

Data Quality in Zooarchaeological Faunal Identification

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Abstract There is no standard for reporting faunal identifications in zooarchaeology. Zooarchaeologists are open to accusations that reported conclusions are invalid. Other sciences counter such problems through use of quality assurance, consisting of quality control (QC), and assessment (QA). QC is a standard for procedures adopted during laboratory practice. A rarely cited standard was published by Driver in 1992. QA focuses on criteria for faunal identification and is becoming more common in zooarchaeology. QC and QA must be integral parts of zooarchaeology if identifications are to be accepted. The stakes are high because paleobiological datasets are now used to study problems in conservation science.

Keywords Zooarchaeology · Faunal identification · Quality assurance · Quality control · Quality assessment

Introduction

In zooarchaeology, validity or lack thereof potentially besets the most basic research process, namely bone, tooth, and shell identification. In a critical examination of faunal analysis method and reporting, Gobalet (2001, p. 377) states that “the reader [of most zooarchaeological studies] has no basis for knowing who made the identifications or the criteria for the identifications.” Thus, he notes that most faunal identifications “must be taken on faith” (see Butler and Lyman 1996). Researchers in other scientific fields strengthen claims based on laboratory research through use of systematized procedures. There are no broadly accepted discipline-wide standards for zooarchaeological lab work. Zooarchaeologists must overcome this flaw in the faunal identification approach if we are to overcome “serious concerns about the accuracy of identifications because of the lack of replicability” (Gobalet 2001, p. 378).

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Lyman (2008 p. 11–13) wrote about the general concept of validity using the concepts of target variable and measured variable in his book *Quantitative Paleozoology*. A target variable is “the variable one is interested in and seeks to measure or estimate” (Lyman 2008, p. 311), such as the kinds of animals people hunted in the past. A measured variable is what is actually measured, and Lyman (2008, p. 11) asks “are the two variables [measured and target] sufficiently strongly correlated that measuring one measures something about the other?” If one is not measuring what one thinks, there is a problem of validity because causal relationships cannot be inferred. Thus, the general concept of validity is perhaps most easily understood through answering the classic question “are we measuring what we think we are?” (Kerlinger 1964, pp. 444–445; see Lyman [2008, p. 12] for discussion related to zooarchaeology). The development of standardized approaches such that reliable interpretations can be made from data is important for all areas of archaeology (e.g., Thomas 1978; Dunnell 1982; Binford 1986; Clarkson 2002; Andrefsky 2005, p. 86; Barker *et al.* 2012), but here, the focus is on zooarchaeology (though the implications of this paper easily extend into paleobiology [see Lyman 2011a]).

In this paper, I discuss two types of validity and their relevance to faunal identification in zooarchaeology; I then introduce the concept of quality assurance and its two constituent parts, quality control and quality assessment. This is followed by discussion of a standard for faunal identification published in 1992 by Driver, which dovetails into consideration of the types of practices zooarchaeologists use and should use to ensure validity of zooarchaeological data.

Validity and Faunal Identification

The most basic forms of validity concern generation of data, and other kinds of validity concern statistical inference, theory construction, and argumentation by generalization (Calder *et al.* 1982; Winter 2000). Descriptive and internal validity are basic forms that are particularly relevant to faunal identification. Maxwell (1992, p. 287) defines the concept of descriptive validity in the context of qualitative research stating that “if different observers or methods produce descriptively different data or accounts of the same events or situations, this puts into question the descriptive ‘validity’ (and other types of ‘validity’ as well) of the accounts.” “Observers” in Maxwell’s assessment are social scientists producing data (“accounts”) about subjects through interviews, surveys, and other instruments. The importance of descriptive validity in faunal analysis should be transparent; if different analysts come to different conclusions regarding the identity of faunal specimens, there is a validity problem. These “rather blatant difference[s] in description demonstrate the highly selective, reductive, and subjective processes involved in all research” (Winter 2000), including faunal analysis.

