

## Mito-communications

SIMON Y. W. HO<sup>1</sup> & ROBERT LANFEAR<sup>2</sup>

<sup>1</sup>School of Biological Sciences, University of Sydney, Sydney, Australia, and <sup>2</sup>Research School of Biology, Centre for Macroevolution and Macroecology, Australian National University, Canberra, Australia

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### Ancient mitogenome from an unknown hominin

There has been much recent genetic work on ancient hominins, made possible by the availability of high-throughput sequencing methods. In a paper published in *Nature*, Krause et al. (2010) have presented the sequence of an unknown hominin from Denisova Cave in southern Siberia, dated to 30,000–48,000 years before present. The authors used two different approaches to sequence the mitogenome, achieving an average 156-fold coverage.

The new hominin sequence is remarkable not only because of the methodological challenges that were surmounted—which in itself represents a creditable achievement—but also owing to the estimated phylogenetic placement of the individual. When analysed alongside sequences from a modern human, a Neanderthal, and a common chimpanzee, the hominin was estimated to have diverged from humans and Neanderthals about 1 million years ago. This timing is intriguing because it substantially antedates the spread of *Homo heidelbergensis*, the species thought to have given rise to Neanderthals and modern humans less than 500,000 years ago (Endicott et al. 2010). The estimated divergence also postdates the spread



### Population dynamics of cave bears in the Pleistocene

The megafaunal extinctions of the late Pleistocene have long fascinated biologists and the wider community.

of *Homo erectus* out of Africa, which occurred about 1.9 million years ago.

The analysis of the Denisova Cave hominin raises the intriguing possibility that there might have been three distinct hominin species co-existing 40,000 years ago in central Asia. However, the new mitogenomic sequence represents only a single genetic locus, and it would be premature to draw any conclusions about species status without additional evidence from the nuclear genome. Further morphological data would also be invaluable. In addition, there is some uncertainty over the dating of the individual, and this will need to be investigated rigorously.

The hominin tree has undergone some dramatic changes over the past decade. Unfortunately, samples from another enigmatic hominin, *Homo floresiensis*, have so far failed to yield genetic data and appear to be beyond the reach of ancient-DNA techniques.

### References

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Ongoing dispute over the causes of these extinctions, focusing on the relative impacts of climatic and anthropogenic factors, has induced researchers to utilise a range of methods to evaluate competing

Correspondence: R. Lanfear, Research School of Biology, Australian National University, Building 116 Daley Road, Canberra, Australian Capital Territory 0200, Australia. Tel: +61 2 6125 7270. Fax: +61 2 6125 5573. E-mail: rob.lanfear@anu.edu.au

hypotheses (Barnosky et al. 2004). In recent years, data from ancient DNA have been brought to bear on this question. For example, studies on bison (Shapiro et al. 2004), lions (Barnett et al. 2009) and other species have revealed substantial changes in genetic structure coincident with climatic change in the late Pleistocene.

In a recent study, Stiller et al. (2010) conducted analyses of ancient DNA to investigate the population dynamics of cave bears and brown bears, two species that have received considerable attention in molecular studies. The authors assembled datasets comprising 42 published and 17 novel sequences from cave bears, and 40 published sequences from brown bears. These two datasets were then analysed using a Bayesian phylogenetic approach that enables the estimation of population history from sequence data (Drummond et al. 2005).

Stiller et al. (2010) found that the population size of cave bears experienced a marked decline from 50,000 years ago until their extinction 25,000 years ago. This suggests that the decline was unlikely to have been driven exclusively by climatic change associated with the onset of the Last Glacial Maximum, which began about 30,000 years ago. Instead, the authors propose that modern humans, who arrived in northern Eurasia about 50,000 years ago, might have competed with cave bears for suitable cave sites. In contrast, the



### Mutational processes differ significantly between closely related nematodes

Understanding the mutational processes that shape genomes is of central importance to many areas of biology. Mutations are implicated in a huge number of diseases, and in the process of ageing (Kujoth et al. 2007). Furthermore, almost all analyses of DNA sequences make assumptions about mutational processes, but in many cases relatively little is known about the validity of these assumptions. A new study (Howe et al. 2010) reports the results of two mutation accumulation experiments that were used to measure mutational processes in the mitogenomes of laboratory strains of the nematode *Caenorhabditis briggsae*. The rates and types of mutation in the two strains were compared with each other, and with those in the closely related nematode *Caenorhabditis elegans* (see Denver et al. 2000). Mutational processes in *C. briggsae* were found to differ from those in *C. elegans* in two important ways. First, *C. briggsae* suffers from significantly higher rates of large deletions than *C. elegans*. Second, although overall rates of single-base-pair substitution mutations in the two species are strikingly similar, the spectra of the mutations that occurred were significantly different. The observation of significant differences in mutational processes between two such closely related species highlights the need for models of molecular evolution that can account for such differences (see, e.g. Baer et al. 2007).

demographic analysis of brown bears did not find any measurable population decline during the same period (late Pleistocene and Holocene).

The study by Stiller et al. (2010) demonstrates the effectiveness of ancient DNA analysis in reconstructing past population dynamics. In coming years, ancient DNA will play an increasingly important role in the debate surrounding megafaunal extinctions in the late Pleistocene.

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Perhaps the most surprising result of Denver et al.'s study is that the mutational spectra appeared to be quite different even between the two *C. briggsae* strains. All six of the observed single-base-pair substitution mutations in one strain (PB800) were from C:G to T:A base pairs, whereas this type of mutation accounted for only one of nine mutations in the other strain (HK104). This difference is not quite statistically significant, but provides a tantalising suggestion of a very surprising result, and it will be fascinating to see whether this result is confirmed by additional data. The measurement of differences in mutational processes between species (and possibly strains) of model organisms such as *C. briggsae* and *C. elegans* provides rich fodder for further understanding the hows and whys of mutation in animal mitogenomes.

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