

Archaeology and DNA

Understanding the human past

Martin Jones *Chairman of the Research Panel; Professor of Archaeology, University of Cambridge*

Recent advances in DNA science have a considerable impact on our understanding of the human past. Projects at the University of Cambridge, the birthplace of DNA science, illustrate the range of that impact.

In the last two decades, archaeology and DNA science have interacted in a remarkably fruitful way. That interaction has brought the 'Out of Africa' model of modern human evolution to prominence, initially through the sequencing of modern samples, and subsequently by the sequencing of Neanderthal specimens. It has raised the profile of many areas of archaeological enquiry, from early diseases, to kinship patterns, to the domestication and breeding of plants and animals, and the movement of different communities around the world. The University of Cambridge is one of several centres in which such research is active. The following examples of its research illustrate the growing range of this new branch of archaeological science.

The spread of farming

There has been much debate over how much the spread of farming took new communities around the world. The clear survival of a genetic signature of the palaeolithic movements show that such a replacement was far from total, and indeed some have argued that farming spread largely as an idea rather than a community. There are however, both genetic and linguistic arguments that the physical spread of extraneous Neolithic communities was substantial. This is an issue that can be explored by comparing and contrasting human genetic patterns with patterns of domesticated plants and animals that clearly moved during the farming episode. Martin Jones' group is part of a newly funded NERC consortium, in which Cambridge institutions partner with the University of Manchester Institute of Science and Technology (MIST) and the University of Sheffield to map precisely the genetic signatures of two key Neolithic crops, emmer wheat and

barley, across the European continent. This project will examine DNA from extant plants and ancient archaeological specimens, and also material from an intermediate group, including herbarium specimens and thatch fragments that might loosely be described as 'stale DNA'.

Most ancient DNA projects are now nested within extensive modern DNA studies. The cereal project above is an example of that, as is the recent work of Peter Forster and Marsha Levine on the origins and spread of horse domestication, working largely from modern mitochondrial DNA. With their detailed global analysis in place, Mim Bower is able to situate an extensive multi-period collection of excavated horses from the Cambridgeshire site at Earith Quarry in context, and two individual horses from Roman Cambridgeshire have already been linked to their European types.

Conquerors and slaves

Written history is almost invariably shaped by the conquerors, but archaeogenetics bears witness to the oppressors and oppressed alike. In collaboration with Mark Jobling at Leicester, Peter Forster's Cambridge group used DNA sequences to trace the spread of African slaves into the Caribbean. A critical feature of this research was the independent tracing of male lines (through the Y chromosomes) and the female lines (through the mitochondrial DNA). The most striking result in the sample studied was that more than 95 per cent of Caribbean mitochondrial DNA is African, whereas more than 25 per cent of Caribbean Y chromosomes are European, the latter presumably derived from the slave owners. Native American DNA comprised only 1 per cent, confirming the large-scale extinction of the indigenous population. Conversely, Native American slaves

have left their trace in the Polynesian Islands, where Matt Hurles managed to connect certain unusual genetic types today to the 19th-century Peruvian slave trade.

Conquerors have very often been male, a feature brought out by Peter Forster's group in the contrasts between Y and mitochondrial signatures in various parts of the world, a point graphically illustrated by the 'Genghis Khan' signature. This is a Y-chromosomal lineage that makes up only half a per cent of the world's male population, but eight per cent between the Caspian Sea and the Pacific Ocean, a modern genetic fossil of the Mongol expansion.

Text genetics

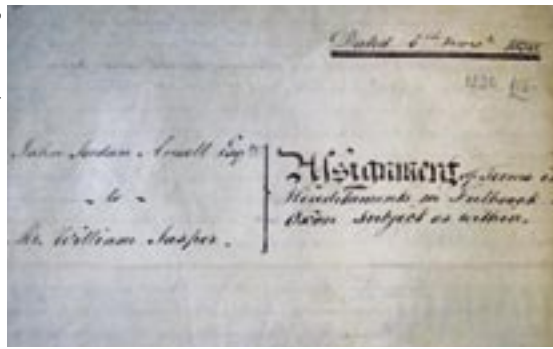
An unusual spin-off of the growth of genetic analyses has been the transfer of family-tracking or 'phylogenetic' programmes, designed for the study of strings of DNA, to strings of words. In Chris Howe's biochemistry lab, alongside the test tubes, molecular reagents and DNA sequences, he is using these programmes to study the 'relatedness' of slightly variant mediaeval texts. His group is also refining methods to study the ancient DNA signatures from mediaeval parchments, not just to determine the animal sources, but also the relatedness of the animals used.

Peter Forster has also extended these programs from molecules to words, to explore the contentious ancestry of certain Indo-European languages. His analysis of the Celtic family group raised alarm bells among certain historic linguists, as it broadly supported Colin Renfrew's hypothesis of linkage with the spread of early farming. However, a similar, more wide-ranging analysis of Indo-European languages, also using phylogenetic programs, has arrived at a similar conclusion.

