

Centre for GeoGenetics 2016

Highlights of the year

In 2016, we published 3 papers in *Nature* (two Articles and one Letter) and a total of 103 papers including journals like *PNAS* and *Current Biology*.

Among these was the first genome study of Aboriginal Australians and highland Papuans (*Nature*). The population history of Aboriginal Australians remains largely uncharacterized because of ethical concerns. By engaging with Aboriginal groups, we managed to obtain 83 samples across Australia and 25 from the New Guinea Highlands. We generated high-coverage genomes from these 83 Aboriginal Australians. We found that Papuan and Aboriginal Australian ancestors diversified 25–40 thousand years ago, suggesting pre-Holocene population structure in the ancient continent of Sahul (Australia, New Guinea and Tasmania). However, all of the studied Aboriginal Australians seem to descend from a single founding population that differentiated ~10–32 thousand years ago. We inferred a population expansion in northeast Australia during the Holocene epoch (past 10,000 years) associated with limited gene flow from this region to the rest of Australia, consistent with the spread of the Pama–Nyungan languages. We estimate that Aboriginal Australians and Papuans diverged from Eurasians 51–72 thousand years ago, following a single out-of-Africa dispersal, and subsequently admixed with archaic populations. Finally, we report evidence of selection in Aboriginal Australians potentially associated with living in the desert. The paper got the front cover of *Nature* (shared with two other papers of which GeoGenetics was part of two out of three). The journal *Science* highlighted the Australian paper among the breakthroughs of the year in 2016.

Another highlight was our work on reconstructing the biology of America's interior ice-free corridor (*Nature*). It has remained debated for centuries if the interior ice-free corridor was the travelling route for the first Americans coming in from Siberia. During the Last Glacial Maximum, continental ice sheets isolated Beringia (northeast Siberia and northwest North America) from unglaciated North America. By around 15 to 14 thousand years ago, glacial retreat opened an approximately 1,500 km long corridor between the ice sheets. It remains unclear when plants and animals colonized this corridor and it became biologically viable for human migration. We obtained radiocarbon dates, pollen, macrofossils and metagenomic DNA from lake sediment cores in a bottleneck portion of the corridor. We found evidence of steppe vegetation, bison and mammoth by approximately 12.6 thousand years ago, followed by open forest, with evidence of moose and elk at about 11.5 thousand years ago, and boreal forest approximately 10 thousand years ago. Our findings reveal that the first Americans, whether Clovis or earlier groups in unglaciated North America before 12.6 thousand years ago, are unlikely to have travelled by this route into the Americas. However, later groups may have used this north–south passageway.