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An arrowhead that belonged to people associated with the Clovis culture, early settlers in the Americas.

carrying artefacts, such as sophisticated projectile points, from a culture known as Clovis began to populate the interior of North America about 13,000 years ago. For decades, scientists thought that people associated with this culture were the continents' first inhabitants.

But the discovery of 'pre-Clovis' settlements — including a nearly 15,000-year-old site at the southern tip of Chile — pointed to an even earlier wave of migration to the Americas.

The first ancient-DNA studies from the region, appearing in 2014, began to add detail to this picture. The genome of a baby boy who was buried roughly 12,700 years ago in Montana alongside Clovis artefacts[3], and genomes from other ancient individuals[4], hinted at two early populations of Native Americans.

The Montana baby, known as the Anzick boy, belonged to a population known as the Southern Native Americans, who are most closely related to present-day Indigenous populations from South America. They split from Northern Native Americans, who are genetically closer to many contemporary groups in eastern North America, around 14,600–17,500 years ago. And the common ancestor of those two groups split from East Asians some 25,000 years ago, as scientists established earlier this year by sequencing the genome of 11,500-year-old human remains from Alaska[5].

But this timeline was based on just a few ancient genomes from the Americas, and scientists expected further data to paint a more detailed, complex picture of the continents' history, as well as reveal later migrations there.

SAME GENES, FAR APART

The two latest studies include genome data from 64 ancient Americans, and provide the first detailed look at the ancient inhabitants of Central and South America and their early movements into the region.

To chart these migrations, Meltzer and his colleague Eske Willerslev, a palaeogeneticist at the Natural History Museum of Denmark in Copenhagen, compared genetic data from the Anzick boy with those from 10,700-year-old remains in a Nevada cave and 10,400-year-old remains from southeastern Brazil.

The genomes were remarkably similar, despite the great geographical distances between them, Willerslev says, pointing to a rapid population expansion from Alaska. "As soon as they get south of the continental ice caps, they're exploding and occupying the land," he says.

An independent team led by David Reich, a population geneticist at Harvard Medical School in Boston, Massachusetts, also found evidence[1] for a rapid expansion into South America, through analysing 49 ancient genomes from Central and South Americans.

Both teams documented multiple later human migrations into South America. Reich's group found, for instance, that the genetic signal of the earliest inhabitants — closely related to the Anzick boy — had largely vanished from later South Americans, suggesting that different groups had by then moved in from the north.

Potter says that the main conclusions of the two papers are broadly consistent. "Complex and realistic are the two adjectives I would use," he says.

Even with dozens more newly discovered ancient genomes from the Americas, important aspects of the region's population history are probably still missing, says Reich. "There are many dots that are not filled in," he says. "I think as these studies scratch the surface, they make things more, rather than less, complicated."

Jennifer Raff, an anthropological geneticist at the University of Kansas in Lawrence, says that the emerging picture of the Americas is less a revision of the earlier models and more an elaboration. "It's not that everything we know is getting overturned. We're just filling in details," she says. ■

1. Posth, C. *et al. Cell* https://doi.org/10.1016/j.cell.2018.10.027 (2018).
2. Moreno-Mayar, J. V. *et al. Science* https://doi.org/10.1126/science.aav2621 (2018).
3. Rasmussen, M. *et al. Nature* **506**, 225–229 (2014).
4. Rasmussen, M. *et al. Nature* **523**, 455–458 (2015).
5. Moreno-Mayar, J. V. *et al. Nature* **553**, 203–207 (2018).

INSTITUTIONS

Sanger whistle-blowers dispute inquiry findings

Leading genomics institute stands by conclusions of an investigation that clears its management of bullying.

BY HOLLY ELSE

Six current and former employees are calling for the Wellcome Sanger Institute in Hinxton, UK — one of the world's top genomics centres — to reopen an investigation that last month cleared its management of bullying, gender discrimination and misuse of grant money.

The group raises concerns about the process of the investigation and questions the decision to clear senior management at the institute of the allegations. Among other things, the group says that the investigation did not interview enough people, and that its scope may have been too narrow. Its members, who say they are among 12 people who contributed evidence to the April complaint that prompted the probe, also question the investigation's transparency.

Their concerns "cast doubt as to whether the investigation was conducted in a manner that was as effective as it could be, given the seriousness of the allegations", they say in a statement seen by *Nature*. On 2 November, Serena Nik-Zainal, a clinical scientist who now works at the University of Cambridge, sent the statement to Genome Research Limited (GRL), which oversees the Sanger and commissioned the investigation from barrister Thomas Kibling. "We firmly believe sufficient evidence was not unearthed to make an appropriate judgement," says the statement.

David Willetts, chair of the board of GRL, told *Nature* that the investigation was independent

and detailed, and that the organization does not plan to review the findings. "We believe Mr Kibling carried out a thorough and independent investigation as he was tasked to do," he says.

The Sanger employs almost 1,000 scientists and other skilled professionals, and played a key part in the Human Genome Project, which concluded in 2003.

