NEWS & VIEWS

EVOLUTIONARY BIOLOGY

Ancient bacteria liked it hot

Manolo Gouy and Marc Chaussidon

Proteins from ancestral bacteria have been modelled and reconstructed. Strikingly, the heat stability of these proteins parallels the temperatures of their ocean habitats, as determined from the geological record.

The study of the environment in which early life evolved has long been the domain of the physical sciences. For example, analyses of the chemical and isotopic compositions of rocks formed during the Archaean (from 3,800 million years ago to 2,500 million years ago) allow precise dating and reconstruction of environmental parameters at that time, such as seawater temperature and atmospheric composition. But the natural sciences have recently discovered other ways to study the habitats of early life. On page 704 of this issue, Gaucher *et al.*[1] describe one such approach. They have 'resurrected' proteins from bacteria of bygone ages, providing clues about the temperatures at which these organisms lived.

The protein targeted by Gaucher *et al.*[1] is elongation factor thermo-unstable (EF-Tu), a crucial player in protein synthesis. Every extant cell contains variants of the genes that encode EF-Tu, and so the factor is expected to have existed in all cells throughout evolutionary history. In present-day bacteria, the temperature above which EF-Tu loses its precise three-dimensional structure is highly correlated to the temperature of each species' habitat — EF-Tu proteins of hyperthermophilic bacteria (which thrive at temperatures of 80 °C or more) maintain their structures at high temperatures, whereas the analogous proteins of mesophilic bacteria (which prefer temperatures between 25 °C and 40 °C) unfold at much lower temperatures.

The sequences of many extant bacterial genomes have been determined, so EF-Tu sequences from species representing various groups and habitats are known. By contrast, ancient protein sequences can only be estimated, using methods based on statistical modelling of the molecular evolutionary process. Gaucher *et al.*[1] have made such estimations for a dozen organisms in the bacterial phylogenetic tree, starting from the last common ancestor and ending with present-day bacteria. They synthesized the corresponding gene sequences and cloned them into *Escherichia coli* cells, which then produced ancestral EF-Tu proteins. The authors then measured the thermostability of the proteins.

The results are striking. In bacteria, there is a clear correlation between age and thermostability for ancestral EF-Tu sequences: proteins from bacteria that lived during earlier periods are more heat stable than those from more recent times. This trend parallels the changes in temperature proposed for Precambrian oceans (which existed between 3,800 million and 542 million years ago) on the basis of analyses of the isotopic composition of Precambrian cherts. These cherts are some of the best-preserved sedimentary rocks from the period. It has been shown that the ^{18}O and ^{30}Si isotopic contents of Precambrian cherts are best explained by a progressive cooling of the oceans — from temperatures of about 70 °C some 3,500 million years ago to 20 °C just 800 million years ago[2,3].

But ancestral protein-sequence estimation is dogged by several uncertainties. The first problem is that such estimates are based on a phylogenetic tree that models evolutionary relationships between organisms, but in which the relationships between large bacterial groups are unconfirmed. The second issue is that statistical models of protein-sequence evolution depend on a simplifying hypothesis, which states that the probability that each amino acid will be replaced by another never changes with time. This may not be true. Finally, for any given tree and evolutionary model, billions of ancestral sequences are possible. But Gaucher and colleagues' results[1] are robust. They performed a series of control experiments that convincingly show their results to be qualitatively insensitive to the intrinsic uncertainties of their technique.