The more common concept of “internal validity” used in quantitative research is perhaps a better fit for assessing zooarchaeology. Internal validity “addresses whether or not an observed covariation should be considered a *causal* relationship” (Calder *et al.* 1982, p. 240, emphasis added). The use of the word “cause” refers to the fact that this concept is often used in reference to correlation analyses that lead to hypotheses as to whether or not X causes Y. Are zooarchaeological identifications causal claims? Yes, when one assigns a taxonomic designation (such as a species or genus name) to a

fragment of bone or shell, one is using morphological similarity (covariation) between the unknown specimen and a reference specimen to infer that the evolutionary biology of that species or genus *caused* the morphological similarity, thus producing a valid identification. Internal validity becomes an issue when other alternative “causes” of morphological similarity are not rejected (Smith and Glass 1987, p. 5), for example, that alternative species/genera exhibiting comparable morphology did or did not cause the similarity on which the identification is based. In zooarchaeology, internal validity is problematic at the most basic level because the process of identification is unavoidably a subjective one of pattern recognition (Driver 1992; Gobalet 2001; Lyman 2002; Bochenski 2008), and “if all reasonable alternative causes [potential biological taxa] cannot be ruled out, the research [identification of specimens] may be inconclusive and invalid” (Wolverton 2009, p. 373).

It is easy to conceive of how internal validity might be problematic with a simple example. At the nominal scale, zooarchaeological data are at times useful in studies of paleobiogeography. I argued that the presence of prairie taxa in the northern Ozarks Highlands of Missouri during the mid-Holocene suggested extension of upland prairies farther to the southeast than previously reported based on the presence of skeletal remains of grassland species in regional archaeofaunal samples (Wolverton 2002). In order to make this argument, I claimed that remains of bison (*Bison bison*), spotted skunk (*Spilogale putorius*), badger (*Taxidea taxus*), and prairie chicken (*Tympanuchus cupid*) indicated open-grassland habitat. There are at least two potential validity problems in this study, one of internal validity and one related to generalization based on and derived from identification of these species.

First, there would be a problem of internal validity if the identifications upon which I based my claims were incorrect. Second, I based my claim on the ecological notion that these species prefer open-grassland habitat as opposed to deciduous forest habitat, which could be incorrect and represents a problem of generalization. I must trust the ecological literature to strengthen the claims I made about the functional, evolutionary, and behavioral ecology of these species (Lindzey 1982; Reynolds *et al.* 1982; Meagher 1986). Assuring the validity of the faunal identifications, however, requires detailed information on zooarchaeological method. The scientific reader of the paper needs to be assured that bison represented bison and not cattle (*Bos taurus*) because the stratigraphic context from which the bones came is mixed, that spotted skunk was not striped skunk (*Mephitis mephitis*), and that badger and prairie chicken indeed were represented in the samples. Finally, the criteria used to identify these species needs to be explicit and subject to evaluation by others. As stated by Lawrence (1973, p. 397), “identification is the foundation on which all subsequent analysis rests. Yet, more often than not, site reports [and publications] devote very little space to discussing the criteria used for making identifications. Somehow it is assumed that differences between species are so well understood that no two workers would identify the same fragment differently.”

Identification of faunal remains, though seemingly basic, is an area in which zooarchaeologists often undermine their claims through unrecognized carelessness (Gobalet 2001). Ensuring valid results and claims in zooarchaeology requires more than simply accepting a scientific and theoretically informed approach to research; it requires additional attention to *quality assurance*, which consists of two components, quality control and quality assessment. Quality assurance represents a “set of planned

activities intended to ensure that the analytical information produced meets the quality requisites ... [of the field] in terms of accuracy and representativeness, which are the two analytical properties that can be directly ascribed to results” (Pérez-Bendito and Rubio 1999, p. 39). Quality assurance is important in analytical chemistry, where target analytes are identified chemically and quantified in terms of concentration. Much like the zooarchaeologist, the analytical chemist starts with a material of unknown identity and quantity and produces an identification of the material. Unlike in zooarchaeology, detailed quality assurance plans are designed and used in analytical chemistry labs. Adoption of a quality assurance standard in zooarchaeology would substantially diminish problems of internal validity and help identify when such problems exist, which is important for two reasons: first, zooarchaeologists often claim to be scientific, thus the results of our basic research process—faunal identification—must derive from a systemized methodological framework, which quality assurance can provide. Second, as the results of zooarchaeological research continues to grow in importance through applications in conservation biology (Lyman 2006; Frazier 2007; Wolverton *et al.* 2011; Rick and Lockwood 2012; Wolverton and Lyman 2012) and forensics (references in Haglund and Sorg 2002), our claims need to be justified in a much wider applied context.

