Credit: mattjeacock/E+

chains of zipcoded oligonucleotides, which can be combinatorially decoded during scRNA-seq. They demonstrated how three separate illumination and addition steps created a grid of 8 × 20 µm regions, although the system could theoretically be multiplexed further in an exponential manner for each further round of addition.

Overall, ZipSeq provides a means for spatial transcriptomics in live tissue samples and can be focused on microscopically defined regions of interest. Key areas for future development will be to enhance the number and fine-scale resolution of differently zipcoded regions.

Darren J. Burgess

ORIGINAL ARTICLE Hu, K. H. et al. ZipSeq: barcoding for real-time mapping of single cell transcriptomes. *Nat. Methods* https://doi.org/10.1038/s41592-020-0880-2 (2020)

> a conserved developmental clock that can translate age … across humans, dogs and mice

The 394 developmental CpGs were used to generate a conserved developmental clock, and its ability to predict ages within and between species was compared with single-species methylome-wide clocks. Single-species clocks were more accurate than the developmental clock when tested on the species on which they were trained (dog *rho* = 0.99 versus 0.81, mouse *rho* = 0.86 versus 0.78). However, the developmental clock substantially outperformed the single-species clocks when trained on one species and tested on another (dogs-to-mice *rho* = 0.73 versus 0.22, mice-to-dogs *rho* = 0.71 versus 0.32).

This new ability to translate age and physiological states across species should facilitate a deeper understanding of the ageing process.

Dorothy Clyde

ORIGINAL ARTICLE Wang, T. et al. Quantitative translation of dog-to-human aging by conserved remodeling of the DNA methylome. *Cell Syst.* https://doi.org/10.1016/j.cels.2020.06.006 (2020)
RELATED ARTICLE Horvath, S. & Raj, K. DNA methylation-based biomarkers and the epigenetic clock theory of ageing. *Nat. Rev. Genet.* **19**, 371–384 (2018)

POPULATION GENOMICS

An odyssey to Oceania

Credit: Mlenny/E+/Getty

The early history of Polynesia — in particular the possibility of contact between Native American and Polynesian populations — has been the subject of much debate. A study analysing genome-wide variation in individuals from islands across eastern Polynesia now reports evidence of admixture with Native Americans related to Indigenous inhabitants of northern South America.

The authors included publicly available genotype data and newly generated SNP array data for 807 (predominantly modern) individuals from 14 Polynesian island populations and 15 Pacific coastal Native American populations. To infer and visualize population genetic structure, the team merged the genotyped Polynesian individuals together with reference panels from across the globe, including European and African panels. They performed a global ancestry analysis using principal component analysis (PCA) as well as the program ADMIXTURE, a tool that provides estimates of the proportion of each individual genome from different populations on the basis of common underlying allele frequencies. Moving from patterns of global to local ancestry, the authors used the modelling approach RFMix to infer ancestry along the genome.

In addition to a large Polynesian component, many islanders harboured genomic regions of European ancestries, likely resulting from colonial admixture. Strikingly, the four easternmost Polynesian islands (Palliser, Marquesas, Mangareva and Rapa Nui) showed two ancestry components characteristic of both modern and ancient central and southern Native American populations.

The central Native American component, characteristic of Indigenous Mexican and Indigenous Colombian individuals, was found to be associated only with the Polynesian component using compositional analysis. This finding suggests that it arrived independently of any European component. Moreover, little variation of the central Native American component across different Rapanui individuals is suggestive of an older admixture event, before the arrival of Europeans in the Pacific region.

The authors applied a novel ancestry-specific PCA to determine the origin of the Native American ancestry component in Pacific islanders, which was revealed to be most closely related to the Zenu people, an Indigenous population from northern South America (corresponding to present-day Colombia). This finding was consistent with previous geographical, historical and linguistic observations.

Finally, by modelling the length distribution of the Polynesian, Native American and European ancestry segments in Pacific islanders, the team was able to infer an initial Native American–Polynesian admixture event dating to around AD 1200, predating the settlement of Rapa Nui. The date estimate was confirmed using a linkage disequilibrium-based dating method. This event seems to have been followed by multiple European admixture events in the late eighteenth and early nineteenth centuries, in line with the European colonization of remote Oceania.

As the authors posit, this study emphasizes the value of using "genetic studies of modern populations […] to unravel complex prehistoric questions."

Linda Koch

ORIGINAL ARTICLE Ioannidis, A. G. et al. Native American gene flow into Polynesia predating Easter Island settlement. *Nature* https://doi.org/10.1038/s41586-020-2487-2 (2020)