

# Beware the Springbok in Sheep's Clothing: How Secure Are the Faunal Identifications upon Which We Build Our Models?

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**Abstract** Lively debate surrounds the introduction of non-indigenous domestic livestock to southern Africa. Despite disagreements regarding process, the archaeological community agrees, with unusual unanimity, on the broad chronology. Indeed, the certainty with which the timing is known (admittedly within the limits of radiocarbon dating) has been celebrated, because with these underpinning data in hand, issues of process can

be explored in a serious and empirically grounded manner. Recently published ancient DNA (aDNA) research in southern Africa now calls into question the reliability of many faunal identifications upon which this debate rests. These data build on earlier ecological data, suggesting that some faunal identifications at sites crucial to the debate may be unreliable. A number of morphologically identified domesticate bones were chosen for aDNA sequencing to explore the relationships among southern Africa's early domestic stock. Unfortunately, a large proportion yielded DNA sequences indicating a wild origin. This led us to consider the potential scale of the problem and the implications for existing models regarding the introduction of herding to the subcontinent. The issue may originate largely from the optimistic identification of specimens retaining too few key morphological markers. We acknowledge that reconstructions of the past are likely to be biased by discarding potential zooarchaeological data through overly conservative identification. We argue, however, that the potential ramifications of building models on unreliable data are far greater than those of being forced to acknowledge gaps in our data and are calling for further research.

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**Résumé** Des discussions animées portent sur la question de l'introduction des animaux domestiques en Afrique australe. S'il existe des désaccords au sujet des processus d'introduction, la communauté archéologique s'accorde néanmoins dans son ensemble sur la chronologie de ces événements, dans le cadre d'un consensus qui est plutôt inhabituel. Ces certitudes (certes dans le cadre des limites de datation radiocarbone)

sont à l'origine de l'élaboration de scénarios rigoureux et empiriques. Toutefois, les dernières recherches sur des échantillons d'ADN anciens venant d'Afrique australe remettent en question la fiabilité de nombreuses identifications fauniques sur lesquelles repose le débat. Ces recherches se construisent sur d'anciennes données écologiques et suggèrent que certaines identifications d'espèces, dans des sites clés, seraient erronées. Un grand nombre d'os d'animaux domestiques identifiés sur des bases morphologiques ont été sélectionnés pour des séquençages ADN afin d'explorer la question des relations au sein des premières populations d'animaux domestiques d'Afrique australe. Or, une grande proportion des séquences d'ADN ancien indiquent une origine sauvage. Ceci nous conduit à envisager l'ampleur potentielle du problème et ses implications sur les modèles actuels relatifs à l'introduction de l'élevage sur le sous-continent. Le problème trouve certainement sa source dans l'identification optimiste de certains spécimens associés à un trop faible nombre de marqueurs morphologiques. Nous reconnaissons que les reconstructions du passé sont biaisées par la disparition de certaines données zoo-archéologiques et par un trop grand nombre d'identifications à l'identique. Mais nous soutenons néanmoins que les conséquences induites par des modèles construits sur des données discutables sont plus importantes que celles pour des modèles volontiers enclins à reconnaître la fragilité des données et appelant à poursuivre la recherche.

**Keywords** Zooarchaeology · Data quality · Ancient DNA · Domestic stock

## Introduction

The introduction of domestic stock to southern Africa about 2000 years ago has been a major focus of archaeological research in recent decades. The manner of introduction(s) to the region, the impacts the introductions had on resident foraging groups, and the nature of the interactions between foragers and food producers have all been examined (Sadr 1998, 2003; Smith 1992, 1998, 2006). Faunal data are crucial in these research issues. Jerardino et al. (2014) have used dated faunal remains from across southern Africa to construct a GIS model of livestock spread across the region. They calculate a rate of expansion of approximately 2.4 km per year and, noting that this is much faster than the rate observed in the European Neolithic of about 1 km per year

(Pinhasi et al. 2005), argue that the spread was primarily driven by cultural diffusion.

Both ancient DNA (aDNA) data and ecological data now show that some significant published faunal identifications cannot be regarded as secure. We first describe the aDNA data and ecological data that led us to believe that faunal remains have been misidentified at a rate that warrants rethinking the chronology. We then discuss the implications of the revealed pattern for the ongoing debate about the processes by which domestic livestock were introduced into southern Africa.

