia in *gray*. *Dotted line* shown east of the Solomon Islands delineates Near Oceania to the west and Remote Oceania to the east

(though note that the Lapita introduction of the dog has been questioned based on limited archaeological evidence of dog remains in Lapita sites (Matisoo-Smith 2007)). The settlement of the Polynesian Triangle, which happened at least 1500 years after Lapita colonization of Samoa and Tonga in West Polynesia (Wilmshurst et al. 2011), continued the spread of these four animals across the Pacific. In 1994, the application of a commensal approach to studying the human settlement of the Pacific was first described (Matisoo-Smith 1994). By reconstructing the genetic phylogenies of animals transported in colonizing canoes, it was argued, we had a proxy for tracking and reconstructing human migration pathways through the Pacific.

The term commensal is derived from Latin and literally translates to "to eat at the same table", yet it has been applied in biology to refer to animals or organisms that exist in a symbiotic state, where one species benefits from the relationship while the other is generally unaffected. In the Pacific, it has been applied to describe the relationships between humans and the plant and animal species they introduced, intentionally or unintentionally, to the islands that were settled. The first commensal study in the Pacific focused on mitochondrial DNA (mtDNA) variation in the Pacific rat (*R. exulans*) (Matisoo-Smith 1994). This animal was chosen because unlike the other three Lapita associated animals carried into the Pacific, this rat was introduced to all islands that were settled by Lapita and later Polynesian colonists. Pigs, dogs, and chickens have a much more patchy prehistoric distribution (Storey et al. 2013a).

In addition, *R. exulans* is a distinct species from the rats that were introduced to the Pacific by European explorers, traders and colonists, *R. rattus* and *R. norvegicus*, and thus did not interbreed with these later introductions. The pigs, dogs, and chickens carried by European ships belong to the same species as those carried by Pacific colonists, and thus quickly interbred with the animals already present on the islands. As a result, modern populations found on the islands are generally no longer representative of those initially introduced by the Pacific colonists. So, it was argued that *R. exulans* provided the best study animal with which to develop a commensal approach for the Pacific. The initial study focused on mtDNA variation in extant populations of *R. exulans* collected from across the Polynesian Triangle (Matisoo-Smith et al. 1998) and indicated that indeed a commensal approach would work for modeling human colonization and interaction patterns in the Pacific.

11.3 Ancient DNA in Commensal Studies

In order to further test the commensal approach and address the question of timing of prehistoric rat introductions and possibly identify multiple introductions through time, we investigated the possibility of obtaining data from archaeological remains of *R. exulans*, through the analysis of ancient DNA (aDNA) (Matisoo-Smith 2002; Matisoo-Smith and Robins 2004; Matisoo-Smith et al. 1997). The first paper describing the analysis of DNA from ancient skeletal remains was published in 1989 (Hagelberg et al. 1989) and methods have developed considerably over the years. One of the main developments from the early studies was the recognition of the problems of contamination in aDNA which resulted in the development of a range of broadly accepted protocols to control for and identify possible contamination (Cooper and Poinar 2000). Many of the early claims for ancient DNA recovery from samples that were hundreds of thousands of years old or older (Cano and Borucki 1995; Golenberg 1991) were indeed shown to be the result of contamination (Austin et al. 1997).

The development of a procedure called the Polymerase Chain Reaction or PCR in the mid-1980s (Mullis et al. 1986), was a major breakthrough for aDNA analysis. PCR is the process by which DNA is amplified, or copied, to obtain enough DNA for sequence analysis, generally using a protocol known as Sanger sequencing (Sanger and Coulson 1975). The nature of aDNA is that it is generally highly degraded and damaged, resulting in very short fragments of DNA in limited quantity, particularly compared to modern DNA. The process of PCR will preferentially amplify DNA of good quality and quantity and the resulting Sanger sequencing of amplified PCR products generates a consensus of the majority of the DNA that was amplified. If the DNA extracted from an archaeological bone or tissue sample is degraded and in low copy number (as is generally the case in ancient DNA), any modern DNA on the sample or in the laboratory can be preferentially amplified and sequenced by mistake. Contamination can be introduced by people handling the samples, leaving their own DNA on the sample; it can be introduced in laboratory

reagents, or it can be introduced by cross-contamination between samples being processed or previously processed in the lab. As a result, one of the main protocols in aDNA research is the running of negative controls—or processing samples with every DNA extraction and PCR amplification in which no DNA has been intentionally introduced. All negative controls should, of course, produce no PCR product—and if they do, all results for samples processed with the negative control should be questioned and, ideally, not used for further analyses.

Obviously, when studying faunal remains, DNA introduced by the handling of the samples by archaeologists or the laboratory staff is identifiable as human DNA and thus is easy to recognize. The use of species specific PCR primers that will not amplify DNA belonging to another species are also useful for reducing the likelihood of contamination. Cross sample contamination and contamination of laboratory reagents, however, can be a problem with analyses of faunal remains. It has been suggested that domesticated animal DNA can be found in some laboratory reagents (Leonard et al. 2007). The use of negative controls and independent replication can help with the identification of contamination and are generally required for publication as over the years, partly due to claims for extreme results such as the recovery of dinosaur DNA, it has become the onus of the researcher to prove that any aDNA results produced are reliable and replicable (Gilbert et al. 2005).

With these developments in aDNA research, the commensal approach could be applied to the other animals transported in the Pacific colonizing canoes, and studies were undertaken on archaeological dog, pig and chicken remains (Larson et al. 2007; Savolainen et al. 2004; Storey et al. 2007). These results have been invaluable for studying the process of human settlement of the Pacific, highlighting that there may be different histories for different commensal species and indicating that the settlement process may be more complex than we initially assumed (Matisoo-Smith 2009). The limitations of using modern domesticated animal DNA to reconstruct prehistoric dispersal patterns of Pacific commensal animals should be considered, as recent husbandry practices and modern dispersals of domesticates may obscure more ancient patterning, making modern samples unsuitable as a point of comparison for aDNA results (Gongora et al. 2008; Shannon et al. 2015). Modern breeds of dogs, pigs, and chickens have been artificially manipulated substantially by humans in the last few hundred years in order to produce the range of phenotypes that define those breeds, and thus they tell us little about the genetic makeup of the populations living prior to these historic breeding programs (Girdland Flink et al. 2014). Archaeological context, the radiocarbon dating, and other biochemical analyses of samples being processed for aDNA remain critical for interpreting aDNA results (Storey and Matisoo-Smith 2014; Storey et al. 2008, 2013a).

11.4 New Methods: Next Generation Sequencing

While ancient DNA methods and applications had improved dramatically over the years, recent developments in technology have revolutionized the field of aDNA research. The development of what has been termed Next Generation Sequencing

(NGS), or high throughput sequencing, has not only dramatically increased the amount of genetic information we can obtain from ancient samples, it has significantly reduced the cost of analyses and eliminates or dramatically reduces many of the issues with the old method of PCR amplification and automated Sanger sequencing (see Knapp and Hofreiter 2010; Millar et al. 2008 for excellent overviews and graphics of NGS methods). NGS encompasses a range of sequencing platforms (Illumina's Solexa, Applied Biosystem's SOLiD, Thermo Fisher's Ion Torrent, and Roche's FLX 454, for example) which all share the property that they quickly and directly sequence in unison millions of short fragments of DNA present in a sample. These tiny sequences of DNA (generally ranging in size from between 50 to 400 base pairs) are then reassembled by computer to provide the sequence of a whole genome or parts thereof. Perhaps the most valuable aspect of NGS for archaeological studies is that just by the volume of data produced, these methods allow for the sequencing of nuclear DNA in ancient samples. Prior to NGS, researchers studying aDNA were limited, for the most part, to analyses of mitochondrial DNA. This was due to the fact that there are many mitochondria in every cell and, therefore, many copies of the mitochondrial DNA. Due to price, the time required, and the limitations of the old technology (particularly with damaged ancient DNA), mtDNA sequencing studies targeted only a few hundred base-pairs of the hypervariable region (HVR). The HVR is the region of the mitochondrial genome, which, it was assumed, carried the most variation due to the fact that it was a non-coding region and could, therefore, accumulate mutations without negatively impacting the organism. Nuclear DNA has always been very difficult to obtain from ancient samples due to the low copy number in each cell. NGS produces so much data that even samples with small amounts of endogenous DNA can result in sequencing of portions, if not the complete nuclear genome (Green et al. 2010; Miller et al. 2008; Poinar et al. 2006). Recently, researchers used NGS to sequence the complete genome of a 700,000 year old horse recovered from permafrost (Orlando et al. 2013), and while this sample was unusual in terms of its preservation, the age range of samples from which we can obtain aDNA is increasing dramatically.

Rather than producing a consensus sequence of the targeted DNA in a PCR amplification, as is the case with Sanger sequencing, with NGS each DNA molecule in a prepared sample is sequenced independently. Thus, all of the DNA in an ancient sample, including endogenous DNA as well as contamination, can be copied and sequenced at the same time. As DNA degrades over time, predictable patterns of damage result. Generally, this is seen as deamination at the ends of the DNA fragments which causes C/T transitions in the resulting sequences. (Ginolhac et al. 2011). Because all fragments are sequenced and not all pieces of DNA extracted from a sample are sheared or broken in the same patterns, all of the fragments of DNA can be aligned, and it can be determined if a variable site is likely to be real or merely the result of damage. Evidence of predicted damage patterns in an ancient sample can be used to support the likelihood of the sequences being ancient endogenous DNA as opposed to contamination from modern DNA, which would not show these typical patterns (Ginolhac et al. 2011). NGS can also show if there are multiple sources of sequences in an extract, which again allows for the identification of possible contamination.

An added benefit of NGS is its ability to sequence short fragments of DNA. Previously, it was virtually impossible to amplify DNA fragments that were shorter than 60–70 base pairs long using standard PCR protocols. Analysis of DNA fragment lengths indicate that most aDNA is sheared to fragments that are less than 70 base pairs in length (Knapp and Hofreiter 2010; Knapp et al. 2012), particularly in environments like those found in the Pacific, where the hot and humid climatic conditions work against DNA preservation. With NGS, very short fragments of DNA and thus much more of the aDNA extract can be sequenced, allowing data to be obtained from highly degraded samples that would not have provided any sequence using Sanger sequencing.

Unfortunately, in addition to sequencing the DNA of the organism of interest, NGS methods also sequence all of the environmental DNA in the sample too, resulting in the inclusion of a large amount of bacterial or other microbial DNA which can then dominate the percentage of obtained sequences. In what is referred to as a shotgun sequencing approach, all of the DNA in a sample, including environmental DNA, is randomly sequenced, and these sequences are then aligned to a scaffold of the known species or the most closely related species. Samples that do not align or match the species of interest are discarded or set aside. This approach can result in the sequencing of complete genomes, but only if the samples are particularly well preserved, such as in material recovered from permafrost. Shotgun sequencing, however, also provides valuable information regarding the quality and quantity of endogenous DNA in a sample. Alternatively, and particularly for samples that are not so well preserved, portions of the genome can be specifically targeted and enriched for sequencing through a range of different methods (Knapp and Hofreiter 2010).

The combination of NGS methods with a process known as hybridization capture, which allows for the targeted enrichment of particular parts of the genome, is increasingly being used in aDNA studies. Using these approaches researchers can, for example, target and rapidly sequence complete ancient mitochondrial genomes with relative ease (Briggs et al. 2009; Knapp et al. 2012; Krause et al. 2010a, b). By incorporating small, sample-specific barcodes (a known and unique sequence of nucleotides) to the ends of each DNA fragment when a sample is being prepared, many samples can be pooled together and run on a single lane of a sequencing machine, significantly reducing the cost per sample. After the sequencing run, each sample can be identified by its barcode using bioinformatic pipelines and all of its sequenced fragments separated from the others and then aligned and assessed to create the final, ideally high coverage, complete sequence of interest.

11.4.1 Ancient Mitogenomics

While the development of NGS allows for the sequencing of the nuclear genome, this still requires a level of preservation that many samples will not meet and is still relatively expensive. The ability to sequence complete mitochondrial genomes, or mitogenomes, however is still particularly valuable for addressing some questions,

such as identifying population origins, diversity, and change through time. In addition, it is still also more likely to obtain mitogenomes than nuclear DNA from archaeological samples recovered from open archaeological sites as opposed to those recovered from more temperate and protected cave sites (Ho and Gilbert 2010). When combined with barcoding and hybridization capture, the use of NGS allows for the relatively quick and inexpensive sequencing of the mitogenomes of archaeological remains. Whole mitogenomes allow for much more complex and potentially insightful analyses than researchers are able to undertake looking at HVR sequences alone. While it was assumed that the HVR produces enough variation for most phylogeographic analyses, it has been shown that there are numerous important and phylogenetically informative variations outside the HVR and these can be important for inferring population history (Duggan and Stoneking 2013; Duggan et al. 2014). The numbers of species and numbers of samples for which complete ancient mitogenomes are being generated is increasing exponentially as are the data for modern populations, which is also useful. I suspect that in the future, studies presenting only HVR data will be difficult to publish.

11.4.2 Application of NGS for Faunal Studies: Domestication

The ability to sequence targeted portions of the nuclear DNA in ancient samples has allowed us to begin to see evolution in action, and while this was possible using traditional Sanger sequencing, the use of NGS makes analysis of the nuclear genome possible for a much wider range of ancient samples, both geographically and chronologically. One of the first studies to investigate the impact of human selection on domesticated species looked at selection for coat color variation in ancient horses (Ludwig et al. 2009). Analyses of six genes associated with coat color in late Pleistocene wild horses from Siberia and East and Central Europe showed that all were bay or bay-dun in color, indicating this was the most likely color of the original wild horses. By the early Holocene horses from the Iberian Peninsula (n = 8) were either black or bay, as were early Neolithic and Copper Age samples from East Europe. Beginning in the fifth millenium BP, a significant increase in the variety of coat colorations was seen in Siberia and East Europe, with mutations resulting in spotted varieties emerging slightly later. Interestingly, no additional color change was identified in the Spanish populations until the Medieval period (Ludwig et al. 2009). While this study was carried out using standard Sanger sequencing, studies of selection will be more common in the future using NGS.

A similar study was undertaken using NGS on ancient canid remains from Asia and Europe to investigate coat color changes associated with domestication of dogs (Ollivier et al. 2013). By studying changes in the Mc1R (Melanocortin 1 Receptor) and CBD103 (canine-β-defensin) genes, the authors showed that variation in dog coat color occurred very early in the domestication process, with both dark and light color-causing mutations present as early at 10,000 BP, at the beginning of the Holocene. This variation may have been present in the wolf gene pool prior to

domestication or may have been caused by a relaxation of natural selective pressure associated with the domestication process itself.

11.4.3 Application of NGS for Ancient Population Genomics

With the constant improvements and developments of NGS, the cost per genome is coming down and the amount of DNA that can be obtained from ancient samples is increasing. While we have learned huge amounts from single genomes of, for example, ancient hominins (Lalueza-Fox and Gilbert 2011; Meyer et al. 2012), the idea of sequencing the genomes of many individuals within a population or species is now possible, and thus ancient population genomic studies are feasible (Parks et al. 2015). Such large scale studies, of course, will rely on availability of large numbers of well-preserved samples and are thus possibly limited to arctic or Antarctic species or those that exhibit unusually good preservation, but will allow for the extension of studies looking at impacts of environmental changes on species and other long term demographic histories. While some indications regarding demographic changes and their likely causes in ancient or extinct populations are possible without full genomic studies (e.g., Hofreiter et al. 2007; Shapiro et al. 2004; Valdiosera et al. 2008), the increase in the amount of data that can be obtained using NGS will only improve the robustness of the results obtained.

11.5 Application of NGS to Ancient Samples from the Pacific

One of the exciting results of the growth of NGS is that we now have much better modern DNA databases with which to compare aDNA results. Recent analyses of complete mtDNA genomes in humans using NGS have indicated that there is much more variation in the mtDNA of Pacific populations than previously thought based on the analysis of just the hypervariable region of the mitochondrial genome (Benton et al. 2012; Duggan et al. 2014). This increased level of variation may help us better reconstruct relationships between different populations. These data also have significant implications for reconstructing ancient demography, such as estimating the size of founding populations. This level of analysis of variation can potentially identify new arrivals in a population or even population replacement as we have recently found on the island of Atafu in Tokelau (unpublished data).

While the sequencing of entire ancient nuclear genomes is still time consuming and expensive, particularly for poorly preserved samples such as those from the Pacific, NGS techniques have been used to sequence complete mitochondrial genomes from ancient human and dog remains from the archaeological site of Wairau Bar in the South Island of New Zealand (Greig et al. 2015; Knapp et al. 2012).

Dogs provide an interesting case study. Previous aDNA research on archaeological dog remains in the Pacific identified the presence of only two haplotypes, Arc1 and

Arc 2 (Oskarsson et al. 2012; Savolainen et al. 2004) based on sequencing just a small (290 base pair) fragment of the HVR. As was the case in analyses of complete human mitochondrial genomes in the Pacific, it has been demonstrated that there is significantly more variation across the mitochondrial genome in dogs (Verscheure et al. 2014). Using NGS hybridization capture techniques, Greig et al. (2015) sequenced the complete mitogenomes of 14 dogs recovered from an oven feature (dated to AD 1320–1350) at Wairau Bar, and identified five different mitochondrial haplotypes in this single New Zealand population. It is therefore possible, if not likely, that complete sequencing of ancient mitogenomes will help elucidate relationships between different archaeological dog populations across the Pacific. In addition to being able to obtain more sequence data using NGS methods, it is possible to get DNA out of Pacific faunal samples that previously did not provide reproducible data using standard PCR and Sanger sequencing (unpublished data from the Matisoo-Smith lab). Such data will not only help identify origins of different dog populations, but can address questions about dog mobility both within an archipelago and across the Pacific, which tells us more about dog/human relationships in the region through time (Greig et al. 2016).

While the pigs, dogs and chickens that were brought into the Pacific by early colonists were already domesticated, evidence for significant variation in snout length in dogs in Hawaii (Clark 1997) suggests possible selective breeding for particular facial characteristics (Clark 1997). In New Zealand, there may have been selection for coat length or color in association with the use of dog fur for cloak production (Best 1899). Given these preferences, it should be possible to investigate coat color in faunal remains through analysis of the Mc1R and CBD103 genes (Ollivier et al. 2013) to determine if changes in gene frequency occur through time. Similarly, aDNA analyses could be conducted on dog burials to determine if there are any unusual or specific phenotypic traits associated with these animals compared to those dog remains found associated with food remains.

Another significant avenue for investigation involves examining genetic changes in Pacific pig populations over time and space and possible evidence of selection for specific traits. Pigs have clearly had a significant role in cultures across the Pacific, and genetic changes associated with tusk development (Lum et al. 2006) or levels of fat distribution (Lee et al. 2011) could provide evidence of selective breeding in different populations. It is also possible that through sequencing of complete mitogenomes, phylogenetically informative mutations not previously found in Pacific pigs will be recognized, as only one haplogroup has ever been identified based on analyses of HVR sequences in ancient Pacific pigs (Larson et al. 2007).

The application of NGS technology could also potentially settle the highly public debate about the pre-Columbian introduction of Pacific chickens to the Americas (Beavan 2014; Bryant 2014; Gongora et al. 2008; Storey and Matisoo-Smith 2014; Storey et al. 2007, 2008, 2013b; Thomson et al. 2014a, b). Prior to 2007, it was generally accepted that the chickens found in the Americas were first introduced by Columbus or other early European explorers. However, when Storey et al. (2007) published evidence for the presence of chicken bones from a pre-Columbian coastal site in central Chile, this presumption was challenged. The remains of at least five

chickens were recovered from the site of El Arenal-1 and one of these bones was initially made available for radiocarbon dating and ancient DNA analysis. The radiocarbon date obtained was 633 ± 35 BP, giving a calibrated age range of AD 1321–1407. Even at two sigma, the sample was clearly pre-Columbian (AD 1304–1424). The DNA sequence obtained from the sample, which was replicated in an independent lab, was identical to sequences found in ancient Pacific chicken bones recovered from archaeological sites in Tonga and Samoa (Storey et al. 2007). This result was challenged in several publications from another research group who questioned both the radiocarbon dates, suggesting that they may have been impacted by a marine diet in the chickens which would make the dates appear older than they were, and the ancient DNA sequences obtained from the Chilean bone (Gongora et al. 2008; Thomson et al. 2014b).

To date, three El Arenal chicken bones have been sequenced and directly radiocarbon dated. All three are clearly pre-Columbian even at two standard deviations. Isotope analyses of these bones also indicate that they had a terrestrial diet, similar to local camelids, and, therefore, no additional corrections due to a marine component in the diet are necessary. The dates for the chicken bones were also thoroughly consistent with the artifactual and stratigraphic evidence and thermal luminescence dates for the site (Storey et al. 2013b). Thus the issue of a pre-Columbian introduction of chickens to South America is well supported. Identifying the source of that introduction is where the DNA evidence comes into play.

Storey and colleagues (2010, 2012) have argued that there were two, chronologically separate, chicken introductions to the Pacific, an early introduction which involved chickens carrying mtDNA sequences belonging to a now common, Asian derived, lineage (Haplogroup E), and a later introduction of chickens into the Pacific from Island Southeast Asia. These later chickens carried DNA belonging a different lineage (Haplogroup D). All archaeological chicken bones recovered from Pacific sites with dates earlier than 1000 BP contain only Haplogroup E chickens. Sites dating later than 1000 BP contain chicken bones with both Haplogroups E and D, with a higher proportion of Haplogroup D in East Polynesian sites such as Hawaii and Easter Island (both likely settled around or post 1000 BP). The three Chilean chicken bones were identified as carrying Haplogroup E sequences, which led some (Thomson et al. 2014b) to argue that these and the early Pacific E sequences were the result of the contamination of PCR reagents with modern chicken DNA, which it was assumed likely belonged to Haplogroup E. The application of NGS could easily solve the issue of possible contamination of reagents used in the sequencing of the Chilean and other ancient Polynesian bones. If indeed the samples or the reagents were contaminated with modern chicken DNA, this would be visible in the quality and diversity of sequence reads obtained. If the sequences obtained all belonged to one haplotype and had typical damage patterns of ancient DNA, it would be difficult to argue that there was contamination. This debate illustrates well how DNA evidence can become a singular focus of dispute to the point of excluding relevant archaeological data (context, radiocarbon dating,

etc.). While DNA evidence can be compelling, the archaeological context of that DNA remains critical. If the right samples from the right locations are not studied, DNA evidence can be misinterpreted.

Perhaps one of the most exciting developments in the application of new aDNA methods to Pacific samples is that we now have the ability to obtain more data regarding diet and health of prehistoric peoples and their animals through aDNA analyses of the microbiomes present in their fecal remains (Tito et al. 2012) and calculus deposited on their teeth (Warinner et al. 2015). Microbiomes are the totality of the microbial communities which inhabit the human or animal body and can undergo observable changes with dietary shifts, such as those associated with transitions involving predominant intake of plant or animal foods (David et al. 2014). As such, analyses of microbiomes represent opportunities for a whole new level of commensal studies. While coprolites are not particularly common in Pacific sites, they do occur and could be a possible source of information regarding the diet of ancient Pacific people, in addition to providing evidence for infectious agents that may have impacted both people and their commensal animals.

Analysis of dental calculus is perhaps more promising for Pacific samples and could include studies of both humans and commensal animals such as pigs. Researchers have recently demonstrated the value of investigating dental calculus for micro-fossils in the Pacific (Tromp and Dudgeon 2015), but dental calculus also provides ideal conditions for the preservation of biomolecules. The calcium phosphate minerals of the calculus trap and preserve both food remains and oral bacteria as well as other disease causing organisms, and these biofilms accumulate throughout the lifetime of the individual, as long as the calculus is not removed by abrasion or other dental treatment. Removal of the calculus from archaeological remains is non-destructive to the actual tooth itself as it can just be scraped off with a dental pick. The yield of DNA recovered from dental calculus is significantly greater than that recovered from bone or dentine (Warinner et al. 2014), again making this an ideal source of DNA for samples found in the Pacific and other warm, wet locations, which are often poorly preserved. Either shotgun sequencing or targeted sequencing for particular species of interest can be applied to NGS analyses of dental calculus from archaeological remains (Weyrich et al. 2015; Ziesemer et al. 2015).

Lastly, NGS methods have been used recently to assess the impact of the arrival of humans and their commensal species on native animals, which often became extinct not long after human arrival on Pacific islands (Allentoft et al. 2014). Even using standard PCR and Sanger sequencing of aDNA, it has been shown that Yellow-eyed penguins (*Megadyptes antipodes*), a species previously believed to have been endemic in New Zealand, were in reality recent arrivals that moved in to the ecological niche left by the loss of a previously unrecognized native species as a result of human arrival (Boessenkool et al. 2009; Rawlence et al. 2015). In the future, full genomic analyses (both mitochondrial and nuclear) of native and extinct species in the Pacific might provide further evidence for similar replacement or hybridization events and help us to fully assess the impact of the arrival of humans and their commensal animals on fragile island ecosystems.

