

AHB Special Issue Editorial: Human Biology and Ancient DNA: Exploring Disease, Domestication and Movement

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Introduction

The development of ancient DNA analysis has radically transformed how we think about and study the past. The use of ancient DNA technology has permeated almost every area of anthropology and archaeology and continues to radically alter how we understand the past (Pääbo et al. 1989; Pääbo et al. 2004; Meyer et al. 2016; Slon et al. 2017). Ancient DNA has both vastly enriched and complicated the mosaic picture of the human story from Neanderthals and *Homo sapiens* interbreeding to the identification of the hitherto unknown Denisovan group (Slon et al. 2017). Ancient DNA has revolutionised the fields of archaeology, population genetics and evolutionary biology, allowing us to directly test hypotheses about past populations which could only previously be inferred from other lines of evidence. Revealing new species, challenging assumptions about admixture, and demonstrating that processes such as animal and plant domestication are even more complex than we had assumed. The oldest ancient DNA (from a horse) is currently 700,000 years old (Orlando et al. 2013) and the oldest human ancient DNA 400,000 years old (Meyer et al. 2016), potentially opening up much of human prehistory to this new field. However, there are also questions which cannot currently be answered by ancient DNA, whether because of the age or nature of a sample, the preservation conditions, or ethical considerations, including engagement with indigenous and marginalised groups. These themes were explored by the participants of the 59th Society for the Study of Human Biology Symposium held in August 2018 at Oxford Brookes University, UK. Work presented at SSHB2018 included pioneering studies which have pushed the origins of human pathogens back to before the emergence of domesticated animals and agriculture

(parvovirus B19 (Mühlemann, Margaryan, et al. 2018)), as well as uncovering the complex evolutionary history of chronic viral infections which will require further ancient genomes to resolve, such as hepatitis B virus (Mühlemann, Jones, et al. 2018; Krause-Kyora et al. 2018). The 59th SSHB Symposium explored how ancient DNA can help us to understand the human biology of disease (both chronic and infectious), the migration of groups and species, personal identity explored using genetics, and domestication - including the ways in which humans have 'self-domesticated' through the origins of behaviours such as language. By bringing together an interdisciplinary team of researchers and practitioners, including not only archaeologists, geneticists and human biologists, but anthropologists, population biologists and experts on the ethics of ancient & population DNA analysis, we tackled questions around what ancient DNA can add to our knowledge of human biology.

This special issue of the *Annals of Human Biology* includes papers from participants and selected papers which highlight the topics explored during the Symposium. The papers range from analysis of introgressed SNPs from Neanderthals (Ham et al. 2019) to identifying genes associated with language disorders, though they can only encompass a fraction of the diverse ways in which ancient DNA technology is changing our views on human evolution years.

Ancient DNA: Exploring Disease, Domestication and Movement

The role of disease in the deep past is one that has often been overlooked but an increasing body of research is revealing a much more complicated pattern of adaptation and selection (Wolfe et al. 2007; Trueba & Dunthorn 2012; Houldcroft & Underdown 2016; Pimenoff et al. 2018). The work of Underdown et al (Underdown et al. 2017) have demonstrated that it is possible to use genetic data from diseases to reconstruct events that are completely invisible to the archaeological and fossil records and well beyond the 400,000 year old age of the oldest ancient human DNA. But many human diseases are regarded as modern phenomena. For example, cancers are generally thought of as a *quid pro quo* of modern life. But are neoplastic diseases effectively a product of post-industrial human society, or can we trace their origins further back into deep (prehistoric) time? It is a common misconception that pathogen-driven oncogenesis was rare or non-existent in human prehistory (Rifkin et al. 2017). Similarly, it is often, incorrectly, argued that cancer was essentially selectively neutral in the past, with oncogenesis normally attributed to the combination of short hominin lifespans and a (perceived) lack of exposure to causative agents inherent to modern human society. However, evidence for neoplastic tumours in Australopithecines c. 2 million years ago, Neanderthals at 120,000 years ago and anatomically-modern humans at 100,000 years ago, establishes the antiquity of human cancers (Randolph-Quinney et al. 2016). The impact of infectious disease

generally, and oncogenic infection specifically, can therefore be traced across multiple hominin species over at least 2 million years. This demonstrates a chain of infection transmission from Pleistocene Africa to Palaeolithic Europe and, ultimately, to modern human populations (Houldcroft & Underdown 2016). While intrinsic risk factors contribute a relatively small amount (<30%) to the lifetime risk of oncogenesis, 70-90% of cancers have been attributed to extrinsic, (largely environmental and also microbial) factors (Plummer et al. 2016). Approximately 45 species of bacteria, viruses and parasitic microorganisms have been implicated directly in oncogenesis. In sub-Saharan Africa, nearly 33% of cancers are thought to be infection-related. However, when combined with data for sub-Saharan African HIV infection-related cancers, these figures suggest a 44% probability that infection with viral, bacterial and parasitic pathogens is driving oncogenesis in sub-Saharan Africa (Rifkin et al 2017). Since many infectious agents not currently thought of as oncogenic (in particular HIV) may play a major role in carcinogenesis (Jacqueline et al, 2017), the incidence of cancer in prehistory is almost certainly hugely underestimated. Similarly, the discovery of multiple examples of cancer in an extremely fragmentary fossil record argues for a much greater incidence of cancer than can be assumed from a simple skeletal 'body-count'. As our understanding of human exposure to pathogens in prehistory becomes clearer (eg Muhlemann, 2018 PNAS, 2018 Nature), a more detailed picture of the role these microbes played in our evolution is gradually developing. The role of ancient DNA will be crucial in shining a light on not just where and when these microorganisms became human pathogens, but also in revealing how they have evolved to exploit human biology and behaviour (Bennett & Baker, 2019, Rascovan et al, 2019, Park et al 2018).

