

Paleoethnobiology

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Abstract Ethnobiology is broadly defined as the study of human-environmental interactions in various times and places, covering such topics as traditional and local ecological knowledge, cognition and language, plant and animal taxonomy, and medicinal uses of plant and animal tissues, but also topics that relate to environmental archaeology. It is these types of topics, such as studies of past subsistence systems, material culture made from plant and animal products, as well as interactions of people with ancient environments, that are the subject matter of paleoethnobiology. In this chapter, we summarize various types of paleoethnobiology from zooarchaeology to archaeobotany to archaeological residue chemistry, and we discuss issues of data quality, taphonomy, and related research problems in the field.

Introduction

Paleoethnobiology is the study of human-biota interactions through analysis of faunal and floral remains from archaeological and paleobiological contexts. Paleoethnobiological research plays the important role of adding an empirical record of time depth to ethnobiology, which examines human-environment relationships within cultures and compares these interactions cross-culturally. The framework of paleoethnobiological research centers on two primary research questions: (1) what types of plants and animals were incorporated into past diets through foraging, pastoralism, or gardening? And (2) what were paleoenvironments like that people interacted with in the past? The two questions are interwoven,

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Fig. 1 Avian bone whistles from Ponsipa'akeri (LA 297), an Ancient Pueblo village in New Mexico, that illustrate the confluence of subsistence behaviors and the past environment from which these specimens were foraged. The whistles are manufactured from limb bones of a large bird, probably turkey (*Meleagris gallopavo*), which may have been hunted from wild populations or raised in captivity. Turkeys were hunted or raised for food but have also provided feathers. Bone whistles might have been used as turkey calls



as archaeobotanical and zooarchaeological remains (whether macroscopic, microscopic, or molecular) represent past human subsistence behaviors and the paleoenvironments from which biota was foraged or produced (Fig. 1). The subfields of paleoethnobiology generally overlap with those of environmental archaeology, historical ecology, and paleobiology. An important distinction is that paleoethnobiologists focus on human-biota interactions across space and time, whereas mainstream archaeological research emphasizes past human behaviors and paleobiological research does not focus on human interactions.

Types of Paleoethnobiology

In this chapter, we organize paleoethnobiology into three different subfields: paleoethnobotany, zooarchaeology, and archaeological chemistry (Table 1). Floral, faunal, and biomolecular-residue remains are identified and analyzed in a variety of ways because

Table 1 Types of paleoethnobiological remains and residues

| Zooarchaeology | Paleoethnobotany | Archaeological chemistry |
|----------------|-----------------------|--------------------------|
| Bone | <i>Macrobotanical</i> | Ancient DNA |
| Teeth | Wood and charcoal | Fatty acids and lipids |
| Horn | Seeds | Alkaloids |
| Antler | Nuts | Proteins |
| Shell | Fibers | Stable isotopes |
| Rock art | Rock art | |
| | <i>Microbotanical</i> | |
| | Pollen | |
| | Phytoliths | |
| | Starches | |

each type of animal remain, plant remain, or molecular residue preserves and is recovered in distinctive ways. In this brief summary, we do not describe the different approaches for each type of analysis; rather, we focus on general challenges that are shared across them. For recent summaries of the fundamentals of paleoethnobotany, see research by Adams and Smith (2011) and Pearsall and Hastorf (2011); for brief primers on zooarchaeology, see Lyman (2005) and Stahl (2011). For a compilation of important ecological papers in zooarchaeology, see Broughton and Cannon (2010). There are several useful volumes that introduce archaeological chemistry of biomolecular residues; a recent one is by Brown and Brown (2011). See Barbarena (2014) for a clear introduction to stable isotope analysis in environmental archaeology. Although research approaches vary within the types of paleoethnobiology, there are shared concerns of data quality, taphonomy, and quantification. In addition, all three areas of paleoethnobiology are increasingly important in applied ecological research, from conservation biology to ecological restoration.

Data Quality

All paleoethnobiological analyses relate closely to particular research questions. The “target population” represents what the researcher seeks to understand about past human-environment interactions (Lyman 2008). For example, if one wants to understand differences in local vegetation and animal paleobiogeography to assess past landscape change, then in many cases flora or fauna may need to be identified to species, which can be difficult with paleoethnobiological remains that may or may not be well preserved. Different species with similar morphology may prefer distinctive habitats; thus, the reliability of conclusions depends on the confidence with which the analyst can make identifications. The paleoethnobiologist, however, does not work directly with target populations and instead works with samples recovered from archaeological or paleobiological contexts. These assemblages of remains are not randomly designed samples of past biological populations, ecological communities, or human behaviors. Instead, they are fortuitous samples recovered during field surveys and excavation. Thus, the validity of paleoethnobiological analysis depends on answering two important questions: (1) how confident is the