11.6 Conclusion: Costs, Benefits and Caveats for aDNA Analyses of Faunal Remains

There is no doubt that the developments in the field of Next Generation Sequencing in the last few years open up exciting possibilities for ancient DNA analyses of skeletal remains. These advances are particularly important for addressing questions in the Pacific region where temperature, humidity, and site locations are not particularly conducive to DNA preservation. Of course these same limitations apply to other regions, such as the islands of the Caribbean and Mediterranean, and similar questions are being addressed and molecular methods applied (Hardy et al. 1994; Foley et al. 2012; Kimura et al. 2016; Ziesemer et al. 2015). We can now obtain complete mitochondrial genomes where previously we were limited to analyses based on small portions of the HVR. This allows for potentially much more data with which to tease out relationships and track migrations patterns between closely related populations like those often found on Pacific islands. We can obtain sequence from the nuclear genome, including in the best preserved samples, complete genomes (Rasmussen et al. 2011). This allows us to potentially answer questions we never thought possible to address through analyses of faunal remains, such as determining if selective breeding for non-skeletal phenotypes (e.g., coat color or plumage characteristics) was taking place, or if animals with these different phenotypes were being disposed of differently (e.g., in middens vs. symbolic burial). Analyses of environmental DNA and the microbiome introduces new commensal species for study, which allow us to potentially better understand health and diet of both humans and their domestic animals. The potential zooarchaeological applications of aDNA studies are numerous. But we must be careful that we do not get overly excited about the genetic data and forget about the importance of archaeological context and other information necessary for the interpretation of aDNA data.

The fact that aDNA data could possibly answer a research question may not be sufficient reason to attempt an aDNA study. A major drawback of aDNA analysis is its destructive nature. Although the amount of material required for sampling is becoming smaller with each passing year, archaeologists have an ethical obligation to weigh the loss of rare or unique specimens against the potential for recovery of significant data. As methods in massively paralleled sequencing progress, the amount of data obtained increases, and the cost of sequencing declines, the number of samples that aDNA researchers will seek to analyze will undoubtedly rise. Where previously, most aDNA studies were conducted on a small number of samples, today, tens if not hundreds of samples can be run on every lane of a sequencing machine (Meyer and Kircher 2010; Neiman et al. 2011), such that it is cost effective to process many samples at a time. It is most important, therefore, that archaeologists and faunal experts are not only consulted in the development of research questions which will be addressed using aDNA, but are directly involved in the selection of appropriate samples and the interpretation of all results. As noted above, the cost in terms of loss or modification of samples must be weighed against the benefits of the information that might be obtained. One must also keep in mind, however, that

large amounts of data can be obtained from a single immortalized library prepared for NGS, so many more questions can be addressed with each ancient DNA sample extraction and preparation than was possible using the previous methods. Regardless of the type or amount of DNA sequence data collected, context is still paramount. It is particularly important to understand and fully assess the archaeological evidence for the timing of animal introductions and the possibilities of multiple or serial introductions, as without this information it is far too easy to misinterpret genetic data obtained from archaeological samples and the implications of those data for reconstructing human behavior (Storey et al. 2013a).

While the opportunities available for aDNA research and the range of new questions that are now possible to address make this a very exciting time for biologists, archaeologists, and zooarchaeologists, we should still proceed cautiously. However, as with any new field, methods develop and improve quickly, and often enthusiasm can get ahead of scientific rigor, as occurred in the early days of PCR and aDNA research (Wayne et al. 1999). While the research prospects of aDNA in zooarchaeological studies seem endless, archaeological samples are a limited resource and we have a responsibility to use them wisely.

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Chapter 12
Zooarchaeology by Mass Spectrometry (ZooMS) Collagen Fingerprinting for the Species Identification of Archaeological Bone Fragments

Michael Buckley

12.1 Introduction

Bone is the most abundant organic tissue found typically to survive on archaeological sites, and in many cases can represent one of the most common types of find. Nonetheless, due to taphonomic and/or anthropologic factors, bone is more often than not fragmented beyond amenability to morphological identification. As a result, vast proportions of archaeological assemblages collected are often not utilized, and, therefore, the zooarchaeological inferences will undoubtedly be subject to some forms of bias. The objective identifications possible through the use of biomolecular information present in bone offer a tantalizing prospect for resolving such issues. The most obvious biomolecular target, ancient DNA (aDNA), has been, and continues to be, used (Burger et al. 2000; Horsburgh 2008; Waugh 2007) (see Matisoo-Smith, Chap. 11). However, this is not often a practical solution for application to the majority of assemblages given the high costs of analysis per sample, requirement for specialist facilities, and highly unpredictable likelihood of success. The success rates themselves are also increasingly poorer in warmer environments (Kahila Bar-Gal et al. 2002; Larson et al. 2007)—the environments more likely to have a wider range of wild taxa and be of greatest interest to those studying early animal husbandry.

Recent years have witnessed the development of an alternative biomolecular method for species identification that addresses the impracticalities of the widespread adoption of aDNA-based methods. The method, described as a form of "Zooarchaeology by Mass Spectrometry" or ZooMS for short, is one that uses

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proteomics-based methods to analyze proteins that survive in faunal remains, primarily for species identification. The analysis of proteins rather than DNA has several advantages: (1) proteins are much more abundant (Tuross 1994; Tuross and Stathoplos 1993); (2) they survive for much longer periods of time (Rybczynski et al. 2013), making their analysis much more successful even in warmer environments (Buckley et al. 2009, 2010); and (3) the analyses can be carried out at very low cost, often as low as the cost for aDNA screening methods themselves (e.g., amino acid racemization (Poinar et al. 1996) and carbon/nitrogen analysis (Götherström et al. 2002).

In bone, the dominant protein is type I collagen, the protein that is typically referred to when describing the carbon source for radiocarbon dating and stable isotope analyses. Collagen is considered the most abundant protein in the vertebrate kingdom (Shoulders and Raines 2009) and is particularly abundant in the extracellular matrix (ECM). It has a wide range of functions that primarily relate to its role as a scaffold in bone mineral deposition. However, despite its presence in many different tissues and interactions with a wide range of other non-collagenous proteins (NCPs), in bone, collagen interacts with NCPs involved with the biomineralization pathway; the small mineral-binding protein osteocalcin is the most abundant of these NCPs in bone. Although many NCPs survive in archaeological bone for long periods of time, some of which are potentially more taxonomically informative (Buckley and Wadsworth 2014), collagen is by far the most abundant and will be the focus of this chapter. More than 28 types of collagen are known to exist within humans throughout the lifecycle (Ricard-Blum 2011), but 80–90% of the collagen in the body consists of types I, II, and III, of which type I collagen is by far the most abundant, as noted above.

The triple helical structure common to all collagens is maintained through the presence of repeating imino acids, proline (Pro) and its modified form hydroxyproline (Hyp), which induces the twisting structure in each of the three chains (Fig. 12.1 inset). However, to maintain this structure, the helix also requires the repeated presence of glycine (Gly), the smallest amino acid, which typically occurs every three amino acids. Most other amino acids would not fit within this structure due to much larger side chains. As a result, collagen is known by its repeated Gly-Pro-Hyp motif and has largely been considered very highly conserved on the whole. Although some collagen types are homotrimers (i.e., formed from three identical chains), collagen type I is a heterotrimer, which in most vertebrates is made up of two identical chains called alpha 1 chains and one genetically distinct chain called the alpha 2 chain (hereafter referred to as α1(I) and α2(I) respectively). Notably, however, in actinopterygian (bony ray-finned) fish species, type I collagen is composed of three distinct chains, but the third (α3(I)) is a duplicate of the (α1(I)) gene (Morvan-Dubois et al. 2003). Recent research (e.g., Buckley et al. 2009) has found that the α2(I) is so much more variable that it does not appear to be restricted to the same requirement for Pro content, therefore making collagen much more useful for species identification than previously thought possible.

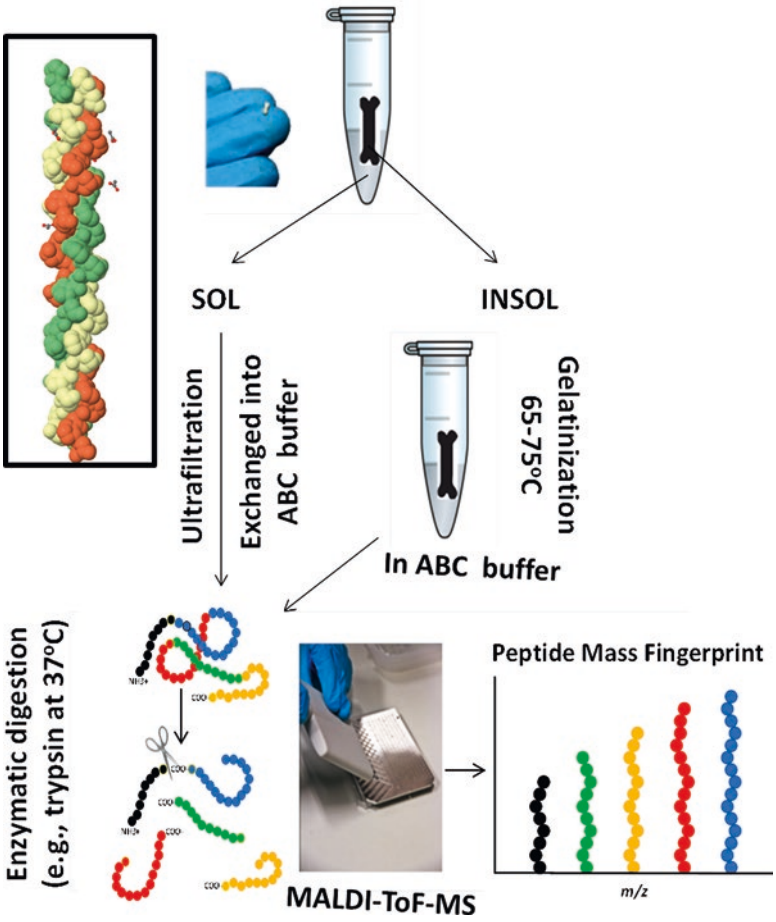

Fig. 12.1 Schematic of the two primary approaches to obtaining a collagen peptide mass fingerprint using either the soluble collagen or by heating and gelatinization of the insoluble collagen (scissors image sourced from www.commons.wikimedia.org, tube image sourced from www.clker.com); collagen triple helix shown in inset (image from 1BKV pdb file viewed online at http://www.rcsb.org/pdb/)

Early developments of the ZooMS method started with the isolation of the collagen α2(I) telopeptide (Buckley et al. 2008) using solid phase extraction (SPE) cartridges following digestion with bacterial collagenase, but this single 18 amino acid peptide alone was not sufficient at separating all of the major domesticated animals. This was particularly problematic for sheep (*Ovis aries*) and goat (*Capra hircus*), whose skeletal elements are morphologically so similar that their separation is considered challenging (Zeder and Lapham 2010). As a result of this morphological similarity, these two taxa have been typically reported together in

zooarchaeological analyses as “caprine” or “ovicaprid”, despite the fact that their remains reflect distinct components of early animal husbandry based on differences in animal behavior, diet, and habitat preferences. Subsequently, a similar SPE-based method following digestion with trypsin was developed to preferentially isolate a single large (33 amino acids) helical peptide from the α2(I) chain that could discriminate between these two taxa (Buckley et al. 2010), which was later verified by DNA analysis (Campana et al. 2013). Since then, the method was simplified into one that yielded two fractions for analysis, where the first fraction eluted with lower organic solvent concentration removed greater numbers of the typical collagen motif-containing peptides, and the second fraction with higher organic solvent concentration subsequently removed less typical collagen peptides from a specialist C18 pipette tip (Buckley et al. 2009).

To date most applications to zooarchaeological studies have focused on mammalian taxa, with early work on domesticates (Buckley et al. 2009, 2010) followed more recently by studies on wild taxa (Buckley and Collins 2011), including marine mammals (Buckley et al. 2014). So far, little consideration has been given to the variability of amino acid sequences across a wider range of vertebrate taxa. This study explores in detail the information content potentially available through collagen sequence analysis, and considers the implications for the simplest form of ZooMS, the collagen fingerprint, given its amenability to high-throughput productivity and status as the most feasible molecular approach for widespread zooarchaeological application. A particular emphasis is placed on divergence times between vertebrate species of each of the major taxonomic groups (classes) as a potential means to highlight which taxa are and which are not likely to be appropriate for application of collagen sequence analysis as a means of molecular-based identification.

12.2 Methods

Essentially, the ZooMS method extracts bone proteins into solution digests, these into peptides, and then measures many of these peptides using mass spectrometry. Getting proteins from biomineralized tissues, such as bone, into solution typically requires some form of decalcification of the mineral phase and/or subsequent gelatinization of the otherwise insoluble “collagen” pellet. These methods can be very similar to the protocols used for radiocarbon dating and stable isotope analyses, but much simpler and shorter. However, there are two general methodological approaches to obtaining a ZooMS collagen fingerprint (Fig. 12.1). One is the more recent approach of decalcifying the bone with an acid (e.g., hydrochloric acid: HCl) and using ultrafiltration to transfer the acid-soluble collagen into a buffer compatible with the enzymatic digestion (van der Sluis et al. 2014), whereas the more traditional approach typically gelatinizes the acid-insoluble “collagen” in a buffer that is compatible with the subsequent enzymatic digestion and mass spectrometric analysis (Buckley et al. 2009). Both approaches typically yield similar peptide mass

fingerprints (PMFs); the former can sometimes yield more collagen, the latter more likely to avoid various forms of contamination. Once the solubilized proteins have been digested (most commonly with the protease trypsin, with an optimum active temperature of 37°C and usually carried out for at least several hours), the peptide solution is acidified and can be further purified using SPE. At this stage the sample solution is ready for proteomic analysis.

A soft-ionization mass spectrometer is typically composed of three parts: (1) the ion source; (2) the mass analyzer; and (3) the ion detector. The two most common ion sources that convert analytes into gaseous ions used in proteomics are Electrospray Ionization (ESI) and Matrix Assisted Laser Desorption Ionization (MALDI). In ESI, the sample solution is dispersed into a fine aerosol and evaporated through a highly charged capillary needle, following which the droplets undergo Coulomb fission, decreasing in size and eventually exploding into smaller, more stable droplets from which ions are eventually liberated into the gas phase (Fenn et al. 1989; Smith et al. 1990). In MALDI, the sample solution is spotted onto a stainless steel target plate and co-crystalized into a solid with a light-absorbing matrix, such as a-cyano-hydroxycinnamic acid. The sample is then irradiated with a laser whereby the analytes sublime and are directed towards the mass analyzer (Karas and Krüger 2003; Zenobi and Knochenmuss 1998).

This chapter will only focus on the MALDI approach, which is much simpler and more cost-effective than the ESI approach and is less prone to contamination issues. The MALDI mass spectrometer can have various types of mass analyzer, but the "Time of Flight" (ToF) mass analyzer is the simplest and most common. By measuring the time for each analyte (peptide ion) to traverse across the flight tube (of known distance), its mass to charge ratio (*m/z*) can be inferred due to the known input energy; larger analytes take longer to travel across the flight tube, whereas smaller analytes travel more quickly. Slight deviations in the initial laser energy applied to each sample can also be corrected through the use of a reflectron "ion mirror", which improves the recorded peak resolution (Cornish et al. 1994). The ion detector converts the ion current into an electrical current, which is outputted as a spectrum of peaks showing the relative abundances of each ion detected. When an amino acid substitution occurs between taxa within one of the observed peptides, this change will be seen as a peak *m/z* difference in the acquired fingerprint, in a similar manner as for DNA fingerprints (Fig. 12.2).

There is a wide range of mammal bone collagen PMFs now published, to facilitate evaluation of taxonomic resolution, the consideration of black rat (*Rattus rattus*) is included here for comparison with the publically available brown rat (*R. norvegicus*) sequence information. Data from one previous publication (Buckley et al. 2009) that identified *conserved* "bird" collagen PMF markers in chicken (*Gallus gallus*), turkey (*Meleagris gallopavo*), and duck (*Anas platyrhynchos*) are updated here, with consideration given to their fingerprint variation and the support provided by additional analysis of the collagen PMF from pheasant (*Phasianus*) bone. Review of the collagen variation in other vertebrate groups — the reptiles, amphibians, and fishes—is

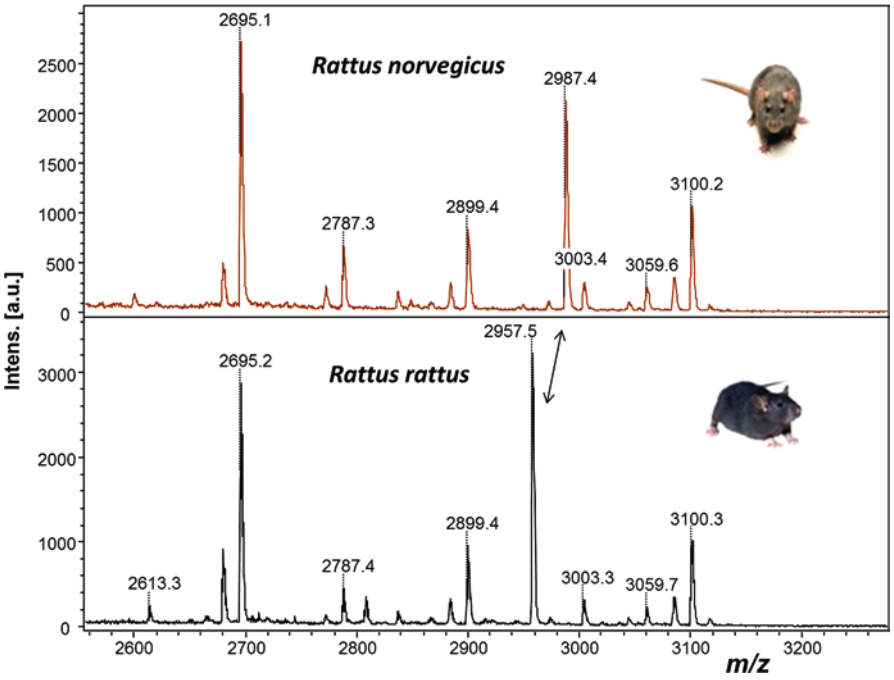

Fig. 12.2 Zoomed in part of MALDI-ToF mass spectra of collagen digests (PMFs) from brown (*top*) and black rat (*bottom*); *arrow* indicates a homologous peptide marker for distinguishing between the two species

based on the published sequence information, with the exception of example spectra for Atlantic cod (*Gadus morhua*) and Atlantic haddock (*Melanogrammus aeglefinus*). All additional modern specimens were sampled from the University of Sheffield's zooarchaeology collections. All publicly available collagen sequences were obtained from the UniProt database (see Table 12.1 for accession information).

12.3 Results

The fingerprints of vertebrate collagens typically include 50–100 peaks, which reflect approximately 40% of the available sequences of α1(I) and α2(I) collagen chains. Much greater sequence coverage of ~70–90% is typically recoverable with more in-depth liquid chromatography-tandem mass spectrometry (LC-MS/MS) methods, which involve peptide separation and subsequent mass spectrometric fragmentation for probability-based match sequencing (Buckley et al. 2011), but these require some known sequence information and are much more costly in both reagents and instrument usage.

Table 12.1 Percentage similarity of aligned mammalian collagen sequences. Shaded numbers indicate α1(I) sequences, unshaded indicate α2(I) sequences

	Bos (cow)	*Ovis* (sheep)	*Sus* (pig)	*Felis* (cat)	*Canis* (dog)	*Myotis* (bat)	*Ictidomys* (squirrel)	*Mus* (mouse)	*Rattus* (rat)	*Nomascus* (gibbon)	*Pan* (chimp-anzee)	*Homo* (human)
Bos		98.5	95.6	93.8	94.0	92.2	92.3	90.4	91.3	93.5	93.5	93.3
Ovis	99.4		95.7	93.6	93.9	92.0	91.9	89.8	90.5	93.5	93.5	93.3
Sus	98.0	98.1		95.2	95.6	91.8	94.1	91.3	92.1	94.3	94.2	94.2
Felis	98.2	97.8	98.1		97.6	92.4	94.6	91.4	92.7	94.7	94.6	94.6
Canis	98.3	97.9	98.1	99.4		93.0	94.6	91.5	92.7	94.5	94.6	94.6
Myotis	96.9	96.9	97.0	97.8	97.3		92.4	90.5	91.6	92.1	92.3	92.1
Ictidomys	97.4	97.3	97.4	98.0	97.9	97.5		93.3	94.7	94.8	94.3	94.3
Mus	95.9	95.7	95.7	96.2	96.1	95.5	96.1		96.1	91.2	91.0	90.8
Rattus	96.1	96.1	96.1	96.5	96.4	96.0	96.5	98.5		92.6	92.2	92.2
Nomascus	98.1	98.0	98.4	98.4	98.5	97.1	97.7	95.5	96.1		99.5	99.5
Pan	98.3	98.1	98.1	98.4	98.5	96.8	97.4	95.5	96.0	99.7		99.6
Homo	98.3	98.1	98.1	98.4	98.5	96.8	97.4	95.5	96.0	99.7	100	

12.3.1 Mammals

Collagen fingerprinting in archaeological remains has so far focused predominantly on mammalian bone (e.g., Buckley et al. 2009, 2010, 2014). During the earliest approaches of separating domesticate taxa such as sheep (*O. aries*) from goat (*C. hircus*) (Buckley et al. 2010), it became clear that differences in the α2(I) sequences are more useful in separating taxa, with up to 8 million years divergence required to make distinctions (Buckley and Collins 2011). Although species-specificity was observed within collagen PMFs of the extant camel species, *Camelus dromedarius* and *C. bactrianus* (Rybczynski et al. 2013), these taxa also diverged approximately 8 million years ago (Ji et al. 2009). Analyses of cetaceans, for which it was possible to distinguish between fin whale (*Balaeonoptera physallus*), sei whale (*B. borealis*), and blue whale (*B. musculus*), reduced the divergence threshold to 5–6 Ma. A sub-family level of taxonomic resolution was also supported for cervids, in which "New World deer" of the sub-family Capreolinae (e.g., *Capreolus*) could be separated from those of the Old World Cervinae, but several members of the Cervinae could not be separated. For example, red deer (*Cervus*) could not be routinely distinguished from fallow deer (*Dama*) using the collagen fingerprint alone. However, small mammals, particularly rodents, are

known to have a higher rate of amino acid substitution which can be expected to facilitate separation of taxa at the sub-family level (Gu and Li 1992). This is supported by recent analyses of myomorph rodents (Buckley et al. 2016), in which the brown rat (*R. norvegicus*) can readily be separated from the black rat (*R. rattus*), reflecting a younger divergence of ~2.8 Ma (Fig. 12.2).

Sequence analysis of publicly available (www.uniprot.org) mammal collagens demonstrates that, although collagen sequences are highly conserved due to the abundance of glycine and proline/hydroxyproline residues, the large size of each chain allows for multiple amino acid substitutions. For example, cattle (*Bos taurus*) has only 0.6 and 1.5% variation in its α1(I) and α2(I) chains, respectively, from sheep (*O. aries*), but this reflects 6 and 15 amino acid substitutions for taxa that diverged ca. 25 Ma (Fernández and Vrba 2005). The α1(I) of humans is identical to that of chimpanzee, but has four substitutions in the α2(I) sequence (a divergence of 7–13 Ma; Langergraber et al. 2012). Across all mammal sequences, the α2(I) is more variable than the α1(I) sequence (Table 12.1).

12.3.2 Birds

In comparison to those of mammals, bird collagen fingerprints appear to be highly conserved. Unfortunately, there are fewer bird collagen sequences publicly available than for mammals, with only one curated α1(I) and α2(I) sequence available for chicken (*G. gallus*). There are several uncharacterised α2(I) sequences available to make a comparison of variation rate, including chicken, turkey (*M. gallopavo*), flycatcher (*Ficedula albicollis*), and zebra finch (*Taeniopygia guttata*).

Within the Phasianidae, *Gallus* separated from the pheasant/turkey lineage sometime between 30 and 40 Ma (mtDNA by Kan et al. 2010), whereas the split between pheasant (*Phasianus*) and turkey (*Meleagris*) is estimated at 16–20 Ma (Helm-Bychowski and Wilson 1986), although more recent mtDNA analyses indicate this is much older at ca. 32–34 Ma. Only a few peak differences were clearly observed between the two (Fig. 12.3). Based on comparison of the publicly available sequences (Table 12.2), there are 15 amino acid substitutions between chicken and duck, which diverged more than 100 Ma (Pereiraa and Bakera 2009), at least five of which are observed in the fingerprints. However, there are potential problems with relying on peak *m/z* alone in this avian example, where two diagnostic peptide markers, representing peptide sequences from different parts of the same pheasant collagen molecule, are coincidentally represented by the same *m/z* (Fig. 12.3). Adding to this confusion is the fact that the peptide responsible for the signals at *m/z* 1578.8 and 1594.8 (the latter being a hydroxylated variant) is different in duck and chicken than it is in turkey.

