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consistent with the climate history from oxygen isotopes and the general notion that CO₂ is a fundamental driver of climate. They use an energy-balance climate model incorporating the proxy record of atmospheric CO₂ to determine tropical sea surface temperatures during the Phanerozoic. The temperatures predicted with this model bear little resemblance to the climate record. Either the CO₂ proxies are flawed, or our understanding of the relationship between CO_2 and climate (as expressed in the climate model) needs rethinking. From the title of their article, "Evidence for decoupling of atmospheric CO2 and global climate during the Phanerozoic eon", the authors evidently feel that CO₂ may not be the climate driver it has been made out to be.

Such a conclusion deserves close scrutiny, because the policy implications are huge. The geological record is our best hope of establishing a correspondence between atmospheric levels of CO_2 and climate, and understanding the likely consequences of fossil-fuel burning. If large changes in atmospheric CO_2 in the past have not produced the climate response we thought they had, that undermines the case for reducing fossil-fuel emissions.

The authors concentrate on two mismatches: the glaciation of the Late Ordovician period (440 million years ago) and the cool climate of the Jurassic and early Cretaceous (approximately 220-120 million years ago), both of which coincided with proxy indications of high levels of atmospheric CO₂. These seeming paradoxes are not new, however, and the Late Ordovician mismatch has been particularly well studied^{6,7}. Solar physicists argue that the Sun was then some 5% less luminous than it is today, so higher atmospheric CO2 would have been necessary simply to prevent runaway 'icehouse' conditions. Moreover, the glaciation was extremely short-lived⁸, so the available proxies may not pick up a possible reduction in levels of CO_2 during that brief period. CO₂ has a short residence time in the atmosphere, and a transient reduction in atmospheric CO_2 is a viable explanation for the glaciation⁹.

The Jurassic mismatch is a more persistent and problematic feature. There is also a notable mismatch during this time interval between the proxy data, which indicate greatly increased concentrations of CO_2 , and more moderate estimates that come from models of the carbon cycle¹⁰. So levels of atmospheric CO_2 may not have been as high as the proxies indicate. Nevertheless, the cool climate of the Jurassic remains something of a mystery.

Clearly, factors other than atmospheric CO_2 can influence climate on geological timescales. Continental drift creates supercontinents and breaks them into smaller fragments, gives birth to mountain belts and high plateaux, and shifts the distribution of continents among latitudinal belts and

hemispheres. All of these factors affect the atmosphere and the ocean circulation, as well as the intensity of the hydrological cycle, which ultimately dictates the cloudiness of the planet and its ice-cap coverage. These changes in the water cycle also alter the reflectivity of Earth as a whole, and can therefore affect global climate.

When we put everything we know into models of the carbon cycle, though, we predict changes in atmospheric CO_2 that largely parallel inferred climate shifts. So the lack of close correspondence between climate change and proxy indicators of atmospheric CO_2 may force us to re-evaluate the proxies, rather than disavow the notion that substantially increased atmospheric CO_2 will indeed lead to marked warming in the future. Lee R. Kump is in the Department of Geosciences and the Astrobiology Research Center, 503 Deike Building, Pennsylvania State University, University Park, Pennsylvania 16802, USA.

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A start for population genomics

S. Blair Hedges

The most thorough analysis yet of the divergence of sequences in human mitochondrial DNA has been carried out. The results support the view that modern humans originated in Africa.

When and where did our species arise? Over the past two decades molecular evolutionists have vigorously pursued this question. DNA evidence from the cell powerhouse known as the mitochondrion has figured prominently in these studies, with mutations providing the raw data for producing evolutionary trees and molecular clocks to time sequence divergence. The mitochondrial family tree of humans has suggested that our roots lie in Africa¹⁻³, but this tree has had only weak statistical support. Conversely, other researchers have proposed that modern humans arose simultaneously in different regions of the world⁴.

Now, on page 708 of this issue, Gyllensten and colleagues⁵ describe an analysis of the complete mitochondrial genomes of 53 people of diverse geographical, racial and linguistic backgrounds. At 16,500 base pairs, each sequence is much longer than those previously studied. The upshot is a robust tree rooted in Africa, which times the exodus from Africa to within the past 100,000 years (recent in evolutionary terms). With this result, the pendulum swings further towards the claim that modern humans, *Homo sapiens*, originated in Africa.

Our closest living relatives are African apes, so why is an African origin for modern humans controversial? The reason is that our immediate predecessors in the genus *Homo*, now extinct, are known to have wandered out of Africa as early as two million years ago. The main alternative to an African origin, the multiregional model, holds that modern humans arose simultaneously in Africa,

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Europe and Asia from these predecessors⁴. Proponents of this view argue that the fossil record indicates transitions between, for example, Neanderthals (*H. neanderthalensis*) and modern humans in Europe, and between *H. erectus* and modern humans in Asia. However, the existence of non-African transitional fossils is debatable^{6,7}, and there is genetic evidence⁸ that Neanderthals did not widely interbreed with modern humans even though the two coexisted for at least 10,000 years. Such coexistence is the strongest evidence for recognizing the two as separate species.