## Faunal Misidentification: Genetic Evidence

Since 2013, three studies have been published, in which DNA sequences from archaeological remains have shown that specimens initially identified by zooarchaeological analyses to be domestic cattle, sheep, or sheep/goat actually originated from wild species (Horsburgh and Moreno-Mayar 2015; Horsburgh et al. 2016; Orton et al. 2013). The studies were not undertaken to test the accuracy of the morphological identifications, but rather, because of the positively identified livestock, they aimed to use aDNA analyses to understand the genetic relationships among southern Africa's domestic livestock. Technical details of the methods employed in the aDNA studies are fully described in the cited papers. We suggest that readers seeking more in-depth discussions of genetic methods and applications in anthropology access one of the many reviews on the subject (e.g., Gilbert et al. 2005; Horsburgh 2015; Kaestle and Horsburgh 2002; Matisoo-Smith and Horsburgh 2012; Mulligan 2006; O'Rourke et al. 2000). Here, we note only that the DNA sequenced in these studies is the maternally inherited mitochondrial genome. The abundance of mitochondria in cells, and thereby the abundance of its genome in biological tissues, means that it is more likely than nuclear DNA to preserve in archaeological remains. It is further worth noting that DNA is not the only biological molecule that encodes phylogenetic information. Known as Zooarchaeology by Mass Spectrometry or ZooMS, mass fingerprinting of preserved protein peptides has also proven valuable in determining species identity and, when the phylogenetic distance is large, determining evolutionary relationships among taxa (e.g., Welker et al. 2015). Proteins have greater stability in the archaeological record than does DNA. Genetic analyses can provide higher-resolution phylogenetic information

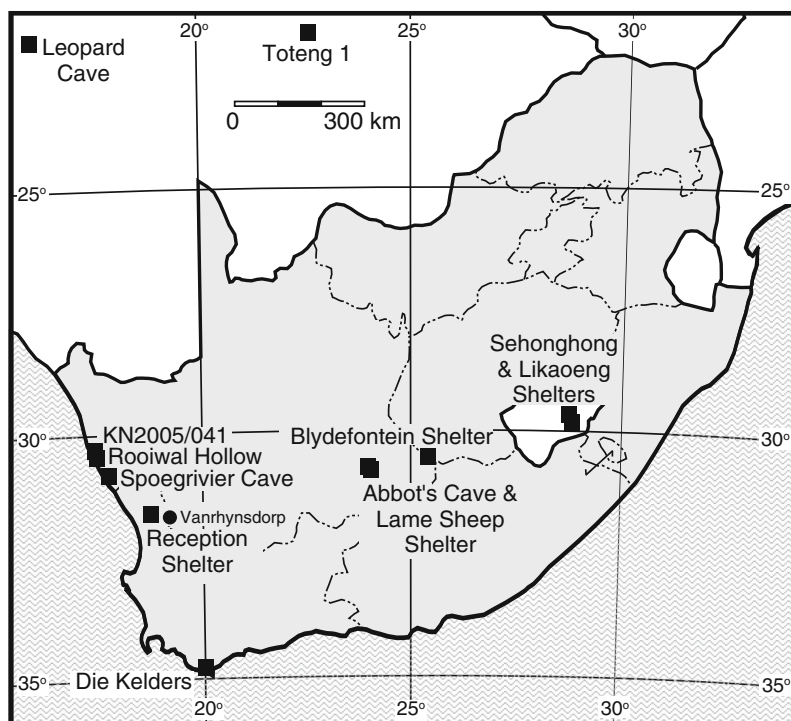
than can ZooMS but only when DNA is sufficiently well preserved.

The first of the relevant aDNA studies examined two specimens excavated from sites in Namaqualand, South Africa (see Fig. 1 for a map of site locations) (Orton et al. 2013). One specimen was from KN2005/041, a coastal shell midden located near the Swartlintjies River that had been excavated in mitigation of mining activities, and the other specimen was from Reception Shelter, in the arid Knersvlakte region some 200 km to the southeast. Initial faunal analyses identified two cattle specimens, the base of a horn core from KN2005/041 and a juvenile upper right maxilla from Reception Shelter. While the KN2005/041 midden was dated on charcoal to the mid-first millennium AD, the level from which the maxilla originated was ca. 2000 years old and offered an exciting opportunity to sequence the oldest identified cattle bone in South Africa. DNA preservation in the horn core was poor, but a little less than 3 % of the mitochondrial genome (just over 300 base pairs [bp]) were recovered. As expected, it was similar to that of known cattle specimens, but the recovery of such a small fragment meant that little phylogenetic information could be recovered. The maxilla, however, was significantly better preserved. Almost 90 % of the mitochondrial genome (~14,500 bp) was recovered. Contrary to a priori expectations, the DNA sequence