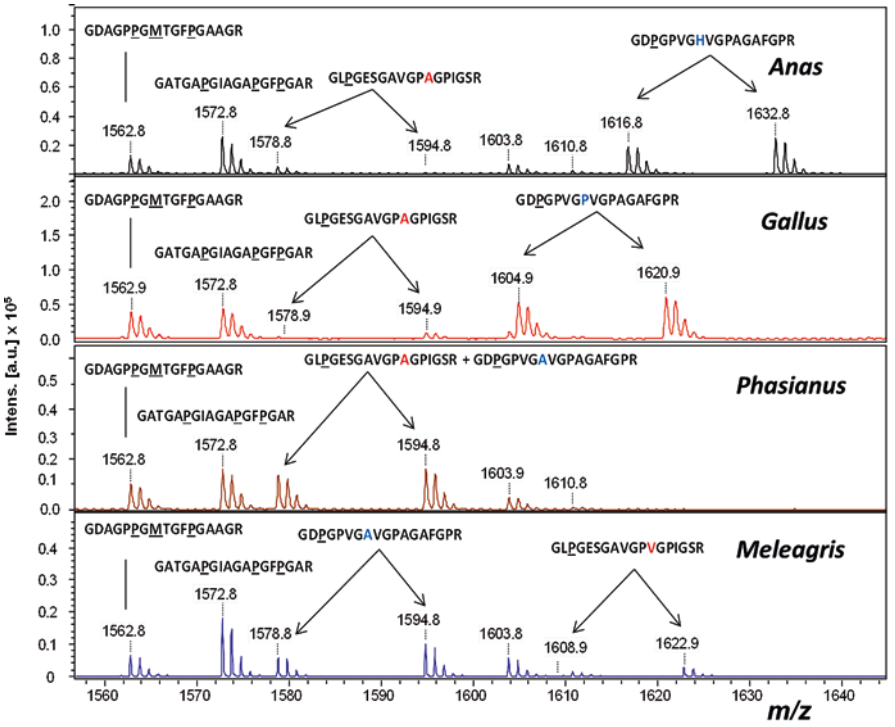

Fig. 12.3 MALDI-ToF-MS spectra of avifauna where the *arrows* indicate homologous peptide markers for distinguishing between the Anseriformes and Galliformes. Inset zoomed in on region of interest for separating duck (*Anas platyrhynchos*) and chicken (*Gallus gallus*) from pheasants (*Phasianus coturnix*) and turkeys (*Meleagris gallopavo*)

Table 12.2 Percentage similarity of aligned collagen α2(I) sequences

	Gallus (chicken)	*Anas* (duck)	*Fidecula* (flycatcher)	*Taeniopygia* (zebra finch)
Gallus		98.4	97.9	97.9
Anas			97.5	97.7
Ficedula				99.2
Taeniopygia				

12.3.3 Reptiles and Amphibians

The more recent analyses of giant tortoise collagen fingerprints indicate that, in this reptilian lineage at least, there is a much greater than expected level of variation in the primary sequence. For sequence analysis, there is only information currently

Table 12.3 Percentage similarity of reptile and amphibian aligned collagen sequences. Shaded numbers indicate α1(I) sequences, unshaded indicate α2(I) sequences

	Pelodiscus (turtle)	*Anolis* (lizard)	*Xenopus laevis* (African clawed frog)	*Xenopus tropicalis* (western clawed frog)	*Lithobates* (bullfrog)
Pelodiscus		81.3	74.3	74.3	72.6
Anolis	87.8		72.1	72.4	71.2
Xenopus laevis	83.0	85.5		91.3	82.0
Xenopus tropicalis	83.6	86.6	95.5		82.4
Lithobates					

available for the green anole (*Anolis carolinensis*) and the Chinese softshell turtle (*Pelodiscus sinensis*), which diverged from each other ca. 270 Ma (Shedlock and Edwards 2009). Although a crude approximation given the deep divergence between these two reptilian groups, the estimated ca. 12% and ca. 20% dissimilarity for these taxa represents almost 130 and 200 amino acid substitutions in the α1(I) and α2(I) chains, respectively, reflecting a combined substitution rate of >1 amino acid per million years that is in keeping with the higher rates seen within previously analyzed tortoises (Van der Sluis et al. 2014).

Very little research has been carried out on protein fingerprinting of amphibian remains despite their great potential as environmental indicators due to their climate sensitivity (Blaustein et al. 2001) and typically short home ranges (Martof 1953). Analysis of the known α1(I) and α2(I) sequences from the western clawed frog (*Xenopus tropicalis*) and African clawed frog (*X. laevis*) indicates nearly 50 and more than 90 amino acid substitutions, respectively, at the species level, although they diverged 30–90 million years ago (Bisbee et al. 1977; Evans et al. 2004) (Table 12.3). Sequence analysis further indicates ~185 amino acid substitutions in the α2(I) chain alone between *Lithobates* (family Ranidae) and *Xenopus* (family Pipidae), which separated ca. 240 million years ago (Bossuyt and Roelants 2009).

12.3.4 Fish

Fish collagens yield the greatest variation of any within species group and have been most widely studied by amino acid and protein analysis methods for discrimination in the food chemistry industry (Gómez-Guillén et al. 2002). Richter et al. (2011) have previously shown that species commonly observed in British Medieval assemblages can be separated using principal component analysis of the PMFs without attempting to identify specific markers, but have not considered the likely taxonomic resolution.

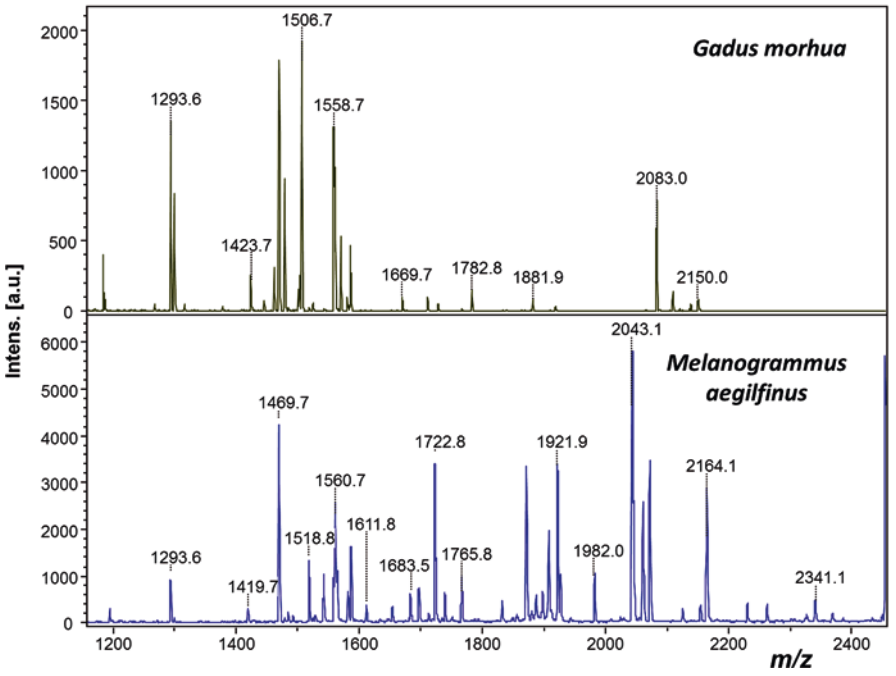

Fig. 12.4 MALDI-ToF mass spectra of collagen digests (PMFs) from Atlantic cod (*Gadus morhua*) and Atlantic haddock (*Melanogrammus aeglefinus*) showing that most visible peaks (representing collagen peptides) differ between the two closely-related taxa

Fig. 12.4 gives some indication of the extent of variation present within the Gadidae family, showing that a large number of the dominant peaks differ between two gadid species, Atlantic cod (*G. morhua*) and haddock (*M. aeglefinus*). Throughout the spectra there appear to be at least 20 markers between taxa that diverged ca. 8.5 Ma (Bakke and Johansen 2005), which is significantly greater than that for most mammal groups of similar divergence.

Sequence analysis of seven actinopterygian (bony ray-finned fish) orders (zebrafish, Cypriniformes; flounder, Pleuronectiformes; tilapia, Perciformes; rainbow trout, Salmoniformes; Amazon molly, Cyprinodontiformes; pufferfish, Tetraodontiformes; stickleback, Gasterosteiformes), which diverged ca. 110–250 Ma (Betancur-R et al. 2013), all show large amounts of variation (10–30% for each chain) representing hundreds of amino acid substitutions between groups (Tables 12.4 and 12.5). At the species level, rainbow trout (*Oncorhynchus mykiss)* is 96.4% similar to chum salmon *(O. keta)* for α2(I), with 38 amino acid substitutions and divergence dating back to at least ca. 8–20 Ma. This indicates a rate of at least 2–4 amino acid substitutions per million years within this group for this single chain. Combined with differences in the other two chains, this rate is more likely to have been at least ca. 6–12 substitutions per million years.

Table 12.4 Percentage similarity of aligned fish collagen sequences. Shaded numbers indicate α1(I) sequences, unshaded indicate α2(I) sequences

	Oncorhynchus (rainbow trout)	*Paralicthys* (flounder)	*Oreochromis* (tilapia)	*Poecilia* (Amazon molly)	*Takifugu* (fugu)	*Gasterosteus* (stickleback)	*Danio* (zebrafish)
Oncorhynchus		78.7	76.9	77.7	74.7	75.4	79.7
Paralicthys	83.4		86.1	84.0	83.2	81.1	79.4
Oreochromis	83.9	88.4		85.3	82.5	80.2	79.4
Poecilia	83.5	86.5	89.7		81.2	79.1	79.8
Takifugu	80.6	86.3	87.0	85.8		77.7	76.9
Gasterosteus	79.8	84.3	84.4	84.5	85.3		73.5
Danio	85.8	84.4	86.6	85.9	83.1	82.1	

Table 12.5 Percentage similarity of aligned fish collagen α3(I) sequences

	Oncorhynchus (rainbow trout)	*Oreochromis* (tilapia)	*Poecilia* (Amazon molly)	*Takifugu* (fugu)	*Gasterosteus* (stickleback)	*Danio* (zebrafish)
Oncorhynchus		72.9	73.0	72.9	75.2	75.2
Oreochromis			84.1	83.6	79.4	79.3
Poecilia				81.1	78.6	79.0
Takifugu					78.6	77.5
Gasterosteus						75.2
Danio						

Some teleost fish also have an α3(I) chain leading to an α1α2α3 heterotrimer, a condition which does not exist in sharks and lampreys (Kimura and Ohno 1987). Molecular sequence analysis of these three chains has indicated that the α3(I) chain is derived from a duplication of the α1(I) gene that has occurred in the actinopterygian lineage (Morvan-Dubois et al. 2003), but sequence comparisons indicate it to be even more variable between taxa than the α2(I) chain (Table 12.5). Tissue-specific existence of this chain has long been known (Miyauchi and Kimura 1990), and in the collagen of some organs, such as the swim bladder, only the typical $(\alpha1)_2\alpha2$ heterotrimers are present, whereas in the collagens of scale and bone the α1α2α3 heterotrimer is rich (Kimura et al. 1991).

12.4 Discussion

12.4.1 Sampling

Sampling practicalities of ZooMS collagen fingerprinting are not typically discussed in publications, yet is perhaps the most obvious concern to the zooarchaeologist and of particular interest for a volume dedicated to methodology. Standard (low-throughput) ZooMS analyses typically yield better results when a powdered sample of bone is used, due to the increased surface area of the bone mineral that is decalcified, increasing resulting collagen concentrations. However, bone collagen can also be removed in sufficient amounts from archaeological specimens without destructive sampling. This latter method is more amenable to high-throughput processing and could result in different approaches to the storage of microfaunal assemblages in which specimens could be archived in multi-well microtitre plates, as exemplified by the analysis of >12,000 specimens from Pin Hole Cave, Derbyshire, UK (Buckley et al. 2017) (Fig. 12.5). In this approach, part or the entire specimen can be submerged in a weak acid, or even in a buffer not intended for demineralization, releasing surface collagen into the solution but keeping the bone morphologically intact. A small amount of collagen that has been extracted for stable isotope analysis could also be subsampled for fingerprint analysis, which can complement the isotopic interpretations, clarifying morphological identifications, or distinguishing between species that could not be clearly separated (van der Sluis et al. 2014).

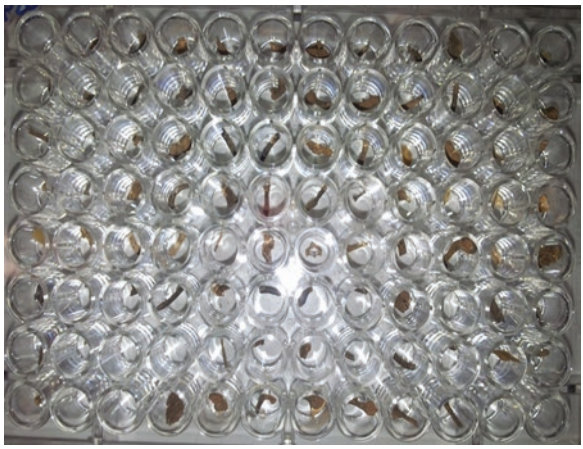

Fig. 12.5 Potential storage option in multi-well microtitre plates of appropriate well size allowing for quick visual access to analyzed specimens; 96 well plate filled with microfaunal remains shown

12.4.2 Success Rates

The main advantage of using collagen fingerprinting as the method of choice for biomolecular species identification is that collagen is not only the most abundant genetically-informative biomolecule in modern bone, but becomes relatively more abundant in archaeological bone following the rapid loss of the majority of DNA and non-collagenous proteins. Insoluble collagen can also be recovered and fingerprinted from bone specimens that have such little collagen that they fail stable isotope analyses (Buckley et al. 2011). Extracting collagen from the acid-soluble fraction further enhances success rates, but at the potential cost of introducing unknown environmental contaminants and endogenous protein break-down products. As such it is possible to still retrieve collagen fingerprints good enough for species identification despite there being insufficient insoluble collagen for suitable radiocarbon or stable isotope results.

To date, collagen fingerprinting has successfully been applied to a wide variety of archaeological assemblages (Buckley et al. 2009, 2014; Buckley and Collins 2011; Buckley and Kansa 2011; Richter et al. 2011; van der Sluis et al. 2014; von Holstein et al. 2014), but these have typically come from regions or time periods known for poor DNA survival, such as the Near East (Buckley and Kansa 2011) or the Paleolithic (Buckley and Collins 2011). It remains to be seen how widely the method will be employed in more temperate regions and for younger assemblages where better aDNA survival is anticipated, although the relatively low cost of collagen fingerprinting makes the method competitive for taxonomic differentiation irrespective of DNA preservation issues.

12.4.3 Taxonomic Resolution

The identification of faunal remains and the level of taxonomic resolution achievable in this task are core components of zooarchaeological practice. Focusing on both domestic and wild vertebrate prey, the review of collagen fingerprinting provided here has demonstrated the ability of this method to distinguish taxa in most cases at the genus level where there is at least ca. five million year divergence, and even at the species level for some large mammal genera (e.g., *Camelus*). However, this is clearly a matter related to the systematics behind defining different taxonomic groupings, where the extent of molecular diversity, and therefore collagen fingerprint specificity, is known to vary between taxa. With smaller vertebrates, where there is much greater population turnover, species-specific resolution is more readily obtained by collagen fingerprinting, reaching its greatest potential in fish (Fig. 12.6). The task of distinguishing between fish taxa is potentially further assisted by fish physiological conditions. The melting temperature of the collagen triple helix is typically within a few degrees of body temperature, with imino acid

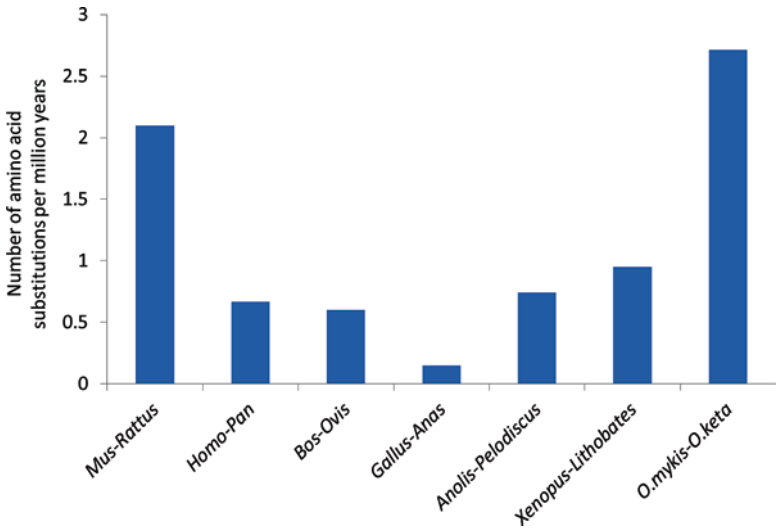

Fig. 12.6 Bar chart showing the number of amino acid substitutions from selected taxa across the animal kingdom

content (proline and hydroxyproline) playing a role in the stability of the protein (Hall and Reed 1957; Jenkins et al. 2003); in fish, as has been noted previously, there is a substantial reduction in the dominant imino acid concentration, with on average 14% less proline and ~30% less hydroxyproline (Szpak 2011), which is thought to be potentially linked with the lower body temperature of a large portion of this group (Leikina et al. 2002).

Throughout the sequence similarity results for each major vertebrate group, it is clear that the α2(I) sequence is much more variable than α1(I). Surprisingly, the α3(I) sequence in fish is typically more variable than both, despite its origins being from a duplication of the more highly conserved COL1A1 gene.

12.4.4 Relevance to Zooarchaeology

This chapter has focused on the taxonomic resolution provided by collagen sequence variation and how this may be used to distinguish between bone fragments of different species. However, the need for collagen fingerprinting-based species identification in archaeological assemblages will undoubtedly differ between sites of different types, time periods, and geographical locations. In deciding whether or not to employ the ZooMS method, the two most relevant considerations are: (1) the types of fauna known to be present in the area during the period of interest (i.e., how well are these likely to be separated using

ZooMS?); and (2) the potential effects of taphonomic processes on relative frequencies of different taxa. The ZooMS method can be used to derive enhanced number of identified specimens (NISP) counts, although it should be noted that morphologically undiagnostic fragmentary remains identified using biomolecular methods may not be equally amenable or appropriate for calculating some measures of species abundance such as minimum number of individuals (MNI). For example, it is well understood that the incompletely mineralized skeletal remains of younger individuals are more affected by the process of diagenesis (Lyman 1994); likewise, the less robust/dense bones of mature bats and fish would also suffer such bias. In the case of the latter, a widely studied subject area is the uptake of fishing, which is considered one of the most significant indicators for the development of human cognition and dates back to at least the Middle Paleolithic (Fiore et al. 2004; Hardy and Moncel 2011; O'Connor et al. 2011; Richards et al. 2001; van Niekerk 2011). Given that the highest levels of variation are seen within the fish, this area is one of the most promising applications of collagen fingerprinting to zooarchaeological applications.

As has been demonstrated in several publications (e.g., Buckley and Kansa 2011; Buckley et al. 2009, 2010, 2014), there are many taxa of interest to the zooarchaeologist that become difficult to separate following minor taphonomic or anthropic processes. In the latter case, the human modification of bones, whether breakage for marrow access, or modification for the creation of tools, etc., can produce greater than average levels of fragmentation or alter the bone beyond taxonomic recognition. Here collagen fingerprinting can be particularly useful for identifying the taxa of choice in subsistence and industrial activities, as illustrated by the use of collagen fingerprinting to identify the source bone—red deer or reindeer—employed in the manufacture of Early Medieval bone combs (von Holstein et al. 2014). The relative utility of ZooMS increases with the increasing antiquity or the object of interest and could be readily applied back to the Paleolithic, where aDNA techniques would be less likely to yield positive results due to preservation issues.

In some cases, where current morphological criteria remain poorly refined (e.g., criteria for the separation of *Bos* from *Bubalus* for domestication studies), obtaining molecular support through collagen fingerprinting could offer an appropriate solution that is low cost and minimally destructive in the confirmation of morphological criteria in different species/populations. In many cases, collagen fingerprinting has the added benefit of being able to be nested within other studies where collagen is being employed for analytical inferences, such as stable isotope analysis or radiocarbon dating. This allows the archaeologist to subsample from such analyses for confirmation of taxonomic identification and limits further destruction of specimens, which can be a particular concern in cases where these are rare or relatively unique (e.g., aforementioned bone combs). For microfaunal remains, the amenability of collagen fingerprinting to

high-throughput processing enables zooarchaeologists to reconstruct paleoenvironments based on more complete taxonomic information about the assemblage than can be potentially obtained by relying on morphological identification (and the required specialist expertise) alone.

12.5 Conclusions

The hierarchical nature of the collagen fingerprint (Buckley et al. 2009) allows for identification in the absence of equivalent reference material. PCR-based DNA methods usually require prior information for the process of designing appropriate primers and/or multiple rounds of analysis that increase costs. When species identification is the primary objective, and in cases where ZooMS collagen fingerprinting is known to be capable of the desired taxonomic resolution, it should be considered one of the most practical methods to use. This is not only due to the robustness of the procedure in the face of poor preservation and degradation of zooarchaeological bone, but also to its very low cost per analysis, which is typically between one and two orders of magnitude lower than for aDNA methods. Although the equipment needed may seem an expensive outlay, most large universities that possess biochemistry departments typically already house soft-ionization instrumentation. The potential taxonomic resolution of collagen sequence analysis makes the method clearly suitable for distinguishing the major domesticate taxa, including domesticate birds. Unfortunately, at this time, the study of wild avifauna using collagen fingerprint analysis is likely to be less beneficial than other taxonomic groups due to the more highly conserved nature of bird collagen. By contrast, the analysis of fish collagen fingerprints is likely to yield a valuable technique for speciation at a much better taxonomic level than even the small mammals with a notoriously high amino acid substitution rate (Gu and Li 1992), ideal for the study of early fishing strategies. Taxonomic identification is a primary objective of zooarchaeology and has traditionally been facilitated by specimen morphology. As the discipline has evolved, newer methods, such as DNA analysis and geometric morphometrics, have become part of the zooarchaeological toolkit. ZooMS is one such new tool, but unlike others it has unprecedented power in terms of the scope and scale of its applicability and, therefore, holds tremendous potential to fundamentally change how zooarchaeologists conduct analysis and the questions they ask.

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Part IV
Toward Practical Applications and Broader Syntheses

Chapter 13
Coming to Terms with Imperfection: Comparative Studies and the Search for Grazing Impacts in Seventeenth Century New Mexico

Emily Lena Jones

13.1 Zooarchaeology and the Challenge of Regional-Scale Questions

The history of archaeology—and zooarchaeology—is marked by a suite of classic questions. Did humans cause the extinction of Pleistocene megafauna (Burney and Flannery 2005; Faith 2014; Grayson 2007; Martinez et al. 2013; Wroe et al. 2013)? Was there a "broad spectrum revolution" prior to the adoption of agriculture (Stiner 2001; Zeder 2012)? Are human hunting impacts on landscape always negative, or do cultures more often show a record of sustainable management (Campbell and Butler 2010; Costanza et al. 2007; Morgan 2008; Wills et al. 2014)? How have plant and animal translocations shaped societies (Crosby 1972, 1986; Jones 2015; Mann 2011; Nunn and Qian 2010)? What all these questions have in common—besides the fact that their answers rely, to one degree or another, on zooarchaeological data—is that they are large in scale, and so answering them requires the integration of multiple data sets. However, the integration of data sets—whether zooarchaeological or other—also poses numerous challenges (e.g., Kintigh et al. 2014). This has perhaps been best illustrated by the debate on the cause of Pleistocene extinctions, which has been raging for well over a century and shows no sign of abating (e.g., Grayson 1984a; Grayson and Meltzer 2015; Haynes 2007; Koch and Barnosky 2006; Martin 1967; Martin and Stuart 1995; Wolverton et al. 2009).

Clearly there is a rich history to large-scale analyses in zooarchaeology. However, in recent years the number of such studies has increased dramatically, likely due to the increasing publication of raw data and the rise of data repositories (Arbuckle et al. 2014; Jones and Gabe 2015; Manning et al. 2013; Orton et al. 2014; Ottoni et al. 2012; Shennan et al. 2013). More data are available now than were even five

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years ago. Sometimes these data are made available through repositories like tDAR (http://core.tdar.org/) and OpenContext (http://opencontext.org/); sometimes they are housed in less formal data-sharing portals (e.g., http://repository.unm.edu/). Sometimes the data are recently generated, and the data's authors are available for consultation; other times the data were collected half a century ago, and the collections from which those data were derived are long since lost or discarded (e.g., Atici et al. 2013).

This wide availability of data presents an unprecedented opportunity for those interested in big questions. Data are now relatively easy to find and incorporate into analyses. This allows for the compilation of large datasets, which in turn provides a robust means of testing landscape-level questions (e.g., Otaola et al. 2015). But the use of these large data sets also introduces pitfalls—none of which are new (see discussions in Grayson (1984b) and Smith (1977)), but which are amplified by the quantity of data now at hand. In this chapter, I use a case study searching for evidence of grazing impacts in seventeenth century New Mexican zooarchaeological assemblages—particularly those from Puebloan and Navajo sites—to illustrate problems that may arise in large-scale zooarchaeological analyses and explore potential solutions.

13.2 Grazing Impacts in Early Colonial New Mexico?

Modern New Mexican grasslands have been heavily altered by grazing of domestic animals, particularly cattle (*Bos taurus*) and sheep (*Ovis aries*). Domestic ungulates are relative newcomers to New Mexico, having first arrived with the Spaniard Francisco Vásquez Coronado's entrada of 1540. Coronado's sojourn in New Mexico was brief (AD 1540–1542), and the fate of the domestic animals he brought with him is unknown. In 1598, however, the first Spanish colony in New Mexico was established, and these colonists brought with them a suite of domestic animals from Spain, including goats (*Capra hircus)*, horses (*Equus caballus*), and pigs (*Sus scrofa domesticus*) as well as sheep and cattle (Barrett 2012; Hammond and Rey 1953). While initially these taxa were confined to Spanish settlements and missions, they were eventually adopted by indigenous communities living outside Spain's reach (Jones 2013b, 2015, 2016).