Quality Assurance

Internal validity of research is strengthened if alternative “causes” are rejected through a process of elimination. The identification of each faunal specimen is, thus, a *hypothesis* as to the taxonomic and skeletal part identity of a particular bone or shell specimen. Quality control (QC) is an explicit set of steps or activities for “continuously checking laboratory” practices (Pérez-Bendito and Rubio 1999, p. 40). QC in zooarchaeology must derive from a transparent accounting of the *procedures* that are applied in the process of identifying skeletal remains. Quality assessment (QA) concerns verification of the laboratory procedures used during the QC process (see below).

Quality Control

Though he did not use the term QC, in 1992 Jonathan Driver wrote a detailed exposé of the faunal identification process; his paper should be one of the first papers that students of zooarchaeology read, and it should be a commonly cited reference in methods sections of reports and research papers. Similarly, Gobalet (2001) wrote a critical examination of zooarchaeological lab procedure based on blind tests of faunal analysts; Lyman (2002) wrote a thorough review of the implications of both papers. As of March 2011, scholar.google.com listed only 18 citations and ISI Web of Knowledge only 14 citations of Driver’s paper; by June 2012, this improved to 26 citations for scholar.google.com, with 7 new citations since 2010. Gobalet’s (2001) critique has been cited 20 times on scholar.google.com, and 16 times in Web of Knowledge as of June 2012. Driver’s (1992) paper was recently

republished with commentaries by other zooarchaeologists in the online, open-access journal *Ethnobiology Letters* (Driver 2011a). Here, I have condensed and modified Driver's discussion into five rules for faunal identification, which form the backbone for QC in zooarchaeology, but I begin discussion of his approach by considering two problematic assumptions that zooarchaeologists may make, which he discussed in detail.

The first assumption is that "single bones exhibit sufficient diagnostic characteristics to allow identification, frequently to the species level" (Driver 1992, p. 39; Bochenksi 2008). We should counter this assumption with an opposing first principle: fragments of bone *rarely retain* diagnostic features that would make them identifiable to fine taxonomic levels, such as Linnaean family, genus, or species (Bochenksi 2008). Those remains that do retain such features should be identified to fine taxonomic units only when detailed, defensible criteria are provided with the identification. This first principle brings to light the second problematic assumption that Driver discussed: "methods for identification are sufficiently well tested that" most identifications do not need to be justified (Driver 1992, p. 39). To the contrary, zooarchaeologists should adopt as a second governing principle that all identifications should be justified and explicated (Lyman 2011a). Should zooarchaeologists adopt these two principles and Driver's five rules to support them, data quality would be better assured. We will have to reach farther, however, to achieve QA (quality assessment), which is discussed later in the paper.

Rule 1 Identify Each Specimen on Its Own Merits

The first rule is in direct response to the tendency to assume that because two (or more) specimens come from the same paleozoological context and appear to represent the same taxon, then by association identification of one means identification of the other. Here, "association" refers to the fact that some specimens are recovered in close spatial context (see Lyman 2012a for a variety of definitions and uses of the term association); it is tempting not to give due attention to all specimens if they appear to belong to the same species, genus, or family. For example, one might encounter the skull of a coyote (*Canis latrans*), which can be identified to the level of species, and perhaps it is associated with several thoracic vertebrae, which compare favorably with those of coyote. If one concludes that the vertebrae are coyote, this would be an example of what Driver terms "identification by association." In fact, the vertebrae might be from a domestic dog or another canid; thus, Driver advocates that such specimens (*e.g.*, the vertebrae in this fictional example) be identified to a broader category, such as Canidae or medium carnivore. The hidden assumption of identification by association is thus avoided, and one can later state that one is assuming that the vertebrae are from coyote *because* they were recovered in association with an identifiable cranial specimen and are identifiable to Canidae or medium carnivore.

A rule countering identification by association is a first step toward a rigorous QC system. Rule 1 simply states that each specimen (bone/tooth/shell or fragment thereof) should be considered independent of every other specimen regardless of recovery context and similarity in

morphology, identified first to element then to taxon. Adoption of this rule precludes cursory examination of some specimens at the favor of others, which is why it adds rigor to the faunal analytical approach.