was significantly very similar to the published sequences of gemsbok (*Oryx gazella*) and not closely similar to that of domestic cattle. After the genetic data became available, the faunal analyst reexamined the specimen and found that the assignment to gemsbok is warranted on morphological as well as genetic grounds (RGK).

Blydefontein Rock Shelter, in the eastern Karoo of South Africa, provides a second example of aDNA results being used to revise the identifications made in the original faunal analysis (Horsburgh and Moreno-Mayar 2015). Initial analyses of the faunal assemblage did not identify any remains of domestic stock (Sampson 1970; Klein 1979; Bousman 1998, 2005) and reported that the majority of the assemblage was too fragmentary to identify (Klein 1979). Subsequent reanalysis of the Blydefontein faunal assemblage identified 10 specimens of domestic caprine. Eight of the specimens that had been morphologically identified as sheep or sheep/goat were subjected to aDNA analysis. Organic preservation was sufficiently good in six of those specimens to permit DNA recovery. Of these, only one specimen, a complete first incisor, proved to be of domestic origin. The other specimens were found to be from two springbok (*Antidorcas marsupialis*), a gray rhebok (*Pelea capreolus*), a mountain reedbuck (*Redunca fulvorufula*), and an eland (*Tragelaphus*

**Fig. 1** Map showing locations of sites discussed



*oryx*). Crucially, the specimen identified by genetic methods to be an eland had been subjected to direct accelerator mass spectrometry (AMS) dating and, had it proved to be a sheep, would have provided evidence for the surprisingly early introduction of domestic sheep into southern Africa at around 2800 cal BP (Bousman et al. 2016). It is possible that the wild specimens listed here had been accurately identified in the original zooarchaeological analysis. We think it more likely, however, that these specimens had been considered unidentifiable on the basis of their preserved morphology. It should be noted that the ancient DNA research at Blydefontein has not gone uncriticized and that both the site's archaeologists (Bousman et al. 2016) and the faunal analysts (Scott and Plug 2016) suggest that the aDNA data should not necessarily be considered reliable. We agree that all researchers make mistakes, ancient DNA researchers included, but nonetheless contend that the nature of genetic and morphological data are such that species identifications by aDNA are likely to be more reliable than those by morphological analysis. The primary advantage of genetic data in determining species is that with DNA, there are about 16,500 points of comparison (i.e., ~16,500 base pairs or bp) in a well-preserved mammalian mitochondrial genome. Morphological methods of distinguishing species, on the other hand, will always be dependent on fewer points of comparison but can be equally reliable if the appropriate morphology is preserved.

Analyses of fauna from Sehonghong Rock Shelter, Lesotho, have likewise shown a significant pattern in which bones of indigenous species were identified as those of domesticates (Horsburgh et al. 2016). Nineteen specimens that had been morphologically identified as cattle, sheep, or sheep/goat were subjected to ancient DNA analysis. Of the 10 specimens from which DNA could be recovered, only one proved to be domestic in origin, specifically cattle. The remaining specimens included six eland, two gray rhebok, and a mountain reedbuck. Among the specimens from which DNA could not be recovered was a single specimen from which a direct AMS determination yielded a date of about 4600 cal BC ( $5870 \pm 30$  bp, Wk-34,784; Horsburgh et al. 2016), and so while there are no DNA results to indicate from which species this specimen originated, we can be confident that it was not a domesticate. This leaves seven of the original 19 specimens. There is no reason to believe that archaeological domestic fauna are less likely to preserve DNA than are

wild fauna and therefore no reason to believe that the specimens from which DNA could not be recovered are preferentially likely to be domestic stock.

