



Sequencing archaic human DNA

SEMINAR PRESENTED BY THE CENTRE FOR ARCHAEOLOGICAL SCIENCE (CAS)

DATE: MONDAY 29 JANUARY
TIME: 12:30-1:30PM
VENUE: 41.G03A, UOW
PRESENTER: MATTHIAS MEYER

Matthias Meyer is a biochemist and head of the "advanced DNA sequencing techniques" group at the Max-Planck-Institute for Evolutionary Anthropology in Leipzig, Germany. He has developed many methods that improve the scope of DNA sequencing in evolutionary studies, a work that has led to the generation of the first high-quality genome sequences from archaic humans as well as the recovery of the oldest DNA sequences known to date from fossils discovered outside the permafrost.



SEMINAR OVERVIEW:

Advances in DNA sequencing technology and sample preparation techniques have greatly improved the scope of ancient DNA research in recent years. High quality genome sequences are now available not only from early modern humans but also their extinct archaic relatives. These include the genomes of Neanderthals and Denisovans living in the Late Pleistocene, the latter of whom were identified as an Eastern Eurasian sister group to Neanderthals based predominantly on the analysis of their DNA rather than fossil evidence. DNA sequences were also recovered from the ~400,000 year-old hominin fossils of Sima de los Huesos, Spain, extending the temporal depth of ancient DNA analysis from the Late to the Middle Pleistocene. Due to the scarcity of the hominin fossil record in the Pleistocene and variability in DNA preservation, archaic human DNA could until recently only be recovered from a relatively small number of sites. This is about to change due to the discovery of ancient hominin DNA in Pleistocene cave sediments. This presentation will summarize the progress that has been made in the analysis of archaic human DNA and highlight some of the insights this work has provided for our understanding of human evolutionary history.



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