Rule 2 Set the Universe

Faunal identification is time consuming and labor intensive, especially if the taxonomic and skeletal part identity of each specimen is treated as a hypothesis. According to Driver (1992, p. 44) “if one begins with no assumptions then identification is virtually impossible.” The faunal analyst should compile a comprehensive list of taxa thought to occur in the region of study (the universe), thus providing an assumptive base for narrowing the pool of candidate species that are likely to be identified. This should include careful reading of regional literature on biogeography and taxonomy (Gobalet 2001, 2005).

Driver (1992) contrasts high arctic canids to those of temperate North America as an example. Including kit fox (*Vulpes macrotis*) and swift fox (*Vulpes velox*) into the universe of canid species likely to be encountered in faunal assemblages from the arctic would make the comparative analysis process logistically challenging because species of fox overlap in terms of size and skeletal morphology (e.g., Monchot and Gendron 2010). Rule 2 must be adopted with the cautionary note that species’ geographic ranges change over time; thus what represented a temperate-latitude or arctic canid during the past may not be the same as today (see Lyman 2002). Therefore, expect rare occurrence of unanticipated species (*sensu* Grinnell 1922). Lyman (1986), for example, discusses remains identified as arctic fox (*Alopex lagopus*) by Gustafson (1972) in southeastern Washington during the early Holocene hundreds of kilometers south of the species’ current range, suggesting cooler summers in the past (see Graham 1984, 1988 for additional examples). Obviously, the veracity of this claim relies on QC of the faunal identification; as it turns out the remains are from red fox (*Vulpes vulpes*) (Lyman 2012b), which changes interpretations about past climate.

Rule 3 Set Diagnostic Criteria

This rule is a procedural step for laboratory practice in which the zooarchaeologist learns and records, and thereby is able to anticipate those criteria that are important for distinguishing species in the analytical universe (Rule 2). It should be distinguished from quality assessment procedures that support the validity of the criteria (see Assessment of Diagnostic Criteria and Assessment of Biometric Criteria sections). Rule 3 is about laboratory practice, whereas assessments of criteria are independent studies to determine the utility of particular criteria for making taxonomic separations making QA (assessing criteria) a step beyond QC (having criteria).

Driver (1992, p. 39) lists three types of general methods for determining taxonomic identifications—use of comparative reference collections, use of published criteria, such as guides and keys, and use of biometric criteria (size and shape). He makes it clear that setting diagnostic criteria is most

important when attempting to separate “relatively rare species” or those taxa¹ that are difficult to distinguish from one another. Use of comparative collections is, theoretically, the industry standard, but “most comparative collections are really inadequate for their intended purpose” (Driver 1992, p. 39). This is so because collections rarely comprise the vast range of species relevant in the analytical universe. As important, however, is that intraspecific variability related to sexual dimorphism, ontogenetic variation, and ecophenotypic plasticity is rarely represented in comparative collections (Lyman 2002). If the limits of existing reference collections are not problematic enough, consider that many museums and universities are progressively less willing to invest infrastructure and personnel resources for maintaining and managing such collections making them less common and their use more restricted (Lyman 2010).

The zooarchaeologist is left with two alternatives: first, he/she can create his/her own comparative collection (Lyman 2002). Second, and less attractive, is increased reliance on guides and keys. Current guides, though important and helpful (e.g., Lawrence 1951; Olsen 1968; Brown and Gustafson 1979), are not adequate replacements for comparative collections. It remains to be seen how successful internet guides can be in the future that use rotating photos and detailed descriptions of identification criteria (e.g., Betts *et al.* 2011; Maschner *et al.* 2011; references in Kansa 2011), which is an important direction for future research. In addition, the relatively new technology of three-dimensional printing may make previously inaccessible comparative materials more accessible in the future.

