

Mito-communications

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(Received 16 November 2008; accepted 18 November 2008)



Report on the 3rd International Symposium on Biomolecular Archaeology

The 3rd International Symposium on Biomolecular Archaeology (ISBA3) was held in York, 14–16 September, bringing together over 175 researchers working on population genetics, stable isotopes, and mass spectrometry. Along with the International Conference on Ancient DNA and Associated Biomolecules, the biennial ISBA meeting is one of the key gatherings of ancient DNA researchers in Europe and beyond.

Not surprisingly, the continued dominance of mitochondrial DNA (mtDNA) in ancient DNA research was noticeable. A variety of mtDNA research was presented, focusing primarily on human evolution and migration, as well as animals of archaeological interest (bovines, goats, horses, chickens, and mice). Some delegates expressed reservations over ancient human mtDNA research, drawing attention to the perennial problem of modern contaminants.

The prize for the best student talk was awarded to Meirav Meiri (Royal Holloway, University of London, UK), who presented a population study of European red deer based on analyses of modern and ancient mtDNA. She used this case study to illustrate the difficulty in recovering complex demographic histories from modern mtDNA alone.

Abstracts from the meeting can be found on the official meeting website (<http://www.york.ac.uk/depts/arch/ISBA3>). Future meetings will be held in Copenhagen (2010) and Amsterdam (2012).



Ursid mitogenomics

The phylogeny of the bear family (Ursidae), comprising eight extant species and a number of extinct relatives, has been the object of extensive research and revision. Recently, three separate groups have attempted to resolve the issue by analysing complete mitochondrial genomes.

In the first paper, Yu et al. (2007) inferred the ursid phylogeny using a dataset consisting of three published and five novel mitochondrial genome sequences. Earlier this year, Krause et al. (2008) sequenced the mitochondrial genomes of two extinct species, the American giant short-faced bear and the cave bear, and analysed these along with the eight modern bears. In a recent issue of *Proceedings of the National Academy of Sciences of the USA*, Bon et al. (2008) described the successful retrieval of the mitochondrial genome of a cave bear from a Paleolithic painted cave. As reported in *Science* by Balter (2008), there has been some dispute over the priority of the two cave bear mitogenomic sequences.

The first three articles share a number of findings in common. Most notably, all three inferred the same evolutionary relationships among ursid species, while noting the presence of incongruent phylogenetic signals among genes. This carries the implication that previous estimates of the bear phylogeny, based

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on partial mtDNA, were probably misled by sampling error.

In all three studies, the estimated divergence times led the authors to conclude that bears underwent rapid speciation. Nevertheless, there is drastic disagreement over the time-scale of ursid evolution. For example, Krause et al. (2008) infer an age of 19 million years for the split between the giant panda and other bears, whereas the Yu et al. (2007) and Bon et al. (2008) analyses actually calibrate their dating analyses by assuming an age of 12 million years for this event. Both the Krause et al. and Yu et al. studies estimate that most of the extant bear species diverged rapidly around 5–6 million years ago, but Yu and colleagues place these divergences around 1–3 million years before present.

Collectively, these papers illustrate the potential of mitogenomic analysis. Their convergence on the same tree is reassuring, but the diversity of date

estimates provides a cogent reminder of the sensitivity of divergence-dating analysis to the choice of calibrations.

References

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(Received 23 November 2008; accepted 1 December 2008)



Ancient human mitogenomics

In 1991, two German hikers discovered the frozen body of Ötzi, the Tyrolean Iceman, high in the Alps between Austria and Italy. Dating from the end of the Neolithic, Ötzi has been the subject of considerable media attention, partly due to an ownership dispute between Austria and Italy, as well as various parties competing over the rights to a finder's fee. Perhaps even more dramatic have been the sensational reports of "Ötzi's curse", which has purportedly seen the deaths of seven people associated with handling and analysing the Iceman's remains.

In a recent issue of *Current Biology*, Luca Ermini and colleagues report the complete DNA sequence of Ötzi's mitochondrial genome, obtained using a combination of Sanger sequencing and pyrosequencing (Ermini et al. 2008). The genome was found to differ from the revised Cambridge Reference Sequence by 30 transitions, and was confirmed as being a member of the west Eurasian mitochondrial DNA haplogroup K. Among 115 modern representatives of this haplogroup, there were no exact matches

to Ötzi's sequence. Indeed, the authors take this, among other factors, as being indicative of the authenticity of the sequence.

Together with the recently published sequence from a Paleo-Eskimo (Gilbert et al. 2008), the Ötzi project has pushed back the boundaries of ancient human mitogenomics. This reflects an increasing confidence in our ability to detect and exclude contamination in ancient DNA studies of humans. Further sequencing efforts will be required in order to gauge the potential for recovering complete mitochondrial sequences from human samples preserved under less favourable conditions.

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(Received 3 December 2008; accepted 4 December 2008)



Goat domestication

The domestication process has been the focus of a number of high-profile genetic studies. These have often involved analyses of large mitochondrial datasets containing hundreds of DNA sequences, which are used to estimate the timing, number, and location of domestication events. Naderi et al. add to this growing literature with their recent investigation of goat domestication, conducted using a comprehensive DNA sample from bezoars, the wild progenitors of goats. Their collection of 600 specimens, obtained from over 40 locations throughout the modern geographic distribution of the bezoar, yielded 469 mitochondrial DNA sequences. By comparing these with the haplotypes of domesticated goats, they place the main centre of domestication in Eastern Anatolia, an estimate that is consistent with the available archaeological evidence.

Naderi et al. find relatively little genetic structure among the bezoar samples, suggesting that there has been extensive human-mediated translocation of animals in the past. The authors then infer the

demographic history of the bezoars by performing a Bayesian skyline plot analysis, which traces the effective population size over time. As with other coalescent-based analyses of domesticated animals (e.g. Finlay et al. 2007; Ho et al. 2008), there is strong genetic evidence of rapid population growth associated with the domestication process. It is likely that ancient DNA and additional data from nuclear markers will be able to offer further insights into goat domestication.

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Partial deletion of the mitochondrial control region

The Genographic Project has been curating a growing database of human mitochondrial genome sequences, of which over 120,000 have been acquired through their public participation programme. Among these genomes, Behar et al. report a 154-base-pair deletion in the control region of an anonymous Japanese woman (haplogroup A1a). The authors confirm the presence of the deletion using a variety of methods, including repetition of the amplification and sequencing procedure using multiple primer pairs.

The deletion is also present in the woman's two sons and does not appear to have a detrimental health

impact, although the authors were unable to exclude the possibility of an unknown or slightly deleterious effect on fitness. Nevertheless, it is interesting that the mitochondrial genome is still able to replicate and function despite the loss of more than 10% of the control region. Behar et al. conclude their report by discussing the implications of the deletion for our understanding of the mitochondrial replication mechanism.

Reference

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Corrigendum

The author would like to apologise for an error that occurred in the iFirst publication of *Mitochondrial DNA*,

DOI: 10.1080/19401730802644994 [ePub 09 January 2009]

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The sentence below should replace what is currently present.

Page 2:

Both the Krause et al. and Yu et al. studies estimate that most of the extant bear species diverged rapidly around 5–6 million years ago, but Bon and colleagues place these divergences around 1–3 million years before present.