Climate science

A complete palaeoclimate picture emerges

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Palaeoclimate data and models have been used to produce a comprehensive report of Earth's temperature changes over the past 24 millennia. The results suggest that modern warming differs from the gradual rise of the past 10,000 years. **See p.239**

John E. Kutzbach, a pioneer of palaeoclimate modelling, had a grand vision for how we might better understand past climate changes — and better predict the climatic future[1]. In his view, climate research should seamlessly combine models and proxy data, which provide an indirect measure of the palaeoclimate when direct data are unavailable, using certain chemical species preserved in the environment that provide an estimate of past temperatures. A geologist could tease out a climate record from a stalagmite in China, for example, while a modeller simulated its growth, drip by drip, in a digital cave. On page 239, Osman *et al.*[2] bring us a step closer to realizing Kutzbach's vision by pairing proxy data with models to reconstruct the evolution of the global temperature over the past 24,000 years, extending back to a period called the Last Glacial Maximum.

Osman and colleagues' study represents a natural continuation of a decades-long effort to reconstruct past climate changes. Growing numbers of proxy records have clarified the general warming trend and probable reasons for the global temperature changes since the Last Glacial Maximum[3,4]. At the same time, models have become more complex through the incorporation of simulations of water isotopes, which can be used to estimate temperature through their sensitivity to changes in phase[5], and by considering transient changes in temperature, rather than just snapshots in time[6].

Techniques for incorporating proxy data into climate models have also become more sophisticated, and researchers in the same team as Osman *et al.* have devised many of these approaches (see, for example, ref. 7). In the current paper, the authors bring these pieces together in an assimilation of models and data that provides an understanding of global temperature changes spanning the past 24,000 years (Fig. 1).

Mapping temperature changes across the globe was previously challenging because of the relatively small and disparate proxy data sets used in earlier studies[3,4], which precluded meaningful interpolation across data gaps. To remedy this, Osman *et al.* built on their previously reported modelling work (see, for example, ref. 8), and amassed a larger temperature data set that included more than 500 marine records, each spanning at least 4,000 years. They then used this data set to update simulated temperatures from a climate model representing different time intervals over the past 24,000 years. The benefit of this hybrid approach is that the proxy data bring the model closer to reality, and the model fills in gaps where no data are available.

> **"Data from relatively few locations might capture average temperature trends on a large scale."**

The authors' most notable contribution is the reanalysis of the evolution of global temperatures over time, which will help researchers who are investigating changes that have occurred in the ocean, ice, vegetation and atmosphere since the Last Glacial Maximum. Intriguingly, the study's findings suggest that the key patterns of average temperature change through time, both across the globe and in both hemispheres, are similar to those estimated earlier using a small amount of data[9]. This observation echoes initial assessments of twentieth-century global warming, which suggested that data from relatively few locations might be needed to capture average temperature trends on a large scale[10].

The authors also identified subtler features that were previously missed, including the effect that gradual changes in the alignment of Earth's axis have on climate. In fact, the authors found that stronger summertime solar radiation that was related to these changes coincided with cooler mean annual temperatures in both hemispheres, contradicting the century-old hypothesis of Serbian geophysicist Milutin Milankovitch. They also found a gradual global warming during the current interglacial period (which started approximately 11,650 years ago) that is unlike other reconstructions over this period[3,11]. If confirmed through further studies, this result would imply that modern warming is extraordinary compared with that of the past 10,000 years (Fig. 1) — adding weight to a similar conclusion made in the most recent report from the Intergovernmental Panel on Climate Change[12].

Osman and co-workers' study also represents a change in the way palaeoclimate

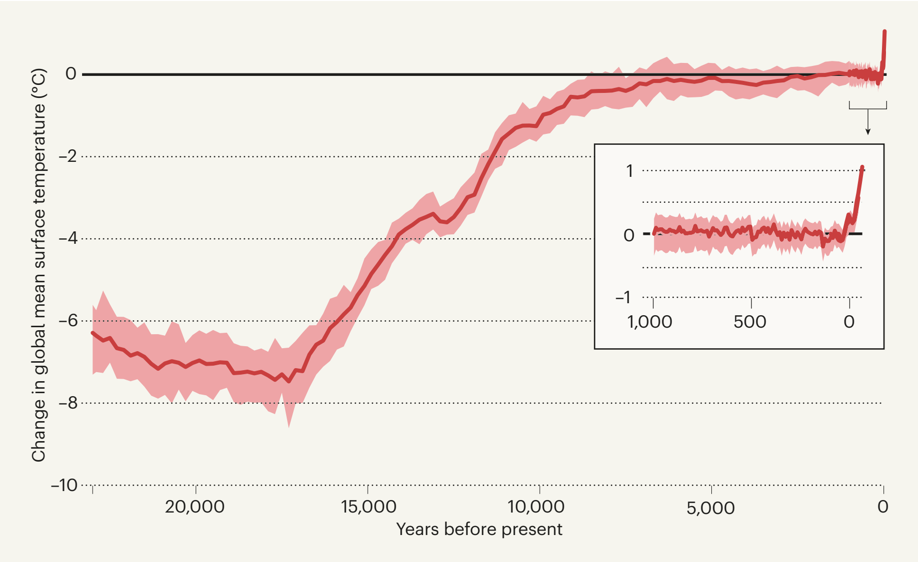

Figure 1 | Changes in the global mean surface temperature over the past 24,000 years. Osman *et al.*[2] combined proxy data — obtained indirectly through palaeoclimate records when direct data are unavailable — with climate models to compute the evolution of the difference in the global mean surface temperature relative to the average for the pre-industrial period of the past millennium (1000–1850). The shaded area represents a 95% confidence interval. (Adapted from Fig. 2 of ref. 2.)

