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Human migration

When early Polynesians migrated eastwards

Patrick V. Kirch

A genome-wide analysis of modern populations in Polynesia suggests the direction and timing of ancient Polynesian migrations. This model bears consistencies and inconsistencies with models based on archaeology and linguistics. **See p.522**

Determining the timing and sequence of people's discovery of and settlement in their island homes in the Pacific Ocean has been an enduring scientific problem. Genetic studies published in the past few years have determined the history of human movements across the southwestern Pacific[1], but the settlement of Polynesia remains the subject of ongoing debate. In a methodologically innovative study, Ioannidis *et al.*[2] (page 522) use genomic data to propose a sequence of migrations, starting in Samoa and progressing rapidly eastwards through the Southern Cook Islands in the ninth century, thence to the Society Islands and Tuamotu Islands, and finally, by the mid-fourteenth century, to the widely separated islands of the Marquesas, Raivavae and Rapa Nui (also known as Easter Island).

Rather than using ancient DNA recovered from skeletal remains, Ioannidis and co-workers' analysis used genome-wide data from 430 contemporary individuals from 21 island populations. The genomes of these modern populations contain a combination (or 'admixture') of ancestries as a result of the region's colonial history. Therefore, to work out the migratory path taken by the Polynesian ancestors of these individuals, the authors 'masked' genomic segments of non-Polynesian ancestry (that is, European or Native American ancestry). They then applied an innovative ancestry-specific analysis exclusively to those segments of the genetic code known to be of Polynesian origin.

The spread of populations across the eastern Pacific is marked by a 'telescoping' succession of genetic bottlenecks, known as founder events, in which small colonizing populations moved from one island to discover and settle on another. Such events lead to founder effects, whereby the small number of individuals who initiate new populations do not encompass the full genetic complement of the parent population. As a result, the subset of genetic variants from the parent population that were carried by individuals who established new populations are expected to be more frequent in the child population.

Ioannidis *et al.* measured the accumulation of the retained gene variants using a statistic called the directionality index – applied for the first time here to reconstruct human migrations. The directionality index therefore provides an arrow that links a child population back to its parent. To estimate the dates for parent–child population separations, the authors identified and analysed segments of DNA that were shared by pairs of individuals on different islands (and that were thus inherited from a common ancestor). This allowed the authors to compute how many generations had passed since the divergence of the individuals' ancestry.

That both the direction and the timing of human population movements can be inferred from the genomes of contemporary populations offers a powerful tool for historical anthropology. Moreover, the Pacific Islands provide ideal opportunities to test the coherence of historical inferences on the basis of independent lines of evidence[3]. Unlike on continents, where populations can readily move

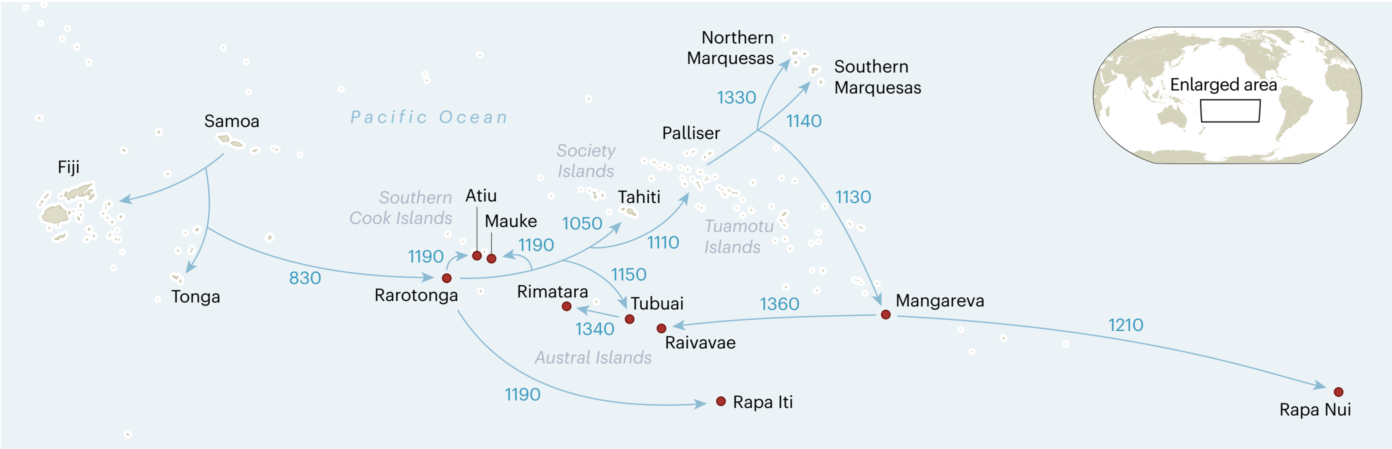

Figure 1 | A map of early eastward migration across Polynesia, informed by modern genomes. The timings and routes of migrations by early Polynesians to their island homes are controversial. Ioannidis *et al.*[2] analysed the genomes of 430 contemporary Polynesian individuals to infer the directions of early Polynesian migrations between islands. Moreover, by analysing fragments of DNA shared by individuals on different islands, the authors could estimate when those individuals' ancestral populations diverged (years AD shown in blue). The authors' model suggests that early Polynesians migrated from Samoa to the Southern Cook Islands in the ninth century and, from there, to the Society Islands and Tuamotu Islands. The model also suggests that the Marquesas Islands, Raivavae and Rapa Nui (also known as Easter Island) were settled by the twelfth to thirteenth centuries.

about and mix, the relative isolation of islands limits the possibilities for frequent population interactions.