The eventual environmental repercussions of the introduction of Old World domesticates to New Mexico include erosion, decreased richness of plant and animal taxa, turnover of native plant communities, and grassland invasion by trees and shrubs (e.g., Coop and Givnish 2007; Diggle and Hieb 2004; List et al. 2007; Smythe and Haukos 2010), but the initial impacts of this introduction are not well-understood. Some argue that impacts such as erosion, decrease in native grasses, and negative impacts on native ungulate taxa occurred by the late seventeenth century (e.g., Bohrer 1975; MacCameron 1994; Weisiger 2009), However, while instances of overgrazing were recorded in parts of Mexico in the early colonial period (Esparza Sánchez 1996), in New Mexico the earliest written documentation

of overgrazing impacts dates to the nineteenth century, making document-based assessment of these arguments a challenge.

However, if there were significant environmental impacts from introduced grazers in seventeenth century New Mexico, the archaeological record should contain evidence of this. Some archaeologically visible corollaries of intense grazing in the American Southwest might include:

- Decreases in native grasses and associated increases in invasive taxa, particularly shrubs (Ryerson and Parmenter 2001; Yanoff and Muldavin 2008);
- Increasing erosion (Diggle and Hieb 2004);
- Increasing widespread presence of domestic ungulates in zooarchaeological assemblages (Jones 2015);
- Decreasing relative abundance of native artiodactyls, such as mule deer (*Odocoileus hemionus*), elk (*Cervus elaphus*), and pronghorn (*Antilocapra americana*), on the landscape and thus in zooarchaeological assemblages (Beck and Peek 2005; Brown et al. 2006).

The first two of these corollaries require paleobotanical and/or geoarchaeological evidence to test; the third and fourth, however, are zooarchaeological in nature. Comparative studies making use of zooarchaeological data from the many Southwestern archaeological collections dating to the late prehistoric and early historic periods are thus one way to test for grazing impacts. Here, I use a test for evidence supporting the fourth corollary—a decrease in abundance of native ungulates—as a means to explore the challenges and opportunities associated with such studies.

13.3 The Data

In the early twentieth century A. V. Kidder was famously advised not to work in the American Southwest because "the Southwest is a sucked orange" (Kidder 1958). This statement is often referenced to demonstrate how incorrect it was (Kidder himself used it in this way), but it also highlights a different point: there has been a vast quantity of archaeological excavation undertaken in the American Southwest (Cordell and Fowler 2005; Snead 2001), and this rich tradition of research has generated in turn a vast amount of archaeological data—including many zooarchaeological collections housed in museums across the USA (see discussion in Jones and Gabe 2015). A reasonable number of these collections have been studied at some point in the past, producing a substantial faunal dataset. As of this writing, tDAR contains 33 faunal datasets from the American Southwest; if all data available through publications, gray literature, and less formal data-sharing portals were included, this figure would easily reach into the hundreds.

However, not all of these data are comparable, or of sufficient resolution to address complex questions. While there are a number of notable exceptions, faunal remains have been relatively less studied in the Southwest than other material

classes (Gifford-Gonzalez 2011); some reports say little more than "zooarchaeological material was recovered." When faunal data are available, they vary significantly in how they are reported, ranging from presence/absence lists (so-called laundry lists), to summary reports with no breakdown by context and numbers reported only as site total minimum number of individuals (MNI), to extremely detailed monographs. This variability limits the types of analyses that can be performed on the data as a whole (Conrad 2015; Jones and Gabe 2015).

In the seventeenth century New Mexico grazing project, I focused my analysis on the early Colonial period, the time between initial Spanish settlement (AD 1598) and the Pueblo Revolt, when the Spanish were ejected from New Mexico (AD 1680). I searched tDAR and the published and gray literature for zooarchaeological data from this period; in addition, I analyzed zooarchaeological faunas from Chamisal Pueblo (Jones 2015) and the Navajo-affiliated Fruitland Data Recovery Project sites (Jones 2013b), using comparative collections at the University of New Mexico's Zooarchaeology Laboratory and Museum of Southwestern Biology to confirm identifications. I compiled these datasets to document the distribution of domestic fauna across central and northern New Mexico in the seventeenth century and to look for changes in abundances of native New Mexican fauna during this period.

The final dataset comprises zooarchaeological data from 29 archaeological sites containing five Old World domestic taxa (pig, chicken, horse/donkey, sheep/goat, and cattle) and five native artiodactyl taxa (bison, deer, pronghorn, and elk) spread across central and northern New Mexico from the Sangre de Cristos to the Four Corners region (Fig. 13.1).

As discussed in the previous section, one predicted corollary of grazing impacts from introduced domestic fauna is declining abundance of native grazers and browsers. The presence of significant numbers of competitors and landscape management for those domestic taxa may have decreased available forage (Beck and Peek 2005; Brown et al. 2006). I therefore calculated relative abundance of native ungulates (*A. americana, C. elaphus, and Odocoileus* spp.) in the Chamisal and Fruitland faunas as a means to test for grazing impacts, using $\sum$ Number of Identified Specimens (NISP) of native artiodactyls/$\sum$ total mammalian NISP to calculate relative abundance (Lyman 2008).

One potential problem with this test is that domestic ungulates were not available in the late prehistoric period. If they were added to the diet in the early historic period, native taxa might appear to decrease simply because there were more resources in total available (see Jones 2007 for an example of this problem in a very different context). I therefore excluded domestic fauna of Spanish origin (as well as all specimens identified to *Bos/Bison*, due to the difficulty in distinguishing between domestic cattle and native buffalo (bison); see discussion later in this chapter) from these calculations. While as calculated here relative abundance thus necessarily underestimates the presence of native ungulates in these archaeofaunas, measuring this way avoids the problem of native fauna appearing to decline simply because there was an increase in non-native taxa.

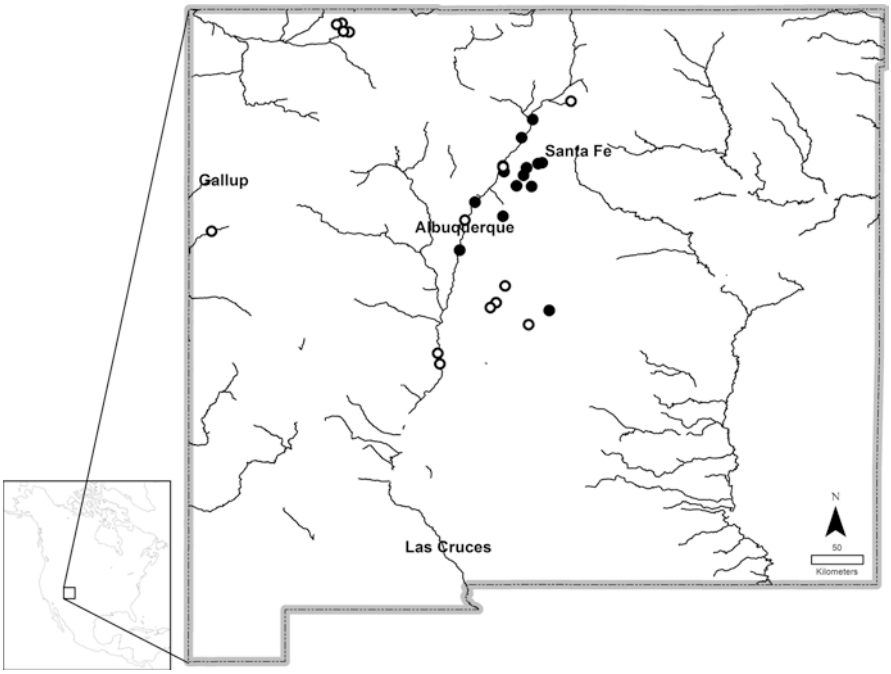

Fig. 13.1 Seventeenth century New Mexican archaeological sites containing analyzed fauna; sites included in the relative abundance analysis are indicated by open circles

What the exclusion of domestic fauna does not address is the possibility that seventeenth century people invested less time in hunting native taxa because they had domestic ungulates on hand. This is the "human filter" problem—because these data are drawn from zooarchaeological collections, it is necessary to establish that these assemblages are representative of environmental change, not just dietary change (e.g., Peacock et al. 2012). In this case, people might have replaced native fauna with domestic fauna in their diets for a number of reasons (including preference and access), and if they did so, a decline in native taxa in these archaeofaunas might simply indicate changing diets, rather than changing landscape abundance. However, previous work has shown there was not a substantial increase in domestic taxa in native diets prior to the eighteenth century (Jones 2013b, 2015, 2016), so this is an unlikely explanation.

I also calculated relative abundance of native artiodactyls for the other sites in the dataset which contained sixteenth century (pre-Spanish colonization) and seventeenth century (post-Spanish colonization) deposits, again omitting domestic fauna (Table 13.1). However, because I did not identify these fauna myself, the collection and recording protocols were different, and I was unable to perform further statistical analyses (see Wolverton 2013). I did, however, qualitatively consider the general trends present in these data. My goal in doing so was simply to establish whether or not a broad geographic trend is present. If it is not, this may indicate landscape

Table 13.1 Seventeenth century New Mexican archaeofaunas. Sites included in the relative abundance analysis are indicated by bold type; ARMS indicates a record on file with the New Mexico Historic Preservation Division (http://www.nmhistoricpreservation.org/arms.html)

Name	Prehistoric component?	Domestic fauna present?	Sources
Abó (LA97)	**Y**	**Y**	Baldwin (1988) and Trigg (1999, 2004)
Agua Fria Schoolhouse (LA2)	N	Y	Payne (1999)
Casa Quemada (LA4955)	N	Y	Trigg (1999)
Chamisal (LA22765)	**Y**	**Y**	Jones (2015)
Cochiti Springs (LA34)	N	Y	Snow (1971)
Gran Quivira (LA120)	**Y**	**Y**	Clark (2003) and Spielmann et al. (2009)
Isleta Convento (LA724)	N	Y	Jones (2015)
LA 16769	N	Y	Levine et al. (1985) and Payne (1999)
LA16768	N	Y	Levine et al. (1985) and Payne (1999)
LA65005	N	Y	Moore (1993)
LA72747	**Y**	**N**	Hovezak and Schniebs (2002) and Jones (2013b)
LA72787	**Y**	**Y**	Hovezak and Schniebs (2002) and Jones (2013b)
LA73582	**Y**	**N**	Hovezak and Schniebs (2002) and Jones (2013b)
LA79462	**Y**	**Y**	Hovezak and Schniebs (2002) and Jones (2013b)
Las Huertas (LA 282)	Y	Y	Earls (1985, 1987)
Las Majadas (LA591)	N	Y	Trigg (1999)
Pa'ako (LA162)	N	Y	Gifford-Gonzalez and Sunseri (2007)
Pargas Pueblo (LA 31746)	Y	Y	James (1987)
Picuris (LA127)	**Y**	**Y**	Emslie (1981) and Harris (1999)
Pueblo del Encierro (LA 70)	**Y**	**Y**	Harris (1976)
Quarai (LA95)	**Y**	**Y**	Clark (2000b) and Spielmann et al. (2009)

(continued)

Table 13.1 (continued)

Name	Prehistoric component?	Domestic fauna present?	Sources
San Marcos (LA98)	N	Y	Lucas et al. (2002) and Pavao-Zuckerman and Reitz (2006)
Sanchez Site (LA20000)	N	Y	Trigg (1999)
Signal Site (LA9142)	N	Y	Trigg (1999)
Tabirá (LA51)	**Y**	**Y**	Clark (2000a) and Spielmann et al. (2009)
Tenabó (LA200)	N	Y	Baldwin (1988)
Torreon Site (LA6178)	N	Y	Snow and Warren (1967)
Yunque (LA59)	N	Y	Caroline Gabe, personal communication
Zuni (LA37)	**Y**	**Y**	Tarcan (2005)

variability, but it may just as easily indicate methodological variability. If, on the other hand, despite all the methodological variability, such a trend is present, this is more likely to represent landscape-level change.

All but two of the archaeological faunas in this dataset contain domestic livestock, confirming their widespread presence across north-central New Mexico in the seventeenth century (Table 13.1). If these new taxa were competing with native artiodactyls for available grassland, one would expect the relative abundance of native artiodactyls in human diets to decrease during the seventeenth century, as Spanish flocks increased. However, this decrease is not evident in the data explored here; instead, the relative abundance of native artiodactyls seems to have increased, rather than decreased (Fig. 13.2). A chi-square analysis supports a significant increase in native artiodactyl abundance between pre- and post- seventeenth century assemblages at both Fruitland sites ($\chi^2 = 48.148$, $p < 0.001$) and Chamisal Pueblo ($\chi^2 = 125.134$, $p < 0.001$). It is important to note that statistical significance may not be an indicator of, in Wolverton's terms, "practical significance" (Wolverton et al. 2016). Although a Pearson correlation analysis shows no relationship between sample size and relative abundance at Fruitland and Chamisal ($r = -0.58$; $p = 0.42$), chi-square analyses are extremely sensitive when the combined tallies for all categories are large, and in these archaeofaunas sample size is relatively high (Fruitland sites: n = 689; Chamisal Pueblo: n = 724). Indeed, effect size is weak ($\varphi < 0.1$) in both these cases.

Still, relative abundance of native ungulates clearly does not decline, as predicted in the case of grazing impacts. And other lines of evidence suggest the apparent increase is not simply an artifact of sample size. Data quality does not allow for a quantitative analysis of the remaining datasets, but the same increase is also present at all the other sites for which there is a late sixteenth century as well as a seven-

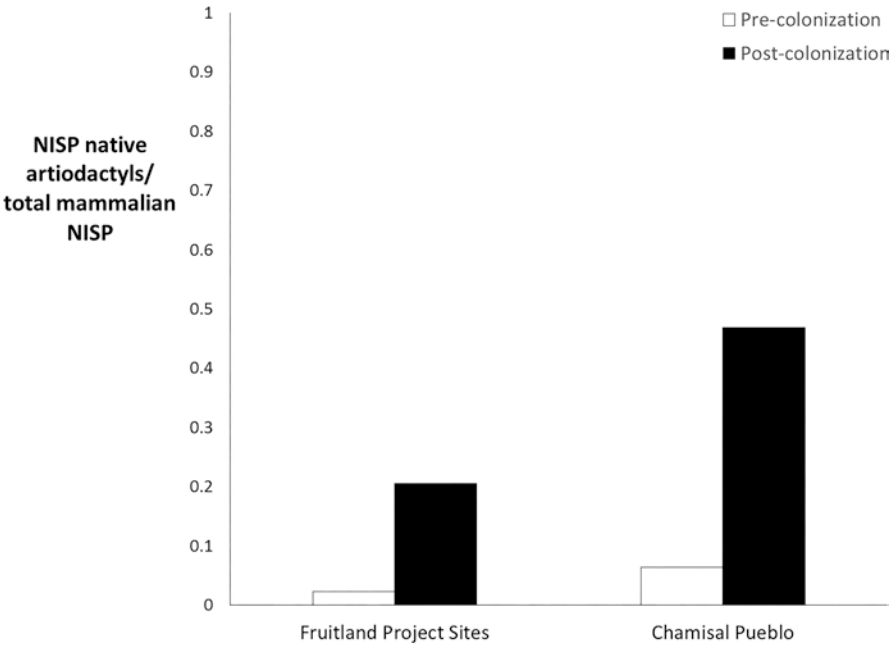

Fig. 13.2 The relative abundance of native artiodactyls before and after Spanish contact at the Fruitland Project sites (Jones 2013a) and Chamisal Pueblo (Jones 2015)

teenth century component (n = 13; see also Jones 2016). The ubiquity of this trend across north-central New Mexico is suggestive. Non-human-deposited rodents also imply an increase in grasses and a decrease in desert vegetation throughout the seventeenth century. At the Fruitland Project sites there is an increase in the abundance of *Neotoma cinerea*, a green vegetation indicator, relative to that of *Dipodomys ordii*, a desert vegetation indicator from the early to late seventeenth century (Jones 2013b). Baldwin (1988) recorded a similar increase in relative abundance of *N. cinerea* relative to *D. ordii* during the seventeenth century at the sites of Tenabó and Abó, although small mammals were not the focus of his study. While more data are needed to confirm the presence of such a trend across the region, these small mammal data may suggest an overall improvement in grassland conditions during the seventeenth century.

In short, the data presented here do not support a decline in grassland health in seventeenth century New Mexico; if anything, they may suggest the opposite, though additional data is necessary to fully assess this.

13.4 The Challenges

Comparative studies have long been undertaken by zooarchaeologists; there is an equally long history of critiques of such studies (Coombes and Barber 2005; Keene 1983; Plunkett et al. 2013). While such critiques have investigated a variety of issues, one major area of concern has been the methodological issues posed by using multiple data sets. The zooarchaeological data on seventeenth century New Mexican landscape change highlights a number of these methodological issues; here I will discuss three: mechanical problems, chronological resolution, and site type diversity.

13.4.1 Mechanical Problems

I define "mechanical problems" as issues biasing the raw data itself, rather than issues arising from data analysis. Such problems include a variety of defects—analyst error (Driver 1992), differential fragmentation (Cannon 2013; Lyman 2008), and screen-size bias (Lyman 2008; Schaffer 1992) to name three—all of which can pose difficulties in a single-size analysis as easily as in a comparative study. Indeed, in meta-analyses, imperfections in individual datasets can sometimes be less problematic than in small-scale studies, because the inclusion of so much data means issues specific to individual datasets will be swamped by the preponderance of the evidence. But on the flip side, if there is a systematic bias to the data, a meta-analysis will magnify what was initially a trivial error.

In the seventeenth century Southwestern grazing case, there are at least two ways in which these data might reflect systematic biases. First, in older excavations (as well as some newer ones), it was common practice to screen different contexts with different size screens (see review in Jones and Gabe 2015). The sites in this case study represent a mix of prehistoric and historic deposits. Archaeologists frequently treat historic and prehistoric sites differently (see, for example, Hovezak et al. 2002); given the practice of differential screening, it would not be surprising if many of the prehistoric deposits in this sample were screened with smaller mesh than the historic ones. If this is the case, the pattern of increase in artiodactyl abundance seen in the sites in Fig. 13.1 could reflect not a true increase, but rather changing archaeological practice. And unfortunately, for much of the data included here specific contextual information is not available.

Another problem arises from the possibility of systematically misidentified faunas. The faunas included in the seventeenth century Southwest grazing project were identified by a wide variety of analysts, some with many years of experience, others with little background and no access to comparative collections (for instance, see Baldwin 1988). In such a case identifications to size class may be solid, but finer-grained taxonomic identifications can be inaccurate, and tricky identifications in particular may not be reliable (Driver 1992). In the data presented here, this issue

becomes especially pressing in contexts where there are Old World domesticates. In many Spanish mission sites, domestic cattle have been identified. However, both archaeological work (i.e., Spielmann 1991) and the documentary record demonstrate that Puebloans did consume buffalo in both the late prehistoric and early historic. It is routine in contact-era literature to see *Bos*/*Bison* from contexts dated before AD 1600 identified as buffalo, while those from early historic contexts are identified as domestic cattle. Although separation of these two taxa is possible (see Balkwill and Cumbaa 1992), without knowing the criteria which analysts used it is impossible to know whether the identification is reliable or not.

For both these issues, screen size variability and misidentification, the ideal solution would be reanalysis: reidentification of the faunas and in-depth work with original field notes. But while individual reanalyses can be a means of testing the overall dataset (Jones 2015; Manning et al. 2013), reanalyzing all data in a large analysis often is not practical (let alone possible). The power of meta-analyses, after all, is in the number of datasets included; the problem is that by including so many datasets, one is necessarily giving up some control over data quality.

To move past the issues posed by mechanical problems, the analyst must identify potential sources of systematic bias, and then find some way to negate them. In the seventeenth century grazing case, testing for biases in individual collections has allowed progress; reanalyses, new analyses, and work with original field notes suggest differences in screen size are not driving the change in artiodactyl relative abundance in at least some of the collections included here (Jones 2013b, 2015, 2016). In the case of possible misidentifications of domestic cattle, however, because this problem is so widespread I have removed this particular taxonomic category from analyses that include sites where analyst methodology cannot be verified (Table 13.2). While reanalysis projects will hopefully eventually allow projects assessing cattle distribution in early New Mexico, with this particular dataset acknowledging the data problem seems the only solution.

13.4.2 Chronological Resolution

Chronological resolution can be a critical problem in comparing site to site; the late prehistoric and early historic period in New Mexico is no exception to this. There are two primary ways in which this problem manifests in the case study presented here. One involves the chronology of the spread of Old World domestic taxa across New Mexico. While seventeenth century archaeological contexts are neatly constrained by Spanish settlement (and accompanying new material culture types) on the one hand, and the Pueblo Revolt of 1680 on the other (Liebmann 2012), finer-grained chronological resolution is not possible with the data in this study. So while Fig. 13.1 does demonstrate that Old World domesticates were widespread in the seventeenth century, the data do not allow us to answer the question of how quickly their range expanded.

The second problem in the chronological resolution category relates to explaining the apparent increase in relative abundance of artiodactyls in the seventeenth

Table 13.2 Presence/absence of Old World domestic taxa across selected seventeenth century New Mexico indigenous sites. Cattle are excluded from all further analyses due to challenges in identification

Name	Site Type	Pig	Chicken	Horse	Sheep/Goat	Cattle?	NISP	Sources
San Marcos (LA98)	Mission	x	x	x	x	x	3420	Lucas et al. (2002)
Zuni (LA37)	Mission	x	x	x	x	x	1273	Tarcan (2005)
Isleta (LA724)	Mission	x	x	x	x	x	172	Jones (2015)
Gran Quivira (LA120)	Mission		x	x	x	x	5392	Clark (2003)
Picuris (LA127)	Mission		x	x	x	x	9500[a]	Harris (1999)
Quarai (LA95)	Mission		x	x	x	x	1299	Clark (2000b)
Abó (LA97)	Mission		x		x	x	>200[b]	Baldwin (1988) and Trigg (2004)
Pa'ako (LA162)	Mission		x	x	x		>300[b]	Gifford-Gonzalez and Sunseri (2007)
Tenabó (LA200)	Village				x		>250[b]	Baldwin (1988)
Tabirá (LA51)	Village					x	4156	Clark (2000a)
Chamisal (LA22765)	Village					x	127	Jones (2015)
LA73582	Residences						169	Jones (2013b)

[a]Harris (1999) is an estimate for the entire collection of Picuris fauna, and thus likely overestimates the seventeenth century component

[b]Authors in these studies did not provide a total NISP; minimum possible total NISP was derived from figures in these publications, but this number likely underestimates total NISP

century. One potential reason for such a trend is increased precipitation, and thus improved graze—something that documentary records suggest did occur, at least in the Santa Fe area, in the seventeenth century (Barrett 2012). Most of the data on precipitation and climate for the Southwest is drawn from dendroclimatological records. While these high-resolution records are an excellent source of information, matching them to the coarse-scale chronological data available for zooarchaeological assemblages presents a challenge. The assemblages in this dataset cannot be directly tied to the dendroclimatological record because, not only are many of these collections not well-dated, most are from time-averaged deposits (Jones 2016).

The solution to these challenges is to relax the scale of analysis. For the spread of Old World domesticates, one can say there was a widespread distribution in the seventeenth century even if more specific conclusions are not possible. Likewise, the change in artiodactyl representation seems to occur mid- seventeenth century; thus, if increased precipitation were driving this change, we should see a strong, consistent signal for a wetter period across the Southwest. The dendroclimatological data suggest this is not the case; rather than consistency, there is a high level of variability (Jones 2016; Salzer 2000; Towner and Salzer 2008). Given that the increase in relative abundance of large mammals is evident across a broad geographic space, precipitation does not seem a good candidate for the ultimate cause of this transition (Jones 2016).

13.4.3 Site Type Diversity

In the seventeenth century New Mexico case study, sites in the dataset represent a variety of different cultural and functional contexts (Table 13.2). Mission sites represent locations with a permanent Spanish church presence; *visitas*, locations with a visiting friar; and villages and residences represent locations where, while Spaniards may have been nearby (Barrett 2002, 2012), there was no sanctioned Spanish presence. Documents indicate that livestock raising was a major activity at the missions; it may or may not have been at other locations (Lycett 2014; Spielmann et al. 2009). Similarly, hunting was almost certainly variable across these site types (Jones 2016). Sites used for different purposes will often have different faunas; so differences in relative abundance can thus represent changes in site type (e.g., Henry 1994; Jones 2013a).

While the seventeenth century New Mexican change in relative abundance of artiodactyls does not seem to reflect changes in site type (Jones 2013b, 2016), the spatial patterning of archaeological deposits containing Old World domesticates suggests the degree of Spanish interaction does have an impact on the distribution of these taxa (Table 13.2; also see Jones and Gabe 2015). Only indigenous sites with 100 or more identified specimens were included in this analysis, which reduces the overall sample, but some interesting correlations are present. The number of domestic taxa in these assemblages does not seem to be driven by sample size ($r_s = -0.27$, $p = 0.55$), but there is a strong correlation between site type and number of domestic taxa ($r_s = -0.85$, $p = 0.00$). Mission sites have all potential domestic taxa; *visitas*, which had a visiting friar but no consistent Spanish presence, have fewer; and villages and residences without a Spanish presence have least of all.

