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POPULATION GENOMICS

Off the beaten track

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Four new next-generation sequencing studies in ancient and modern humans report genomic insights from a large number of geographically diverse populations, adding greater detail to our picture of human genetic variation and population history.

The development of next-generation sequencing technologies has provided unprecedented power for inference in the field of population genetics, fuelling hopes that answers to long-standing questions regarding the origins of anatomically modern humans may be close at hand. One of the recurring themes has been the dispersal of anatomically modern humans out of Africa, which has been the subject of substantial debate.

With a focus on demographically smaller populations ignored by previous sequencing projects, Malaspinas *et al.* provide a comprehensive catalogue of human genetic diversity in Australia. The authors sequenced 83 Pama–Nyungan-speaking Aboriginal Australians and 25 Papuans from the New Guinea Highlands. Their analysis of Aboriginal Australian genomic diversity reveals shared genomic signatures of a single out-of-Africa dispersal with Eurasians, with the two populations diverging shortly after, estimated to be about 51–72 thousand years ago (kya). The team also found that Pama–Nyungan speakers and Highland Papuans descended from the ancestral population that first colonized Australia, and that they diverged about 37 kya.

Charles Wollertz/Alamy

In a second study, Mallick *et al.* find that present-day non-Africans descended from a single ancestral population. The authors present the Simons Genome Diversity Project (SGDP), the high-quality genome sequences of 300 individuals pertaining to 142 populations. The chosen populations were selected so as to cover a broad range of human genetic, linguistic and cultural diversity. The authors posit that their results are in keeping with skeletal and archaeological evidence showing the presence of early modern humans outside of Africa if early migrations occurred but did not contribute notably to present-day populations.

In a third study, Pagani *et al.* present the Estonian Biocentre Human Genome Diversity Panel (EGDP), a dataset that comprises 483 high-coverage human genome sequences from 148 global populations, including 379 new genomes from 125 populations. The EGDP findings match a multiple-dispersal model, as an early expansion of anatomically modern humans from Africa can be detected today in Australasia. Specifically, a genetic signature in present-day Papuans indicates that at least 2% of their genome originates from an ancestor that separated from Africans earlier than other Eurasians, estimated to be around 120 kya. This result is not necessarily contradictory to the first two studies, as these do not entirely exclude minor contributions from earlier migration waves.

A fourth publication by Skoglund *et al.* focusses on Oceania, analysing both ancient DNA from four individuals who lived on the South Pacific islands of Vanuatu and Tonga around 2.3–3.1 kya and DNA obtained from 778 modern-day individuals from East Asia and Oceania. The team found that the four ancient individuals had little to no Papuan ancestry, suggesting that existing Papuan ancestry in the South Pacific resulted after the first peopling of the islands through later human population migrations. These findings based on ancient DNA are in contrast to those of previously published genetic studies, highlighting the utility of and the need for systematic analyses of ancient DNA to detail population migrations and admixtures that have shaped the ancestry of present-day humans.

Taken together, this vast catalogue of novel high-quality genomes from diverse populations will allow new inferences to be made and existing models of human migration patterns to be refined, furthering our understanding of human history.

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ORIGINAL ARTICLES Malaspinas, A.-S. *et al.* A genomic history of Aboriginal Australia. *Nature* http://dx.doi.org/10.1038/nature18299 (2016) | Mallick, S. *et al.* The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. *Nature* http://dx.doi.org/10.1038/nature18964 (2016) | Pagani, L. *et al.* Genomic analyses inform on migration events during the peopling of Eurasia. *Nature* http://dx.doi.org/10.1038/nature19792 (2016) | Skoglund, P. *et al.* Genomic insights into the peopling of the Southwest Pacific. *Nature* http://dx.doi.org/10.1038/nature19844 (2016)

FURTHER READING Veeramah, K. R. & Hammer, M. F. The impact of whole-genome sequencing on the reconstruction of human population history. *Nat. Rev. Genet.* **15**, 149–162 (2014)