Ham et al (this volume) examine patterns of Neanderthal allele variation in modern humans in order to explore hypotheses for selective pressures. The SNP rs3917862 is associated with hypercoagulability and while it can be deleterious it can also help to prevent blood loss. Ham et al test two very different selective pressures; death from interpersonal violent trauma (or what might be thought of as the orthodox view of male-led violence) and death from blood loss during childbirth. Their results suggest that women are more likely to die in childbirth in populations lacking rs3917862 while deaths due to violence show no correlation with rs3917862. Their results challenge the assumption that Neanderthal admixture has negatively impacted on modern human health and that maternal survival may have been an important selective pressure for the persistence of hypercoagulability alleles in modern Europeans.

Mountford (this volume) examines the genetics underlying our ability to communicate and interact with the world. They ask whether small population isolates help us to detect genes associated with developmental disorders of language, and thus better understand their

evolution in ancient genomic data. Language is not a phenotype which fossilises well and studies of modern populations are crucial if we are to properly understand what data from the fossil, archaeological and ancient DNA records reveal about the development of language and how humans effectively self-domesticate through niche construction.

Donoghue et al (this volume) use ancient DNA to examine variation in ancient strains of tuberculosis (MTB) and leprosy (ML). While both diseases are well known from the paleopathological record what is less well understood is how the diseases differed across time and space. Using data from 18th century Hungary they report that many individuals were co-infected with up to three MTB sub-genotypes. In C8th– C14th Europe significant differences in ML genotypes were found between northwest Europe compared with central, southern, or eastern Europe. Co-morbidities can also be detected using aDNA, as several co-infections of MTB and ML were detected in historical samples. This provides an important layer of detail that is all but invisible to macroscopic examination of skeletal lesions.

Santander et al (this volume) review the state of research for archaic introgression in African populations and explore recent developments. They make the important point that while much research has focussed on the modern human populations that left Africa and subsequent introgression between *Homo sapiens*, Neanderthals and Denisovans little attention is paid to the deep genetic diversity of African human populations. They compellingly argue that future studies should concentrate on unravelling the complicated demographic history of Africa through means of ancient DNA where possible and through more focused efforts to sequence modern DNA from more representative populations across the African continent, an approach other researchers are already taking to heart (eg Lorente-Galdos, 2019, Genome Biology).

Silva et al (this volume) demonstrate how a detailed mtDNA phylogeographic approach, using both modern and ancient variation, can provide evidence of population movements. They focus on the phylogeographic patterns of mitochondrial haplogroups H2 and H13 in the Indian Subcontinent and incorporate evidence from recently released ancient genomes from Central and South Asia. Their results indicate signals of Neolithic arrivals from Iran, and later movements in the Bronze Age from Central Asia that derived ultimately from the Steppe. Their approach shows that even in the face of strong male-bias such as during the Bronze Age Steppe dispersals, mtDNA analysis can shed light on complex population movements and help to answer key questions about the shaping of the South Asian gene pool over the last 10 Kyr.

Scheib et al (this volume) uses aDNA to understand kin relationships in an East Anglian Neolithic burial, supporting recent hypotheses that patrilineal burial were common in Atlantic facade and British megalithic burials, and providing genetic predictions of key phenotypes such as lactase persistence which can inform the dietary isotopic data which this study also provides. This study is a perfect example of the power aDNA has to inform skeletal biographies which are already possible for human remains, by adding data on predicted hair, eye and skin pigmentation, dietary intolerances and even susceptibility to selected infectious and chronic diseases [Pfeiffer, 2019].

Conclusions

The themes explored and the questions posed at the 2018 SSHB symposium reflect the exciting directions the field is moving in: ancient population genetics, sedimentary and pathogen aDNA, and the integration of phenotype and function with aDNA discoveries. Ancient DNA is able to answer old, and ask new, questions across the breadth of human biology and the interdisciplinary nature of this symposium reflects the complexities of trying to understand the selective pressures that shaped modern humans.

The 59th SSHB Symposium successfully brought together researchers from a wide range of disciplines and research methods, but who were ultimately all focussed on the role that ancient DNA has in understanding what it means to be human. This special issue of the Annals of Human Biology is intended to mirror the themes and questions posed at the symposium and hopefully to showcase new ideas, thinking, and research applications for ancient DNA to human biology and beyond.

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