Rule 4 Anticipate Difficult-To-Separate Taxa

A step beyond setting the universe and diagnostic criteria is to consider in detail those species with skeletal morphologies that make them difficult to separate. The identification process begins with skeletal part and might proceed from there to taxon. For example, post-cranial remains of white-tailed deer (*Odocoileus virginianus*), mule deer (*Odocoileus hemionus*), pronghorn (*Antilocapra americana*), and bighorn sheep (*Ovis canadensis*) are notoriously difficult to separate, though criteria exist (Lawrence 1951; Jacobson 2003, 2004). Another example from North America is separation of post-cranial remains of *Bos* and *Bison* (Balkwill and Cumbaa 1992); crowded families of rodents, such as Muridae may require cranial remains, even teeth, to identify (Chomko 1990; Hager and Consentino 2006). In some cases, it may not be possible to identify skeletal remains to the desired taxonomic scale; for example, it would be useful to be able to reliably separate white-tailed and black-tailed jackrabbits (*Lepus townsendii* and

¹ Here, “taxa” refers generally to species. However, it could refer to genera, families, or higher-order taxa, as at times it is not possible to distinguish between them when studying fragmentary remains (e.g., post-cranial remains of *Antilocapra* and *Odocoileus*, or skeletal remains of multiple genera and families of marine or freshwater fishes). Throughout the paper, the seemingly imprecise use of the terms taxa and taxon are meant to reflect that identification of zooarchaeological remains is often imprecise and should be conservative.

Lepus californicus) from assemblages in the Mesa Verde region because each species prefers a different habitat. As it turns out, one may not only have trouble separating these species, but also the snowshoe hare (*Lepus americanus*) and two species of cottontail rabbit (*Sylvilagus*) (Yang *et al.* 2005).

We can add to the challenge of separating similar taxa, the fact that skeletal morphology varies with age and sex within species; thus, there is a range of variability for each species, not simply an archetype (Bochenski and Tomek 2000; Bochenski 2008). The point here is not to adopt a defeatist position but to anticipate in which situations separation criteria are necessary and to familiarize oneself with those criteria so that valid identifications are produced. Obviously, one's ability to apply this rule increases with experience (Driver 1992; Lyman 2002). Although the examples discussed here relate to mammals, rule 4 applies to fish (Butler 2001; Gobalet 2001; Rick *et al.* 2001), birds (Searjantson 2009; Bovy 2011, 2012), shellfish (Szabo 2009; Moss and Erlandson 2010; Randklev and Lundeen 2012), and other animals.

Rule 5 Write a Systematic Paleontology

Every faunal report should include a section that describes the basis for taxonomic and skeletal part identifications (Lyman 2011a). This section should consist of narrative description explaining the criteria for identification and the reasons for coarse-scale designations. It should describe categories that are not Linnaean taxa, such as “medium mammal,” which is based on size of skeletal parts. In addition, each description should provide illustrations, when necessary, to highlight criteria. Zooarchaeologists may lament that this section of the report is cumbersome, and that cultural resource managers usually only want a table. The zooarchaeologist should always write a systematic paleontology, even if it is separate from the final document submitted for the site report. Another way to simplify the cumbersome job of writing the systematic paleontology is to make it common practice to publish peer-reviewed research papers, communications, and notes on the criteria we use to make identifications (*e.g.*, Lyman 2012b), which falls under the rubric of quality assessment (see below). Lyman (2002), for example, mentions that many editors (especially in the past) considered publication of faunal identification data to be descriptive and expensive, which should be progressively easier with the publication of supplementary data in online repositories. Nonetheless, it is much easier to cite a paper covering detailed criteria than it is to describe those criteria in each report.

Quality Assessment

Quality assessment (QA) refers to research activities that evaluate the ability of analysts to use QC practices to generate replicable results (Pérez-Bendito and Rubio 1999, p. 41). There are several ways that QA can be accomplished in zooarchaeology, four of which are discussed below. The examples are those with which I am most

familiar and tend to be for taxa found in North American faunas. The rationale for QA, however, applies to faunal analysis from any part of the world.

Assessment of Diagnostic Characters

In order to address QA, zooarchaeologists must determine the replicability of diagnostic criteria for producing valid identifications of skeletal parts. Character descriptions of morphological features of portions of skeletal elements thought to provide an ability to separate skeletal remains of similar species do not count as QA. Lawrence's (1951) criteria for separating post-cranial elements of *Bison bison* and *Bos taurus* is a classic example; she also published criteria for distinguishing post-cranial remains of *Odocoileus*, *Antilocapra*, and *Ovis*. In similar fashion, Hargrave and Emslie (1979) provide a description of characteristics that can be used to separate sandhill crane (*Grus canadensis*) and turkey (*Meleagris gallopavo*) post-cranial elements. However, these authors did not assess the validity of criteria statistically, thus their studies are not examples of QA.