#### Faunal Misidentification: Ecological Evidence

There have been a small number of isolated, and little noticed, cases in which published faunal lists have been at odds with available ecological information. In reporting the results of their excavations at Rooiwal Hollow on South Africa's Namaqualand coast, Orton et al. (2005) note that the only species of small bovid identified at the site was steenbok (*Raphicerus campestris*) and argue that the remaining small bovid bones determined to be unidentifiable are likely to derive from steenbok, rather than grysbok (*Raphicerus melanotis*) because the local environment is not well suited to the latter species. Indeed, the grysbok is a denizen of thick shrubland and ecologically should not occur anywhere north of Vanrhynsdorp (Shortridge 1942; Skead et al. 2011). In particular, Orton et al. (2005) draw attention to the contrast between the fauna from Rooiwal Hollow and nearby Spoegrivier Cave, where 1037 grysbok specimens were identified from a total identifiable faunal assemblage numbering 3614 specimens (Webley 2002, Tables 17 and 18). They suggest that a high-frequency presence of grysbok is improbable at both Rooiwal Hollow and Spoegrivier. Extrapolating from what appears to be a significant error rate among the small bovids at Spoegrivier, we consider it likely that the remains identified as domestic stock are equally likely to have been misidentified. While revising the identifications of grysbok at Spoegrivier Cave to the more likely steenbok might little alter interpretations of prehistoric behavior at the site, the morphological identification, and direct AMS dating, of domestic sheep is critical to our existing understanding of the chronology of domesticate arrival in southern Africa, especially since the oldest directly dated sheep in South Africa originates there (Sealy and Yates 1994). We will return to the issue of the reliability of the sheep identifications at Spoegrivier Cave later.

Faunal analyses of remains from Abbot's Cave and Lame Sheep Shelter, both rock shelters in the semi-desert Karoo of South Africa, have likewise indicated the presence of ecologically unlikely species in deposits considered to date largely to the second millennium AD (Plug 1993). The presence of the remains of the blue duiker (*Philantomba monticola*) have been reported



among the fauna recovered from both sites. The blue duiker, however, is a forest-dwelling species (Klein 1984; Skinner and Chimimba 2005) and unlikely to have existed near the site within the last few thousand years when regional climate and probably vegetation were similar to those of today. Minor increases in rainfall have caused grassland expansion (Scott and Bousman 1989) but have not allowed for the introduction of forests to the area. Plug (1993) acknowledges the improbability of finding blue duiker there, but suggests that the inhabitants of the sites had contact with groups living on or near the coast, where blue duiker are found, or themselves visited the coast and acquired the animals there. It is further suggested that blue duiker would have been an unimportant food animal and so “may have had some important meaning to hunter-gatherer societies” (Plug 1993, p. 20). No citation is given for any ethnographic evidence of the cultural importance of blue duiker, and we are unaware of any such evidence. There are occasions where isolated examples of certain species might have been collected for some symbolic value, like the lion teeth cited by Fagan (1967) and Orton et al. (2011), while other bones may have been transported because they were curated to serve specific functions like the modified *Raphicerus* metapodial noted by Smith (2006). However, such reasons for the inclusion of blue duiker in the Abbot’s Cave and Lame Sheep deposits would surely have been noted. Furthermore, one of us (RGK) has examined one of the fragments from Abbot’s Cave that has been identified as blue duiker and is of the opinion that it was not identifiable to species or even genus. Given the growing body of ancient DNA evidence that faunal remains have been commonly, if not routinely, misidentified, we consider it more likely that the remains did not derive from blue duiker.

### Error in Archaeology

In material sciences, we expect observer-error and inter-observer variabilities. In archaeology alone, there has been abundant documentation of these kinds of problems in lithic analysis (Beck and Jones 1989; Lyman and VanPool 2009; Young and Bamforth 1990), cutmarks (Domínguez-Rodrigo et al. 2012), and satellite imagery coding (Sadr 2015), as well as in zooarchaeology (Gobalet 2001; Lyman and VanPool 2009). In his now classic paper “Identification, Classification, and