To what extent does this genetic model agree with the latest inferences from archaeology or historical linguistics (Fig. 1)? Archaeological dating of Polynesian settlement has advanced greatly through the application of radiocarbon dating of short-lived plant materials using accelerated mass spectrometry, and high-precision dating of coral artefacts using uranium–thorium analysis[4,5]. The most recently proposed archaeological chronology for the settlement of the Eastern Polynesian region suggests that sites in the Cook Islands, Society Islands, Marquesas Islands and Mangareva were all settled between AD 900 and AD 1100. The discovery and settlement of all of Eastern Polynesia, including Hawaii and New Zealand, is suggested[6] to have occurred no later than AD 1250. This archaeologically attested time frame accords well with the chronology proposed by Ioannidis and colleagues, although there are some inconsistencies.

One disparity concerns the dating of the settlement of the Northern Marquesas Islands, which Ioannidis *et al.* put at AD 1330, nearly two centuries after their date of AD 1140 for the settlement of the Southern Marquesas Islands. Radiocarbon dating of the Hane archaeological site on the island of Ua Huka in the Northern Marquesas, however, establishes[7] that Polynesians settled there by about AD 900–1000. Moreover, it seems improbable that only the southern islands of the relatively small Marquesas archipelago would have been occupied for two centuries after the first arrival of people. Ioannidis *et al.* point out that their divergence times should be taken as the latest possible dates for settlement. Thus, using both the archaeological and genetic-divergence estimates to constrain each other, the timing of Polynesian settlement can be confidently bracketed to a remarkably precise historical span.

Ioannidis and colleagues' genetic model implies that the settlement of central Eastern Polynesia proceeded in a series of discrete island-to-island founder events, without substantial contact and gene flow between island populations after initial settlement. However, such a model is not entirely consistent with linguistic or archaeological findings.

The methods of historical linguistics provide models for the sequence in which languages have branched or diverged over time from an ancestral speech community. The Eastern Polynesian languages form a subset of a larger Nuclear Polynesian group of languages that also includes Samoan and the languages of the Polynesian outliers (that is, islands to the west of the 'Polynesian Triangle' that encompasses most of the Polynesian islands, with New Zealand, Hawaii and Rapa Nui at its corners). A revised subgrouping of the Eastern Polynesian languages[8] suggests that these closely related dialects diverged from each other in the context of considerable and continuing inter-island contact during the early period of eastward migration into the Eastern Polynesian archipelagos.

Similarly, archaeological evidence of the long-distance exchange of stone tools between early Eastern Polynesian communities reinforces the idea of substantial interactions between these populations[9]. Adzes (axe-like tools) made from stone quarried in the Marquesas and Austral islands were widely transported and exchanged between early communities across the rest of Eastern Polynesia. Reconciling the genetic model of discrete, sequential founder events with these linguistic and archaeological models of inter-island interaction across relatively extensive areas is thus an issue calling for further interdisciplinary collaboration.

The anthropomorphic stone statues and other exemplars of stone working and stone carving of the Marquesas, Raivavae and Rapa Nui are thought to have arisen later than the initial settlement migrations, and to reflect later inter-island contacts and influences[6]. A provocative hypothesis of Ioannidis and colleagues' study, however, is that these statues might instead be a consequence of a shared ancestry that originated in a southeastern part of the Tuamotu Islands, or possibly Mangareva, which is southeast of the Tuamotu Islands.

Although they are rare, similar stone statues and cut-and-dressed stone working (in which stones are cut to a required shape and size) are also present in Hawaii[10]. Genomic data from Hawaiian individuals were not included in Ioannidis and colleagues' study. When such data are included, it will be informative to see whether the settlement of Hawaii derives from this same branch of the Eastern Polynesian genetic tree.

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Virology

Ebola virus can lie low in human survivors

Robert F. Garry

A genomic comparison of Ebola virus from the 2021 outbreak in Guinea with sequences from the West African outbreak that ended in 2016 suggests that the virus can remain latent in human survivors for an extended period of time. **See p.539**

Infection by Ebola virus can be fatal, so understanding what drives human outbreaks might offer better ways to control it. On page 539, Keita *et al.*[1] provide evidence that the 2021 outbreak of Ebola virus in Guinea, West Africa, was triggered by reactivation of an infection that had been dormant in a person without evoking symptoms. Although reawakening of such clinically latent Ebola virus infections has been observed previously, the length of the latency period — nearly five years from the end of the 2013–16 West African Ebola outbreak — is surprising. The unexpected observation that the virus can persist in the human body for such a long time has considerable implications for public health and care of survivors of Ebola.

Keita *et al.*[1] analysed Ebola virus genomes from the 2021 outbreak in Guinea. They found that fewer mutations had accumulated in the viral genome than would be expected if it had continued to replicate and be transmitted from host to host since the earlier West African outbreak. This suggests that the virus had come from a survivor of that outbreak, rather than from its transmission to humans from animals (Fig. 1). Further evidence came from