Genes and beyond

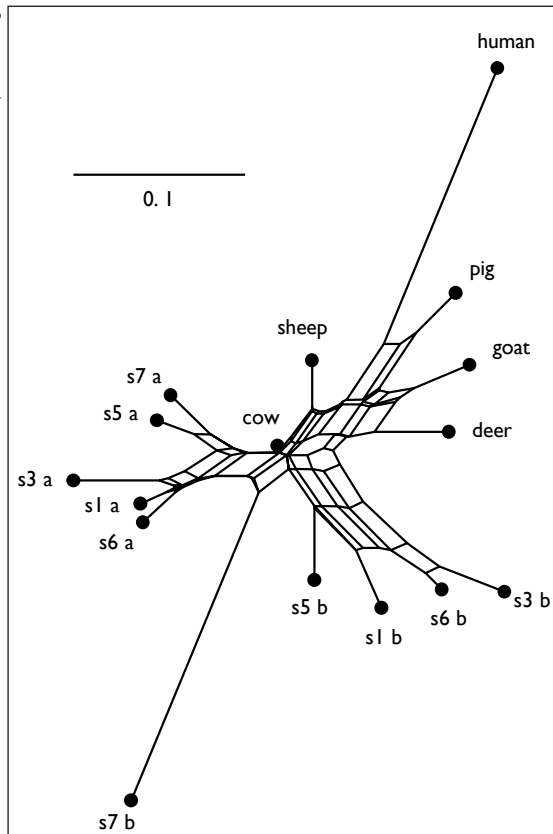
Much of the interface between DNA science and archaeology has exploited DNA sequences as a kind of neutral tracker, charting family relationships without getting too confused by other issues. However, DNA sequences are also a driver of our form and structure, and one of the exciting directions of the archaeology / genetics interface is an exploration of the links between DNA, active genes and the tangible world of human life and its varied forms. Robert Foley and Marta Lahr are pioneering the study of the genetic basis of human physical variation. Their Leverhulme Centre of Human Evolutionary Science, soon to move into a new, state-of-the-art building, will take forward modern and

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One of the parchment specimens with which the University of Cambridge has been experimenting: a legal document, written in Oxford in 1830.

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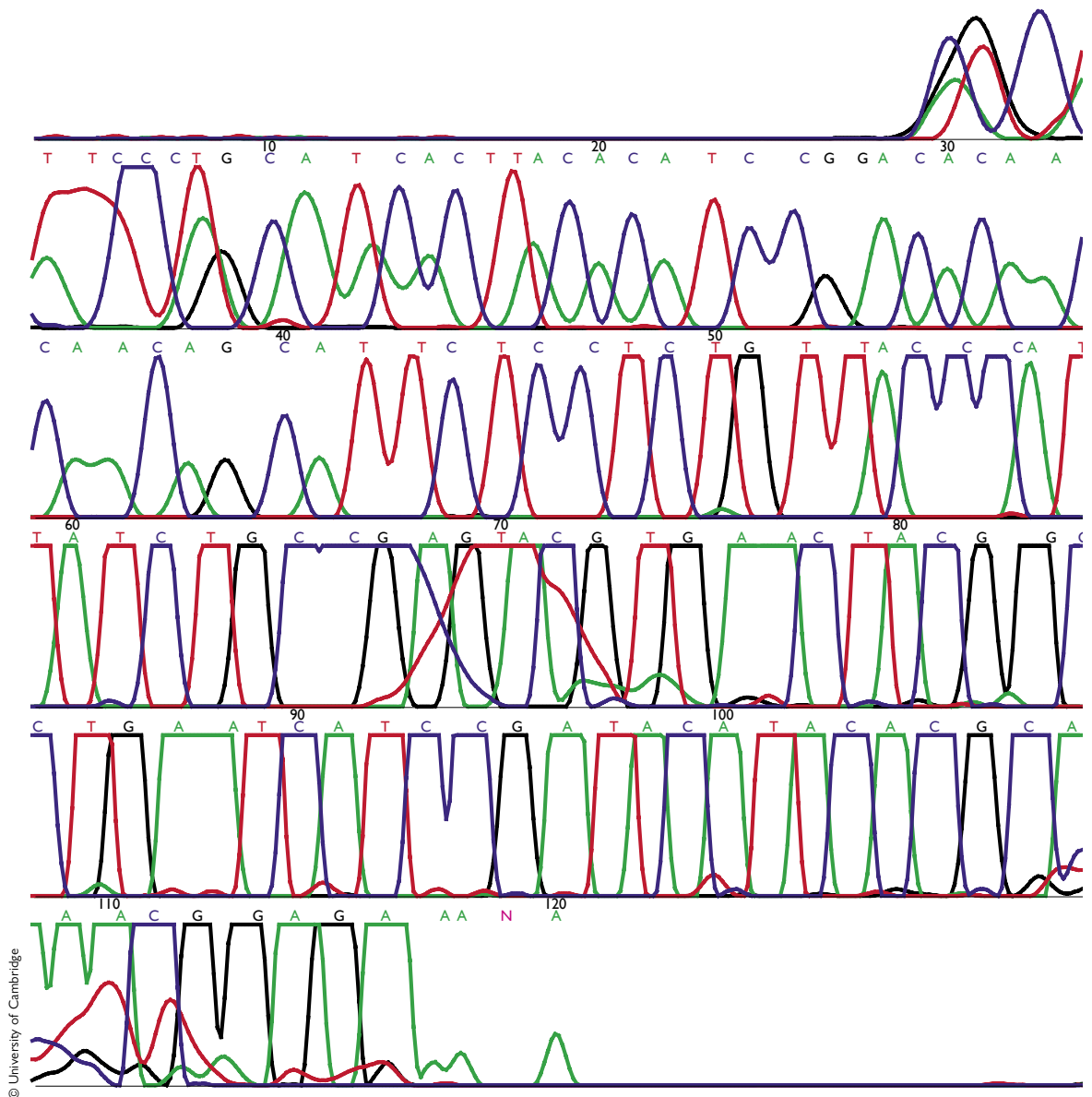


