

## **Supplementary Text to accompany**

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### **On Taxonomic Identification and the Changing Status of “Diagnostic” Skeletal Traits**

Most paleozoologists who comment on the topic argue that taxonomic identification is fundamental to most analyses (e.g., Baker and Shaffer 1999; Chaplin 1971; Emery 2004; LeFebvre and Sharpe 2018; Parmalee 1985; Peres 2010; Salemme et al. 1991), and a few add that an inaccurate identification is worse than no identification (Lawrence 1957; Olsen 1959; Peres 2010); “Identification must not be forced” (Chaplin 1971:39). Many also make three principal observations about the process. First, the Linnaean biological taxonomy is a nested hierarchy of levels (species within a genus, genera within a family, etc.) or an “aggregative hierarchy” (Valentine and May 1996). Second, not all skeletal elements (humeri, mandibles, ribs, tibiae, etc.) are equally taxonomically diagnostic (Baker and Shafer 1999; Bochenski 2008; Chaplin 1971; Davis 1987; Driver 1992; Gifford-Gonzalez 2018; Gilbert 1973; Gobalet 2001; Hillson 1992; Klein and Cruz-Urbe 1984; Lyman 1979, 2005; Morales-Muñiz 1993; O’Connor 2000; Olson 1961, 1971; Salemme et al. 1991; Stahl 1996, 2008; Wheeler 1978; White 1953, 1956; Ziegler 1973) and identifying the skeletal element represented by a specimen is typically a requisite first step to identifying the taxonomic family, genus, or species it represents (Driver

1992; Hillson 1992; Lyman 2002; Meadow 2000; Medlock 1975; O'Connor 2000; Reitz and Wing 2008; Smith 1979; Stahl 2008; Ziegler 1965, 1973). Finally some anatomical traits seem to be highly taxonomically diagnostic whereas others seem to only be diagnostic sometimes, that is, occur in less than 100% of the reference specimens consulted, in part a result of variability across semi-isolated populations of a species (Barr 2008; Bochenski 2008; Gifford-Gonzalez 2018; Graham and Semken 1987; Lawrence 1973; Lyman 2002; Navarro et al. 2018; Nims and Butler 2017; Polly and Head 2004). Together, these three things mean that there are different taxonomic “levels” to which any given skeletal specimen might be identified, and taphonomic modification of ancient skeletal remains simply exacerbates our inability to identify specimens to high resolution. Thus, when the remains of different taxa of similar body form and size are believed to potentially be present in a collection, it likely will be most prudent to identify the less distinctive of them to genus or some group of less taxonomic resolution than species (e.g., large bovid).

Surprisingly few (in our view) researchers worry that intraspecific variability in skeletal anatomy is insufficiently documented to recognize which traits are unambiguously taxonomically diagnostic (are *deterministic* traits), which traits are only sometimes taxonomically diagnostic (are *probabilistic* traits), and which traits are never diagnostic. It is precisely this lacuna in our knowledge that prompts most analysts cited above to urge that reference collections be large both in terms of species included and in terms of multiple individuals of each species (e.g., ~30 of each sex of both adults and juveniles,  $\Sigma = \sim 120$  [Findley 1964]). The reason is that it has been shown within many species there is not only within-population variability but also between population variability. As more of the total geographic range of a species is sampled, more anatomical (including skeletal) variation is found (Bell et al.

2010; Plug 2017; Polly and Head 2004; Stewart 2005). As intraspecific variability increases, the potential this variability will begin to overlap with that observed in other species will increase. Greater intraspecific variability translates to less interspecific difference and, therefore, fewer robust, high resolution identifications.

As many zooarchaeologists have observed over the years, individual variability of skeletal anatomy within a species tends to be poorly documented and thus is a major obstacle to strongly warranted identifications (Driver 1992; Gilmore 1949; Harris 1963; Hildebrand 1955; Hillson 1992; Lawrence 1951; Lupo 2011; Parmalee 1985; Plug 2017; Zeder 1991). Thus Polly and Head (2004:198) caution that without study of numerous skeletons of each species, the identification results comprise a “‘small [reference] sample’ typology.” This point of view is readily justified by describing instances wherein what were believed to be taxonomically diagnostic traits were subsequently shown to not be diagnostic. Here we provide three examples illustrating this uncertainty, underscoring the importance of testing of our identification protocols in zooarchaeology.