Zooarchaeology,” Driver (1992, p. 35) records “a tendency for the more experienced to be less willing to differentiate between closely related species” and cautions that comparative collections will, inevitably, fail to display the full range of intra-specific variation. Further, he notes that zooarchaeologists seldom subject themselves to blind tests of their accuracy, resulting in neither empirical nor theoretical justification for assuming that most identifications are accurate. Since Driver’s paper was published, however, Gobalet (2001) has undertaken just such a blind-testing study. Unfortunately, Gobalet’s study is not reassuring. He enlisted five faunal analysts who specialize in fish and asked them each to evaluate a fish faunal assemblage from San Luis Obispo County, CA, and found a high level of disagreement between analysts. To preserve anonymity, he provides Greek letters as pseudonyms for each of the analysts and reports that “[t]he fact that alpha collectively identified 27 clupeid bones [the fish family including herrings and sardines, among other species] (specifically *Sardinops sagas*), beta found 11, gamma 12, and delta 18 (Tables 3–11) leads to the conclusion that these investigators *do not know what is going on* despite doctoral degrees and approximately 50 years of collective professional experience” (Gobalet 2001, p. 380, emphasis added). He further notes that “[b]ecause the identity of the fish from which the elements came cannot be absolutely determined there are no right or wrong answers, just differing opinions” (p. 378).

We suggest that, provided organic preservation is sufficient—a criterion that is certainly not going to be met across all sites—there can be the determination of right or wrong answers. Ancient DNA analyses are not flawless, but DNA sequences are objectively superior to morphological analysis for the identification of species, and it would be valuable to subject an assemblage such as the one Gobalet tested to ancient DNA analysis. Discerning which, if any, of the analysts was able to accurately determine species among the analyzed fish remains, and to quantify and qualitatively describe the ways in which analysts erred, could provide crucial insights. Understanding the nature of the mistakes could show the way forward in attempting to correct for them.

Although similar inter-observer studies have not been conducted in South Africa, Sealy and Yates (1994) (Table 1) provide numbers of sheep bones identified by one of us (RGK) from levels older than ca. 1600 BP at three sites. They total 15 bones. Prior

to obtaining their direct AMS dates, they had these bones reexamined by the same analyst in order to be sure that they were selecting the most reliable specimens for their project. With the application of a greater degree of caution, just four were considered at that time to be unquestionably sheep. Variations in the circumspection applied by the analyst at any given time can therefore also play a role in the numbers of each species eventually presented.

Driver (1992) calls for the provision of data tables documenting the numbers of each element that have been recorded for each taxon to allow meta-analyses to combine data across sites in a systematic fashion and to allow zooarchaeologists to assess the methods employed by other workers. Specifically, he draws attention to the practice of identifying elements by association, such that undiagnostic elements, like ribs, are identified to species by virtue of there being diagnostic elements of an appropriate species present. Driver argues that such “identification by association” practices should be avoided but notes that the availability of detailed faunal tables allows others to detect when it has occurred. In calling for the provision of faunal tables, Driver makes the now quaint suggestion that perhaps floppy disks or microfiche could be used to combat the tremendous amounts of space such tables would demand. Now that the provision of online supplementary materials is standard at most journals, making these kinds of data available should be trivial. Indeed, many of the more reputable journals require that genetic data be submitted to an online database before publication. Perhaps it is time to require the same of zooarchaeologists.

## Southern Africa

Sophisticated mathematical modeling of spatial data has been undertaken to discern the trajectory, speed, and mechanism of the first movement of livestock into southern Africa (Jerardino et al. 2014; Russell 2004). These models, however, are only as good as the raw data upon which they are built. Given the high frequency of misidentification of domestic stock in the southern African record, we cannot now regard such models as informative. See Table 1 for a summary of the data included by Jerardino et al. (2014) with indications of their relative reliability. Although these researchers were acting in good faith, using the data available to them,

their most valuable contributions are more likely to be in the establishment of methodologies that could be reused. Indeed, it is now our view that building models using morphological data in the absence of aDNA verification often incorporates too much unreliability. Of course it is unfeasible to sample all bones because of the prohibitive costs, but key specimens, like the 2105 BP sheep from Spoegrivier Cave (Sealy and Yates 1994) and caprine teeth from Leopard Cave (Pleurdeau et al. 2012), should certainly be tested as it is these particular specimens that have the greatest effect on devised models. We discuss here the data employed by Jerardino et al. (2014) because it is the most recent of the spatial studies and incorporates the largest number of specimens. Of the 17 radiocarbon determinations used by Jerardino et al. (2014), only one—from KN2005/041—is associated with an aDNA confirmation of species identity. There has been aDNA work conducted on some of the sheep remains from Die Kelders 1 (Horsburgh and Rhines 2010), but the dated second phalange was not in the sample subjected to genetic analysis. It is notable that all the sheep specimens from Die Kelders 1 that were analyzed for aDNA were tooth rows with at least two teeth. The specimens analyzed from Blydefontein and Sehonghong, and which proved to have been misidentified, were either isolated teeth or postcrania (Horsburgh and Moreno-Mayar 2015; Horsburgh et al. 2016). We suggest, therefore, that the 100 % accuracy of the morphological species identification of the genetically analyzed Die Kelders 1 specimens is likely to be, at least in part, a consequence of the relative completeness of the specimens and their acknowledged reliability for species identification. We therefore cannot assume the phalange to be sheep just because all of the mandibles were confirmed to be sheep.