13.5 What Can We Know?

Mechanical problems, chronological resolution, and site type variability all pose significant challenges to the analyses presented here, some more so than others. In this case study, the influence of site type on the distribution of Old World domesticates is an interesting finding, but in other situations (Garcia 2013; Jones 2013a, b), a diversity of site types in the analytical set can confound results. Conversely, in the case presented here, mechanical problems and chronological resolution pose challenges that cannot be fully addressed. The only solution is to relax the scale of analysis.

These challenges mean that one cannot use all data to answer all questions all of the time. There is only so much that can be done with older datasets (Atici et al. 2013). To avoid error, it is imperative to avoid pushing conclusions too far, or trying to make the data say more than they can. I would argue that the most critical aspect of working with imperfect data is this: accept the things you cannot change. Big data will always be messy. What is important is to know *how* the data are messy—and so knowing may mean certain questions cannot be answered. In the case presented here, I see no solution to the *Bos*/*Bison* identification problem other than reanalysis.

However, these challenges do not mean comparative studies cannot contribute to archaeology, or that they should not be conducted. On the contrary, the seventeenth century New Mexican grazing study shows some ways in which imperfect data can be used to shed new light on old questions. One benefit of this type of analysis is that imperfections drawn from single studies that can confound smaller-scale studies often will be swamped by data; as long as one addresses potential systematic biases, meta-analyses can avoid these issues (see Jones and Gabe 2015). Similarly, "big data" can be extremely useful as a type of exploratory analysis, testing general assumptions prior to in-depth, single-site analyses (Conrad 2015; Jones 2016). Without larger-scale analyses, many of the classic questions in archaeology never would have been raised. With the increasing availability of data, we have the means to explore these questions further. But our excitement over data availability should not blind us to challenges with particular datasets; nor should it lead us to ignore single-site analyses, which can complement larger-scale studies.

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Chapter 14
Zooarchaeology Method and Practice in Classical Archaeology: Interdisciplinary Pathways Forward

Michael MacKinnon

14.1 Introduction

Given the historical intrigue devoted to the study of Greek and Roman antiquity, it comes as no surprise that a central contributor to this investigation—the discipline of classical archaeology—attracts a wealth of scholarly attention. Zooarchaeological remains certainly factor among the host of material categories available to classical archaeologists, but not until more recent times, arguably since the rise of paleoeconomic and processual theoretical foci in general archaeological scholarship in the 1970s and 1980s, has deeper attention surfaced as regards method and practice of zooarchaeological work in classical archaeology (MacKinnon 2007). Agendas have developed tremendously since that time, to the point where collection and reporting of the full range of biological, ecological, and cultural data available from investigations of faunal remains at ancient sites are increasingly commonplace. These have in turn fueled great initiatives to integrate zooarchaeological results more widely in the construction of broader syntheses about animals in Greek and Roman antiquity. At one level, such momentum has certainly affected the current quantity of available faunal data, which are themselves drawn from an equally impressive registry of ancient sites. Simultaneously, however, the richness of this ever-increasing faunal record is intensified by incorporation of the vast amounts of cognate evidence from ancient textual, historical, artistic, and archaeological sources that are available to classical archaeologists, although not always integrated as such.

Zooarchaeologists investigating Greco-Roman antiquity are certainly privileged with multifarious lines of evidence to explore. Drawing upon the potential of this interdisciplinary framework, nevertheless, brings both successes and challenges. This chapter reviews the relationship of zooarchaeology to the broader discipline of

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classical archaeology, outlining some of its contributions in reshaping and refining our knowledge of how animals factored in the world of antiquity. Attention focuses on several key issues: (1) zooarchaeological input to the complicated debate centering upon "sacred" and "secular" reasons behind why meat was consumed in Greek antiquity; (2) the interrelationships of ancient textual, iconographic, and zooarchaeological information to our knowledge of the great diversity of livestock "breeds" in antiquity; and (3) advancements in zooarchaeological method and practice, including isotopic research, that are refashioning the questions asked, and directions pursued, in classical archaeology as a whole.

14.2 Zooarchaeology and the "Sacred/Secular" Debate for Meat Consumption in Greek Antiquity

Considerable debate has focused upon the issue of ancient Greek animal sacrifice. Based on available literary, epigraphical, and iconographical evidence largely derived from Archaic and Classical time frames (ca. eighth to fourth centuries BC), many purport that meat was typically (perhaps exclusively) consumed within a ritual/sacrificial context during Greek antiquity (see Ekroth 2014 and Faraone and Naiden 2012 for wider discussion and further references). This position has been largely championed through research by scholars such as Vernant (1989), Durand (1989), and Burkert (1985) in wider philosophical deliberations about the role and practice of ancient Greek sacrifice. Essentially, "sacred" here refers to meat consumption that formed part of some (often public) sacrifice, while "secular" might entail handling and consumption of meat in contexts which seem incompatible with sacrifice, such as in everyday household use or in more "common" settings, such as bars/taverns, workshops, and slaughterhouses. Some flexibility was accommodated. For example, the nature of ancient Greek ritual events, as regards their size, scale, and public/private aspects, could certainly vary, as might the distribution of meat at such festivals, or its sale and/or provisioning afterwards, through whatever type of mechanism. However, meat consumption in the ancient Greek world has traditionally been argued as somehow linked to sacrificial contexts or practices. Curiously, the situation does not extend rigidly into Roman antiquity, where "secular" consumption of meat is widely noted alongside ritualized feasting, sacrifice, or consumption involving animals (Ekroth 2014; Huet and Scheid 2004; Rüpke 2009).

Tradition has loomed large in this established practice. Zooarchaeological evidence had historically been marginalized (and at worst, ignored) in earlier debates about the role of meat in Greek antiquity, as attention sought to construct grand, moralizing philosophies about Greek cult practices, many of which centered on an implied or demonstrable division between "sacred" and "secular" consumption of meat. Many advocated that since meat was arguably expensive and rare in Greek antiquity (given that most slaughtered animals were inconveniently large for individual or household dining), its consumption was consequently relegated to sacrificial, festival settings, themselves mired in social symbolism, tradition, and ritual.

Fig. 14.1 Location of sites mentioned in this chapter

While shades of doubt infiltrated these arguments, exceptions for consumption of meat from hunted animals and other taxa not otherwise considered fit for sacrifice blurred any strict differentiation among concepts. Increasingly, however, incorporation of the ever-growing body of zooarchaeological data from a range of archaeological contexts—some seemingly "ritual," others less so—augments the degree of complexity and variation displayed as regards Greek animal sacrifice, in turn squarely challenging any firm division between rudimentary categories of "sacred" and "secular" (Ekroth 2007, 2009, 2013, 2014; Faraone and Naiden 2012; Scullion 2013). The addition of zooarchaeological work, therefore, has greatly illuminated our understanding of the role of animals in Greek cult beyond that which could be reconstructed from ancient textual and iconographic evidence alone. This methodological expansion has also shaped the practice of zooarchaeology in classical archaeology, resulting in a much greater drive to recover faunal remains more completely and a deeper appreciation of the richness of data that holistic approaches to faunal remains can provide.

Two examples illustrate these developments. The first concerns the reconstruction of meat consumption practices during the Archaic period (primarily the sixth to fifth century BC) at the cult and festival center of Nemea, Greece (MacKinnon 2013) (see Fig. 14.1 for site locations). Examination of excavated faunal materials from both secular and sacred contexts for this time frame at the site yields clues about the distribution of meat to gods (e.g., Zeus, the patron deity of the area), heroes (in this case, Opheltes, on whose death the legendary Nemean Games were

founded), and the mortal officials, spectators, and athletes participating in the events at Nemea. As regards "sacrificial" assemblages, most of which consisted of bone remains (often burnt offerings) collected from altars and other ritual-type contexts (the latter, chiefly pits that were directly connected to such altars), the data indicate a preference for sheep (*Ovis aries*) as the standard sacrificial animal. These data also show a definite penchant for the hind limb sections of the left side for sacrifices to the hero Opheltes, as opposed to the god Zeus, whose sacrificial remains contained a mix of entire animals (i.e., *holocaust* sacrifice), limb portions (i.e., *thysia* sacrifice), and tails (i.e., *osphys* sacrifice).

Deeper inspection of the nature of burning and breakage on these bones suggests that the sacrificial fires for Zeus and Opheltes were wood fires, possibly olive wood, stoked periodically to maintain a constant temperature of about 400 °C. Fires were additionally fueled through the sacrifice of bones surrounded by fatty and fresh cuts of meat rather than defleshed, degreased, and dry (MacKinnon 2013). Also a possibility is the wrapping these materials in some type of covering, perhaps the fatty stomach lining as is seemingly depicted in Greek vase paintings (Ekroth 2013; Forstenpointner et al. 2013; Van Straten 1995). Higher relative frequencies of fully calcined bones among the samples associated with the Altar of Zeus, compared with those related to deposits for Opheltes, further imply that combustion of materials was more pronounced when it came to sacrifice for the god as opposed to the hero. The preference for left-sided elements in the cult of Opheltes is also unique among Greek sacrificial assemblages and presumably may relate to the association of Opheltes, in his guise as Archemoros, with an underworld figure—heroic, but not godly. A few examples of right-side choice in Greek sacrifice do register among zooarchaeological samples, but in each of these cases veneration is to a god, typically Apollo (MacKinnon 2010). The duality of left/underworld/dark/hero and right/heavenly/light/divine, consequently, may factor in symbolic choices for cult practices involving animal sacrifices in Greek antiquity, the specifics of which are not detailed explicitly in ancient texts or iconography.

"Secular" deposits at Nemea—including faunal remains from pits, hearths and fills outside the temple, and altar precincts at the site—show different trends, such as the presence of unburnt bones, representation of skeletal parts from across the wider skeleton (including more ribs, vertebrae, and cranial elements), no bias in choice of side, and the presence of wild animal and fish remains. The latter are animals not typically sacrificed in Greek antiquity (Ekroth 2013, 2014). Certainly, as regards zooarchaeological method and practice, the comparison of all types of faunal deposits from Nemea, with deeper appreciation to the nature of their context of recovery and the impact such may have in shaping patterns observed, proved critical to a more holistic interpretation of the range of cultural events that took place at the site. This has arguably helped cultivate a much better environment for recovery of faunal materials across ancient sites than existed in the past. Moreover, it has fueled a host of innovative experimental archaeological ventures, most notably studies linked to butchery and burning of fleshed and unfleshed carcass sections (e.g., Ekroth 2007, 2009; Forstenpointner et al. 2013), to help reconstruct and clarify the features and procedures noted.

The second example of how zooarchaeological method and practice is reshaping our notions of cult practice in antiquity concerns animal remains from a cistern in the Sanctuary of Poseidon at Kalaureia, on the island of Poros (Mylona 2013) (Fig. 14.1). This sanctuary complex appears to have had a long history, from Archaic times (ca. eighth/seventh century BC) into the second/third century AD. The particular cistern in question here went out of use as a source of water in the first century BC, but subsequently became a place where various types of dead animals, loose animal bones, and complete or fragmented glass vessels were deposited. Stratigraphic and taphonomic evidence suggests that these materials were interred in one episode or over a very short period of time. Investigators were able to exclude the possibility these remains represented random refuse or cleared debris from surface cleaning. Taphonomic conditions among them are quite uniform; the largest concentration of material occurs tightly within two strata (5 and 6), and the composition of materials, skewed towards bones and glass vessels, with near absence of other remains, appears relatively special and deliberate. The impression is that these materials are linked to one or more sets of ritual activities occurring within the sanctuary. The collection included butchered, disarticulated parts of cattle (*Bos taurus*), pig (*Sus scrofa* dom.), sheep, and goat (*Capra hircus*), materials that might typically reflect ritual dining carried out within the sanctuary precinct. Despite expectations derived from the ancient texts indicating these agro-pastoral taxa were commonly offered on an altar and consumed at sacrificial meals, this suite of domesticated fauna were not the only animals recovered. In addition to cattle, pig, sheep, and goats, excavation at Kalaureia also recovered thousands of bones and shells of a very wide range of animals, including molluscs, fish, birds (and their eggs), mice, rats, snakes, frogs, lizards, and adult and juvenile dogs. None of these fauna, save perhaps frog, could occur naturally in the cistern. Rather, the collection was deliberately deposited in this cistern, and requires a cultural explanation for its composition. The adult dog carcasses were already disarticulated prior to deposition, and some of their elements showed traces of butchery and burning. Several snake and frog bones also displayed burn marks (Mylona 2013, p. 154).

The inclusion of such a wide array of otherwise "unusual" animals as food or ritual items within this deposit seems less odd if we expand the concepts of sacrifice and ritual in antiquity to encompass the broader roles such animals fulfilled to encompass magic, divination, death, superstition, medicine, and social and physical marginality (Mylona 2013, pp. 160–161). The edibility/inedibility and ritual status of different products could vary among cultures in antiquity. Those on the social and geographical periphery of the Greek world, for example, are more commonly referenced as consumers of chickens and eggs (Parker 1983, pp. 357–365). Symbolic realms of place, space, and function further register. Shells, fish, water snakes, and frogs link to aquatic environments—the domain of Poseidon, the deity venerated at Kalaureia—but ties to chthonic worlds simultaneously are invoked through incorporation of dogs, puppies, lizards, snakes, and bird eggs. Roles overlap and become even more multifaceted. Dogs, snakes, and chickens factor in medicinal realms, but then again divisions between medicine and magic were not always distinct in antiquity (Mylona 2013, p. 160). The assemblage of animals represented in the cistern at

Kalaureia thus yields a more multidimensional picture of cult activity, one that extends beyond simple sacred/secular descriptions to more complex worlds of diet, ritual, sacrifice, magic, superstition, and social practice. This degree of detail would be lost without contributions from zooarchaeological methodology that ensured, for example, the careful retrieval of all faunal material from deposits at the site and concomitant meticulous exploration of taphonomic factors that affected assemblages. A large portion of the Kalaureia faunal assemblage, notably the wealth of materials from small animals, such as snakes, frogs, and fish, would otherwise have been lost had not stringent screening and flotation protocols been in place. In their absence a totally different (and perhaps more routine) picture of animal sacrifice at the site may have been presented—one that concentrated principally on larger domesticates such as cattle, sheep/goat, and pig.

Moreover, had not the taphonomy of the bones been scrutinized, subtle nuances about the sequence of deposition, the incorporation of materials from different ritual events/practices, and the post-depositional disturbances that variously affected the faunal assemblage and resulting cultural reconstructions, would have been compromised. Taphonomy has long been an integral component in zooarchaeological scholarship (Lyman 1994), but has traditionally seen less application in the field of classical archaeology. This incorporation of more zooarchaeological work in classical archaeology has thus generated greater appreciation of the overall importance of taphonomy in our studies of ancient sites.

The examples from Nemea and Kalaureia certainly highlight the value of zooarchaeological findings to reconstructions of life in antiquity, but also underscore how methodologies have been modified (especially through greater attention to recovery and taphonomy) to achieve results. Such potential is increasingly recognized and voiced. Scott Scullion (2013, p. 253) stresses that incorporation of zooarchaeological evidence can go beyond this and indeed revolutionize our understanding of Greek cult practice, essentially forcing us to rethink the whole matter "from the ground up," that is, on the basis of the actual remains of the animals used in such activities and the cultural choices that shaped the selection, butchery, treatment, and consumption of these animals. Zooarchaeological contributions to this debate not only have widened our understanding of what may be distinctive, local idiosyncrasies of ritual practice in particular sanctuaries or cults (e.g., the case of left hind limb elements of sheep offered for the hero Opheltes at Nemea), but also fostered crucial dialogue at the core of how we might define and construct animal sacrifice altogether. Picking up on the latter, Gunnel Ekroth (2013, p. 22) suggests that a distinction between "sacrificial" and "sacred" meat among Greek ritual practices might be more informative. Animals killed at the altar, in communion with the divine, would constitute "sacrificial" meat, while "sacred" could denote any remaining meat consumed in the sanctuary, in whatever fashion such was accessed or acquired. Although such categorization might aid in explaining the variety of animals and animal parts consumed by the ancient Greeks among "ritual" contexts, meaning can be further enhanced from greater exploration of zooarchaeological materials whose context is disassociated (perhaps entirely) with sanctuary antecedents. A wider array of such contexts marks many zooarchaeological samples collected from sites that date to

periods outside of Archaic and Classical times (ca. eighth to fourth centuries BC) in Greek antiquity, with intriguing results of complexities surrounding animal use in the Bronze Age Aegean world (ca. 3000–1000 BC).[1]

Venturing forward, one area in need of more attention in zooarchaeological method and practice within classical archaeology is the enhanced retrieval and analysis of potentially "non-ritual" faunal deposits, such as assemblages linked to households, workshops, and bars/taverns, especially those dating to Archaic and Classical times. Advances along this path represent a shift in excavation and recovery priorities within the field of classical archaeology, not always an easy measure, but the potential benefits can be quite enlightening. Investigation of faunal remains recovered from various wells in association with taverns and workshops in the Athenian Agora, and dating to Archaic and Classical times, for example, revealed patterns that seemed discordant with what might have been expected had strict guidelines for animal sacrifice, as provided in the ancient sources, been followed exactly (MacKinnon 2014). Specifically, these contexts contained higher frequencies of pig (of all ages) and juvenile cattle than typically requested as part of sacrificial calendars and proceedings in ancient Athens. These patterns challenge notions that all consumed meat was sacrificial in nature and create strong incentives to pursue the issue of sacred/secular divisions in classical archaeology from a much more multifaceted lens.

14.3 Interrelationships of Ancient Textual, Iconographical, and Zooarchaeological Evidence in Determining "Breeds" of Animals in Antiquity

The examples of zooarchaeological contributions to understanding of Greek cult practice outlined above demonstrate components of conformity and tension that may exist among the analysis of faunal and ancient textual and iconographic datasets. Accounts and images of Greek sacrificial practices do register, but clearly what is available from such sources may not be complete and must always be assessed critically. Such reflective caution is essential in any integrated reconstruction of the role of animals in antiquity. Overall, ancient texts, iconographic works, and archaeological materials (bones or otherwise) often reflect different activity domains, locations, and timescales in the past, which in many cases inflicts serious challenges on interweaving their accounts into a single comprehensive narrative (Foxhall 2004; MacKinnon 2004). Notwithstanding practical issues of preservation, recovery, and the like, that affect each of these three lines of evidence, effective investigation of

[1] Zoorchaeological literature and studies for Bronze Age sites in the Greek world typically outnumber those for Archaic and Classical timeframes by comparison. Moreover, they often show greater depth of coverage and synthesis across types of deposits, and exploration of wider themes beyond ritual use and consumption of animals. To this end, the studies collected in Kotjabopoulou et al. (2003) provide a measure of reflection for general assessment.

ancient texts and iconography, for example, further requires thorough understanding of the temporal and social context surrounding the creation and purpose of the work. Details of the author's/artist's intentions, experiences, skills, knowledge, messages, and manner of reliability and embellishment in crafting the work are integral to assess the value, role, and purpose of each, which are themselves often closely tied with the demands and expectations of the audience to which the work is directed. Similar considerations surround the understanding of context and its effects on meaning, intention, and integrity of the recovered dataset and are critical to the investigation of archaeological materials, including faunal remains. Zooarchaeological evidence must be considered in light of sometimes multifaceted, complex natural and cultural conditions and agents shaping its creation, deposition, preservation, recovery, and ultimate interpretation.

Exploration of animal "breeds" in Greek and Roman antiquity represents one field for which the integration of ancient textual, iconographic, and zooarchaeological datasets shows tremendous promise. Often we consider species generically, overlooking that cultures often can breed stock to promote certain features. All cattle are not alike: varieties or "breeds" created are cultural products, and as such, akin to new and different amphora forms or types of pots, one might argue. Still, modern genetic manipulation of physical and behavioral traits underscores today's definition of "breeds." Certainly ancient cultures bred animals to promote selected features, but in documenting varieties through media such as ancient texts and art, they often distinguished types by their geographic location (e.g., Umbrian cattle, Campanian cattle), rather than upon strict genetic and reproductive criteria as used today. The relationship between a geographically-distinguished "breed" and a truly genetically-recognized "breed" need not match completely. While geography can act to separate stock and lead to the creation of breeds, it might be better at this point to classify this concept as "varieties" of livestock, as opposed perhaps to "breeds" as defined today.

Notwithstanding definitional variation, traits of interest as regards various animal species and "breeds" of these are documented in ancient textual sources (Table 14.1). The Romans, for example, emphasize concepts including appearance (typically size and color) and working capacity (e.g., power and durability) in describing and distinguishing types of cattle (MacKinnon 2010, p. 58). Among pigs, the Romans highlight fecundity, meat quality, fat content, and ability to walk over distances among traits of interest (MacKinnon 2001). Comments about wool quality largely dominate references to varieties of sheep in Roman antiquity (MacKinnon 2015). Overall, a range of traits likely factored in cultural selection of stock for various purposes or duties (e.g., as sacrifice, for milk production, for wool or hide, for meat, for work purposes, as pets, etc.). Artificial selection of such traits in Roman livestock, therefore, should lead to genetic changes and clustering, provided of course that gene pools of geographically and/or culturally separated individuals remained largely closed. Similar selection might result by importing stock, which contained the desired traits, to another zone where they could mate with local varieties, and in turn introduce new traits.

Table 14.1 Selection of ancient references that provide descriptions and characteristics of various "breeds" of cattle, sheep and pig

Taxon	"Breed"/variety/type/region	Traits of interest mentioned in ancient texts	Sources
Cattle	Campanian (Italy)	Smaller size, white, strong for cultivation	Col., 6.1.1–3, Varro, *Rust*. 1.20.4
	Ligurian (Italy)	Small	Col., 6.1.1–3; Varro, *Rust*. 2.5.10
	Umbrian – large (Italy)	Large, white	Col., 6.1.1–3
	Umbrian – small (Italy)	Small, red, spirited, strong	Col., 6.1.1–3
	Etruria/Latium (Italy)	Thick-set, powerful, hard-working	Col., 6.1.1–3
	Apennine (Italy)	Tough, unattractive, strong bulls bred in southern regions	Col., 6.1.1–3; Cassiod., *Var*. 11.39
	Alpine (Italy, North)	Low stature, unattractive, multipurpose, but good milkers	Col., 6.24.5; Plin., *NH* 8.70.179; Verg., *G*. 3.143–4, 3.175–6
	Phoenician (North Africa/Near East)	Tall, excellent milkers	Ael., *NA* 16.33
	Euboean (Greece)	White	Ael., *NA* 7.35
	Gallic (France)	Good breed, good workers	Varro, *Rust*. 2.5.9–10
	Epirus (Greece/Albania)	Acclaimed breed	Varro, *Rust*. 2.5.10
Pig	"Larger" type	Smooth-skinned, great-bodied, large hips, white-bellied, long in shape, ample and round; pastured in warmer, sunnier regions	Col., 7.9.1–3; Pallad., 3.152; Petron., *Sat*. 47; Juv., 13.117–18
	"Smaller" type	Smaller–sized; hard, dense, black bristles; similar to wild boar	Col., 7.9.1–3
Sheep	Arabian/Syrian (Near East)	Two kinds – one with long & fat tail; other with broad tail; white, strong, coarse wool	Ael., *NA* 10.4; Plin., *NH* 8.72.198; Strabo, *Geog*. 16.4.26
	Ceos (Greece)	Good milkers for cheese	Ael., *NA* 16.32
	Ligurian (Italy)	Important sheep region, milk producers; black/dark brown color	Strabo, *Geog*. 5.3.1; Col. 7.2.4
	Daunian/Apulian (Italy)	Soft wool, breed of outstanding excellence	Strabo, *Geog*. 6.3.9; Col. 7.2.3
	Laodiceian (Turkey)	Soft, white wool	Strabo, *Geog*. 12.8.10
	Milesian (Turkey)	Soft, black wool	Strabo, *Geog*. 12.8.10
	Tarentine (South Italy)	Fine, short-stapled wool; excellent quality	Col. 7.2.3–5; Varro, *Rust*. 2.2.18
	"Rich, flat country"	Tall sheep	Col., 7.2.3
	"Lean, hilly region"	Sheep of square build	Col., 7.2.3
	"Wooded, mountainous region"	Small sheep	Col., 7.2.3

Manipulation of livestock varieties/types/breeds certainly occurred in antiquity, but exploration of the temporal and regional extent, variation, and fabric of such practices is an aspect where zooarchaeological method and practice is proving instrumental, notably through advancements in osteometrics (Albarella 2002) and geometric morphometrics (Owen et al. 2014). Classical archaeology has been slow in the uptake and application of geometric morphometrics (GMM) in zooarchaeology. Rather than representing any overall dismissal of the value of GMM, this is likely due to the limited applicability in the discipline of current GMM studies, which tend to focus on identifying prehistoric extinct fauna or distinguishing wild from domestic taxa in analyses of initial animal domestication, as well as accessibility concerns (equipment, training, costs, etc.). Currently, a great deal of data about animal size and shape in antiquity can be gleaned, fairly readily and economically, through traditional osteometric analyses, and it might suit classical archaeology best to explore these methods more thoroughly at this stage to help provide a baseline of information. Measurements of bone lengths within individual livestock categories (i.e., cattle, sheep/goat, pig), variously converted to withers' heights, for example, typically register a temporal increase towards larger animals throughout antiquity (MacKinnon 2004, 2010). Some of the largest gains as regards average withers' height occur during Roman antiquity, notably Roman Imperial times. While one sees height increases across the empire, Italy, as the core of the Roman world, seems to capitalize on this earlier than its provinces (MacKinnon 2004).

