

News & views

Ancient DNA

Ancient migrations uncovered in California

Alan Izarraras-Gomez & Diego Ortega-Del Vecchyo

Genomic data from ancient humans who lived up to 7,400 years ago, sampled from across California and Mexico, unveil patterns of migration that could explain how some Indigenous languages spread in parts of North America. **See p.122**

Migration and the sharing of cultural information between generations and groups have contributed to the proliferation of languages around the world. Before the arrival of the first European colonizers in the sixteenth century, the region that now encompasses California harboured a huge diversity of Indigenous languages. On page 122, Nakatsuka *et al.*¹ report the analysis of ancient DNA sampled from individuals in locations that now belong to northwest Mexico, Baja California (a Mexican peninsula) and California (Fig. 1) – work that sheds light on the movement of people and languages, as well as other characteristics of Indigenous populations, in this part of the world.

Northwest Mexico, Baja California and California are part of an ecological region known as Aridoamerica. In the past decade, researchers have started to analyse the demographic history (the chronology of migrations and changes in population size) of Aridoamerica using genomic information from present-day and ancient individuals^{2,3}. The cultural practices and settlements of the mainly hunter-gatherer civilizations that inhabited Aridoamerica were different from those of the mainly agricultural civilizations that existed in the adjacent regions of central and southern Mexico. To understand the culture, languages and migration dynamics of individuals who lived in precolonial Aridoamerica, insight is needed from researchers across disciplines.

Analysis of ancient DNA plays a key part in this multidisciplinary research because of the rich information it can provide about historical population dynamics, such as migration events. Using genomic information from both ancient and recent human sources, Nakatsuka and colleagues provide detailed evidence for a northward migration from

Mexico into central California that happened around 5,200 years ago. This migration might explain how one Indigenous language family, Uto-Aztecan, spread in California, in that those who moved from northern Mexico to California were probably speakers of Uto-Aztecan languages⁴. Interestingly, the authors argue that this migration occurred before the spread of agricultural practices for cultivating maize (corn), which took place around 4,100 years

ago – suggesting that the migration of people who were likely to have spoken languages of the Uto-Aztecan family to central California probably did not happen at the same time as agriculture began spreading there.

Analyses of ancient genomes can also provide information on how population sizes have changed over time. In 2023, a study found that communities in precolonial Aridoamerica were smaller than those in central Mexico³. Nakatsuka and colleagues took samples of ancient DNA from individuals dating to less than 1,600 years ago, and found that settlement sizes were smaller on the Californian Channel Islands than in mainland California. This finding could be explained by the much greater area of mainland California, allowing for larger populations than existed in the islands.

By contrast, the authors found that population sizes were smaller overall in California compared with those of northwest Mexico. Notably, population sizes were larger in the southern settlements than in the northern settlements of northwest Mexico. This result suggests that people in the southern parts of northwest Mexico might have had more access to fertile land and water, and so