Jacobson (2003, 2004) provides an excellent example of QA through statistical verification of criteria separating white-tailed deer (*O. virginianus*) and mule deer (*O. hemionus*). From her study, one can obtain multiple criteria for distinguishing post-cranial element portions; importantly, one can also determine how well each criterion works based on her probabilistic assessment of the criteria through analysis of modern individuals (see Balkwill and Cumbaa [1992] for *Bos* and *Bison*). She based her analysis on that of Lister (1996, who cited Gee [1993]), which was a consideration of roe deer and red deer remains. This kind of quality assessment study is becoming increasingly important in zooarchaeology with multiple examples published in 2010 (e.g., Monchot and Gendron 2010; Zeder and Lapham 2010) and 2011 (e.g., Huber *et al.* 2011; Munro *et al.* 2011). One envisions notebooks worth of criteria in zooarchaeology labs worldwide; these need to be assessed probabilistically and published more regularly.

Assessment of Biometric Criteria

Quantitative biometric studies assess differences in size and shape of elements or portions of elements for taxa with similar skeletal morphologies. Hager and Consentino (2006) present a novel example of such a procedure for taxonomic identification of rodent genera from areas of the USA. They measured the arc of upper and lower incisors of rodent specimens from owl pellets to determine "incisor diameter," which is taxonomically distinctive. Validity of the identifications can be assessed probabilistically. This technique can be accurately applied to fragmented specimens for which an arc can be accurately measured.

A second example is the recent work on separating post-cranial remains of arctic fox (*A. lagopus*) and red fox (*V. vulpes*) by Monchot and Gendron (2010). Morphologically, the two species are similar, and in southern areas of the arctic fox's range, the species overlap biogeographically. Accurate identification of arctic fox remains from paleozoological contexts in areas that are extralimital and south of their modern range can be valuable in terms of paleoenvironmental reconstruction, assuming that the ecological tolerance of the species in terms of temperature has not changed much over time.

A limitation of Monchot and Gendron's (2010) approach is that it was developed for application to complete elements, in this case showing that the species can be separated in terms of size in areas of overlap. However, zooarchaeologists must also design measurements that can be accurately applied to portions of robust regions of skeletal elements (Wolverton 2008). Zooarchaeologists must be wary about over-application of standardized measurements designed from complete elements (von den Driesch 1976). Undoubtedly, these standards are useful; however, they may not be designed for portions of elements that are likely to survive taphonomically. As with morphological characters, an advantage of biometric approaches is that they can be assessed probabilistically with a variety of statistical approaches. For example, Huber *et al.* (2011) published a morphometric method for statistically distinguishing some species and super-species groups of salmonids. Similarly, Jacobson (2004) complemented her morphological criteria with multivariate metric analyses of white-tailed deer and mule deer skeletal elements successfully separating several elements and element portions. These few examples do not begin to cover the vast range of biometric studies that have been done and are intended to provide some illustrative examples. In addition, biometric criteria may work for some skeletal elements and for separation of some taxa but not for others, which further accentuates the need for probabilistic assessment of criteria.

Verification and Reanalysis of Random Samples

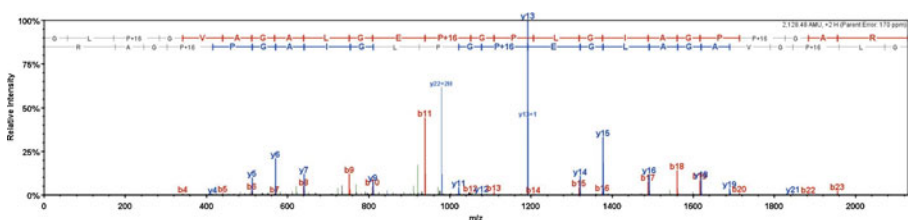
It is common practice in organismal biology for researchers to request independent verification of identifications (Resh and Unzicker 1975). Rea (1986) called for storage of zooarchaeological collections so that specimen identification could be "reverified" when needed, but this is not quite the same practice. In zooarchaeology, verification means sending materials that are difficult to identify to taxon (despite the presence of what ought to be diagnostic criteria) to other experts in the field. Another important QA practice that could regularly be introduced into the faunal identification process is random sub-sampling of previously identified specimens. Fothergill (2003, pp. 72–73; see Driver 2011b) discovered that she had a 2 % error rate in terms of those specimens she identified to species in her reanalysis of roughly 30 % percent of the Bluff Great House fauna (southeastern Utah). She felt that "in order for [her] identifications to be considered reliable, [her] results should be replicable" (Fothergill 2008, p. 73). Similarly, Gobalet (2001) advocates for blind tests of identification ability among zooarchaeologists using specimens of known identity; blind tests and reanalysis provide error rates, which can then be used for QA. It is important to acknowledge that morphological identification is a subjective process that is affected by experience level of the analyst. A scientific standard of quality assurance encourages students, professionals, and authority figures in the field to identify specimens to the level possible given their experience and training (Driver 1992).