While increases in overall average heights may signify a general level of temporal "improvement" among animals in antiquity through breeding of larger stock, varieties or "breeds" of animals can be also explored through detailed studies using bone measurements, a huge corpus of which already exists among zooarchaeological studies for classical archaeology. Incorporating measurements of various dimensions—bone lengths, widths, depth, etc.—as well as ratios among such dimensions provides a better calculation of morphology and enhances observations drawn from withers' height comparisons alone. Thus, as regards cattle, research indicates that although widespread increases in sizes occur throughout Roman Italy during Republican and Imperial times, coincident with marked increases both in agricultural expansion and in the general human population, distinct clusters of cattle "breeds" further develop at these times, with evidence for this found in both zooarchaeological and textual databases (MacKinnon 2010). Differential selection of traits is evident, with features such as stockiness, leanness, height, and leg length, among others, variously manipulated to suit specific cultural and environmental needs and conditions. Several factors interplay to cause size and shape changes, including an augmented market and military demand for grain and other foodstuffs, local necessities for more powerful plow and traction oxen, as well as the import and export of cattle brood-stock into and out of Roman Italy (MacKinnon 2010).

Size and shape variation, as revealed from zooarchaeological metric data for sheep, also indicate an increase in height as a consequence of manipulation of livestock across much of the larger Mediterranean world during Roman times; however, tremendous variation is noted (MacKinnon 2015). Smaller breeds are often never eliminated, while the introduction and spread of taller, slender types, heavier,

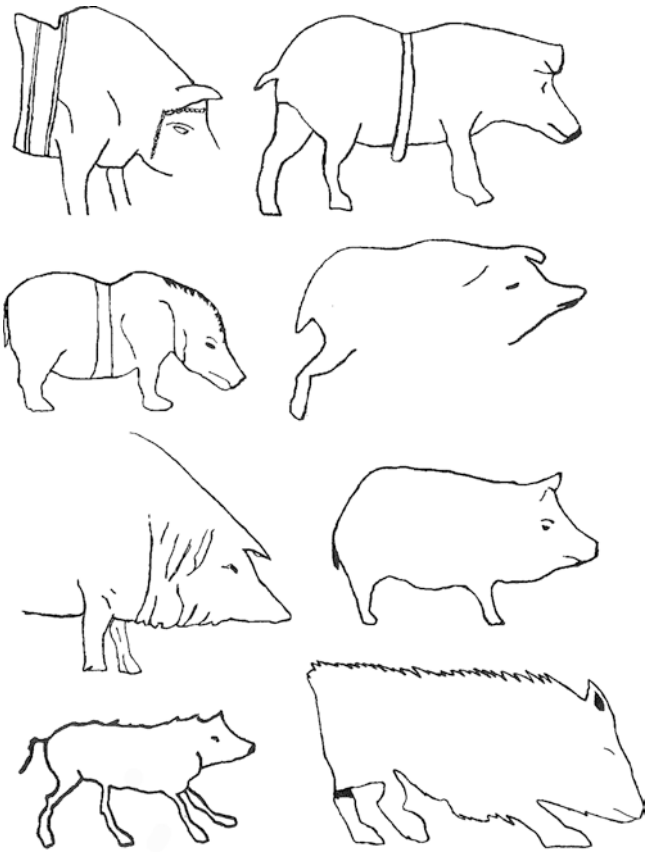

Fig. 14.2 Outline drawings of pigs as represented from various *suovetaurilia* sacrifice scenes from Roman iconography (modified from MacKinnon 2001)

thicker-set types, smaller, compact types, among other varieties of sheep in different areas of the Roman world, attests to the shrewd and productive, but also flexible and often regionally-specific, breeding tactics conducted during antiquity.

Similar complexity registers in the analysis of pig "breeds" in Roman antiquity. As in the cases involving sheep and cattle, zooarchaeological evidence shows an increase in the average height of pigs across much of the Empire, particularly during Imperial times. Presumably, such links to enhanced selection of bigger brood stock (MacKinnon 2001). Moreover, a larger variety sees further development during Roman antiquity—the fat, lop-eared, short-snouted kind. This type may link with sacrifice, as it is often the variety depicted on *suovetaurilia* (sacrifice of bull, sheep, pig) scenes in Roman iconography (Fig. 14.2). In this capacity, animal sacrifice sends a stronger message of imperial propaganda: a large, fat pig better symbolizes prosperity, duty, and godly reverence than a meager-looking pig. Nevertheless, zooarchaeological remains show a smaller, long-legged variety dominated dietary pork.

This latter type occurs across the bulk of archaeological contexts in Roman Italy. It is worth noting that the development of breed diversity in the Classical World was not limited to mammals. De Cupere et al. (2005), for example, employed morphometric assessments of domestic fowl to recognize three "breeds" of chicken (*Gallus gallus*) at the Roman-Byzantine (ca. first century BC to seventh century AD) site of Sagalassos, Turkey. They were able to do so by limiting analyzed specimens to those of female fowl (as determined from the presence of medullary bone, a build-up of calcium in egg-laying birds), which allowed the researchers to avoid problems of sexual size variation that might otherwise complicate results (De Cupere et al. 2005).

The example of the pig, outlined above, may act in another capacity to highlight integration of zooarchaeological and iconographical evidence for antiquity. The anthropology of art/visual culture is a complicated field; any complete analysis of its social function must seek to place art within the holistic world of human culture and do so from a culturally relative perspective free of ethnocentrism. One must contend with layers of assessment: (1) how was the animal depicted? (e.g., naturalistically, stylized, abstractly, etc.); (2) what is the function of the work? (e.g., symbolic, religious, decorative, didactic, commemorative, expressive, etc.); (3) what meaning was intended, and is that same meaning ultimately what is extracted by the viewer (both today and in the past)? Understanding all such facets of ancient art is daunting but can be made more manageable if analytic categories are narrowed. For example, focusing upon *suovetaurilia* scenes in which pigs are depicted in a relatively natural manner (as opposed to heavily stylized) provides some common basis for interpretation, helping in turn to standardize biases and hopefully find patterns of interest. Similar foci may be shaped through other means, such as constraining works by temporal period, geographic region, artistic medium, technology of manufacture, workshop, composition, theme, etc. Certainly, there is a manner of inductive reasoning in such analyses; one gathers a wide pool of images, frames each within its particular context (e.g., when, how, why, it was made), then seeks patterns by which to connect different works (e.g., "image 1, 2 and 4" are similar, but "2" is a later copy of "1", while "4" is a contemporary work from another region). The resulting comparative analyses about animal size, shape, and appearance such work produces can be quite fruitful, however, particularly if linked to morphometric evidence drawn from other sources, such as zooarchaeology.

In sum, cultures of antiquity bred multiple types of animals, selecting and promoting a range of physical and behavioral features within different livestock taxa, as suited local and regional demands and settings. Weight, stockiness, color, hide and wool quality, strength, hardiness, docility, and fecundity, were among a range of characteristics under selection, all of which the ancient Greeks and Romans manipulated as suited their needs. Ancient texts provide some information, but are generally silent on many of these details, especially among available records for Greek antiquity. Iconography yields potential for future investigation, but, notably, its analysis may be hampered by variations in artistic styles and questions about accuracy in depictions. Zooarchaeology increasingly surfaces as a preeminent means with which to investigate and understand animal "breeds" and breeding tactics in Greek and Roman antiquity. No doubt, its role in this capacity will increase

immensely among future projects, especially with advancements in geometric morphometric techniques. As noted earlier, this field has thus far been little explored in classical archaeology. Nevertheless, research using enhanced 3D imaging to aid in the discrimination of types of pig crania provides a great exploratory venture of interest for classical archaeology (Owen et al. 2014) given the importance of pigs, especially in Roman antiquity.

14.4 Isotopes and Other Advancements in Zooarchaeological Method and Practice and Their Potential Within Classical Archaeology

Zooarchaeological interpretations are obviously structured upon sound methodologies in how faunal data are retrieved, recorded, and evaluated. In essence, how investigators determine information about species, element, age, sex, butchery, taphonomy and so forth, act as the essential building blocks to subsequent pattern recognition and larger interpretation and synthesis. Zooarchaeology has witnessed significant strides in how such data are assessed, and certainly refinements across the spectrum in methodology can only enhance the contribution of the discipline, creating more focused, nuanced, detailed reconstructions of the role and use of animals among cultures of the past. While classical archaeology can benefit from any such methodological development in zooarchaeology as a whole, several lines arguably may stand out as key pathways to explore with greater vigor.

One such avenue concerns refinements in our knowledge of age and seasonality in faunal remains. The ubiquity of seasonal schedules and calendrical events in antiquity, encompassing components such as festivals, rituals, sacrifices, agricultural duties, among many other behaviors, highlights its research importance. At a macroscopic level, refinements to dental aging methods and correlations of age at death sequences for animal taxa have assisted in narrowing down potential seasonal culling schedules. Such techniques work best for younger animals where age patterns can be observed in dental wear stages within the first year of life (Lemoine et al. 2014; Zeder et al. 2015). Available evidence for Roman Italy indicates that rural sites register more deaths among sheep/goat in the 3–6 month dental-age group than do urban sites (14% vs. 7%), which, by contrast show a slightly higher percentage of deaths in the 7–12 month category (14% vs. 9%) (MacKinnon 2004, p. 108). Assuming autumn births (as prescribed in the ancient texts: Col. 7.3.12; Varro, *Rust*. 2.1.19, 2.2.14; Plin., *HN* 8.72.187), such a pattern supports the hypothesis of enhanced late-winter or early-spring culls at rural sites, but a preference for predominantly summer- or autumn-culled ovicaprids at urban sites.

Age and season at death in animals may also be investigated by examining incremental structures in the cementum of teeth through the preparation of microscopic thin-sections. Such techniques have assisted greatly in clarifying seasonal rounds in various animal taxa (Klevezal 1996; Lieberman 1994; Pike-Tay 2001; Pike-Tay and

Ma 2011), but as yet have seen little application in classical archaeology, perhaps in part due to practical limitations in processing and analyzing materials. Studies of cementum banding and dental microwear among sheep and goats from the site of Sagalassos, for example, provided greater resolution to seasonal scheduling in pastoral schemes during antiquity (specifically, that sheep mated in early summer in that region and fed on less palatable plants when pasture was stressed during dry seasons), aspects which compared favorably to patterns observed among modern ovicaprids from the region (Beuls 2004; Van Neer and de Cupere 2013). Results bode well that these less established routes for extracting animal age and season of death from archaeological materials offer much potential and should see greater use in classical archaeology, especially as a means to connect past and present animal husbandry regimes.

A second methodological development in zooarchaeology with great potential for application in classical archaeology focuses upon stable isotopes. Elements and their stable isotopes cycle through the biosphere driven by physical, chemical, and biological processes, but at different rates dues to their different atomic masses. This leads to different ratios of these substances in organisms, which in turn help provide signals for aspects such as varying diets, home ranges, breeding and foraging areas, and migrations routes. Commonly used stable isotopes in archaeology today include those of carbon ($\delta^{13}C$), which typically correlates with vegetation; nitrogen ($\delta^{15}N$), which correlates with trophic levels, commonly the contribution of meat to one's diet; strontium ($^{87}Sr/^{86}Sr$) and lead ($^{208}Pb/^{204}Pb$, $^{207}Pb/^{204}Pb$ $^{206}Pb/^{204}Pb$), which reflect local flora, fauna and geological deposits; and oxygen ($\delta^{18}O$), which serves as a proxy indicator for temperature, altitude, and hydrology (Bentley 2006; Farnum and Sandford 2008; Katzenberg 2000; Krigbaum 2008; Pilaar Birch 2013). Correlating and cross-referencing isotopic signatures in animal remains with those of different environmental settings permits the recognition of faunal outliers, foddering and herd management practices, trade, and reliance on foreign imports. Moreover, comparing isotope ratios in tooth enamel (which forms during early years of life, except in animals with ever-growing teeth) to those in bone (which remodels until death) or the local environment helps evaluate the mobility of an animal on both a seasonal and lifetime basis, depending on specific techniques used (e.g., Balasse et al. 2002; Minniti et al. 2014).

Case studies from two sites help illustrate the potential of such work. The Roman-Byzantine (ca. first century BC to seventh century AD) site of Sagalassos, Turkey, has acted as somewhat of a pioneer for zooarchaeological stable isotope research in classical archaeology, with several influential studies. First, oxygen and strontium isotope ratios were measured in archaeological freshwater fish (carp) remains to address issues of provenance. Results from the stable oxygen studies excluded a riverine origin for these fish in favor of a lacustrine environment, while those from the strontium investigation eliminated some local lakes as a potential source of the carp (Dufour et al. 2007). Second, stable carbon and nitrogen isotope results across livestock taxa at Sagalassos indicated a shift in isotopic ratios for sheep, suggesting that they were herded together with cattle in Roman times, but with goats during the Early Byzantine period. Finally, results from stable strontium analysis of ovicaprid teeth from the site

document variation in where these animals were born, as well where they may have moved to throughout their lives, in turn providing a more nuance picture of herding strategies and seasonal transhumant schedules (Van Neer et al. 2010).

The second case study for consideration explores pasturing regimes in Neolithic (ca. 7000–3000 BC) Anatolia (modern-day Turkey). Here, evaluation of carbon and nitrogen isotopes in archaeological sheep and goat bone collagen indicates that flocks used to provision the site of Çatalhöyük moved over a much more extensive territory, encountering multiple, isotopically distinct plant regimes, than did flocks from the nearby site of Asikli Höyük (Pearson et al. 2007). Studies involving oxygen isotopes and dental microwear studies at Çatalhöyük additionally demonstrated that (1) neither long-distance, seasonal transhumance, nor fully separate, nomadic pastoralism was practiced at the site during the Neolithic; (2) flocks grazed on dedicated seasonal pastures and did not suffer from resource stress; and (3) most sheep were slaughtered in early spring after fattening on autumn grass re-growth (Henton 2010, pp. 406–409).

Although this Anatolian example predates the timeframe of classical antiquity, the results are of tremendous interest as a model for framing similar questions about livestock movements in Greco-Roman antiquity. Considerable debate, for example, exists surrounding the various scales of pastoralism in antiquity (Halstead 1996; Lemak 2006). Schemes can vary from localized, small, non-transhumant herding at a permanent site to large-scale, long-distance transhumance. Implementing archaeometric means to track an animal's movement over the course of its lifetime, increasingly accomplished through isotopic analyses, provides an objective measure that focuses upon the actual participants in these processes (i.e., the animals themselves), as opposed to cultural recordings, reflections, or descriptions of such operations (in whatever format these might exist, e.g., ancient textual references, inscriptions, iconography, etc.). Perhaps the best region in which to test the relationship between these different types of evidence is Roman Italy, where our largest pool of ancient references pertaining to transhumance exist, although even then these are still rather minimal (MacKinnon 2004, p. 114). Ironically, Roman Italy remains largely unexplored in this respect, with researchers only beginning to map the isotopic variability of surrounding geology for comparison with archaeological isotopic data.

Although incorporation of more isotopic assessments among zooarchaeological materials in classical archaeology provides great promise, more nuanced interdisciplinary investigations of the current roster of isotopes available for study can add greater texture to our knowledge of antiquity as well. Nitrogen levels, for example, may also be affected by manuring, the practice of which is underexplored in classical archaeology, but is recognized as having been vital for crop and animal husbandry across the ages (Forbes 2012). Paleobotanical research confirms the impact on cereal crops of manuring, which enriches stable nitrogen in these plants (Fraser et al. 2011). The effect among pulses is less noticeable, given these plants can fix atmospheric nitrogen, and tend towards higher stable nitrogen ratios to begin with. One potential investigatory avenue stemming from such work involves assessments of stable nitrogen ratios in herbivores, which in turn might reflect distinctions in dietary schemes among these animals, such as variations in the consumption of pulses and legumes in their diet, or feeding regimes that centered upon grasses grown on well fertilized

fields (i.e., manured ones), versus poorer pastures. This would advance our understanding of how peoples in antiquity integrated agricultural and pastoral schemes. At this stage, continued progress requires intensifying and linking paleobotanical and zooarchaeological isotopic analyses so that more holistic understanding of human-environment relationships in antiquity can be pursued.

Clearly, research utilizing stable isotopes can greatly enhance our knowledge of transhumant scales and routes, herding strategies, relations of stock to ecological zones, exploitation of coastal, riverine, and lacustrine resources, imports and exports of animals across regions of the ancient world, and differential feeding regimes. These are very powerful tools in classical archaeology and areas of incredible potential for zooarchaeological input. Currently, however, more attention has focused on isotopes in human bones, and human dietary investigations (MacKinnon 2007). Existing studies involving animals have concentrated more on Roman or prehistoric contexts, as the Anatolian cases of Çatalhöyük and Sagalassos discussed above illustrate. While disciplinary divides in how classical archaeology is viewed, taught, and administered among different regions has stalled or complicated the application of isotopic techniques, their implementation across the wider temporal and geographic extent of the ancient Greek and Roman worlds is strongly recommended.

14.5 Conclusions

Certainly, zooarchaeology has much to contribute to classical archaeology, but in what ways specifically is the discipline of classical archaeology (as opposed to other fields of archaeology or study) shaping zooarchaeological method and practice (and vice versa for that matter)? One key area affected in this dynamic concerns a more prominent role for zooarchaeology in classical archaeological practice overall, with much greater attention devoted to the more complete recovery of faunal remains across all contexts and a deeper appreciation of how taphonomic factors shaped assemblages. This seems like an obvious step forward within classical archaeology. However, momentum along that path has varied, with the prioritization of artifact retrieval in some projects still potentially biasing zooarchaeological results due to less stringent recovery techniques for faunal remains or even the discard of faunal materials altogether. When recovered in a more responsible fashion, however, faunal samples from classical archaeological sites can sometimes be massive due to the large spatial extent covered by sites and the great amount of debris and waste that can accumulate within this area. The size alone of such assemblages provides great impetus to conduct a thorough analysis, not only so that the results achieved may be more statistically reliable, but also that the depth and breadth of information obtained may be explored more systematically as regards the underlying cultural and natural factors that affect any given archaeological assemblage (see Crabtree, Chap. 9). Multiply these merits across the huge database of classical archaeological sites that have been or will be investigated, and the potential of zooarchaeological work in broader syntheses of the ancient world (over space, time, site type, culture,

etc.) shows tremendous promise (MacKinnon 2007). Such positive aspects, nevertheless, must be weighed alongside added costs in terms of labor, resources, and time devoted to enhanced recovery and analysis of finds. These concerns are not specific to classical archaeology, but they can be especially challenging in a discipline where zooarchaeological input is minimized or stifled through various means, including the separation of specialists in the design and goals of classical archaeological research projects; the publication and funding priority of certain material categories, such as architecture and ceramics; the lack of zooarchaeologists who specialize in classical archaeology; and the administrative, intellectual, and practical barriers to conducting specialized scientific tests on faunal remains, etc. The world of antiquity was complex and multifaceted. As such, any number of established practices and advancements in zooarchaeological method can be applied to its understanding, be this work on recovery, taphonomy, identification, quantification, aging, sexing, pathology, butchery marks, isotopic work, or whatever one might employ to generate data of interest. In large part, classical archaeology represents perhaps a vast, uncharted territory for the application of a host of methodological applications and advancements in zooarchaeology.

The case studies and examples highlighted in this current assessment effectively provide a taste of how advancements in zooarchaeological methodology and interpretation have influenced (and even transformed) discourse in classical archaeology. Detailed assessments of faunal remains from ritual deposits reveal a much more complex framework that underlies the association between "sacred" and "secular" explanations or divisions pertaining to meat consumption in Greek antiquity. Indeed, the contributions of zooarchaeology to our whole understanding of ancient cult practices now shares prominent footing alongside long-entrenched investigatory pathways of these phenomena as largely drawn from studies of ancient textual and artistic evidence. Such interdisciplinary spirit, moreover, sees further potential in classical archaeology with zooarchaeological contributions in our understanding of livestock breeds in antiquity—another forum for which results from animal bone analyses add greater detail to a general foundation of information as provided from other sources. Studies of livestock "breeds" for antiquity reveal targeted, shrewd, and dynamic manipulations of animals during Greek and Roman times, adding texture to our understanding of cultural choices and the interplay of culture and nature in the past. Methodological advancements in zooarchaeology, such as progress in studies involving stable isotopes, trace elements, osteometrics, and aging techniques of bones and teeth, also yield further means with which to refine our understanding of the role and use of animals in Greco-Roman antiquity. Overall, the complexity inherent in the range and composition of datasets available to classical archaeologists, coupled with the wide body of methodological trajectories encompassing the analysis of such sources, forges a vast field of potential for researching and reconstructing the world of antiquity. The discipline of zooarchaeology now stands as a critical player in such work, a role that has developed enormously over a relatively short period of time and for which its future course harkens tremendous promise.

Glossary of Works of Classical Authors Referenced in the Text (Following Oxford Classical Dictionary)

Ael., *NA*. Aelian, *De natura animalium.*
Cassiod., *Var*. Cassiodorus, *Variae.*
Col. Columella, *De re rustica.*
Juv. Juvenal, *Satires.*
Pallad. Palladius, *Opus agriculturae.*
Petron., *Sat*. Petronius, *Satyricon.*
Plin., *NH*. Pliny (the Elder), *Naturalis historia.*
Strabo, *Geog*. Strabo, *Geographica.*
Varro, *Rust*. Varro, *De re rustica.*
Verg., *G*. Virgil, *Georgics.*

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Chapter 15
Assessing California Mussel (*Mytilus californianus*) Size Changes Through Deep Time: A Methodological Case Study from San Miguel Island, California

Todd J. Braje, Breana Campbell, and Hannah Haas

15.1 Introduction

Investigations of human impacts on ancient ecosystems have long been an important avenue of research for archaeologists (e.g., Allen 1997; Broughton 1994, 1999; Grayson 2001; Kirch 2004; Kirch and Hunt 1997; Kohler 2004; Martin 1984; Redman 1999; Redman et al. 2004). In recent years, this research has become increasingly important and relevant for modern management applications. Nearly 15 years ago, for example, marine biologist Daniel Pauly (1995) coined the term "shifting baselines syndrome" to describe the ahistorical approach of modern fisheries science as a major contributor to global fisheries collapse and mismanagement. Pauly (1995) argued that every new generation of marine scientists tended to accept the stock sizes and species composition at the start of their careers as the baseline for evaluating subsequent changes. Earlier periods were ignored or disregarded, and the new generation of scientists assumed data collected by prior researchers was inadequate for complex, modern modeling techniques. What resulted was a disaster in slow motion and the decay and collapse of some of the most important commercial fisheries around the globe (see the historical collapse of Atlantic cod for an excellent example; Hutchings and Ferguson 2000; Kurlansky 1997).

For Pauly (1995) and many other marine scientists (e.g., Dayton et al. 1998; Jackson et al. 2001, 2011; Kittinger et al. 2013, 2014; Lotze and McClenachan 2014; McClenachan et al. 2012; Pauly et al. 1998), one solution to the shifting baselines problem is to consult deeper historical records such as archaeological reconstructions of ancient fisheries (Rick and Erlandson 2008). Analysis of archaeological shell

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middens offers the potential for reconstructing baselines over century to millennial timescales and can provide insights on the effects of ancient peoples on marine ecosystems. Deep historical records offer valuable perspectives that can help aid modern restoration efforts and evaluate the health and structure of modern ecosystems.

Marine shellfish make excellent candidates for historical ecological research agendas for four primary reasons: their remains are often well preserved in archaeological shell middens; they have been exploited by Anatomically Modern Humans for at least 165,000 years (Erlandson 2001; Jerardino and Marean 2010; Marean et al. 2007); they often are ubiquitous in coastal archaeological deposits; and they can be excellent proxies for local environmental conditions (Richardson 2001). A variety of archaeological studies have demonstrated the potential impacts of human foraging and natural climatic changes on marine shellfish populations around the world by tracking size changes through deep time (e.g., Allen 2012; Anderson 2001; Braje 2010; Braje et al. 2012; de Boer et al. 2000; Erlandson et al. 2008, 2011; Faulkner 2009; Giovas et al. 2010, 2013; Jerardino 1997; Lasiak 1991; Mannino and Thomas 2001, 2002; Milner et al. 2007; Morrison and Cochrane 2008; Morrison and Hunt 2007; Raab 1992; Swadling 1976; Whitaker 2008). Fluctuations in shellfish sizes through time can result from a variety of factors, including predation by humans and other predators, competition with conspecifics and other species, disease, and natural climatic variation (e.g., Harley 2011; Menge et al. 1994, 2008; Smith et al. 2006).