DNA sequences from parchment samples (labelled s1 a, s1 b, ...) compared to those from common domestic animals. Lines on the graph represent possible evolutionary relationships, with lengths proportional to the number of nucleotide differences. Parchment samples are closest to those from cow, with differences probably caused by post-mortem damage.

ancient DNA studies in the context of traditional human skeletal and behavioural studies.

Human health and disease

Another Cambridge anthropologist, Leslie Knapp, explores the relationship between health, disease and genetics among the wider primate group, which included humans. Her research group is studying the major histocompatibility complex (MHC) group of genes among a variety of primates. These are genes that are fundamental to our immune system, providing resistance to malaria, tuberculosis, HIV infection and even SARS. However, they not only affect our resistance to diseases, as Dr Knapp's work demonstrates that they also have a discernible effect on our social and mating behaviour. Thus, a complex series of patterns is interconnected. At one end



Typical DNA sequence results. Each coloured line represents the amount of one of the four kinds of nucleotide at a particular point in the sequence. An unambiguous sequence will have a clear pattern of peaks without overlaps, but ancient DNA sequences are often damaged and hard to read. The letters above the peaks indicate the corresponding nucleotides in the sequence.

lie those subtle, unspoken signals that attract us to one another and to the social worlds we build around that attraction. In the middle is the ecology of disease resistance that will be strengthened in the offspring that attraction generates. At the other end is the complex but tangible chemistry of sequences of DNA, which to a great extent we share with many of our animal relatives.

SELECTED PAPERS

- Barbrook A C *et al* 1998 'The phylogeny of the Canterbury Tales'. *Nature* **394**, 839
- Forster P & Toth A 2003 'Towards a phylogenetic chronology of ancient Gaulish, Celtic, and Indo-European'. *Proceedings of the National Academy of Sciences USA* **100**, 9079–84
- Grob, B *et al* 1998 'The major histocompatibility complex and mate choice: inbreeding avoidance or selection of good genes?' *Clinical and Experimental Immunology* **15**, 119–29

- Howe C J *et al* 2001 'Manuscript evolution'. *Trends in Genetics* **17**, 147–52; Reprinted in *Endeavour* **25**, 121–26
- Jansen T *et al* 2002 'Mitochondrial DNA and the origins of the domestic horse'. *Proceedings of the National Academy of Sciences USA* **99**, 10905–10
- Jones M K 2004 'Archaeology and the genetic revolution', in Bintliff, J (ed) *A Companion to Archaeology*. Oxford: Blackwell, 39–51
- Jones M K & Brown T A 2000 'Agricultural origins: the evidence of modern and ancient DNA'. *Holocene* **10** (6), 775–82
- Knapp L A 2002 'Evolution and immunology'. *Evolutionary Anthropology* **11**, 140–44
- Lahr, M M & Foley R A 2001 'Genes, fossils and behaviour: when and where do they fit?', in Donnelly P and Foley R A (eds) *Genes, Fossils and Behaviour: An integrated Approach to Human Evolution*. Brussels: IOS Press, 13–48
- Roy-Choudhury, S & Knapp L A 2001 'Human Reproductive Failure II: Immunogenetic and Interacting Factors'. *Human Reproduction, Update* **7** (2), 135–60
- Underhill, P A *et al* 2001 'The phylogeography of Y chromosome binary haplotypes and the origins of modern human populations'. *Annals of Human Genetics* **65**, 43–62