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Series Editors: Keith Dobney, Peter Rowley-Conwy and Umberto Albarella

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Colonisation, Migration and Marginal Areas

A zooarchaeological approach

Edited by
Mariana Mondini, Sebastián Muñoz
and Stephen Wickler

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2. Understanding Human Movement and Interaction through the Movement of Animals and Animal Products

Steven P. Ashby

In recent years, the concept of human migration has re-emerged in archaeological discussion. However, to date there has been no explicit review of the role that zooarchaeology may be able to play in this field of debate. A variety of zooarchaeological techniques may be exploited; species biogeography, metric and non-metric variation are all important areas of research. Furthermore, several other techniques may help to elucidate the problem of related human and animal movement, including the recognition and sourcing of animal products, and genetic analysis of modern animal populations and ancient faunal remains. The integration of these fields of study with other methods (including some often considered to be outside of the archaeological canon) is fundamental to the understanding of human movement and interaction, and the current lack of a theoretical framework for the study of such phenomena is a major problem.

Introduction

This paper outlines ongoing work which began as a dissertation written for the University of York's Master of Science course in Zooarchaeology. That piece of work (Ashby 2001) consisted of a critical review of the literature relating to the use of animal remains and products in the recognition of human movement and interaction. In this paper, I will focus on the use of faunal remains in the recognition of human migration.

Renewed archaeological interest in migration in the last decade has fostered considerable research into the process and nature of population movement, and models for its comprehension have been proposed (Anthony 1997; Burmeister 2000). However, before the utility of such models can be tested, a good understanding of the archaeological patterning that may indicate human movement is necessary. The differentiation of migration and exchange is notoriously difficult, and we have yet to develop satisfactory methods for the recognition and study of these phenomena (see Burmeister 2000, 539–541).

If we are to begin to understand and recognise human movement in antiquity, it is paramount that all avenues of research are exploited. Faunal remains are a medium which may be effectively utilised in this manner. In this paper I will discuss the application of a variety of techniques to the study of human migration.

Species Biogeography

Perhaps the clearest indication of animal movement and concomitant interaction of peoples is through the presence of species recorded beyond their known geographic ranges. The remains of such species may be recognised in faunal assemblages, while the raw materials of animal products such as textiles and worked bone may also be identified. By noting chronological changes in species distribution we may track the spread of animals and begin to understand patterns of human interaction. This technique has been famously employed in the study of the spread of domestication (*e.g.* Harris 1996) as well as the movement of domestic animals in later periods (*e.g.* Hoffman 1994). The movement of commensal species (see Armitage 1994), and the importation of wild game animals (see Yalden 1999, 153, 158–160) may also help to reveal patterns of human interaction.

A good example is the case of the black rat, *Rattus rattus* (see Rackham 1979; Armitage *et al.* 1984; O'Connor 1991; Armitage 1993; 1994; Ervynck 2002). Populations of *Rattus rattus* were present in Roman Britain, but seem to have declined with the demise of their urban habitat that preceded the Roman withdrawal (O'Connor 1991). They appear to have been absent from Britain between the 6th and 8th Centuries, but large populations were renewed by the end of the first millen-

nium; a time when long range trade clearly seems to have been more important. Notably, their distribution expanded further in the postmedieval period, when settlement of the Americas began (Armitage 1993). Thus, it seems that the success of *R. rattus* populations closely mirrors changes in human movement and interaction. The distribution of *R. rattus* remains may therefore be a useful proxy for long range exchange and movement.

Work by Elizabeth Reitz (1999) provides a nice contrast with this work. When studying faunal assemblages from first nations sites in colonial Florida, Reitz failed to find evidence for significant uptake of domestic animals by Native Americans. This can be explained in ecological and cultural terms, but it seems possible that the social change that a move to the husbandry of domestic animals required was not justified by the potential gains. Reitz's work shows that in cases where human choice is involved, social identity may sometimes prove too resilient for us to recognise the impact of overseas contact through faunal remains. Thus, studies of the commensal and parasitic fauna (particularly small mammal remains) become extremely important.