Along the New World Pacific Coast, California mussel shells (*Mytilus californianus*) are often abundant in archaeological deposits, and mean size changes through time have been used by some researchers as a proxy for identifying natural climatic fluctuations and human impacts on near shore ecosystems (e.g., Braje 2010; Braje et al. 2007, 2012; Erlandson et al. 2004, 2008; Jazwa et al. 2012; Rick 2007; Sharp 2000; Whitaker 2008). Two primary methods have been used to reconstruct mean mussel sizes through time. The most popular for Californian archaeologists has been the use of a mussel hinge size template (e.g., Braje et al. 2007; Jazwa et al. 2012; White 1989). California mussels have relatively delicate shells compared to the larger, more robust shells of abalone, and although many archaeological deposits along coastal California contain California mussel shells, they are often fragmented by a variety of taphonomic processes (e.g., trampling, compaction, argilliturbation; see Claassen 1998). A mussel template developed by White (1989) allows researchers to group mussels into size classes based on the visual inspection of the mussel hinge and comparison to a template derived from modern mussel shells. Experimental studies demonstrate that this technique is statistically unreliable (Bell 2009), however, and results can vary tremendously from one trained zooarchaeologist to another or even over multiple trials by the same zooarchaeologist using the same sample (T. Rick, personal communication 2013).

On California's Channel Islands where sites tend to be better preserved than on the mainland, archaeologists have measured whole California mussels to track size changes through time (Braje 2010; Erlandson et al. 2004, 2008; Rick 2007). This method mitigates many of the problems posed by the template, but introduces others. Two methodological challenges are most apparent. First, studies using whole California mussel measurements from archaeological deposits (e.g., Braje 2010; Erlandson et al. 2004, 2008; Rick 2007) make no distinction between mussels

measured from surface collections versus subsurface samples. Surface and subsurface mussels may fragment at different rates due to a variety of taphonomic processes. Are there, then, statistically significant differences between the average sizes of mussels from surface versus subsurface samples? Secondly, it is possible that smaller shells may be less likely to break from taphonomic processes such as trampling and compaction (Muckle 1985; Wolverton et al. 2010). Since fragmented mussels are not accounted for using this technique, does selecting only whole mussels introduce a sampling bias?

In this chapter, we explore these two methodological questions using data from California's Northern Channel Islands. Erlandson et al. (2008) published their results from a long-term study to track shellfish size changes over 10,000 years on San Miguel Island, the western-most of the Northern Channel Islands (Fig. 15.1) . Their study included 8719 whole California mussel shell measurements from 32 temporally discrete shell midden components across the island (Erlandson et al. 2008, Table 1). We reanalyzed a subsample of these to investigate: (1) if average mussel sizes from surface and subsurface deposits show statistically significant variation; and (2) if a reliance on whole shell measurements biases mean mussel length. Ultimately, our results have important implications for using archaeological samples to build deep historical baselines and for evaluating the health and structure of modern California mussel beds along the Pacific Coast and around the world.

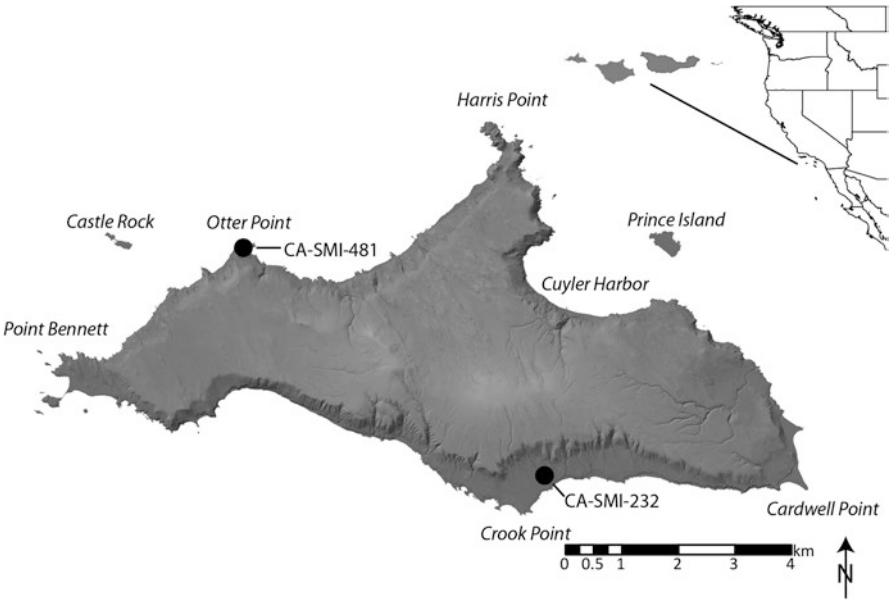

Fig. 15.1 Location map of the Santa Barbara Channel region, the Northern Channel Islands, San Miguel Island, and CA-SMI-481 and -232

15.2 Background

At 37 km^2, San Miguel Island is the second smallest island in the Northern Channel Island chain, located 42 km off the California Coast along the Santa Barbara Channel. Compared to the ecologically diverse mainland, San Miguel Island has a relatively impoverished terrestrial ecosystem with only 198 native taxa of plants, one amphibian, two reptiles, 15 resident birds, and three land mammals (Schoenherr et al. 1999, Table 1). The near shore marine ecosystem surrounding the island, however, teems with a diverse and complex food web of flora and fauna, fueled by deep-water upwelling and nutrient-rich kelp forests.

This rich marine ecosystem attracted the first island inhabitants some 13,000 (or more) calendar years ago (Johnson et al. 2002). The number and size of archaeological sites increased throughout the Holocene as more people occupied island habitats (Rick et al. 2005). During the last 1500 years, many of the quintessential Chumash cultural traits, first described by Spanish explorers, took shape. Native Islander subsistence strategies were adapted to exploit the bounty of the oceans, although terrestrial carbohydrates were an essential part of the diet (Noli and Avery 1988). At European arrival in AD 1542, the Island Chumash lived in large coastal villages and had developed a sophisticated fishing based maritime economy (Arnold 2001; Kennett 2005; Rick 2007) that included sea-worthy redwood plank canoe technology (Arnold 1995; Bernard 2004; Gamble 2002), shell money-bead exchange networks (Graesch 2004), cross-Channel trade systems (Arnold 1992; Rick et al. 2005), and an intensive shellfishery (Braje et al. 2011, 2012). The material remnants of their lifeways are recorded in thousands of archaeological shell middens that dot Northern Channel Island landscapes. Many of these sites are exceptionally well preserved; the relatively arid climate and alkaline archaeological soil matrices suppress biodegradation and promote good site preservation. The lack of burrowing animals (e.g., gophers, badgers, squirrels, etc.) also has helped maintain stratigraphic sequences at multi-component deposits.

While Native American diets and subsistence adaptations fluctuated based on a variety of cultural and natural influences, California mussels remained a central component of the protein diet for over 10,000 years (see Braje et al. 2012). Mussels are abundantly available along Channel Island rocky intertidal habitats, which constitute approximately 50% of island coastlines (Erlandson et al. 2008, p. 2145). California mussels are filter-feeding bivalves that live in aggregations of up to 1000 individuals per square meter and can range in size between a few millimeters to 250 mm long (Jones and Richman 1995). Mussels favor locations of moderate to heavy surf action and live up to 18 m below sea level (Suchanek 1981). They cling to the rocky intertidal substrate via byssal threads, are readily accessible during low tides, and are highly susceptible to population reductions resulting from human predation, storms, El Niño Southern Oscillation (ENSO) events, disease, or other factors (Jeradino et al. 2008). California mussels can be harvested and processed in large quantities with very little tool technology and by a wide variety of human foragers, young and old.

The shell and meat of a California mussel will continue to grow throughout its life, making shell length a reliable proxy for the age of an individual. There are a number of factors, however, that can alter growth rates including tidal height, food availability, sea surface temperature, salinity, and resource stress. But overall, growth is rapid during the first 3 years of life. Coe and Fox (1942) conducted a controlled experiment in southern California and found that California mussels reach lengths of 70 mm and sexual maturity in their first year, 105 mm in their second year, and 123 mm in their third year. After this, growth continues but the rate slackens.

15.3 Methods and Materials

In order to address our two research questions, we reanalyzed California mussel size measurements from San Miguel Island archaeological deposits reported by Erlandson et al. (2008). Our analysis includes Erlandson et al.'s (2008) measurements, plus additional measurements since the manuscript's publication. Erlandson et al. (2008) reported robust samples of whole mussel size measurements from both surface collections and subsurface excavations at only two localities, CA-SMI-481 and -232. The majority of sites reported by Erlandson et al. (2008) produced mussel size measurements from either surface collections or subsurface excavations, but rarely both.

CA-SMI-481 and -232 have multiple radiocarbon dates and artifact analyses that date the deposits to the Late Holocene (<3500 cal BP), with CA-SMI-481 radiocarbon dated to ca. 1220 cal BP (Rick 2007, pp. 64–65) and CA-SMI-232 to ca. 1200 cal BP (Braje 2010, pp. 81–82). CA-SMI-481 is located in a large dune complex on San Miguel's northwest coast and contains at least ten discrete archaeological deposits spanning 7300 years (Rick 2007, p. 61). The 1200 cal BP deposit is located at the top of the dune, where Torben Rick (Rick 2007, pp. 61–65, 138) excavated a small unit and measured whole mussel shells from the surface and subsurface. The deposit is positioned so that surface collections could be confidently associated with the discrete 1200 cal BP deposit.

CA-SMI-232 is a dense, single component shell midden visible in eroding exposures along two gullies on San Miguel's south-central coast. Braje (2010, pp. 77–82, 118) excavated three units in the eastern gully exposure and measured whole mussel shells from these units and from the surface of the eastern and western gullies. While only two sites, a total of 1936 individual mussel measurements were collected, 22.2% of the mussel measurements reported by Erlandson et al. 2008, Table 1. A 2 × 2 analysis of variance (ANOVA), a procedure that analyzes whether differences between more than two groups are statistically meaningful (Sokal and Rohlf 1981), was performed using SPSS 22.0 to analyze differences in average length between mussels collected on the surface versus those from excavated deposits at the two localities.

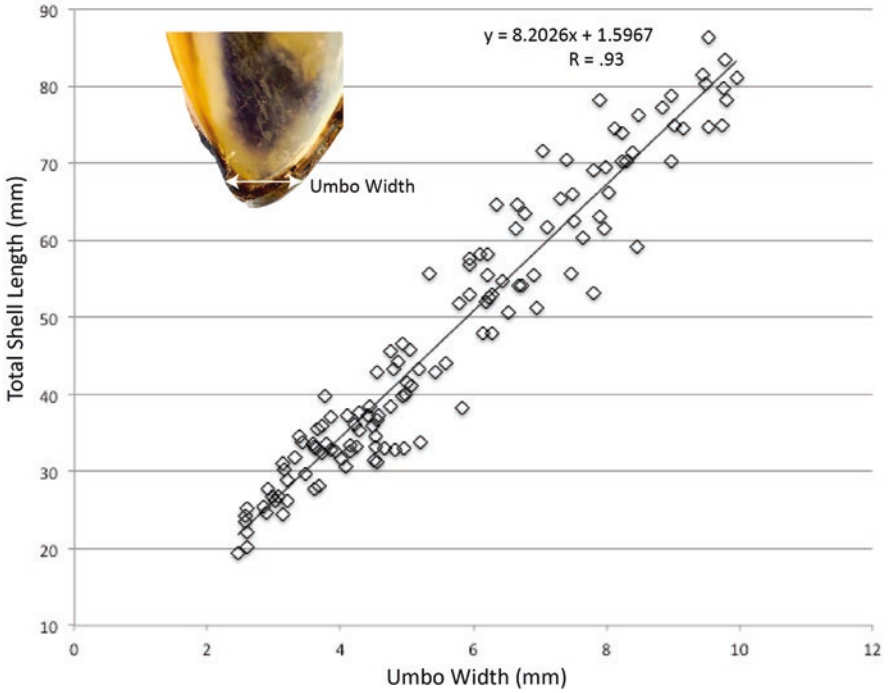

Fig. 15.2 Regression plot and the derived regression formula for California mussel shell length versus umbo width (see Campbell and Braje 2015). Inset: Photograph demonstrating how to measure California mussel umbo width

To test whether a reliance on whole mussel measurements introduces a methodological bias, we employed a new technique for estimating whole California mussel sizes from hinge fragments. Using modern California mussels collected from coastal southern California and archaeological samples from San Miguel Island, Campbell and Braje (2015) calculated regression formulas for three hinge measurements that accurately predict whole mussel length (see also McKechnie et al. 2015; Singh and McKechnie 2015). The regression approach offers an accurate method for estimating the original size of whole shells from shell fragments and commonly uses the least-squares regression method to determine the relationship between two variables (Johnson and Bhattacharyya 1992). While all three of their techniques proved reliable on modern samples, Campbell and Braje (2015) recommended measurement of the umbo width, combined with the regression formula $y = 8.2026x + 1.5967$, where x is the umbo measurement and y is whole shell length (Fig. 15.2), as the best method for archaeological samples. The inset image in Fig. 15.2 demonstrates how to calculate umbo width from a California mussel hinge fragment, measured where the hinge plate is at its greatest width.

We used hinge fragments of California mussel shells from two column samples excavated at CA-SMI-232 (see Braje 2010, pp. 77–96). Only left or right hinges

(whichever produced the largest sample) from each column level were included in our analysis. Following methods by Campbell and Braje (2015), Campbell, Haas, and two trained San Diego State University undergraduate students used digital calipers to measure umbo width for each hinge three times (to account for possible measurement error), averaging the results. The regression formula was applied to produce the average prey California mussel size. An independent samples *t*-test was performed to identify potential differences between average California mussel lengths derived from excavated whole mussels versus excavated hinge fragments.

15.4 Results

Prior to conducting a 2 × 2 analysis of variance, we examined the data to ensure it met the statistical assumptions of an ANOVA (normal distribution and homogeneity of variance). Scatter plots confirmed that the data were normally distributed. The data also met the assumptions of homogeneity of variance as Levene's test was non-significant. After compiling and averaging the results of whole California mussel size measurements in Microsoft Excel, we found a less than 1 cm difference in mean California mussel shell size between surface (50.8 mm) and excavated (43.7 mm) samples at CA-SMI-481 (Table 15.1 and Fig. 15.3). At CA-SMI-232, however, there is a nearly 2 cm difference in mean California mussel shell size from surface (48.2 mm) and excavated (32.2 mm) samples. Our 2 × 2 ANOVA analysis yielded statistically significant differences between mean mussel lengths from surface versus excavated samples at both CA-SMI-481 and -232 (Table 15.2). This difference reflects a large effect size for CA-SMI-232 (Cohen's $d = 1.01$, see Cronk 2008) and a moderate effect size for CA-SMI-481 (Cohen's $d = 0.38$). Consistent with Erlandson et al. (2008, Fig. 2), averages from CA-SMI-481 are larger than CA-SMI-232, a pattern evident from both surface and excavated mussels. The scale of this mean size reduction, however, is quite different; average mussel size from surface deposits exhibits only a slight decrease, while excavated samples show a dramatic decline in average size (Fig. 15.4).

The average size of California mussels at CA-SMI-232, based on 885 whole shell measurements from excavated samples, is 32.2 mm. If whole surface measurements are also included, the average is 34.1 mm. Average California mussel size at CA-SMI-232 from estimates based on 878 umbo width measurements from subsurface deposits is 36.1 mm. This estimated average is less than 5 mm different than whole shell measurements. An independent samples *t*-test produced statistically significant differences between average California mussel size estimated from hinge measurements and those taken from whole shell measurements ($t = 5.6$; $p < 0.01$), and this difference reflects a small to moderate effect size (Cohen's $d = 0.27$). Despite significant differences between mussel means, then, the results should be interpreted with caution as *p* values can be sensitive to large sample size. Effect size is a better measure of the magnitude of differences between groups.

Table 15.1 Age, size, and measurements (mm) of California mussels recovered from surface and excavated samples at CA-SMI-481 and -232

	Age	Surface collections					Excavated collections					Combined				
CA-SMI-	(cal BP)	n	Mean	Min	Max	St. Dev.	n	Mean	Min	Max	St. Dev.	n	Mean	Min	Max	St. Dev.
481	1220	182	50.8	14	119	18.8	751	43.7	7	145	18.6	933	45.1	7	145	18.9
232	1200	118	48.2	21	90	13.8	885	32.2	6	94	15.1	1003	34.1	6	94	15.8

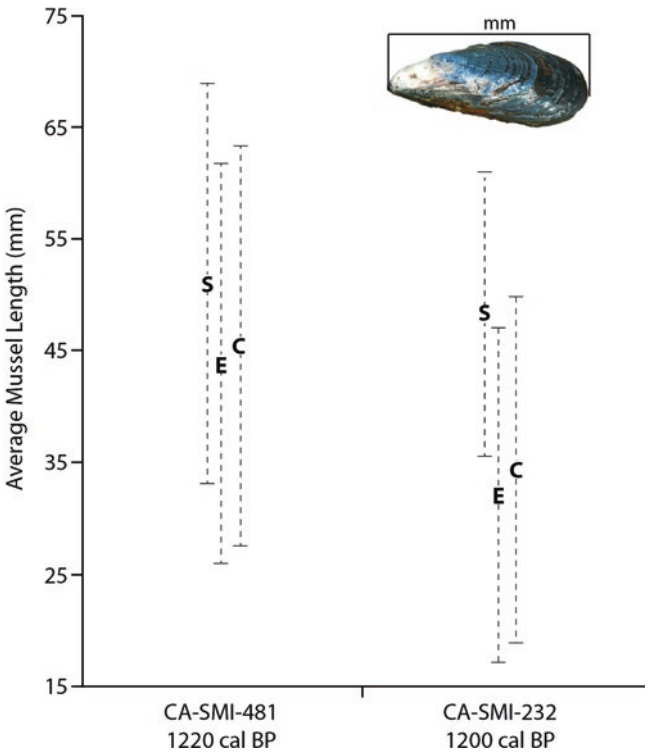

Fig. 15.3 Average length of whole California mussel shells from surface (S), excavated (E), and combined (C) samples at CA-SMI-481 and -232. Error bars represent one standard deviation from the mean

Table 15.2 Results of our 2 × 2 ANOVA

Variable	df	*MS*	*F*	*p*
Site	1	11909.4	42.0	<0.01
Sample type	1	32572.9	115.0	<0.01
Site × sample type	1	4764.4	16.8	<0.01

15.5 Discussion

Based on our comparison of whole California mussel shell size measurements of surface collected versus excavated samples from two San Miguel Island archaeological sites (CA-SMI-481 and -232), we identified significant differences between the average sizes of mussels from surface versus excavated deposits. Even after controlling for sample size, our analysis suggests that a potential methodological bias is introduced if surface collected California mussel size averages are compared with subsurface size averages. At CA-SMI-481, this size difference was less than

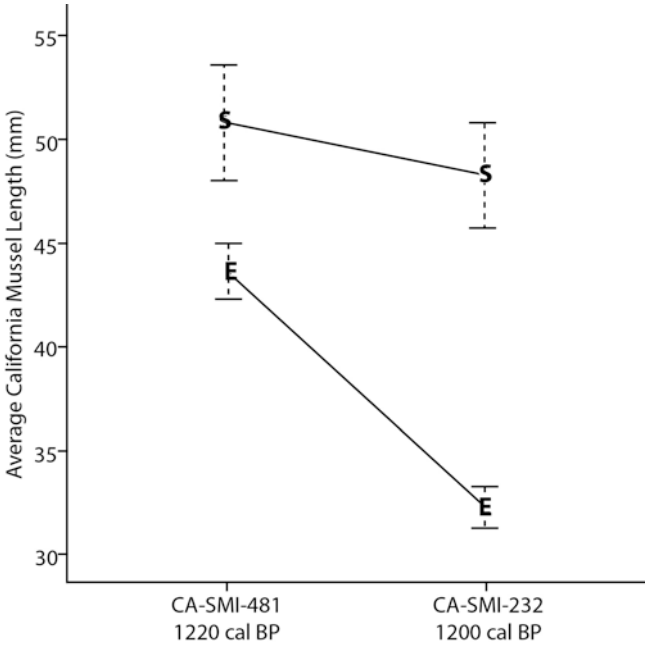

Fig. 15.4 Results from our ANOVA analysis of average California mussel length from samples collected on the surface (S) versus those from excavated (E) deposits at CA-SMI-481 and -232. Error bars represent two standard errors from the mean

1 cm and of little concern. At CA-SMI-232, however, the size difference between average mussel sizes from surface versus excavated deposits is nearly 2 cm. This suggests that, at least at some site deposits and due to differential taphonomic processes, surface shells are not an accurate reflection of average size and subsurface samples should be incorporated. CA-SMI-232 is visible in the eroding exposures of a steep arroyo wall on San Miguel's south coast (see Braje 2010, pp. 77–96). At least a half-meter of historical dune sand caps the site and the top of the deposit is sealed from the elements. California mussel shells eroding out of this deposit tend to cascade down to the gully floor, where they are washed downslope during wet seasons. The 1220 cal BP component at CA-SMI-481 caps a massive dune on San Miguel's northwestern coast. The margins of the deposit are rapidly eroding, but mussels and other shell tends to erode onto the dune surface and gently slide downslope. It may be that delicate mussel shells from the CA-SMI-232 surface tend to fragment more easily than those from CA-SMI-481 due to the positioning of the site and the unique post-depositional processes this creates. Regardless, our analysis suggests that the overall patterning through time remains consistent. There is a size reduction between CA-SMI-481 and CA-SMI-232 whether measured by surface or excavated samples. The scale of this size decline is much more dramatic, however, when consulting excavated samples.

Erlandson et al.'s (2008) study of average California mussel size over 10,000 years on San Miguel Island employed a conservative approach to look at long-term patterning and the general relationship between natural sea-surface temperature changes and human foraging impacts. Their study recognizes that mussel growth rates can be influenced by "temperature, food availability, turbidity, and other factors" and ideal studies would include age of death analysis (Erlandson et al. 2008, p. 2145). Since age of death analysis (see Bailey et al. 2008) can be problematic and introduce its own set of methodological biases, Erlandson et al. (2008) rely on *general* size patterning through time, while recognizing the potential effects of storms, ENSO events, non-human predators, disease, and other processes that can impact mussel populations (Jeradino et al. 2008). With a large sample size and an interpretation that centers on broad scale patterning across the Early, Middle, and Late Holocene, Erlandson et al.'s (2008) interpretations of long-term, island-wide declines in mean California mussel size resulting from increased human foraging pressure as human populations and territoriality increased is likely accurate, despite potential methodological pitfalls. Ideally, based on our results, trends in average mussel sizes through time would only be made by comparing surface mussels through time or excavated mussels through time, and not some combination.

While our study included only two archaeological deposits from San Miguel Island (CA-SMI-232 and -481), sample sizes were robust and should provide an accurate reflection of California mussel size patterning and potential methodological biases. Our analysis, however, only included two Late Holocene deposits from relatively large and well-preserved shell midden sites. Sites that are older, smaller, or significantly altered by natural or cultural taphonomic processes may contain mussels in differential states of preservation and at various fragmentation levels. The methods by which ancient foragers gathered, processed, or discarded mussels, as well as post-depositional processes such as trampling, crushing, and chemical weathering can all have significant effects on the preservation of whole mussel shells (e.g., Ford 1989; Muckle 1985; Nielson 1991; Stein 1992). In addition, large shell middens release carbonates from decomposing shells on midden peripheries which helps counteract soil acidity (Sanger 1981), promoting the preservation of whole mussels that can erode out onto the surface over time. While outside the scope of our study, future work might focus on the relationship between these temporal, spatial, and taphonomic factors and the average size of shellfish from surface versus subsurface deposits. Despite all this, Erlandson et al.'s (2008) focus on broad temporal scales and large sample sizes likely mitigates these potential complications.

Even considering the many ways California mussels might fragment during collection or after deposition, our analysis of average California mussel size from hinge fragments at CA-SMI-232 suggests that the reliance on whole mussel measurements from excavated samples provides an accurate estimation of mean prey size. Our sample of nearly 900 hinge measurements predicted the California mussel mean to within 0.5 cm of the mean calculated using whole shells. At well-preserved shell midden sites, then, our analysis suggests that a reliance on subsurface whole mussels to estimate average prey size through time may be adequate. In such cases, there is little need to take the added step of measuring hinge fragments and

estimating whole shell length. At sites with poor preservation and in the absence of robust samples of whole excavated mussel shells, however, hinge measurements offer an excellent proxy for whole shell measurements. Average mussel size calculated from hinge measurements can be compared against average sizes at other archaeological sites derived from excavated samples of whole shells. That is, hinge measurements and whole shell measurements from excavated deposits are comparable. Further study should confirm these findings, that hinge and whole measurements (under the appropriate conditions) are effectively equivalent when it comes to measuring mussel size. However, continued testing will be critical to validate our findings.

15.6 Conclusions

Over the last decade, zooarchaeologists have become increasingly interested in contributing insights for modern conservation and restoration. The result has been the blossoming of new interdisciplinary fields of inquiry, including applied paleozoology, conservation archaeobiology, and historical ecology (e.g., Braje and Rick 2013; Lyman 2006; Rick and Lockwood 2013; Wolverton and Lyman 2012; Wolverton et al. 2011). All of these subfields attempt to apply deep historical data, collected from such sources as archaeological and paleontological fauna, to modern conservation issues (Braje and Rick 2013; Rick and Lockwood 2013). These perspectives have become increasingly important in the management and restoration of marine ecosystems. One of the significant challenges of this type of interdisciplinary and applied research is finding opportunities and developing methodologies that integrate archaeological or deep historical datasets into modern management strategies. Shellfish size measurements from archaeological sites can provide deep historical baselines on the structure and health of near shore marine ecosystems through time.