| | |
|--|----------------------------------|
| P08535 HBB_LEPEU (100%), 16,062.0 Da | |
| Hemoglobin subunit beta OS=Lepus europaeus GN=HBB PE=1 SV=2 | |
| 2 unique peptides, 2 unique spectra, 2 total spectra, 22/147 amino acids (15% coverage) | |
| MVHLSGEEKS | AVTALWGKVNVEEVGGETLGRLLLVVYPWTQ |
| RFFESFGDLS | TASAVMGNPKVKAHGKKVLA AFSEGLSHLD |
| NLKGTFAKLS | ELHCDKLHVD PENFRLLGNV LVIVLSHHFG |
| KEFTPQVQAA | YQKVVAGVAN ALAHKYH |
| P08535 HBB_LEPEU (100%), 16,062.0 Da | |
| Hemoglobin subunit beta OS=Lepus europaeus GN=HBB PE=1 SV=2 | |
| 3 unique peptides, 4 unique spectra, 4 total spectra, 39/147 amino acids (27% coverage) | |
| MVHLSGEEKS | AVTALWGKVNVEEVGGETLGRLLLVVYPWTQ |
| RFFESFGDLS | TASAVMGNPKVKAHGKKVLA AFSEGLSHLD |
| NLKGTFAKLS | ELHCDKLHVD PENFRLLGNV LVIVLSHHFG |
| KEFTPQVQAA | YQKVVAGVAN ALAHKYH |
| P08535 HBB_LEPEU (100%), 16,062.0 Da | |
| Hemoglobin subunit beta OS=Lepus europaeus GN=HBB PE=1 SV=2 | |
| 2 unique peptides, 2 unique spectra, 2 total spectra, 29/147 amino acids (20% coverage) | |
| MVHLSGEEKS | AVTALWGKVNVEEVGGETLGRLLLVVYPWTQ |
| RFFESFGDLS | TASAVMGNPKVKAHGKKVLA AFSEGLSHLD |
| NLKGTFAKLS | ELHCDKLHVD PENFRLLGNV LVIVLSHHFG |
| KEFTPQVQAA | YQKVVAGVAN ALAHKYH |

Fig. 2 We analyzed proteins in ca. 800-year-old archaeological long bones from the Goodman Point complex in Southwestern Colorado, USA, using liquid chromatography-mass spectrometry (Barker et al. 2015). Three lagomorph samples (*above*) yielded hemoglobin, a blood protein that was identified as originating from the European hare, *Lepus europaeus*. The amino acid sequence of hemoglobin is listed for each of three samples, with identified peptides highlighted in yellow. Taxonomic confusion was generated by species homology and a lack of reference species (e.g., *Lepus californicus*) in commonly available databases. One peptide (VNVEEVGGETLGR) was recovered in all three samples and thus may be an ideal candidate for more sensitive, targeted methods. The green-highlighted valine (V) in the third sample was chemically modified (acetylation), presumably via long-term weathering and/or extraction and processing techniques in the lab, making identification more difficult. These data illustrate several of the current challenges in archaeological protein analysis

analyst in the taxonomic identifications? (2) How representative of past populations, communities, and behaviors do remains appear to be given preservation, sample size, and recovery context (returned to below under “Taphonomy”)?

Identification of archaeobotanical, zooarchaeological, and molecular-residue remains follows the same basic principles. State-of-the-art identification procedures in each of the three areas require a reference collection or database of known contemporary or historically documented specimens. For example, the paleoethnobotanist will have large reference collections of wood samples, pollen, seeds, nuts, phytoliths, and other types of plant tissues for species that are common in their region of study. The zooarchaeologist will assemble a reference collection of skeletons of species in her/his region of study. Many paleoethnobiologists rely on large natural history collections at universities and museums. Similarly, the archaeological chemist relies on large databases that record molecular structures of known examples of compounds that derive from plant and animal tissues, whether these are fatty acids, proteins (Fig. 2), or other types of residues. A constant challenge in

laboratory analysis is the degree to which molecular structure or tissue morphology is conserved in terms of evolutionary biology (homology) across similar species. Thus, an important area for growth in paleoethnobiology is not only the construction and maintenance of reference collections but also the probabilistic assessment of molecular and morphological characters for determining whether or not closely related species or genera can be identified (Wolverton 2013).