Zoologist and part-time paleozoologist Barbara Lawrence’s (1951) description of skeletal traits she believed to be taxonomically diagnostic of American deer (*Odocoileus* spp.), pronghorn (*Antilocapra americana*) and bighorn sheep (*Ovis canadensis*) has been cited more than forty times (Google Scholar, Feb. 24, 2020). Perusal of some of those cited pieces of literature indicates researchers used the skeletal traits Lawrence describes to identify zooarchaeological remains. We are aware of no zooarchaeologist who explicitly indicates he or she tested the validity of the skeletal traits Lawrence describes before using them to make new identifications (Lawrence’s descriptions were often used when reference skeletons were unavailable), but this may be a function of the fact that most zooarchaeologists working in North

America do not describe the identification protocol they follow, and very rarely indicate which skeletal traits were used to make identifications. Some of the alleged taxonomically diagnostic traits Lawrence described have been found to be of questionable validity (e.g., Hildebrand 1955), and others thought to be taxonomically diagnostic by one researcher have been disputed by another (e.g., Chavez 2008; Walker 1992).

In another example paleozoologist Stanley Olsen (1960) described what he believed were skeletal traits that allowed the distinction of North American bison (*Bison bison*) bones from those of domestic cattle (*Bos taurus*). Numerous individuals apparently used those traits without testing (Olsen [1960] cited 86 times; Google Scholar, Feb. 24, 2020); poor reporting of the identification protocol followed prompts us to use the qualifier “apparently.” Later research demonstrated various traits proposed by Olsen were not always valid (Balkwill and Cumbaa 1992). The last underscores why some researchers have chosen to report the probability that a particular trait is taxonomically diagnostic among examined reference skeletons (e.g., Balkwill and Cumbaa 1992; Jacobson 2003, 2004; Lubinski and Hale 2018). The magnitude of such probabilities depends on the reference specimens examined, and so far as we know no one has evaluated those probabilities with other reference specimens.

A third example involves the North American meadow vole (*Microtus pennsylvanicus*). More than a century ago, neozoologist Gerrit Miller (1896:63, fig. 33) illustrated a quite visible posterolingual dentine field (later referred to as the “fifth loop”) on the M2 (second upper molar). He did not mention the fifth loop’s possible taxonomic status, but later neozoologists (those who study modern living animals) did (e.g., Hall and Cockrum 1953; Hall and Kelson 1959; Hooper and Hart 1962; Reich 1981). Subsequently, several paleozoologists (including zooarchaeologists such as coauthor RLL) used the M2 fifth loop trait to identify Pleistocene- and Holocene-age

specimens (e.g., Davis 1975; Guilday 1982; Guilday et al. 1978; Indeck 1987; Johnson 1977; Klippel 1987; Lyman 1997; Morlan 1984; Semken 1980, 1984; Walker 2007; Williams 2009; Woodman et al. 1996), all without additional testing of the validity of the M2 fifth loop.

The supposed status of the M2 fifth loop as taxonomically diagnostic was likely reinforced by a zooarchaeological publication specifically devoted to describing such anatomical traits among rodents (Chomko 1980, 1990). Perhaps testing with newly acquired reference specimens of known taxonomy seemed unnecessary given that neozoologists had suggested the M2 fifth loop was taxonomically diagnostic of meadow voles within this taxonomically rich genus (17 extant species recognized in North America [Lyman 2019]). But reports that the M2 fifth loop was not taxonomically diagnostic have appeared irregularly for decades; those reports indicate both that the absence of the M2 fifth loop does not necessarily mean the tooth is from a non-meadow vole *Microtus* and that the presence of the M2 fifth loop does not necessarily mean the tooth is from a meadow vole (e.g., Bell and Repenning 1999; Oppenheimer 1965; Weddle and Choate 1983; Zakrzewski 1985).

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