Identification Using aDNA and Other Paleoresidues

Paleoresidues in bone, such as ancient DNA (aDNA) and protein residues, may eventually be valuable for separation of bone specimens that are difficult to identify. For example, Barker (2010) has argued that protein residues may be useful for

purposes of paleobiogeography (Hyland *et al.* 1990; Wolverton *et al.* 2011). There are a variety of hurdles in analytical chemistry that must be surmounted to be able to identify specimens to fine taxonomic levels (*e.g.*, family and below), but Barker *et al.* (2012; Barker 2010) have had success with protein residues from jackrabbit tibiae from Goodman Point pueblo in southeastern Colorado (Fig. 1). It may be possible to identify these specimens to genus or species, but the current proteomics mass spectrometry databases only include proteins from the European rabbit (*Oryctolagus cuniculus*), which has been studied extensively in biomedical fields. However, this identification is at the family level, and thus suggests promising potential.

Ancient DNA is another paleoresidue that may provide taxonomically specific identifications. Lyman (1988) argued that conservation biologists had introduced the wrong morphotype of sea otter (*Enhydra lutris*) to the Oregon coast; he suggested that the phenotypic/genetic source population for the reintroduction was from the wrong geographic portion of the species range. The reintroduction failed, and recent aDNA analysis confirms that Lyman's impression about the reintroduction may well have been correct (Valentine *et al.* 2008; Lyman 2011b). Yang *et al.* (2005) assessed leporid remains from a Pueblo II site in southwest Colorado. Rabbit bones from the site had been separated biometrically, based on size, into cottontail (*Sylvilagus*) and jackrabbit (*Lepus*) groups. The authors were unable to separate *Sylvilagus* by species, *Sylvilagus nuttallii* and *Sylvilagus audobonii*. Ancient DNA analysis demonstrated that biometric separation into cottontails and jackrabbits was correct 90 % of the time, and misidentification to genus was problematic for specimens that exhibited intermediate size. Analysts were also surprised to find that snowshoe hare (*L. americanus*) remains were identified from specimens that were large and intermediate in size. Snowshoe hare occurs in the region today, but at relatively high elevations. Tarcan (2005, p. 77) used aDNA analysis to check identifications of bighorn sheep from the Zuni Pueblo fauna and found that she misidentified one innominate as *Ovis* that should have been *Antilocapra*. Ancient DNA analysis has been applied in a variety of



Q28668|CO1A2_RABIT (100%), 53,129.5 Da
 Collagen alpha-2(I) chain (Fragment) OS=Oryctolagus cuniculus GN=COL1A2 PE=2 SV=1
 2 unique peptides, 3 unique spectra, 19 total spectra, 70/526 amino acids (13% coverage)