However, we need not always look for the movement of animals to recognise human migration. Local extirpations, such as that of Cyprus's pygmy hippopotamus (*Phanourios minutus*) may be linked with the arrival of humans (Simmons 1988; MacPhee and Burney 1991). Conversely, animals dependent on the environment created by man may become extinct when humans desert a region (see Brothwell and Jones 1978).

Animal products may also prove to be of use if we can recognise and source the species from which the material of a craft object comes. This has been attempted on antler material at Birka (Ambrosiani 1981) and Novgorod (Smirnova 1997, 139, 145). Similarly, the physical nature of textile fibres may be of use in determining the location of manufacture. When distinctive fibres are discovered beyond their known biogeographical ranges, such as the finds of bison hair in medieval Greenland (Walton Rogers 1998), they may be seen as imports or introductions. Although the movement of such products may often be related to trade rather than explicitly to migration, it may act as supporting evidence if other indications of population movement are observed.

Unfortunately, there are a number of problems with these biogeographical approaches. In addition to considering the possibility of natural animal migration, it is important that we assess the likely effects of temporal change in topography, climate, or habitat, rather than simply assuming a human role in the introduction or extirpation of a species (see MacGregor 1985, 40–41; Vigne 1999, 310). Furthermore, we cannot assume that the absence of a given species in the record indicates a real absence in the past. The true absence of an animal from a region may only be confirmed through meticulous sieved recovery (see O'Connor 1991). We should also be wary of postulating the introduction of species on the

basis of a small number of osteological finds, given the fact that archaeological assemblages rarely give an accurate indication of ancient wild fauna. Notwithstanding these problems, the approach shows promise and, when identification based on morphology is possible, has the advantage of being relatively inexpensive.

Metric Variation

It may also be possible to apply biogeographical techniques to variation below the species level, though it should be pointed out that we are not searching for evidence of breeds in the modern sense, but merely regionally distinct genetic types. One way of proceeding is through the analysis of metric variation. The measurement of bones and teeth is important in the inference of animal movement on a range of scales, but it is fundamental that we first account for the effects of all biological variables. Age and sex may be controlled to some extent by the exclusion from study of strongly sexually polymorphic elements and bones with unfused epiphyses (*e.g.* Maltby 1979, 35; see Reitz and Wing 1999, 170). Unfortunately, environmental factors are more difficult to control for, and it is well known that nutrition may affect growth, particularly during the first years of development (see, for example McMeekan 1940).

In an attempt to control for environmental variables, many analysts have used dental measurements as a marker for genetic difference, under the assumption that tooth growth is relatively environmentally independent (see Payne and Bull 1988; Albarella *et al.* 1997). However, this belief has not been satisfactorily proven, and it is conceivable that malnutrition or serious infection prior to calcification may affect tooth growth (see Mays 1998, 78). There is some experimental evidence for retarded tooth development as a result of stress *in utero* and during the period of tooth formation (*e.g.* Paynter and Grainger 1956; Tonge and McCance 1965). Thus, while it may eventually be shown to be a valid assumption, the environmental independence of tooth size should not be accepted without evidence from controlled experiments. However, ethics limit dietary variation, and mean that today's experiments are more often based on dietary improvement than depletion (*e.g.* Kim *et al.* 2001).

An alternative is to look at bone shape variation, which may be expressed as the difference in relative measurements (see Albarella 2002). While this may be largely unaffected by nutritional factors (although see Bridges 1989), other variables such as sex, age and pathology must be considered (see Albarella *et al.* 1997; Jurmain 1999).

Taking these factors into account, Murphy *et al.* (2000) noted that Roman Age cattle metapodials from Great Hols Farm, Essex were considerably larger, though only a little more robust, than those found at other Roman sites in the

area, and suggested that they represent imported livestock. Thus, when we can account for the various confounds, the study of bone shape variation seems promising, and may lead to interesting insights (see Albarella 2002), but much more research is required if we are to ascertain the reliability and usefulness of this approach.

