

in southern Europe until around 30,000 years ago<sup>2</sup>, thus potentially overlapping with modern humans. As a result, there has long been interest in whether Neanderthals might have interbred with early Europeans. In the 1990s, the first comparisons of DNA sequences from modern humans and Neanderthals<sup>3,4</sup> suggested a rather simple story: that modern humans emerged from Africa during the past 100,000 years, and spread around the globe without receiving genetic contributions from hominins that had left Africa much earlier.

These early studies were based on sequences from mitochondrial DNA, which is easier than nuclear DNA to capture in ancient samples but represents only a tiny fraction of the human genome. However, the past few years have seen a revolution in our ability to obtain nuclear-genome sequences from ancient samples<sup>5–9</sup>, and these data are providing startling insights. One surprise was the first clear evidence for interbreeding between Neanderthals and modern humans<sup>5</sup>; another was the discovery of a second type of archaic hominin in Eurasia in addition to Neanderthals. This group, dubbed the Denisovans, is known mainly from the genome sequence of a single finger bone found in a cave in the Altai Mountains in Siberia<sup>6,7</sup>.

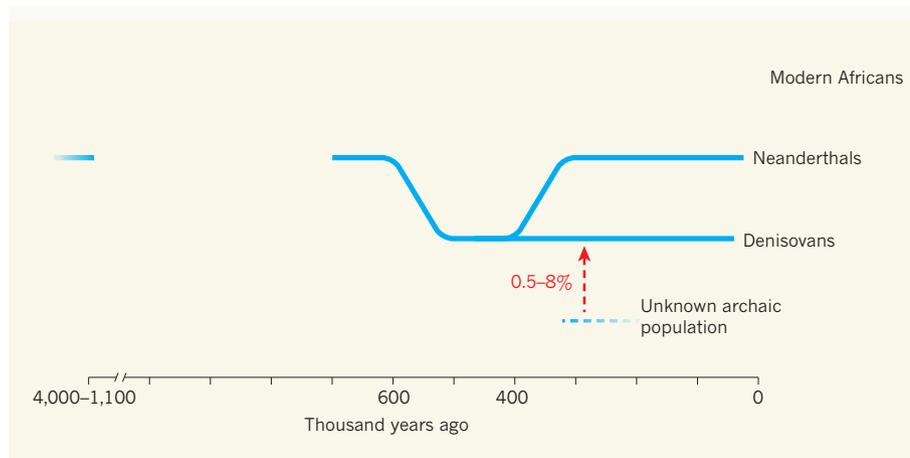
Although the Neanderthal bone from which Prüfer *et al.* derived their genomic sequence was found in the same Siberian cave, its owner is estimated to have lived several thousand years earlier than the Denisovan individual, and the two populations that the individuals represent are not closely related. The ancestors of Neanderthals and Denisovans diverged from the main human lineage about 600,000 years ago, and then split from each other around 400,000 years ago (Prüfer *et al.*

discuss these estimates and associated caveats in detail). Thus, Neanderthals and Denisovans were quite distinct populations, having been separated for roughly three times longer than any modern human populations.

Prüfer and colleagues' sequence comparisons provide further detail about the extent of interbreeding between the different hominin groups living during the Pleistocene period (see Fig. 8 of the paper<sup>1</sup>). The authors offer a more confident estimate of the Neanderthal contribution to the genomes of modern humans: about 2% for non-Africans (Africans have no detectable Neanderthal ancestry). They also report gene flow from Neanderthals into Denisovans that includes input at functionally important genomic regions involved in immunity and sperm function. Earlier work had shown that the main Denisovan contribution to modern humans is found in some populations in Oceania and, to a lesser extent, in east Asians<sup>6,7</sup>.

Most provocatively, Prüfer *et al.* find evidence for modest levels of gene flow into Denisovans of sequence that is different from that of any known group, implying that there is at least one more, so far undiscovered, archaic-hominin group (Fig. 1). Low levels of gene flow have been observed in other radiations of species, so evidence for inter-hominin breeding should not be a tremendous surprise<sup>10</sup>; however, it does seem that Eurasia during the Late Pleistocene was an interesting place to be a hominin, with individuals of at least four quite diverged groups living, meeting and occasionally having sex.

The Neanderthal and Denisovan genomes also share another intriguing feature: they both have extremely low genetic diversity, with only about two heterozygous sites



**Figure 1 | Gene flow from an unknown ancient population.** Prüfer *et al.*<sup>1</sup> calculate that modern Africans show greater genomic similarity to Neanderthals than to Denisovans. Average sequence divergence along the lineage leading to modern Africans is 7.47% since the last common ancestor with Neanderthals, and 7.71% since the last common ancestor with Denisovans (both numbers represent the percentage of divergence since the human–chimpanzee split). This difference is highly significant, and is inconsistent with a simple model in which the entire Neanderthal and Denisovan genomes come from the same source population. The best alternative model identified by the authors is that there was flow of a small contribution of genomic material (0.5%–8%) into Denisovans from a highly diverged, unknown population.



## 50 Years Ago

The Continental Shelf Bill, which received its second reading in the House of Lords on December 3, originated in the Conference on the Law of Sea at Geneva in 1958, which resulted in the Continental Shelf Convention and the High Seas Convention. The former, which the Government intends to ratify if the Bill becomes law, clarified international law concerning those large submarine areas outside the territorial seas where the depth of the water allows the natural resources of the sea-bed and subsoil to be exploited ... In the North Sea ... Britain will have rights over any deposits up to a line half-way across to Holland, Belgium and other coastal States, subject to any adjustments resulting from the negotiations that the Government proposes to undertake after ratifying the Convention.

From *Nature* 4 January 1964

## 100 Years Ago

Major H. G. Joly De Lotbinière has contributed to *The Quarterly Review* for October a valuable and timely article on the position of forestry in England and abroad, in which he reviews the principal timber resources of the world, and the steps that have been taken in England and elsewhere to provide for the future. As he points out, experts in every country are agreed that the world's supply of timber is rapidly diminishing, and that unless vigorous steps are taken in the afforestation of suitable waste lands a shortage of material must be experienced long before the close of the present century. The author indicates in a general way the lines on which the work of afforesting the sixteen million acres of mountainous and heath land in this country should be proceeded with, and urges the necessity for immediate action.

From *Nature* 1 January 1914