

trees across 13 provinces in the country's north since the programme began in 1978.

Around 2000, deserts across the country were expanding by 10,400 square kilometres a year, says the government. But in 2017, it reported that China's deserts were shrinking by more than 2,400 square kilometres a year.

A 2018 study¹ of satellite data from the US National Oceanic and Atmospheric Administration found that forest cover has increased in line with government statistics, but suggested that changes in logging policy were more important than afforestation — planting forests where none were before.

In 1999, the Chinese government began planting millions of trees in its Grain for Green Program, intended to repair damaged farmland in the northern Loess Plateau, which is roughly the size of France.

And the afforestation drive is continuing apace: in 2018, the government announced a target of 30% forest coverage by 2050. At the moment, the coverage is around 22%.

It's still too early to determine whether it has solved the problem, says Congbin Fu, director of the Institute for Climate and Global Change Research at Nanjing University. Land restoration can take several decades or even 100 years, he says.

There are pitfalls to mass tree-planting. Large parts of China — including some areas where trees are being planted — are getting drier. A paper² co-authored by Sternberg found that arid areas in China had increased by roughly 1.6 million square kilometres, about the size of Iran, since 1980 — probably due largely to anthropogenic climate change.

Many of the plants introduced to the Loess Plateau use more water than native vegetation. A 2016 study³ found that the revitalized ecosystem is already sucking up rainfall and reducing the amount of water that runs off to rivers; a drier climate could exacerbate the situation and trigger water shortages for humans. A modelling study⁴ co-authored by Fu and published last month reached similar conclusions, and cautioned against continuing the Grain for Green Program.

Considering water shortages is important, says Shixiong Cao, an ecologist at Beijing Forestry University. He thinks the national forestry department has recognized the error of planting trees in arid areas, and that in recent years, it has moved towards planting shrubs with lower water requirements.

The head of the forestry department, Zhang Jianlong, told state media in March that efforts should go to keep vegetation healthy, rather than simply planting trees. ■

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3. Feng, X. *et al. Nature Clim. Change* **6**, 1019–1022 (2016).
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An artist's impression of a young female Denisovan, based on skeletal traits derived from ancient DNA.

ANCIENT HUMANS

Denisovan portrait drawn from DNA

Reconstruction based on epigenetics reveals broad, Neanderthal-like facial features.

BY EWEN CALLAWAY

For the first time, scientists analysing the DNA of Denisovans — an extinct group of ancient humans that was discovered around a decade ago — have offered a glimpse of what they might have looked like.

Ever since archaeologists uncovered the first fragmented Denisovan remains in a Siberian cave, researchers have scoured the globe for clues to how the mysterious hominins looked. Denisova Cave has yielded a few more small fossils, and a jawbone from the Tibetan Plateau added detail this year. But none of these fossils is large or complete enough to reconstruct many anatomical details.

Now, computational biologists have produced a rough sketch of Denisovan anatomy based on epigenetic changes — chemical modifications to DNA that can alter gene activity. Their approach reveals that Denisovans were similar in appearance to Neanderthals but had some subtle differences, such as a wider jaw and skull (D. Gokhman

et al. Cell <http://doi.org/dbqk>; 2019).

“It does help to paint a clearer picture of how they might have looked. Just the idea that it's possible to use the DNA to predict morphology so well is very impressive,” says Bence Viola, a palaeoanthropologist at the University of Toronto in Canada who has analysed Denisovan remains, but was not involved in this research.

MAPPING METHYLATION

Epigenetic modifications to DNA have a profound influence on most biological traits throughout life. They can help to determine differences between cells with otherwise identical genomes. One of the best-studied epigenetic changes is the addition to a DNA base of a methyl chemical group — made up of one carbon atom and three hydrogens — which often quells the activity of a gene.