scientists approach their research. Previous global-scale reconstructions of the past 24,000 years either focused on narrow time intervals to develop a full spatial picture of temperature changes[13], or studied changes in temperature averaged over the globe to determine the evolution of the climate[4,6]. Osman *et al.* have effectively combined these approaches to produce a complete reconstruction of climate change through space and time.

There are, of course, limitations to the authors' work. No terrestrial data were included in the data set compiled, and few data are available for the central Pacific, Indian and Southern oceans, leaving some questions as to how accurate the reconstruction is across these large expanses of water and continents. This is particularly important when considering the warming that the study reports for the current interglacial epoch, because a reconstruction published last year using several hundred terrestrial climate records instead shows a cooling trend[11], albeit without the help of model simulations. Osman *et al.* also relied on a single climate model, which might bias their results, because different models can produce different spatial patterns of climate change.

Drawing on the innovative data compilation and modelling methods of Osman and colleagues as a foundation, future work should focus on adding more terrestrial records to similar global temperature reconstructions. There is also a need for more model simulations that include water isotopes, so that the authors' approach can be repeated with different climate models. This will help researchers to better assess the degree of uncertainty associated with the temperature reconstruction.

Nonetheless, the work by Osman *et al.* is a triumph, and sets a new standard for the development of large-scale temperature reconstructions of the geological past. It should inspire climate scientists to undertake similar analyses, and perhaps even to consider temperature changes that occurred before the Last Glacial Maximum — fulfilling Kutzbach's vision of combining models and data to fully decipher the climate of the palaeo world.

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Evolution

Rhinoceros genomes uncover family secrets

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Genomes from living and extinct rhinos reveal that different species evolved as a result of geographic isolation. A comparison of DNA from different species also shows that rhinos have long displayed low genetic variability.

Historically, rhinos were once abundant throughout Europe, Asia and Africa[1]. Today, five species of rhinoceros survive as small populations in Asia and Africa, and are all threatened with extinction[2]. Although well studied, there is debate in the literature about evolutionary relationships between modern and extinct rhinos, with three hypotheses being proposed (Fig. 1a–c). Writing in *Cell*, Liu *et al.*[3] analyse contemporary and ancient rhinoceros DNA to piece together the puzzle of the rhino's evolutionary history.

The authors analysed the genomes of five living rhinoceros species — namely black (*Diceros bicornis*), white (*Ceratotherium simum*), Sumatran (*Dicerorhinus sumatrensis*), greater one-horned (*Rhinoceros unicornis*) and Javan rhinoceros (*R. sondaicus*). They also analysed ancient DNA from the Late Pleistocene (the period of time ranging from about 126,000 to 11,700 years ago) obtained from bone and tooth samples of three extinct rhinoceros species: the woolly rhinoceros (*Coelodonta antiquitatis*), the Siberian unicorn (*Elasmotherium sibiricum*) and Merck's rhinoceros (*Stephanorhinus kirchbergensis*). The genomic data revealed that the rhinoceros lineage split approximately 36 million years ago, with the Siberian unicorn separating from a group that included all the other rhino species examined in the study.

The genomic analysis suggests that, approximately 16 million years ago, in the Miocene (which lasted from about 23 million to 5 million years ago), this group then split into two groups: African and Asian. This might have happened when the ancestor of living black and white rhinos moved from Eurasia into the African continent either because of changes in climate or when a land bridge formed between the two land masses approximately 20 million years ago[4]. According to Liu and colleagues' analysis, the Asian group, located in Eurasia, further split into two groups approximately 14.8 million years ago (Fig. 1d). One group consists of the greater one-horned rhinoceros and the Javan rhinoceros (which is found only in a small part of the island of Java in Indonesia); the other includes the Sumatran rhinoceros (living on the neighbouring island of Sumatra), Merck's rhinoceros and the woolly rhinoceros — all of which have current or past geographical ranges that include parts of Asia.

However, Liu *et al*. obtained conflicting signals regarding the position of the different species in the family tree. Depending on the chromosomal region they analysed, the branching of the tree was similar either to that suggested by analysis of DNA in a cellular organelle called the mitochondrion (Fig. 1c) or to that based on geographical distribution (Fig. 1b). The authors attributed the inconsistency between analyses of different chromosomal regions to incomplete lineage sorting, whereby different rhinoceros species might have retained ancestral forms of genes and maintained gene flow between each other after these species formed. The occurrence of these phenomena can lead to the generation of trees that do not show actual relationships between species.

Following extensive analysis that took into account incomplete lineage sorting and gene flow, the authors report that the current genomic data set indicates that rhinoceros species evolved through geographical isolation (Fig. 1b), as previously proposed[5]. However, the authors noted that, to fully