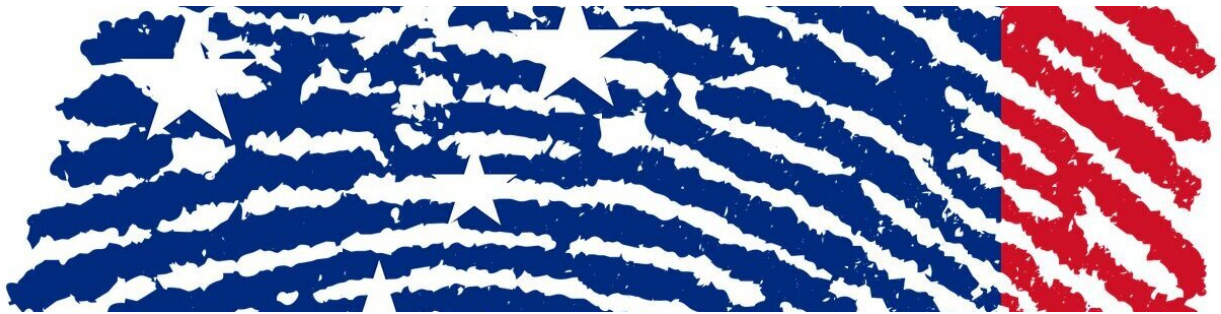


Researchers use 21st-century genomics to estimate Samoan population over 3,000 years

April 15 2020



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Reconstructing how many individuals first settled the many small islands in the Pacific and when they arrived remain important scientific questions, as well as an intriguing ones for understanding human history. Human migrations into the islands of Remote Oceania—from circa 3,000 to 1,200 years ago—mark the last major movement into locations previously uninhabited by humans.

These questions are also crucial as part of scientific efforts to understand the role of early history of Pacific islanders on contemporary public health problems including obesity and associated [non-communicable diseases](#) such as hypertension and Type 2 diabetes.

A new study in *Proceedings of the National Academy of Sciences*

analyzed the genomes of 1,197 individuals in Samoa and found that the effective [population size](#) of the first Samoans was small—ranging from 700 to 3,400 people during the time period from approximately 3,000 to about 1,000 years ago. Starting about 1,000 years ago, [population](#) size rapidly increase to about 10,000 individuals, coinciding with increasing agricultural and socio-political complexity, but also with previously hypothesized contacts with other Oceanic peoples.

This population history scenario for Samoa is consistent with the existing [archaeological evidence](#) of few, widely scattered and small-sized settlements in the first 2,000 years after Samoa's initial settlement. But it contrasts with archaeological population reconstructions of much larger population sizes for adjacent Pacific peoples in Tonga and Fiji during that first 1,500 to 2,000 years after initial discoveries around 3,000 years ago.

The research team's conclusions could help in understanding health conditions of particular importance to people in Samoa, home to some of the highest rates of obesity, heart disease and diabetes in the world.

"These findings are relevant for our ongoing public health research in Samoan populations because they highlight the importance of population history and size in influencing our ability to identify the effect of novel genetic variations, and their interactions with 21st century environments on population health," said Stephen McGarvey, study co-author and a professor of epidemiology and of anthropology at Brown University.

McGarvey has [studied extensively](#) obesity and diseases that stem from obesity—including diabetes, cardiovascular disease, kidney disease and cancer—in Samoa, which are not only a threat to individual health, but to the nations' economic and social development.

"Smaller populations and the evolutionary mechanisms resulting from

them, including genetic drift from bottlenecks and natural selection from novel challenging environments such as experienced by the first settlers of Samoa, make it easier to detect new gene variants and different frequencies of known variants that affect cardiometabolic disease risk factors now in the 21th century," he said.

The new study also found that modern Samoans derive largely from the Austronesian lineage, including the aboriginal peoples of Taiwan, Island Southeast Asia, coastal New Guinea and other island groups of Oceania—but share 24% of their ancestry with Papuans, the descendants of the people who settled Papua/New Guinea, an estimate markedly lower than found in neighboring Polynesian groups.

The researchers also found strong evidence of population reduction coincident with outside contact from European-derived groups, presumably from infectious diseases new to Samoan immune systems and societal shocks from such epidemics. The whole genome sequence data from participants' DNA also enabled findings about some genetic diversification within Samoa that may be reflective of regional and local social processes. The genomic data also showed an increase in population size about 150 years ago.

"These findings indicate that the modern Samoan population is a result of these demographic dynamics from the earliest times 3,000 years ago to the very recent colonial period in the 19th century," McGarvey said. "Any questions about putative genetic influences and their interactions with modern ways of life must be asked in the context of population history."

McGarvey is the overall principal investigator of the Samoan research and collaborated with Daniel Harris and Timothy O'Connor of the University of Maryland on the study, among other co-authors, with support from the TOPMed program of the National Heart, Lung and

Blood Institute (NHLBI) of the U.S. National Institutes of Health (NIH).

The TOPMed program supplied the Samoan whole genome sequences studied by McGarvey and colleagues from the University of Pittsburgh, the University of Cincinnati and Yale University, with ongoing support from NIH/NHLBI. Harris and O'Connor led the effort to use Samoan whole genome sequence data deploying population genetic methods to estimate shared ancestry of present day Samoans with other human groups, degree of shared genetic similarity within the Samoan sample and then estimation of the effective population size over time of Samoans.

More information: Daniel N. Harris et al. Evolutionary history of modern Samoans, *Proceedings of the National Academy of Sciences* (2020). [DOI: 10.1073/pnas.1913157117](https://doi.org/10.1073/pnas.1913157117)

Provided by Brown University

Citation: Researchers use 21st-century genomics to estimate Samoan population over 3,000 years (2020, April 15) retrieved 18 April 2024 from <https://phys.org/news/2020-04-21st-century-genomics-samoan-population-years.html>

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