On 30 October, GRL released a redacted executive summary of Kibling's investigation report. The summary said that the investigation considered "various whistleblowing concerns" in a document submitted by one staff member that alleged that the institute and its director, the geneticist Mike Stratton, had committed gender discrimination, wrongful exploitation of scientific work for commercial purposes and misuse of grant monies. The summary also says that the investigation considered an allegation that Stratton had bullied someone. And it says that Kibling, of Matrix Chambers in London, cleared Stratton and the Sanger's management of all these accusations.

The authors of the 2 November statement are Nik-Zainal; Inês Barroso, a human geneticist who has worked at the Sanger since 2002 and who says she wrote the initial whistle-blowing complaint; Jyoti Choudhary, a proteomicist now at the Institute of Cancer Research in London; and three people, including a former member of the senior management team, who wish to remain anonymous to protect their careers.

Their statement questions the level of information that the investigation considered. It also questions the investigation's finding that there is no evidence for some allegations, and suggests that this might be because crucial evidence fell outside the scope of the investigation.

In his summary, Kibling notes that he was not required to determine the merits of any individual's grievance "which are not in the nature of a whistleblowing complaint or advanced by others" — and that such grievances are to be dealt with in a separate process.

Kibling told *Nature* that he stands by his investigation, and it was his "judgement call" to decide who would assist him and therefore who to interview. "The investigation needs to be proportionate and focused on the whistle-blowing complaint made and not the individual grievances that some of those I spoke to harboured," he says. He adds that he believes that he spoke to those who had a valuable contribution to make and were necessary for the investigation.

The investigation did identify failings in how people have been managed at the Sanger, and a lack of diversity at senior levels of the organization. The 2 November statement acknowledges these findings, but the authors still say that they are "disappointed by the investigation process".

They call on the Wellcome Trust in London, which owns the Sanger, "to reconsider whether the principles of this investigation lived up to its own standards".

Wellcome says that it is "satisfied with the investigation that has been carried out", and has no plans to reopen the probe.

Stratton did not respond to *Nature*'s request for comment. ■

NEUROSCIENCE

'Invisible' mice reveal anatomical secrets

Technique that turns dead rodents clear uncovers surprising details about injury response.

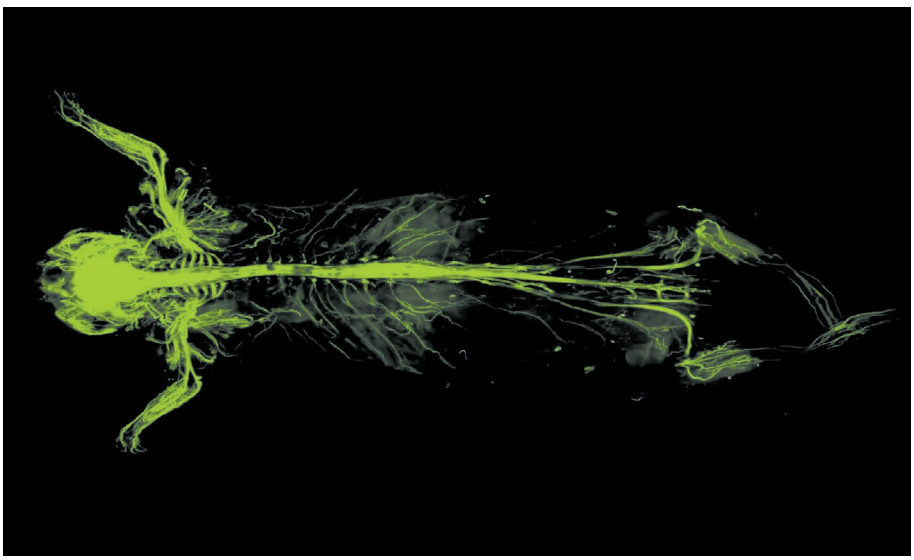
BY SARA REARDON

A new technique that makes dead mice transparent and hard like plastic is giving researchers an unprecedented view of how different types of cell interact in the body. Scientists can pinpoint specific tissues while scanning an animal's entire body.

The approach, called vDISCO, has already revealed surprising structural connections between organs, including hints about the extent to which brain injuries affect the immune system and nerves in other parts of the body. That could lead to better treatments for traumatic brain injury or stroke.

Methods that turn entire organs clear have become popular in the past few years, because they allow scientists to study delicate internal structures without disturbing them. But removing organs from an animal's body for analysis can make it harder to see the full effects of an injury or disease. And if scientists use older methods to make an entire mouse transparent, it can be difficult to ensure that the fluorescent markers used to label cells reach the deepest parts of an organ.

The vDISCO technique overcomes many of these problems. By making the dead mice rigid and see-through, it can preserve their bodies for years, down to the structure of individual cells, says Ali Ertürk, a neuroscientist at Ludwig Maximilian University of Munich in Germany, who led the team that developed vDISCO. He presented the work this month at a meeting of the Society for Neuroscience in San Diego, California.



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The nervous system of a mouse treated using the vDISCO technique glows green.

The process begins by soaking a mouse's body in organic solvents to strip it of fats and pigments. This preserves the structure of cells, even as the mouse shrinks by up to 60% (ref. 1). ▶