Non-Metric Variation

Animal populations, and thus their movement, may also be recognised through the occurrence of non-metric traits. Unfortunately, this subject has suffered from a general lack of research until recent years and many zooarchaeological references to them have been little more than reportage (see O'Connor 2000, 119). However, certain traits have been subject to a little more study, and the field seems to be growing. Here is not the place to go into their details explicitly, but a brief summary is appropriate.

Once again, teeth are of particular interest, as their characteristics may have potential as indicators of genotype (see O'Connor 2000, 120–21). The absence of the second mandibular premolar in bovids has frequently been commented on, but is not yet well understood. The development of the lower third molar may also be useful, as the distal hypoconulid is sometimes underdeveloped or absent.

Also in cattle, the genetic or environmental origins of perforations in the neurocranium have caused debate (Brothwell *et al.* 1996; Manaseryan *et al.* 1999), while the shape of the sagittal profile has also been commented upon (Grigson 1976), although apparently not commonly studied in recent years. In sheep, the position of the femoral nutrient foramen may also be useful, perhaps as an indicator of restricted gene flow or isolation (Noddle 1978, 138; O'Connor 2000, 121–122).

Another potentially informative bovid trait is the presence or absence of horns. Mark Maltby (1994) studied assemblages from Winchester, and noted that early Roman deposits contained a mixture of horned and polled sheep, while assemblages from the hinterland were clearly dominated by the horned variety. This disparity is supported by metrical data, and it seems possible that most of the sheep at Winchester were of a polled variety and were generally larger in size than those from the excavated rural assemblages. It thus seems that the town was provisioned by at least two sources.

Clearly then, there are a number of avenues for research into non-metric variation. Moreover, this field of study may have advantages over metrical analysis (Sjøvold 1973, 212). Firstly, work may still be possible if the material is heavily fragmented or deformed. Secondly, it is possible that the occurrence of many non-metric traits is largely sex-independent. If this can be substantiated, then it will allow the recording of traits from skeletal fragments for which sex cannot be determined.

It is also possible that non-metric traits are less subject

to environmental variables than metric traits (see Sjøvold 1973, 206; Berry 1979, 670). However, neither seems to be under such strict genetic control that it is unaffected by other factors. Indeed, experiments on mice found that development of the third molar was affected by maternal nutrition (Searle 1954). Thus, on the whole, the environmental independence of non-metric traits is unconfirmed, and further research into this area is needed. If such an independence can be established for certain traits, then they may prove to be of considerable utility in the recognition of animal populations. However, a greater understanding of their origins, together with more systematic recording are needed if we are to exploit these phenomena to the full.

DNA Analysis

While future advances may help us to unravel the complex relationship between genotype and phenotype briefly discussed above, a solution now seems less pressing, as the advent of DNA analysis has enabled us to use new techniques in the understanding of culture contact.

Although as yet under-exploited, there is potential for the study of genetic variation in present day animal populations to tell us about human movement. This is particularly true of animals that are closely associated with man and the environment that he creates. Work by Matisoo-Smith and colleagues on Pacific pigs and rats (*Rattus exulans*), and Susan Haynes's study of the origins of the distribution of the Continental (or Orkney) vole *Microtus arvalis* are of particular note (Matisoo-Smith and Allen 1997; 2001; Haynes 2000).

However, work on modern populations is problematic. When attempting to source the migrants to a region, be they animal or human, we must accept that recent migrations and genetic drift may have taken place, and may have had a significant effect on the gene pool (see Mays 1998, 203). The study of ancient DNA thus becomes paramount, as it allows us to add a temporal perspective to the data obtained from the genetic study of present day populations.

