scrambling while causing only a minor perturbation in the structure. The result (although low-resolution) was the first infrared spectrum of CH_5^+. But theoretical calculations[11] have already indicated that although their $CH_5^+(H_2)$ complex is weakly bound as expected, it still has unrestricted internal degrees of freedom: multiple structures with H_2 bound to one of the protons of the three-centre/two-electron bond are predicted to have essentially the same energy, allowing again practically unrestricted rotational and scrambling motion of the H_2 about the CH_5^+. So extracting precise structural information for the core CH_5^+ unit from this $CH_5^+(H_2)$ complex could be extremely difficult.

It seems, then, that the concept of a molecular 'equilibrium geometry' is not valid for CH_5^+. Rather than a picture of a single structure about which the atoms vibrate, a model in which 'delocalized' vibrational modes allow atoms to move almost freely over large regions of space is probably more appropriate. The representation of CH_5^+ stemming from the calculations of Schreiner *et al.* is that of a floppy molecule without a definite structure. Far from being the prototypical nonclassical carbocation, the authors conclude, CH_5^+ is unique. □

Gustavo E. Scuseria is in the Department of Chemistry, Rice University, PO Box 1892, Houston, Texas 77251, USA.

1. Schreiner, P. R., Kim, S.-J., Schaefer, H. F. & Schleyer, P. v. R. *J. chem. Phys.* **99**, 3716–3720 (1993).
2. Olah, G. A. *Carbocations and Electrophilic Reactions* (Verlag Chemie, Weinheim, 1973).
3. Klopper, W. & Kutzelnigg, W. *J. phys. Chem.* **94**, 5625–5630 (1990).
4. Schleyer, P. v. R. & Carneiro, J. W. de M. *J. comput. Chem.* **13**, 997–1003 (1992).
5. Olah, G. A., Prakash, G. K. S. & Sommer, J. *Superacids* (Wiley, New York, 1985).
6. Scuseria, G. E. & Lee, T. J. *J. chem. Phys.* **93**, 5851–5855 (1990).
7. Scuseria, G. E. *J. chem. Phys.* **94**, 442–447 (1991).
8. Bauschlicher, C. W. & Langhoff, S. R. *Science* **254**, 394–398 (1991).
9. Raghavachari, K. *A. Rev. phys. Chem.* **42**, 615 (1991).
10. Boo, D. W. & Lee, Y. T. *Chem. Phys. Lett.* **211**, 358–363 (1993).
11. Kim, S.-J. *et al. J. phys. Chem.* (in the press).

ANCIENT DNA

Less cause for grave concern

Bryan Sykes

IT'S been a busy time for those involved in analysing ancient DNA since That Film came out this summer. Having spent a few months reassuring the public that cloning dinosaurs, as portrayed in *Jurassic Park*, is science fiction, they met in Washington* to reassure each other that at least the survival of DNA beyond the grave was anything but.

Gone, thank goodness, are the days when merely obtaining an amplification product from some biological antique was grounds for celebration, especially when its sequence vaguely resembled something in the nucleotide databases. In the two years since the first international conference in Nottingham[1], when everyone in the field woke up to the unpleasant fact that contamination with modern DNA was all too common, the mood has become one of caution rather than exuberance. All of the speakers in Washington stressed the need for stringent precautions for avoiding contamination, including the vigorous surface treatments of specimens to remove DNA-rich fingerprints.

This is, of course, a particular problem when dealing with human bones, but there are several examples of apparently authentic recoveries of human DNA that have survived rigorous decontaminating procedures. Among these are an impressive series of 98 skeletons excavated from a 2,000-year-old Amerind site in Norris Farms, Illinois (A. Stone, Penn State University), a smaller series from an older palaeoindian site at Port au Choix, Newfoundland (B.S.), several Central and South American mummies (A. Merriwether, University of Pittsburgh; C. Kolman, Smithsonian Tropical Research Institution) and remains from Easter Island (E. Hagelberg, University of Cambridge). These are all amplifications of mitochondrial DNA which, despite some widely publicized statistical setbacks (see, for example, ref. 2), continues to be a most informative marker for at least relatively recent human population movements.

Accepting these derived sequences as genuine is easier because they all fit into an appropriate phylogenetic context; indeed, the construction of these contexts using DNA from extant populations is proving to be absolutely vital. Another good sign that sequences are genuine is a concordance between anthropometric and DNA-based sexing, which was achieved in both Norris Farms and Port au Choix populations using either Y-chromosome-specific repeats or sex-chromosome-specific differences in the amylogenin gene.

Contamination neurosis is understandably less severe among those who work on animal and plant remains, and there were convincing accounts of credible sequences from, among others, the giant ground sloth (M. Höss, University of Munich), extinct cave bears (C. Hanni, Institut Pasteur de Lille), long-dead rabbits (M. Monnerot, CNRS, Paris) and extinct Hawaiian birds (A. Cooper, Smithsonian Institution). The over-enthusiasm of nineteenth-century collectors has been put to good use when comparing the genetic diversity in museum collections with that of extant populations which, like the whooping crane (T. Quinn, Smithsonian Institution) and the red panda (R. Wayne, Zoology Society of London), have gone through a population bottleneck in recent times.

Phylogenetic fidelity, however, is the least of the worries as far as the amazing claims that DNA survives in amber for over 100 million years are concerned. Both G. Poinar (University of California, Berkeley) and R. Cano (California Polytechnic, San Luis Obispo) catalogued the painstaking precautions they had taken during extraction of DNA from entombed weevils[3] and bees[4]. Nothing obvious had been overlooked, and the sequences of both the insects and their indigenous enterobacteria (interestingly confined to the abdomen) are plausibly different from their modern equivalents.

The opposition was in the form of the spiritual (but not physical) presence of T. Lindahl, whose disbelief that DNA can survive time-dependent, mainly oxidative, decay much beyond 50,000 years stems from extrapolations of experimentally determined rates of damage in solution[5–7]. This clash between pride and prejudice will not be resolved until there is ample independent verification of the amber data. On a hopeful note, it seems that the damaged DNA from ancient specimens is not beyond repair, using glycosylases to sand down the DNA, then polymerases and ligases to fill and polish it (L. Grossman, Johns Hopkins University); and there has been at least one successful attempt at reviving Pleistocene DNA using the repair systems of *Escherichia coli* (Höss).

The power of ancient DNA is at its greatest when it can answer historical questions posed by other disciplines, such as the colonization of the Americas and the Pacific and, in Europe, the Anglo-Saxon settlement of England. After the shock of Nottingham enough careful, rigorous and reproducible work has been done to at least reassure those present that this really is going to work and that we are not, after all, dealing with the molecular biological equivalent of cold fusion. □

Bryan Sykes is in the Institute of Molecular Medicine, University of Oxford, Oxford OX3 9DU, UK.

1. Sykes, B. C. *Nature* **352**, 381–382 (1991).
2. Templeton, A. R. *Science* **255**, 737 (1992).
3. Cano, R. J. *et al. Nature* **363**, 536–538 (1993).
4. Cano, R. J., Poinar, H. N. & Poinar, G. O. Jr *Med. Sci. Res.* **20**, 249–251, 619–623 (1992).
5. Lindahl, T. *Nature* **362**, 709–715 (1993).
6. Lindahl, T. *Nature* **365**, 700 (1993).
7. Poinar, G. O. *Nature* **365**, 700 (1993).

*Second International Conference on Ancient DNA, Smithsonian Institution, Washington DC, 7–9 October 1993.