Taphonomy

Taphonomy is the study of the transition of organic matter from the biosphere (the living world) to the lithosphere (the geological world). Taphonomic research within paleoethnobiology has been developed most within zooarchaeology, in which studies have been done to determine processes and agents that modify skeletal remains in various settings over time (Lyman 1994). Taphonomic processes that influence bone include weathering, carnivore gnawing, processing of bone for within-bone nutrients by people, soil chemistry, and other factors that modify or destroy bone. Most taphonomic research within zooarchaeology has focused on vertebrate remains, and there has been limited work on invertebrate remains (Wolverton et al. 2010). Taphonomic research in paleoethnobotany is considerably less synthetic (compared to Lyman's 1994 volume) and tends to focus on attempting to find ways to improve analysis for purposes of reconstructing paleoenvironments and past cultures, though studies also focus on preservation, identifiability, and sampling (see a recent review by Collinson 2011). For a recent compilation of paleobotanical taphonomic studies, see the special issue in *Palaios* by Ferguson (2012). Much of taphonomic research in zooarchaeology and paleontology concerns recording the taphonomic history of remains from a particular context to address whether or not those remains can serve as an adequate sample for addressing specific research questions. For example, one might wish to determine if butchery patterns of Great Plains bison (*Bison bison*) changed over time; in order to interpret any observed changes in frequencies of skeletal parts as indicative of human butchering behavior, the analyst must first determine that differential preservation from other nonhuman processes did not influence the tallies (see examples in Lyman 1994). Very limited research has been done on the taphonomy of molecular residues in archaeological chemistry, which remains an important avenue for future research (e.g., the effects of weathering, cooking, digestion, or other processes on bioresidue preservation). In summary, there are at least two perspectives on the role of taphonomy in paleoethnobiological research: (1) that taphonomic research can aid the researcher in removing biases from samples or (2) that taphonomic effects should be considered as working hypotheses to explain observed patterns in paleoethnobiological data. Given the contingencies of paleoethnobiological sampling (e.g., paleoethnobiologists do not directly or randomly sample target populations of plants and animals by design), the second perspective may prove the most fruitful for future research.

Quantification

The quantitative revolution in archaeology embedded in the new archaeology of the 1960s and 1970s led to increased application of statistical approaches (e.g., Binford 1964; Clarke 1968). However, regarding zooarchaeological remains, Grayson (1979, 1984) illustrated that quantitative data of taxonomic and skeletal part abundance (tallies of bone, shell, antler, or horn specimens) are at best ordinal scale (see a detailed summary by Lyman 2008). Grayson's logic extends to paleoethnobotanical remains, and what he meant is that differences in abundance of, say, pollen grains in a stratum of a core between one taxon of plant and another may suggest that one type of plant was *more* or *less* abundant than another. However, the magnitude of difference in abundance is unknown. Despite twice as much pollen from one taxon compared to another, it should not be concluded that the former was twice as abundant as the latter on the past landscape. This logic extends to many types of paleoethnobiological quantitative data (e.g., tallies of zooarchaeological, archaeobotanical, and paleobotanical remains as well as biomolecular residues), and it stems from a fundamental problem with paleoethnobiological sampling. Inferential statistical approaches are designed to be applied when sampling error is known to be randomly generated, which can be controlled through sampling design when drawing specimens directly from the target population of interest (e.g., an animal or plant population). However, paleoethnobiological populations are never sampled directly or randomly and are subject to diverse taphonomic histories. Thus, statistical approaches should be adopted with caution, making as few assumptions as possible. A conservative approach is to use only descriptive statistical approaches; a more liberal approach is to use robust, resistant, inferential tests, such as nonparametric statistics. The most liberal approach is to use powerful parametric tests, which, if Grayson's recommendation is heeded, should be avoided (Wolverton et al. 2014).

Applied Paleoethnobiology

Within the last two decades, paleoethnobiologists have contributed to scholarship in conservation biology and restoration ecology. Formal research contributions have been made in both applied zooarchaeology (e.g., Wolverton and Lyman 2012) and applied paleoethnobiology (e.g., Lepofsky et al. 2003), and the potential for conservation research through analysis of biomolecular residues in archaeological chemistry is recognized (Barker 2011). Paleoethnobiology contributes a perspective of disclosure to conservation research (see Borgmann 2000); such a perspective is one that shifts the scale of understanding. For example, conservation science aims to support a mission of sustainability, which entails use of natural resources today at a rate that ensures future generations of people the same opportunity. Sustainability explicitly concerns a temporal consideration of human-environment interactions. However, contemporary people live their daily lives at much shorter

time scales through economic, social, and political activities. Paleoethnobiology provides an empirical data source with which to study human-environment interactions over deep time.

Conclusion

Paleoethnobiologists are in a unique position to address issues of sustainability and improve understanding of human impacts on the environment at broad, temporal, and biological scales. Such a perspective is increasingly important as human impacts on the environment reach unprecedented levels. Not only can we more fully understand the past with paleoethnobiological data, but with the continued attention to issues regarding data quality, taphonomy, and quantification, we can better anticipate future challenges that may result from the behaviors of modern societies.

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