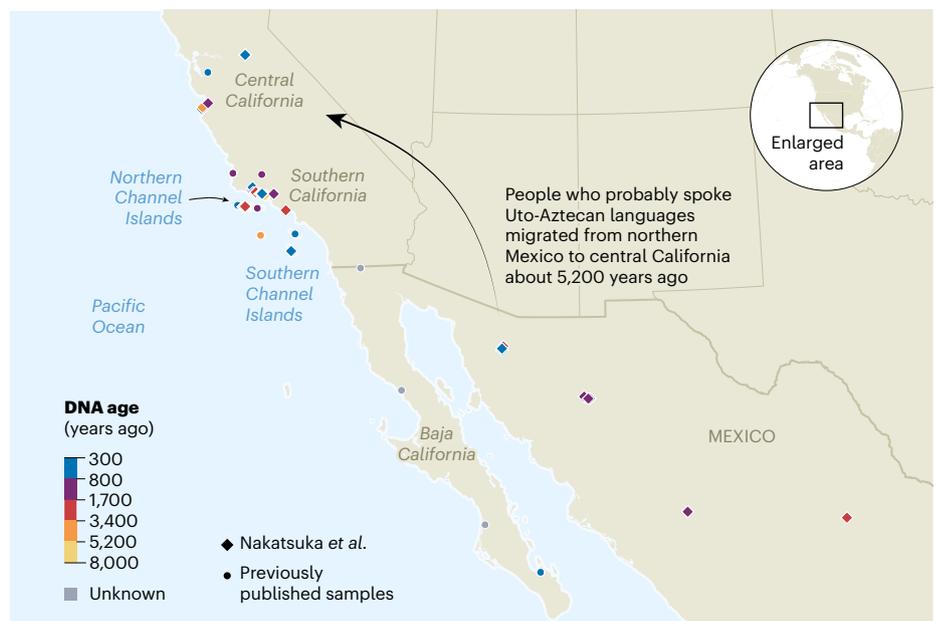


Figure 1 | A map of where ancient DNA was sampled across California and northern Mexico. Nakatsuka *et al.*¹ analysed the genomes of individuals from regions of what are now California and Mexico, including the Baja California peninsula of Mexico and the Californian Channel Islands. By comparing the genomes of ancient and present-day (not shown) individuals, they find evidence of a northward migration from Mexico into central California that happened roughly 5,200 years ago, which was probably responsible for bringing Uto-Aztecan languages to that region. The map shows the locations from which ancient DNA was sampled (either in the current study or in previous studies), and the colours indicate the estimated maximum age of the samples in years before present.

have been able to sustain bigger populations.

Nakatsuka *et al.* also report that modern Native American Chumash people are direct descendants of individuals who inhabited the northern Californian Channel Islands and the Santa Barbara coast around 7,400 years ago. In many regions of America, genomic analyses suggest that present-day Native American individuals tend to be direct descendants of individuals who inhabited the same regions in the past⁵. Interestingly, this trend seems to contrast with patterns seen in Europe, where individuals living in a particular area tend not to be direct descendants of those who lived there thousands of years ago⁶.

There is evidence to suggest that ancient individuals in South America and Polynesia made contact with each other before the arrival of European colonizers⁷. A similar contact might have been established between Polynesians and Native Americans of North America, given that a type of canoe used by people in ancient California is thought to reflect the influence of Polynesian cultures⁸. However, Nakatsuka and colleagues found no genetic evidence for contact between individuals of Polynesia and North America. This finding challenges theories of possible Polynesian genetic and cultural influence before colonization in North America.

Analysis of ancient DNA has allowed scientists to study migrations that took place across the Americas^{9,10}. However, a complete story describing the movement of people and cultures across every region of North, South and Central America requires studies that incorporate large numbers of samples from across space and time, and that use both present and ancient DNA. This gap has started to be filled by thorough sampling of genomic data from present-day individuals across Mexico¹¹. Similar efforts in other countries across the Americas will hopefully take place in the future.

By taking samples of DNA from different regions of Aridoamerica, from individuals dating to between 7,400 and 200 years before the present, Nakatsuka and colleagues can infer information about past migration events that would be difficult to detect using only present-day DNA. Therefore, it is probable that further ancient DNA studies, incorporating samples from individuals who lived across different times and regions in the Americas, will help to paint a fuller picture of the movement of ancient civilizations here. In Mexico, for example, there is archaeological evidence of people leaving certain areas because of environmental factors, such as droughts³. The collaboration between geneticists and archaeologists is essential to understand why large migrations might have taken place.

The study by Nakatsuka *et al.* includes co-authors who belong to Indigenous communities with connections to the ancient individuals whose genetic data were analysed.

Such an effort is deserving of recognition. Future ancient DNA studies should similarly strive to avoid ‘helicopter science’ – in which researchers from privileged settings carry out studies in areas where historically marginalized groups live, without involving local communities or researchers. In the case of ancient DNA research, it would be particularly encouraging to see studies that promote the development of local research facilities and training programmes, and the meaningful involvement of academics and communities who are from the regions from which ancient DNA is sampled¹².

