

DNA analysis of ancient remains to uncover origin mysteries

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Griffith University researchers will analyse DNA sequences from ancient human remains, some dating back 45,000 years, to determine the origins of the peoples of South-east Asia and Australia.

In collaboration with the Universities of Auckland, Copenhagen and [New South Wales](#), the researchers will analyse human remains from continental and oceanic Asia and Australia using more powerful newly developed [ancient DNA](#) sequencing methods.

Chief Investigator Professor David Lambert from the School of Environment says understanding where the earliest people of Asia and continental Australia came from is critical to understanding modern [human evolution](#).

"The recent sequencing of the Australian Aboriginal genome has identified two waves of [human migration](#) through Asia," he said.

"Aboriginal Australians descended from an early human dispersal into eastern Asia, possibly 62,000 to 75,000 years ago.

"This dispersal is separate from the one that gave rise to modern Asians 25,000 to 38,000 years ago, although there is evidence for hybridisation between them."

The researchers aim to identify descendent individuals from both lineages and detect historic patterns of [interbreeding](#) among these early

people.

Professor Paul Tacon from Griffith University's Place, Evolution & Rock Art Heritage Unit said the research was a world-first study to attempt to recover human [DNA sequences](#) from more than 80 ancient human remains collected from a range of time points.

"We aim to identify the mitochondrial DNA lineage of each sample of human remains, the migration wave they represented and evidence of biological interactions, such as hybridisation with other groups.

"Although complete or draft genomes have been recovered from extinct species such as Neandertals and Woolly Mammoths, there are no existing populations of these species available for comparison.

"But an increasing number of complete human genomes in our study provide the foundation for this work."

Professor Tacon said the study was possible because of recent advances in second-generation DNA sequencing and parallel developments in DNA target capture technologies.

"These developments provide extraordinary new possibilities in the field of ancient human genomics."

The study is part of a \$550,000 three-year Australian Research Council Linkage Grant.

Provided by Griffith University

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