The crux of the mitochondrial evidence for an African origin has been the presence of several African lineages deep in the evolutionary trees, even though they have only had weak statistical support. Gyllensten's team⁵ also found this pattern, but obtained a robust tree by collecting a larger data set than in previous studies. The three earliest branches in their tree lead exclusively to Africans, and two of the splits are statistically significant. Interpreted literally, the tree indicates that some Africans are closer to Europeans and Asians than to other Africans. However, the history of a single gene or molecule may not always mirror that of the population, and other molecular studies place Africans in a single group9. Together, these studies suggest that the founding population leaving Africa carried with it a subset of mitochondrial alleles alternative forms of the same gene - and that African populations continued to interbreed after the exodus.

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Figure 1 The origin and dispersal of modern humans, *Homo sapiens*. The time of origin of modern humans is not well known but may have been about 200,000 (130,000–465,000) years ago. New evidence from mitochondrial genomes⁵ bolsters the hypothesis that the place of origin was sub-Saharan Africa and that the dispersal from Africa occurred within the past 100,000 years. The earliest known fossil and archaeological evidence on each continent¹⁴, shown on the map, is consistent with this view.

Gyllensten and colleagues estimate that the divergence of Africans and non-Africans occurred 52,000 \pm 28,000 years ago, shortly followed by a population expansion in non-Africans. This date may even be a bit too recent. Other genetic markers indicate an exodus from Africa around 100,000 years ago⁹⁻¹¹, which would be more consistent with fossil and archaeological evidence of modern humans outside Africa (Fig. 1). But no single genetic marker can time that event precisely, and the mitochondrial date is in the right ballpark. Some nuclear DNA markers have suggested earlier dates for the exodus from Africa¹², so more data are needed to provide a fuller picture. Nonetheless, most of the genetic evidence indicates that there were only about 10,000 breeding individuals for a long time before the recent expansion of modern humans outside Africa¹³. Such a small population size is incompatible with the multiregional model, which would require many more individuals to maintain gene flow among continents.

A different question is when H. sapiens arose in the first place. Molecular clocks would be well suited to address that question if our closest relative were living. But our closest relative in the genus Homo, whether H. erectus or some other species, is unfortunately extinct. The earliest fossils of modern H. sapiens are 130,000 years old¹⁴, however, so that is the upper bound on the origin of our species. Studies of ancient DNA provide hints to a lower bound. The split between H. neanderthalensis (a species which is not necessarily our closest relative) and H. sapienshas been timed by a DNA clock at 465,000 years ago⁸. So our species probably arose somewhere between 130,000 and 465,000 years ago. An estimate of 200,000 years ago

is not unreasonable given the transition seen in the African fossil record between archaic and modern humans around that time¹⁴.

Gyllensten and colleagues⁵ have used sequences from a large number of complete mitochondrial genomes to address these evolutionary questions, an approach that could be called population genomics. The number of such genome sequences will surely grow rapidly in the near future, and complete

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sequences of nuclear genomes, from more than one human, are to be expected. Genes responsible for physical and behavioural traits will probably be found and their allelic histories will provide additional information. Molecular evolutionary trees and time estimates will have greater precision, all of which will help to clarify our evolutionary history.

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On the threshold of success

Richard De La Rue and Chris Smith

Tiny crystals that interact strongly with certain frequencies of light can be used to make semiconductor lasers. They can now be stimulated electrically, and thus be integrated with conventional electronic devices.

hotonic crystals occur naturally as semiprecious opal and the microscopic structures on the wings of some tropical butterflies. They are repeating structures that inhibit the propagation of some frequencies of light. They often produce brilliant colour effects by selecting narrow parts of the spectrum of white light falling on them. If the selection effect is strong enough, the crystal can completely exclude photons of a particular wavelength, creating a threedimensional 'photonic bandgap'^{1,2}. Any defect in the structure will bottle up the forbidden light — like a tiny optical cavity by blocking the propagation of light in all directions. To be useful in optoelectronics, the light has to be allowed to escape from this cavity.

incorporating a photonic bandgap was created by shining a laser beam on the device to stimulate light emission³. In a paper in *Electronic Letters*, Zhou *et al.*⁴ now report a photonic bandgap laser that can be excited electrically, allowing it to be incorporated into electronic devices. Such photonic lasers are only a few micrometres in size, opening up new possibilities for optoelectronics and fibre-optical communications.

The photonic-bandgap effect, first proposed just over a decade ago, is the optical equivalent of the 'forbidden energy bandgap' found in the electronic structure of semiconductor crystals. The electronic bandgap excludes electrons of certain energies, an essential feature of semiconductor devices from transistors to lasers. Semiconductor lasers based on electronic bandgaps are well-

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