The past comes alive

Bryan Sykes

"Pig Brings Home The Bacon on DNA." Thus was the readership of one newspaper alerted to the revelation that Henry VIII's pork chop came from a pig. Hardly a triumph of historical reconstruction this, but nonetheless an important step in the process of authenticating the amplification of DNA from all sorts of dead things. Everybody is having a go — and apparently succeeding — at getting DNA from museum specimens, dried insects, mummies, old bones and fossil plants and, quite rightly, the press loves it. A meeting* last month provided a further outlet for reporting these efforts.

It all began in 1984 when Russell Higuchi and his colleagues managed to clone mitochondrial DNA (mtDNA) sequences from a 140-year-old museum skin of quagga, an extinct beast which looks like a cross between a zebra and a horse¹. The following year Svante Pääbo reported his cloning from 5,000-year-old Egyptian mummy skin and liver². This was hard cloning from exotic sources. Access to the field was widened by the polymerase chain reaction and by the discovery of amplifiable DNA in old bone³, which forms the great bulk of surviving organic material from the past.

Generally, ancient DNA is in pretty bad shape. It comes in short pieces, looks crosslinked under the electron microscope and is damaged to the extent that bases are often oxidized or missing. The *Taq* polymerase copes with such poor quality material by skipping between overlapping extension products if no continuous segment is present, but it has the habit of substituting adenines when it jumps from one strand to the other (S. Pääbo, University of Munich). The amplification products thus contain random errors, which can be averaged out by direct sequencing, and are chimaeric in the sense that they are not copies of a single contiguous target. This does not matter if the target is haploid (mtDNA for instance), but for diploid and higher ploidy nuclear genomes, which are not uncommon in plants and fishes, the products might well be from more than one allele. This has led to complexities in reconstructing *HLA-DQ* haplotypes from the remarkably preserved human brains from the Windover peat pit in Florida (ref. 4; W. Hauswirth, University of Florida). The site contains 91 well-preserved brains from a total of 177 skeletons buried 6,000–8,000 years ago. By both dot-blotting of amplified *HLA-DQ* alleles with specific oligonuc-

leotides, and amplification of cytosine-adenine dinucleotide repeats in the *Apo-A2* gene, the same alleles have been detected in individuals buried 1,000 years, or about 50 generations, apart.

Unusually good preservation conditions, when a basalt flow dammed a steep wooded valley creating a deep anoxic lake which silted up rapidly, have produced the record for the oldest DNA so far. This was from a magnolia leaf between 17 and 20 million years old (ref. 5; E. Golenberg, Wayne State University). Leaves of other species from the same deposits, including cypress, oak and tulip tree, have also given DNA. The sequences of the chloroplast rubisco genes are recognizably specific and the results have now been verified in three different laboratories. This means these compression fossils defy the prediction, from *in vitro* estimates of the rate of spontaneous hydrolysis, that no DNA would remain intact much beyond 10,000 years. What a good job not everybody knew that, grant reviewers included.

The *Clarkia* fossil sequences from the Miocene are being used to construct their molecular phylogenies, and this is clearly an area in which ancient DNA will help tremendously. A nice example is the examination of the moas from New Zealand. There were eleven species of these flightless birds, ranging from 3 to 11 feet in height, and they were all

eliminated by AD 1500 after the arrival of the Polynesians. Sequences of 12S ribosomal RNA from bone and soft-tissue remnants from four of the eleven species showed them to be very closely related despite the considerable morphological differences, a phenomenon common in island populations, and not at all close to New Zealand's other living ratites, the three species of kiwi (A. Cooper, Victoria University, Wellington). Neither were the moas closely related to the Australasian emu and cassowary, which are in turn closer to the ostrich.

Dried skins from a very large museum collection of kangaroo rats (a topic covered in News and Views⁶) were used to bring home the point that the extent of variation needs to be matched by sample size if any sense is to be made of ancient population surveys (K. Thomas, University of California, Berkeley). Mitochondrial D-loop sequencing from rats collected between 1911 and 1930 defined 23 mtDNA haplotypes or 'mitotypes'. Present-day sampling from the same site showed some mitotypes had been replaced by others but, because of the large number of variants, this was still not sufficient to be able to say that gene frequencies had changed significantly. The problem will be a considerable one for all those attempting to interpret the genetic structure of past populations and draw conclusions about, for example, the maintenance of genetic diversity following population bottle necks. Projects to do just that with, at one extreme, the Hawaiian goose (R. Fleisher, Smithsonian Institute,

Jerry Young

IMAGE UNAVAILABLE FOR COPYRIGHT REASONS

In December 1989 the skeletal remains of a young female murder victim were discovered by workmen in the garden of a terraced house in Cardiff, Wales. She had been dead for several years. With little more to go on than her hair and approximate age from dental records, a remarkable reconstruction led to the unequivocal identification of the girl by bone DNA typing, as described by Hagelberg, Gray and Jeffreys on

page 427 of this issue. The initial breakthrough came from the facial reconstruction by Richard Neave, a medical artist at Manchester University. Neave made a plaster cast of the skull and then meticulously built up the facial muscle using modelling clay (left). In little more than a day, the model was complete (right). Two days after pictures of it were released a Cardiff social worker telephoned the police believing the victim to be Karen Price, who had run away from a children's home in July 1981. Although dental records strongly supported the identification, final confirmation came when Jeffreys and coworkers amplified and typed DNA from bone samples using the polymerase chain reaction (PCR). The results were entirely consistent with the victim being the daughter of the presumptive parents, and marked the first instance of PCR-derived forensic evidence being accepted by a British court. **Kevin Davies**

*Ancient DNA, University of Nottingham, 8–10 July 1991.