A team co-led by Liran Carmel, a computational biologist at the Hebrew University of Jerusalem, discovered a way to identify parts of ancient DNA that had once been ▶

► methylated, by analysing patterns of chemical damage that accrues to the DNA over time. In 2014, Carmel's team mapped methylation patterns across the genomes of Neanderthals and Denisovans, and identified a limb-development gene for which these patterns differed between the extinct groups and modern humans (D. Gokhman *et al. Science* **344**, 523–527; 2014).

In the latest study, Carmel and computational biologist David Gokhman, also at the Hebrew University of Jerusalem, led a team that identified thousands more regions of the genome in which the methylation patterns of Denisovans and Neanderthals were distinct from those of modern humans. They compared these with databases of epigenetic modifications in human tissue — where the impacts on gene expression are known — and produced a list of hundreds of genes for which expression levels probably differed between archaic groups and modern humans. To connect this list to anatomical traits, the researchers looked at another database, which catalogues the physical effects of genetic mutations in people with rare conditions, reasoning that the reduced gene expression caused by DNA methylation was roughly analogous to the effects of the disease-causing mutations.

Before applying the method to Denisovans,

Carmel and Gokhman's team first tested whether it could successfully predict the anatomy of Neanderthals, which is known from hundreds of fossils.

The predictions about physical appearance made using this approach are qualitative and relative, Carmel explains. "I can tell you that fingers are longer, but I cannot tell you they are longer by 2 millimetres," he says. The team

"The idea that it's possible to use the DNA to predict morphology so well is very impressive."

found 33 Neanderthal traits that could potentially be predicted from methylation patterns. The results accurately predicted 29 of those traits, for instance that the species had broader faces and flatter heads than modern humans.

The researchers then turned the technique on Denisovans. They predicted that these hominins shared many traits with Neanderthals, such as their low foreheads and wide rib cages, but identified some differences, including wider jaws and skulls. Although it is impossible to know how accurate their picture is, some of the predictions are supported by evidence from Denisovan remains. The best-characterized Denisovan feature in the fossil record is gigantic molar teeth. Although

the researchers weren't able to predict this — because molar size was not in the database they used — they did determine that Denisovans had long dental arches, a potential adaptation for big teeth.

The 160,000-year-old lower jawbone from the Tibetan Plateau matched Gokhman and Carmel's predictions for three out of four traits. And a piece of skull from Denisova Cave that Viola has presented at meetings (but not yet described in a paper) suggests the group had wide heads — which matches the epigenetic reconstruction.

"I think the big picture is correct, but with the individual traits, there is a lot of leeway," says Viola. Although he is impressed by the predictions, he is unsure how they will help to determine what Denisovans actually looked like. Potential Denisovan bones are so rare that most are already tested for DNA or protein — currently the only way to link remains to the extinct group.

In the future, scientists might use epigenetics to reconstruct the anatomy of hominins known from fragmentary fossils, or perhaps even DNA from dirt, says Pontus Skoglund, a population geneticist at the Francis Crick Institute in London. But he thinks the approach could be most useful in predicting traits, such as behaviour, that don't leave an impression in the fossil record. ■

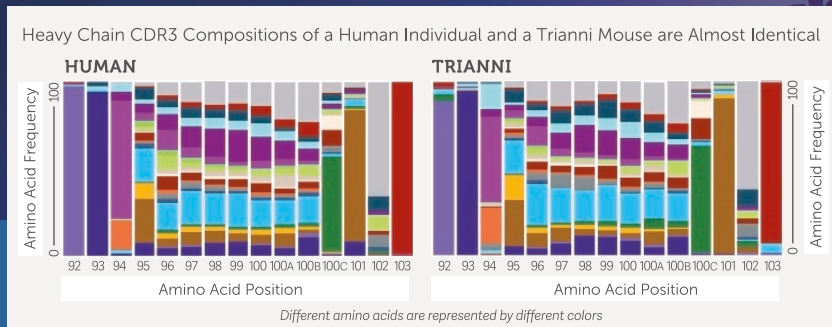
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