We have strong circumstantial evidence to doubt the accuracy of faunal identifications at three other of the sites employed in Jerardino et al.’s (2014) analysis. These are Spoegrivier Cave, Likoaeng, and Toteng 1. As discussed above, the faunal tables from Spoegrivier Cave included the ecologically unlikely species grysbok and klipspringer. Additionally, the fauna from Spoegrivier Cave were analyzed using the same methods and comparative collections as at Sehonghong Rock Shelter, where 10 of the 11 analyzed specimens were incorrectly identified by morphological analysis. Likewise, Likoaeng, a site near Sehonghong, was also analyzed with the same methods, and we have no reason to believe that the fauna there were more reliably identified

**Table 1** The fauna used by Jerardino et al. (2014, p. 6) with notes on their likely reliability. Opinions expressed about likely reliability in this table are informed speculation and ought not be construed as

certainty that these specimens have been misidentified, but rather that sufficient doubt exists about the accuracy of the identifications to warrant caution in employing them in model construction

Site name	Country/region	Morphological species identification	Element	Likely reliability
Toteng 1	Botswana	<i>Ovis aries</i>	Right astragulus	Unreliable <sup>a</sup>
Toteng 1	Botswana	<i>Bos taurus</i>	Second and third right carpal	
Leopard Cave	Namibia	Caprine	Upper right M2	Likely reliable <sup>b</sup>
Leopard Cave	Namibia	Caprine	Lower right M3	
Likoaeng	Lesotho	<i>Ovis aries</i>	Right ulna	Unreliable <sup>c</sup>
Ai Tomas	South Africa	<i>Ovis aries</i>	Associated wild form	Potentially unreliable <sup>d</sup>
KN2005/041	South Africa	<i>Bos taurus</i>	Horn core	Reliable <sup>e</sup>
Spoegrivier Cave	South Africa	<i>Ovis aries</i>	Third phalanx	Likely unreliable <sup>f</sup>
Kasteelberg A	South Africa	<i>Ovis aries</i>	Thoracic vertebra	Potentially unreliable <sup>g</sup>
Tortoise Cave	South Africa	<i>Ovis aries</i>	Associated charcoal	Potentially unreliable <sup>h</sup>
Die Kelders 1	South Africa	<i>Ovis aries</i>	Second phalanx	Potentially unreliable <sup>g</sup>
Byneskranskop	South Africa	<i>Ovis aries</i>	Mandibular condyle	Likely reliable <sup>i</sup>
Blombos Cave	South Africa	<i>Ovis aries</i>	Left mandible	Likely reliable <sup>i</sup>
Blombos Cave	South Africa	<i>Ovis aries</i>	Calcaneum	Potentially unreliable <sup>g</sup>
Boomplaas	South Africa	<i>Ovis aries</i>	Associated charcoal	Potentially unreliable <sup>h</sup>
Hawston	South Africa	<i>Ovis aries</i>	Associated charcoal	Potentially unreliable <sup>h</sup>
Hawston	South Africa	<i>Ovis aries</i>	Associated charcoal	Potentially unreliable <sup>h</sup>

<sup>a</sup> The published photographs do not show sufficient morphology to diagnose species (RGK personal observation)

<sup>b</sup> Photographs of the specimens would be preferable, but the published drawings (Pleurdeau et al. 2012) show sheep morphology

<sup>c</sup> This bone was analyzed using the same methods and comparative collections as the Sehonghong fauna, among which a 9 % accuracy rate has been determined (Horsburgh et al. 2016). Of additional relevance is that the faunal assemblage from Likoaeng presents the same complexities, specifically a wide diversity of wild fauna, as does the assemblage from Sehonghong