This is especially true for New World Pacific Coast California mussels, which can be measured easily and quickly by modern intertidal ecologists and are readily found in many coastal archaeological shell middens, often adjacent to modern mussel beds. On the Northern Channel Islands, very little monitoring work on California mussels was done until relatively recently. Since California mussels have seen little commercial harvest and sport fishing pressure, compared with other shellfish such as abalones (*Haliotis* spp.) and sea urchins (*Strongylocentrotus* spp.), intensive long-term monitoring has not been a priority. In recent years, however, Channel Islands National Park (CINP) marine biologists have recognized the need for increased monitoring as anthropogenic climate change and the associated impacts have altered marine ecosystems, warmed our oceans, and introduced new threats such as ocean acidification. As part of a biyearly survey of marine resources within CINP, managers have begun to systematically collect size data for California mussel populations. While these data can be used to track future changes, they have no points of comparison and offer little information on the health and structure of contemporary mussel populations compared to those of the past.

Calculating the average prey size of California mussels from archaeological sites, then, offers an excellent opportunity to connect archaeological with modern ecological data and aid in contemporary management decisions. Average prey mussel sizes through the Holocene, compared against paleoenvironmental data such as sea-surface temperature fluctuations, can offer a set of baselines and benchmarks to help evaluate the structure and health of modern mussel beds. Our research suggests that archaeological data must be recovered, however, from one of two sources: (1) robust samples of whole mussels from excavated shell midden deposits, or (2) robust samples of mussel hinge measurements from excavated shell midden deposits. Due to varying degrees of preservation of surface samples, surface collected whole mussels cannot be reliably compared with modern mussel measurements.

The application of zooarchaeological data to modern management issues is positioned to be an increasingly important part of zooarchaeological methods as we grapple with how to best manage local, regional, and global ecosystems in the Anthropocene. It will be vital, however, for zooarchaeologists to continue to refine their methodologies and critically evaluate their methodological assumptions. In doing so, interdisciplinary research, which includes zooarchaeologists, stands to make important contributions to conservation and sustainability that integrate research agendas with policy decisions.

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Chapter 16
Concluding Remarks

Umberto Albarella

16.1 Introduction

Zooarchaeology has deep roots in the history of scientific research, but its development in the last two decades has been particularly remarkable. Its maturity is well illustrated in the first, only apparently anodyne, sentence of the editors' introduction to this volume: "As a branch of archaeology, zooarchaeology …" (Chap. 1). This is indeed what zooarchaeology very simply is: "a branch of archaeology". Although to many young researchers this may sound like a truism, those who have been around for longer will know only too well that the path to make such a statement without fear of being challenged has been long and hard. Zooarchaeology is indeed not some kind of zoology of past animals or a scientific investigation in support of archaeological research, but rather a core part of archaeology, aiming to address big questions about past humanities and their behaviors. Zooarchaeology does not study animals *per se*, but rather the *relationship* between animals and people; we study animals because we want to understand people. This does not mean that zooarchaeological research does not have overlaps with sister disciplines such as zoology or paleontology; rather, our research questions are different from those other disciplines, and are firmly rooted in archaeology. Hopefully a zooarchaeology confined to "appendices", or carried out by practitioners of other disciplines—veterinarians, anatomists, zoologists, paleontologists—who double up for the sake of helping their archaeology colleagues, represent things of the past. In this chapter I explore the way contributions to this book provide a sense of the current and future development of the discipline.

Zooarchaeology in Practice clearly and boldly endorses the concept of a *zooarchaeology as archaeology*—not only through its editorial choices and approaches but also in the style of the individual contributions. This is also confirmed by the choice

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of the term "zooarchaeology", as opposed to "archaeozoology", thus emphasizing the position of the discipline *within* archaeology.

Like in all mature disciplines there is a need for zooarchaeology to reflect periodically on its methodological approaches. The best way to do this is to let practitioners, who operate at the forefront of zooarchaeological research, share their experiences, dilemmas, questions and potential solutions. In many respects this is what this book does—provide the opportunity for researchers across the globe to write about their methodological approaches and come up with suggestions that are potentially relevant to practitioners operating in different geographic and archaeological contexts.

There are several zooarchaeology textbooks in existence. Some represent pioneering efforts (Chaplin 1971; Cornwall 1956; Ryder 1968), while others have been published in more recent years (Beisaw 2013; Davis 1987; O'Connor 2000; Reitz and Wing 1999). They represent an important body of reference for students and professionals alike. Their diversity is a bonus, as it allows us to get an idea of the many different perspectives that can be adopted in the analysis of faunal remains from archaeological sites. *Zooarchaeology in Practice* hardly overlaps with such literature. It shares with it a methodological approach, but it is here multi-vocal, without aiming for full methodological coverage. As such it is an important and valuable addition to current zooarchaeological literature—it has its unique place in the history of the discipline. Many collections of zooarchaeology articles have been published in the past, but these have tended to focus on specific themes or geographic areas, rather than providing an *excursus* of methodological approaches. The very recently published Oxford Handbook of Zooarchaeology (Albarella et al. 2017) provides an overview of world zooarchaeology, but in that case too, the focus is not methodological.

Another consideration should help us to realize the value of this effort. As the editors mention in their Introduction, universal analytical solutions are generally not feasible. The world of zooarchaeology has debated this for several decades and it delights me that the most sensible approach has finally prevailed—the concept of "minimum standards" is not helpful and we should rather cherish the ingenuity of researchers in adopting different approaches to solve zooarchaeological issues of a most diverse nature. This means that the future of methodological research in zooarchaeology does not lay in the production of fully comprehensive manuals that propose "one size fits all" solutions, but rather in publications such as the present one, which provide thoughtful considerations of some specific aspects of our methods. These can be of interest regardless of the nature of the assemblages that are being studied and represent a far cry from the imposition of methodological standards, which run the risk of curtailing the creativity of our research approaches. This issue is elaborated in particular in the chapter by LeFebvre and Sharpe (Chap. 3) who, though at some point pleading for some form of standardization, eventually conclude that flexibility is the best possible approach to the study of zooarchaeological assemblages. Judging from the content of her chapter, the other editor (Giovas (Chap. 4)) clearly agrees.

As I mentioned, an effort of this nature cannot realistically aim for completeness and will inevitably be biased in its coverage. Such bias is interesting to explore, as it may provide an insight into the current more urgent concerns in zooarchaeology. I will therefore now dedicate some time to explore what the book includes—and, as a consequence, what it does not.

Since zooarchaeology deals with "faunal remains" it can reasonably be expected that any animals should be the subject of its investigations. Strictly speaking, this is indeed the case but it is obvious that in archaeology some animal groups have a much greater profile than others—because of their visibility, preservation, and potential in answering research questions that are archaeologically relevant. Taxonomic groups that are largely made of soft tissues will rarely survive in archaeological sites and are therefore generally not within the radar of the zooarchaeologist. For instance, species of phyla such as Annelida (earth-worms and the like), Nematoda (round worms) and Platyhelminthes (flat worms), though potentially interesting, are only occasionally studied in archaeology. It is, however, important to bear in mind that bones and teeth (i.e., the remains of vertebrates) are not the only animal remains of interest for archaeological investigations—invertebrates can play an important role too. Like in many other zooarchaeology books, vertebrate studies have the lion share of *Zooarchaeology in Practice*, though two chapters (Jerardino (Chap. 8) and West et al. (Chap. 10)) are exclusively dedicated to molluscs. Among vertebrates, mammals feature in most chapters, birds in a few (Matisoo-Smith in particular (Chap. 11)), one chapter is entirely dedicated to fishes (Giovas), while amphibians and reptiles are barely mentioned.

This distribution of interest is fairly typical and does reflect reasonably accurately the main materials studied by zooarchaeologists today. A large part of zooarchaeology is indeed focused on vertebrates. Among invertebrates, studies of molluscs—particularly marine—are those that are most likely to feature alongside animal bones and teeth. Shells are made of hard tissues and, although their histological composition is different, have preservation patterns that are similar to those of skeletal and dental remains. Also many of the research questions associated with malacological remains are similar to those applicable to vertebrate remains, such as diet, economy, craft, and rituals. Crustacean carapaces can play a similar role but are less commonly found. Other invertebrates that are also very important for archaeological investigations, such as land snails and insects, tend to be less commonly associated with the rest of zooarchaeology and their potential is mainly in paleoenvironmental studies. Their average size is such that they require rather different analytical approaches. Thus the combination of mollusc and various vertebrate categories featured in this book reflects faithfully current priorities in zooarchaeology.

Regardless of the discussed material, this book is, however, first and foremost about methods. I will later elaborate more on the discussion of specific methodological approaches, but here I will report briefly on coverage. Most key zooarchaeological methods are mentioned and, in some cases, discussed in depth, though aging, sexing, butchery, and paleopathologies only manage to get cursory references in a couple of chapters. On these topics there is, however, ample literature available elsewhere (Baker and Brothwell 1980; Bartosiewicz and Gál 2013; Binford 1981;

Ruscillo 2006; Wilson et al. 1982). Taphonomic analysis features strongly, with several chapters partly or entirely dedicated to it (Rainsford and O'Connor (Chap. 5); Faith and Thompson (Chap. 6); Fisher (Chap. 7); Jerardino; MacKinnon (Chap. 14); Braje et al. (Chap. 15)). That old conundrum and fiercely debated subject in zooarchaeology—quantification—is the main theme of chapters by Lyman (Chap. 2) and Giovas and also features in Fisher's. The subject had gone rather quiet in the last few years and it is good to see it making a return. As Lyman says, "although we might believe that there is little left to learn about zooarchaeological quantification, this is far from true". Other topics include: identification (LeFebvre and Sharpe—a chapter that also ventures into epistemology); body part distribution (Faith and Thompson); sample size (Crabtree (Chap. 9)); scale of analysis (Jones (Chap. 13)); biometry (MacKinnon; Braje et al.); seasonality and paleoenvironments (West et al.); and inter-disciplinarity (MacKinnon). Bio- and geo-chemical applications are discussed by West et al. (isotopes—a subject also touched upon by MacKinnon), Matisoo-Smith (DNA) and Buckley (proteins (Chap. 12)).

Though coverage is therefore inevitably punctuated, there is a wide and impressive range of zooarchaeological methods discussed, with most papers heavily reliant on one or more case studies. Lyman and LeFebvre and Sharpe's chapters are slightly different in dealing more with theoretical considerations and less with practical examples.

It is possible to link the discussed topics, as well as the adopted approaches, with national and regional traditions. It is therefore worth pondering a little on the geographic origins of the contributors. First of all we must emphasize that the book is highly international, and that in no way it may be taken as representing just one single research tradition. In term of authors' addresses at the time of writing, the following countries are represented: Australia, New Zealand, UK, Canada, US, Panama and South Africa. Even the editorial team represents an inter-continental collaboration! Nevertheless, it is also worth pointing out that, with one exception, all contributors originate from English-speaking countries. This bias is not surprising when one considers that the book stems from a session of the Society for American Archaeology (SAA) conference, which, though highly international, is not so likely to attract researchers from outside the Americas and the English-speaking world. In evaluating the range of methodological approaches on display in the book, it is therefore necessary to bear in mind that some scholarly traditions are unrepresented.

The worldwide coverage of the book becomes, however, even more impressive when one considers the different archaeologies that are featured in the case studies that are on display. All five continents are represented with faunal assemblages deriving from locations as diverse as Grenada, US, Canada, New Zealand, South Africa, Iran, Britain, Russia, Greece and Turkey. Such range gives us also the opportunity to reflect on the fact that research traditions are not only dependent on the place of origin of individual scholars and their mentoring legacies but also on the geographic focus of their research. It can even be suggested that the latter plays the greatest role. For instance, I would argue that the approach of MacKinnon and Crabtree—North Americans working in the Old World—is fairly typically "European". Conversely the approach of Lyman and Fischer, US-based researchers

investigating American archaeology, appears to be rooted in the North American tradition (e.g., compare their approach to taphonomy with that of UK-based Rainsford and O'Connor, who investigate a British site).

16.2 Taphonomy

One of the big questions regarding taphonomic analysis in archaeology concerns the extent to which its aim is limited to assessing bias in faunal assemblages (an important enough purpose!) or is also intended to provide independent archaeological evidence. To be more precise, the dilemma only applies to post-depositional taphonomy (diagenesis; see Efremov 1940) rather than to the preceding events (biostratinomy), for which there can be no doubt about their usefulness in reconstructing human behavior.

Rainsford and O'Connor are most definitely in the latter camp and, in fact, they go even further by suggesting that taphonomic information represents the most important contribution that faunal assemblages can provide in the urban context. Personally, I believe that this takes the point too far, but I have to admit that they build a very solid argument in defense of the value of taphonomic analysis. The potential for faunal material to help in reconstructing depositional processes and stratigraphic relations is definitely underestimated. One aspect that remains slightly ambiguous in their otherwise very lucid analysis is the distinction between "redeposition" and "residuality", which has caused so much confusion in the zooarchaeological literature (Albarella 2016), particularly that associated with urban contexts.

Although the chapter includes an excellent discussion of sample bias, the effect of differential recovery—arguably the largest bias that affects faunal assemblages—is barely mentioned. The subject is, however, picked up later in the volume by LeFebvre and Sharpe, Fischer and, particularly, Giovas and MacKinnon. I still believe, however, that after so many years of discussion of the issue, the importance of implementing appropriate sieving programs has not been sufficiently elaborated in zooarchaeology. As often is the case, the reasons are complex and difficult to unpack, but there is a definite need to expose students more to the issue. This should happen both in fieldwork training and at the stage of data interpretation.

The effect of taphonomic biases for our interpretation of the zooarchaeological evidence is the core subject of the chapters by Faith and Thompson and Fisher. The former effectively connect that to recording strategies, highlighting how what we record will affect what biases influence our data. They do not go, however, far enough to suggest the adoption of a "diagnostic zone" system (Watson 1979), which would have been the logical consequence of their results. They do recommend, however, a focus on high-survival elements.

Jerardino's chapter deals with a different taphonomic aspect, and a highly problematic one—fragmentation. The focus is on molluscs and it attempts to propose an efficient and time-effective way to establish fragmentation patterns. I can see the

parallel with vertebrate remains and I liked the approach very much. I also found the comparison between left and right valves to assess the solidity of the method to be ingenious.

16.3 Quantification

Despite a plethora of publications on the subject produced between the '70s and the 90s', quantification, and the measures on which it relies (recording and counting), remain some of the most misunderstood and problematic areas in zooarchaeology. Though researchers have carried on publishing on the subject, this appears to have somewhat dried up, not because the topic had been exhausted, but rather because it seemed to have reached a dead end. It would require an essay specifically dedicated to the problem to discuss why that has been the case, but here it will suffice to say that it is positive to see a resurgence of the subject with two papers specifically dedicated to it (Lyman and Giovas) and several others making reference to it. In his assessment of the value of the minimum number of individuals (MNI), Lyman takes a historical perspective, which I found very helpful. He emphasizes the point, with which I wholeheartedly agree, that, to make progress, we must be aware of the history of research. Not to do so will lead us to repeat the same processes and, often, the same errors of past researchers. We must be respectful of the research tradition. This is a point that applies to any aspect of research but it is particularly relevant to quantification issues, which can count on a highly complex body of published material.

Another valuable point that emerges from Lyman's paper is the consideration that the appropriateness of different quantification systems will depend on the nature of the assemblage. This represents another reminder that it is unhealthy to have rigid rules about zooarchaeological methods and that these need to be adapted to circumstances. On the specifics of the MNI, Lyman reminds us that, as Grayson (1984) and others before him had pointed out, the method is affected by the issue of "aggregation". Basically the value of the MNI will vary according to the way different parts of the assemblage will be "aggregated". For instance, according to whether the MNI is calculated separately for three different areas of a site and the numbers then added up, or the calculation is based on the combined assemblage from the three areas, the results will be different. This issue has been considered to be so serious by some researchers that it has led them to conclude that the MNI is an invalid system of quantification. This has always puzzled me, as I would be inclined to see the issue of aggregation as an *opportunity* rather than a *problem*. By calculating the MNI in different ways we gain an insight into the factors that led to certain results and the different values also allow us to estimate the robustness of our evidence. The greater the difference in MNI between two aggregation methods, the more we need to be wary of taking the results at face value. I suspect that the reason why I have this more positive interpretation of the aggregation issue is because, unlike some

other researchers, I see the MNI as a statistical measure that helps us in assessing relative proportions of taxa, rather than a way to get as close as possible to the actual number of animals present on site.

Giovas' chapter, focused on fish bones, explores a rather different theme. A selective recording system traditionally used in New Zealander ichthyoarchaeology (Leach 1986) is compared with a more comprehensive system of recording, including a greater diversity of anatomical elements. The main value of Giovas' contribution is in my view the emphasis on the importance of being explicit about what is being recorded. Our choices clearly influence our results and will affect the way taphonomic factors act on them. In that respect Giovas' chapter shares a common theme with Faith and Thompson's contribution. Personally, I would be very wary to conclude that an "all fragments" approach is better than a selective one—my interpretation would rather be that Leach's system is too selective and a wider range of "zones" should be considered. To move towards a system in which any unspecified fragments are recorded would take us back to the "wilderness" of not having any clear control or clarity of what is exactly being recorded.

16.4 Identification

Identifying body parts and taxa is generally the first and most fundamental job of the zooarchaeologist; yet, beyond identification manuals, the subject is surprisingly little discussed in the literature. The theoretical reflection on the issue as provided by the chapter by LeFebvre and Sharpe is therefore most welcome. There are many important considerations raised in this paper, which would take too long to sum up. Among those, the point that identification will substantially vary according to the level of experience of the analyst is particularly important. Endless other factors can, of course, affect accuracy and detail in identifications, which fortifies further the point made above about being transparent about what is being recorded. Identification variability also leads the two authors to stress the importance of reanalyzing studied assemblages. The point here is not so much the verification of previous identifications, but the acceptance that identification inevitably represents a fluid process which requires constant re-assessment. Animal bone assemblages must be retained; like books in a library, they represent archives to which we should regularly return to in order to extract additional information. To claim to have analyzed an assemblage fully comprehensively represents nothing more than a self-delusional chimera.

Linked to the identification issue is Buckley's chapter. His ZooMS' technique provides a valuable additional tool to verify taxonomic identifications, without the often exorbitant costs of DNA analysis.

16.5 Biometry

Using a rather "Old World" approach, Michael MacKinnon has for many years demonstrated the value of biometrical analysis for our understanding of the human-animal relationship in the classical world (e.g., MacKinnon 2001, 2010). He provides further valuable examples in this book. He also shows how biometry—far from being a biological application of little archaeological relevance—can in fact be integrated with other sources of evidence, such as iconography and ancient texts. Inter-disciplinarity has been the hallmark of his work in the ancient Mediterranean, a lesson from which we can all learn. The need for inter-disciplinarity is also strongly emphasized by West et al.

Dealing with molluscs, Braje et al.'s is the chapter most specifically focused on biometry. They demonstrate how biometry is closely related to other areas of zooarchaeological investigation, for instance suggesting that mussel size is, to some extent, the product of taphonomic factors. Another interesting aspect of their work is the connection that is made with modern specimens and conservation issues. They show how zooarchaeology can help us in the understanding of contemporary environmental concerns, following a tradition that has become more firmly established in the last few years (Lyman 1996; Lyman and Cannon 2004; Wolverton et al. 2016).

16.6 Sample Size and Scale of Analysis

In her chapter Pam Crabtree mounts a highly persuasive defense of traditional zooarchaeology and laments the scarcity of opportunities that today exist in analyzing very large assemblages. She stresses the importance of building large data sets from individual sites and explains the invaluable degree of evidence that they can provide. I am prepared to admit academic bias—this is music to my ears. A lot of zooarchaeology nowadays relies on small sample sizes, which tend to be rather hazardously interpreted. This issue notoriously also affects many of the bioarchaeological and isotopic applications, as also pointed out by West et al. Intensive, high-resolution analyses of large assemblages are necessary—despite the labor and cost involved. Crabtree is also rightly concerned with the educational drawbacks of not providing students with the opportunity to experience the analysis of large dataset. One point on which she does not, however, elaborate is that the dearth of large assemblages is also the consequence of current excavation strategies; rescue excavations are reduced to the bare minimum on the basis of the other highly delusional concept of "preservation *in situ*". Such "preserved" sites only stand a highly remote chance to be ever excavated, and contiguous disturbance often leads to their deterioration anyway. Increasingly limited funding opportunities also reduce the opportunity for large-scale research excavations.

I would argue that the archaeological literature is becoming inflated with insufficiently significant bodies of evidence also as a consequence of the pressure to publish, often before time. Even within a highly specialized subject such as zooarchaeology the amount of published literature is becoming unwieldy. Although on the one hand we should be happy with such intensity of research activity, on the other it is clear that a lot sub-standard work is published ahead of time, even in prominent journals. We should publish less, but more accurately, and using larger bodies of data.

One way to ease the problem of small sample sizes is to approach zooarchaeological analysis using large scale analysis, as in Jones' chapter. Large and not so large dataset can be combined or, better, compared, to identify regional patterns. This is a very important part of our work and it is essential that we carry it out in the awareness of its potential pitfalls. An important point made by Jones is that the degree of precision of our interpretations must be proportionate to the confidence we have in the data. This will apply to the degree of chronological resolution as well as the size of our datasets. In other words, we must be careful not to over-interpret our evidence. Regional analysis is, however, an essential part of our work. It provides a framework for the interpretation of individual sites and it is, at the same time, fed by such smaller scale analyses. In zooarchaeology there is a constant interplay between researches carried out at different scales (see, for example, Otaola et al. 2015), and it is important to be aware that biases at the level of the individual site will be mitigated but not neutralized by the large scale; however, outliers can be more easily identified when a regional pattern is reconstructed.

16.7 Biomolecular and Isotopic Applications

Biomolecular and isotopic applications have been providing us with a valuable new body of evidence, which would have been unthinkable only a couple of decades ago. Many challenges remain—those of a technical nature are gradually being resolved, while the more intellectual ones are proving trickier to overcome. Principal among the current concern is the need of a greater understanding of the biological, anthropological and archaeological contexts, which can only be achieved through close collaboration between isotopic specialists and molecular biologists with archaeologists. It is thus heartening to see that the importance of such close collaboration is clearly made by Matisoo-Smith in her DNA chapter. I was also pleased to see that the expression "scientific rigor" manages to creep in her paper—a clear acknowledgement of the need for biomolecular research to check carefully the reliability of its results and interpretations. It really is an excellent contribution, which gives us hope of a brighter future for the application of biomolecular applications to (zoo)archaeological questions.

Matisoo-Smith also explains that DNA specialists have a special responsibility as concerns the rigor of their research because their analysis is destructive. It is a good point (which applies to archaeological excavations too) to which we should

add that a further problem is that the publication of evidence that is based on shaky foundations slows down the pace of genuine progress in scientific research.

The need for better integration is clearly seen also in Buckley's chapter, outlining the opportunities of protein analysis for taxonomic identifications. His ZooMS method, developed in York with Matthew Collins and others (e.g., Buckley et al. 2010), is providing zooarchaeologists with an excellent new tool for the verification of taxonomic identifications. It is, however, important to apply it sensibly, as stated by Buckley himself. The aim of zooarchaeology is not to identify as many fragments as possible from a faunal assemblage. This is useless at the best, and misleading at the worst. A much more valuable way to use ZooMS is to work alongside zooarchaeologists in establishing good identification criteria based on morphometry and then verify them through biomolecules. Additionally, ZooMS, particularly when it will become more developed in discriminating between rarer taxa, has the potential to resolve the issue of "mystery specimens" that are singled out for their importance but are hard to identify with certainly on the basis of their morphologies.

An important additional message that we can take away from West et al.'s chapter is that isotopic analysis—as well as many other zooarchaeological applications, including genetics—does require verification with modern samples of known origins. This kind of calibration of our results should be of constant concern for zooarchaeologists. Analogy with modern animals carries its own risks, but this can be assessed and it should not discourage us from monitoring our methods through regular observation of current living conditions.

16.8 Summing Up

Zooarchaeology in Practice contributes substantially to the current development of zooarchaeology as a vibrant and informative branch of archaeology. The book has the right balance of innovation and tradition—new directions are indicated, but without forgetting the foundations generated by decades of past research. A survey of different methods represents an overdue output in zooarchaeological literature and one that is likely to lay the foundations for similar reflections in the near future. The success of the book is in no small part due to the skill of the editors, who have masterfully orchestrated its production. The refreshing style of the book goes hand in hand with their own research approach, which is at the cutting edge of the discipline. This is amply demonstrated by Giovas' and LeFebvre's contributions to the volume, which are both hugely stimulating.

The relationship between humans and animals has many facets, which never fail to surprise and amaze us. Our ability to understand it for the past has inevitable limitations and requires rigor of approach as well as constant re-evaluation of the analytical tools available to us. It is only through a constant reassessment of the way we investigate the archaeological evidence that we can hope to understand what linked human and animal lives in the past. There are many wonderful stories to be told, but not all of them are genuine. It is our role as scientists to be able to discriminate between fiction and reality. This book provides useful leads for that ambition to be fulfilled.

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