Interesting work has already been accomplished in this relatively young field. There is a considerable body of work on the introduction of the rabbit (*Oryctolagus cuniculus*) to the Mediterranean, as deduced from aDNA analysis (Hardy *et al.* 1994a; 1994b; 1995), while Allen *et al.* (2001) are currently attempting to clarify the genetic history of pigs in the Pacific region. By detecting the transfer of suid stock, it is possible to gain some understanding of human population contact in the Pacific, and the introduction of new breeds into Polynesia following western contact clearly affected native pig populations (Allen *et al.* 2001, 4–5). A DNA analysis may thus soon begin to improve our knowledge of Pacific migration and trade (Allen *et al.* 2001, 9,12).

However, it should be remembered that the success

rate of ancient DNA analysis is generally very low. In addition to precluding the analysis of small assemblages, this may hamper attempts to answer questions regarding temporal or spatial variation in large assemblages, and may make the generation of generalising hypotheses impossible (see Haynes 2000, 164). Moreover, until the cost of DNA analysis decreases, such investigations will often be unavailable to many projects (Barnes 1998, 80).

Furthermore, DNA extraction necessarily damages bone. At present we have little understanding of preservation processes (Hagelberg *et al.* 1991), and cannot readily recognise samples that are likely to yield 'good' DNA, or decide on the best method of extraction, although Susan Haynes and others seem to have recently made some inroads into this field (Haynes *et al.* 2002). Moreover, contamination is a serious concern, and extreme measures must be applied to minimise the risk of its occurrence (see Brown and Brown 1992, 20; Haynes 2000, 29).

All in all the potential of genetic techniques in this field is clear, but there are still some problems to be resolved. We are not yet in a position to say whether these techniques are likely to supersede traditional approaches, and it is clear that we must work towards a better understanding of both morphological and DNA-based analysis.

Discussion

How do any of these techniques further our knowledge of human migration? One of the most important questions we can ask is how we differentiate the phenomena of exchange and population movement. To generalise, the deliberate and widespread introduction of foreign species or genotypes may suggest some level of population movement, while more isolated occurrences may be interpreted as the products of trade or individual travel. In order for this distinction to be made, a thorough knowledge of the excavated and historically recorded fauna for the area and time period of interest is fundamental.

In the case of taxa that may not have been deliberately imported, the scale of the introduction may not be helpful. The reproductive rate of rats, for example, together with the size, fragility and concomitant sampling issues of small mammal bone make it difficult to use numbers as criteria for the inference of migration rather than trade (see Elton 1958; Armitage 1994). Thus, while commensal animal finds may clearly suggest overseas contact, they must be used as part of a system together with domestic animal remains, artefacts and other forms of evidence if we are to differentiate between exchange and population movement. Some progress may be made if context and ethology are carefully considered. For example, we may ask if the animal in question was likely to have been transported with traded commodities, such as furs or grain, or whether its first appearance coincided with

human migrations known from other sources of evidence.

Thus, the most sensible approach seems to be one of integration, with context considered as a major component of interpretation. The zooarchaeological and biological methods discussed in this paper should be combined wherever possible, through the collaboration of multiple analysts. Each line of evidence should be studied individually, and subjected to a series of validity checks, before being compared and combined with other forms of evidence (*e.g.* Harlan and de Wet 1973). Furthermore, evidence garnered from these studies should be explicitly considered alongside material from other areas of archaeological and non-archaeological study, so that the archaeological, physical and chemical studies of animal, botanical and human remains may be integrated with the study of buildings and artefacts, and documentary, epigraphic or linguistic evidence. These multifarious analytical techniques will not always support each other, but neither should they be expected to. The comparison of the findings of various approaches can only lead to a better understanding of the processes of human movement and contact (see Morales Muniz 1997; Albarella 1999).

Above all, it is vital that we apply these techniques within a clear theoretical framework. A better understanding of the process of migration is necessary if we are to be able to reliably differentiate between processes of movement and contact. It is important that we take into consideration the models of migration devised by social anthropologists and geographers (see for example Ravenstein 1885; Zelinsky 1971; Massey *et al.* 1993), and use these to construct our own framework for the understanding of migration. Such a theoretical underpinning will help to improve our recognition of the signs of population movement that appear in the archaeological record. Thus it is hoped that an integrated strategy for the understanding of culture contact may be constructed.

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