Alan Izarraras-Gomez and **Diego Ortega-Del Vecchyo** are in the International Laboratory for Human Genome Research, National Autonomous University of Mexico, Querétaro, 76230, Mexico.

Health care

Diabetes prevention programme put to the test

Edward W. Gregg & Naomi Holman

Causal evidence shows that referring people who are at risk of developing diabetes to a nationwide lifestyle-change programme can result in health improvements – but only if programme participation can be sustained. **See p.138**

For the past seven years, England has taken one of the world’s boldest approaches to the prevention of type 2 diabetes. The National Health Service Diabetes Prevention Programme (NHS DPP) is a community-based, structured lifestyle programme, which offers at least 13 sessions to participants. The programme is designed to help adults at high risk of developing diabetes to improve their diet, increase their physical activity and attain a healthy weight¹. On page 138, Lemp *et al.*² report a multi-faceted analysis that evaluates how impactful this kind of large-scale intervention really is.

Type 2 diabetes is a metabolic disease associated with excess sugar in the blood that can lead to diverse complications, including diseases of the eye, kidneys, feet and cardiovascular system. Although the risk of developing type 2 diabetes varies from person to person, it is heavily influenced by lifestyle factors such as diet and exercise.

Almost three decades of randomized controlled trials (in which study participants are assigned randomly to a treatment or control group) have shown that structured lifestyle interventions (Fig. 1) can reduce the

e-mails: alanizarraras3@gmail.com; dortega@ligh.unam.mx

1. Nakatsuka, N. *et al.* *Nature* **624**, 122–129 (2023).
2. Verdu, P. *et al.* *PLoS Genet.* **10**, e1004530 (2014).
3. Villa-Islas, V. *et al.* *Science* **380**, eadd6142 (2023).
4. Mabry, J. B., Carpenter, J. P. & Sanchez, G. in *Archaeology Without Borders* (eds Webster, L. D. & McBrinn, M. E.) 155–183 (Univ. Press of Colorado, 2008).
5. Ávila-Arcos, M. C., Raghavan, M. & Schlebusch, C. *Science* **382**, 53–58 (2023).
6. Günther, T. & Jakobsson, M. *Curr. Opin. Genet. Dev.* **41**, 115–123 (2016).
7. Ioannidis, A. G. *et al.* *Nature* **583**, 572–577 (2020).
8. Jones, T. L. & Klar, K. A. *Am. Antiq.* **70**, 457–484 (2005).
9. Moreno-Mayar, J. V. *et al.* *Science* **362**, eaav2621 (2018).
10. de la Fuente, C., Moreno-Mayar, J. V. & Raghavan, M. in *Human Migration* (eds Muñoz-Moreno, M. L. & Crawford, M. H.) Ch. 3 (Oxford Academic, 2021).
11. Sohail, M. *et al.* *Nature* **622**, 775–783 (2023).
12. Ávila-Arcos, M. C., de la Fuente Castro, C., Nieves-Colón, M. A. & Raghavan, M. *Front. Genet.* **13**, 880170 (2022).

The authors declare no competing interests. This article was published online on 22 November 2023.

risk of diabetes by up to 58% (refs 3,4). Such interventions have also been shown to improve cardiorespiratory fitness and physical function, and decrease the likelihood of participants developing diabetes complications such as chronic kidney disease or symptoms of depression⁵.

However, many specialists have questioned whether scaling up targeted lifestyle-change programmes will be effective in tackling the type 2 diabetes epidemic. Cultural and community factors play a big part – these range from the foods that people prefer and have access to, to the methods of transport available and the leisure activities that people engage in⁶. Doubts stem from the logistics and cost of such programmes, and their diluted effectiveness when they are implemented in the real world⁵. Indeed, small ‘translational’ trials have shown that adapting these interventions to community settings does promote behaviour change and weight loss, but less effectively than the most intensive trials carried out in research settings^{5–7}.

Only a few countries and large health systems have tried to make preventative measures available to the whole population of at-risk