GFPGEKGPSSG	EAGTAGPPPT	PGPQGLLGAP	GILGLPGSRG	ERGLPGVAGA
LGEPGPLGIA	GPPGARGPPG	AVGSPGVNGA	PGEAGRDNPP	GSDGPPGRDG
QPGHKGERGY	PGNAGPVGAA	GAPGPQGSVG	PTGKHGNRGE	PGPAGSIPGPV
GAAGPRGPSSG	PQGIKRDKGE	PGDKGPRGLP	GIKGHNLQGG	LPGLAGQHGD
QGAAPGAVGPA	GPRGPAGPTG	PAGKDGSRSGH	PGTVGPAGLR	GSQGSQGPAG
PPGPPGPPPGP	PGASGGGYDF	GYDGDFFYRAD	QPRSPPSLRP	KDYEVDTLTK
SLNKKIETLL	TPEGRSKNPA	RTCRLDLRLSH	PEWSSHYWGI	DPNQGCTMDA
IKVYCDFSTG	ETCIRAQNP	ISVKNWYKSS	KAKKHVWLGE	TINNGTQFEY
NVEGVTSKEM	ATQLAFMRL	ANHASQNITY	HCKNSIAYMD	EETGNLNKAV

Fig. 1 Mass spectrum and peptide sequences of jackrabbit collagen recovered from roughly 800-year-old archaeological bone from the Goodman Point Pueblo (5MT604), southwestern Colorado (This mass spectrum was originally published by Barker 2010, p. 62, Fig. 2 in *Ethnobiology Letters*)

analyses that are not covered here; the approach has great potential for strengthening QA in zooarchaeology (*e.g.*, Moss *et al.* 2006; Horsburgh 2008).

The degree to which aDNA, protein residue analysis, and other forms of archaeological residue analysis are incorporated as QC/QA in zooarchaeological research will depend on a variety of factors: cost, the research potential of faunal remains in question, the level of difficulty of biometric or character-based identification, *etc.* Clearly, there is much potential in terms of QC/QA in zooarchaeology and residue analysis.

Discussion and Conclusion

There are several important points to be made in this paper. First, faunal identification is unavoidably a subjective process of morphological and biometric pattern recognition. However, this does not mean that the process is doomed to be pseudo-scientific and invalid. On the contrary, it is how the analyst engages in this subjective process that influences data quality. In fact, it is because the process requires accumulation of subjective experience that quality assurance is of paramount importance; that is, how the zooarchaeologist goes about this subjective process can either compromise or enhance internal validity of results. The student of zooarchaeology can take a big step forward by familiarizing themselves with the biological literature, including biogeography and taxonomy, for the region she/he studies (Gobalet 2001, 2005). However, this is not the same thing as adopting a laboratory standard that focuses on problems of internal validity. In practice, it is recognized that experience and reputation of the zooarchaeologist and related mentoring of students is a marker of data quality, but this is also not a replacement for quality assurance (Driver 1992; Lyman 2011a). Such solutions represent the status quo in which data quality is accepted “on faith.”

Second, zooarchaeologists have left themselves open to suspicions of problems of internal validity because data from faunal reports rarely address quality assurance in terms of QC or QA. Claims that the faunal identification practice varies across members of the zooarchaeological community and, thus, complaints about any particular example of faunal analysis are difficult to refute. Second, zooarchaeologists should explicitly adopt and perhaps improve Driver’s quality assurance standard as the basis for data quality in faunal analysis. Scholarly publications in academic journals as well as zooarchaeological sections of cultural resource management reports should provide a brief statement concerning data quality. An example of this might be: “the faunal identification process during lab work related to this project adheres to the quality assurance standard developed by Driver (1992); particular examples of QC/QA that relate to identification of remains from closely related, difficult to separate taxa are discussed throughout the report.” However, such explicit statements will have no effect if zooarchaeologists do not first assess the laboratory process and accept and/or improve upon existing standards, such as Driver’s. At a minimum, in the absence of such statements, one is left to question whether or not zooarchaeologists hold a common standard at all.

Short notes and long review QA papers on identification criteria should be published (*e.g.*, Jacobson 2003, 2004; Monchot and Gendron 2010; Zeder and Lapham 2010). Publication of such papers is equally meaningful to papers that delve

into zooarchaeological research on past cultures and environments because the validity of the latter relies on data quality (e.g., Lyman 2012b). QA bolsters QC. When criteria are published, it is a simple matter to cite the appropriate resources to amplify the reader's confidence in any particular example of faunal analysis. Finally, zooarchaeologists should address data quality using the terms *quality assurance*, *quality control*, and *quality assessment*, which should make consideration of data quality explicit and meaningful. However, unless the full meaning and extent of quality assurance procedures are integrated into the culture of zooarchaeological faunal identification, which concerns laboratory training, use of such language will only have minimal effect on data quality.

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