<sup>d</sup> We have no evidence about the likelihood of error in the identification of the sheep specimen; however, from a reading of the site description (Webley 1992), it is far from certain that the relationship between the bone and the date is guaranteed, and in the absence of a direct date, the bone should not be used in model building

<sup>e</sup> The species identity of this specimen was confirmed with by aDNA analysis, and it was directly dated

<sup>f</sup> Faunal tables from Spoegrivier report high frequencies of blue duiker (NISP = 1037; total faunal NISP = 3614). The blue duiker is not found in the region around Spoegrivier Cave, and we think that it most likely that the specimens identified as blue duiker actually derive from steenbok. One of us (RGK) has looked at one of the bones identified as blue duiker and think that it is identifiable to mammal but to no lower taxonomic level. Such high rates of error in the identification of the wild fauna suggest that the domestic fauna may have been equally inaccurately identified. See the main text for further discussion

<sup>g</sup> We have no evidence to suggest that this identification was in error; however, as we found a high frequency of error among postcranial remains, employing the specimens with caution is warranted

<sup>h</sup> It has been well documented that the association between the livestock bones and stratigraphically connected radiocarbon determinations (Sealy and Yates 1994, 1996) is unreliable with sufficient frequency to warrant concern

<sup>i</sup> We cannot be sure that this specimen was accurately identified; however, the emerging pattern suggests that cranial remains are more frequently accurately identified than are postcranial

than those at Sehonghong. Finally, the photograph of the dated bones from Toteng 1 (Robbins et al. 2005) shows specimens without enough preserved morphology to allow reliable identification to species level (RGK personal observation).

We have no direct evidence that any of the other specimens included by Jerardino et al. (2014) have been

misidentified. The emerging pattern, however, is striking. Among the tooth rows containing at least two teeth ( $n = 21$ ), molecular analyses have found an error rate of only 4.7 % (Horsburgh and Rhines 2010; Orton et al. 2013). Among the isolated teeth and postcrania ( $n = 17$ ), however, the error rate is 88.2 % (Horsburgh and Moreno-Mayar 2015; Horsburgh et al. 2016). The fact

that among the remaining specimens included in the Jerardino et al. (2014) analysis, only one is a mandible—the rest are postcrania ( $n = 4$ ), isolated teeth ( $n = 2$ ), a mandibular condyle ( $n = 1$ ), or not directly dated ( $n = 4$ )—suggests that there may be considerable error associated with these data points.

## Discussion and Conclusions

Sealy and Yates (1994, 1996) carried out a useful study to determine whether livestock bones dated by association really were as old as suggested. They found a range of ages confirming the well-known problem of archaeological material “moving between layers” or perhaps having not been excavated correctly in the first place. Nobody would contradict the notion that any model related to the introduction of herding and based on a livestock bone associated with a date of, for example, 2000 BP would fall apart if a direct date on that bone later returned an age of 1300 BP. By the same token, we argue that unless genetic confirmation of a species identification is undertaken on such key specimens, models built on them—even with reliable dating—cannot be fully trusted. The Spoegrivier specimen dated by Sealy and Yates (1994) turned out to be older than expected at  $2105 \pm 65$  BP (OxA-3862) and, together with the recently reported and even earlier caprine teeth (directly dated but also not genetically confirmed) from northern Namibia (Pleurdeau et al. 2012), is a key element in the discussion of early herding in southern Africa (see, for example, Orton 2015). The 2-sigma calibrated age of the Spoegrivier specimen has a range of 465 years, which already lends a degree of uncertainty to any interpretations based on it, but given the identification error rates discussed above, we feel that the lack of an accompanying molecular identity lends further unreliability to the interpretations.

Prehistorians untrained in faunal analyses are dependent on the primary data generated by zooarchaeologists. We hope to have convinced our readers of the need to apply judicious use of aDNA and ZooMS studies in order to substantiate models related to the introduction of herding into southern Africa. While morphological identification of faunal remains can never be replaced, directly dated and genetically identified specimens will help to build a solid foundation for early herder studies in the region and help

to eliminate some of the residual uncertainties surrounding key specimens that have not been so treated.

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## Compliance with Ethical Standards

**Conflict of Interest** The authors declare that they have no conflict of interest.

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