Other procedures for estimating ancient environmental temperatures from extant

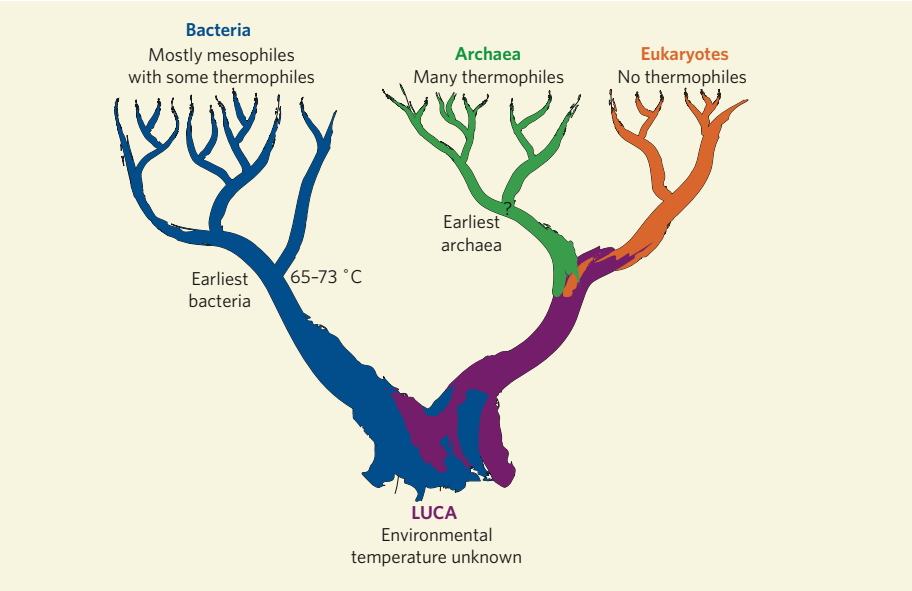

Figure 1 | Environmental temperatures at pivotal points in early evolutionary history. The tree of life stems from the last universal common ancestor (LUCA), which evolved into bacteria, archaea (microorganisms similar to bacteria) and eukaryotes (organisms with nucleus-containing cells). Extant bacteria are mostly mesophilic (they thrive at temperatures of about 25–40 °C), but some are thermophilic (preferring temperatures greater than about 60 °C). Many extant archaea are thermophilic, but no such eukaryotes exist. Gaucher *et al.*[1] modelled and reconstructed proteins from ancestral bacteria, and from their heat stability conclude that the earliest bacteria lived in oceans at temperatures of 65–73 °C. Previous studies[4,5] based on models of ancient RNA suggest that LUCA was either mesophilic or thermophilic. The temperature at which the earliest archaea flourished has not been estimated.

molecular-sequence data are known. For example, the amounts of the nucleic-acid bases guanine and cytosine found in certain RNA sequences of modern-day bacteria and archaea (a group of microorganisms similar to bacteria, but which evolved separately) strongly correlate with environmental temperatures. So by determining these RNA sequences for ancestral microorganisms, the temperatures of ancient habitats can be estimated (Fig. 1). But this method has yielded conflicting results, suggesting that very ancient life-forms were hyperthermophilic[4] but also that the last universal common ancestor (LUCA) of all modern life was mesophilic[5]. Previous statistical estimations of protein sequences support the idea that LUCA was hyperthermophilic[6].

Some of these conflicts might result from the inadequacy of the hypotheses used in evolutionary models. Emerging statistical methods that account for variation in the probabilities of DNA- or protein-sequence mutations with time[7] should help in accurately estimating the features of ancestral protein sequences. The recently discovered correlation between environmental temperatures and the average content of seven specific amino acids in bacterial and archaeal proteins[8] also provides a promising opportunity for future research.

Gaucher *et al.*[1] propose two possible scenarios to explain the striking agreement between the thermostability of bacterial EF-Tus and ocean temperatures in the Precambrian. The first is that bacteria from the Archaean lived in hot oceans, and progressively adapted to cooler oceans. Alternatively, bacteria could have started out in hot springs or thermal vents before expanding their territory into the cooler, global environment.

Sadly, geological evidence that might discriminate between these possibilities is scarce — Archaean microorganisms are poorly preserved compared with those of the late Precambrian (2,500 million to 542 million years ago). Geologists have, however, found laminated, sedimentary structures that are 3,430 million years old in the Pilbara Craton of Western Australia. By comparison with modern analogues, these 'stromatolite' structures are interpreted as reefs constructed by cyanobacteria[9,10]. In addition, carbonaceous microstructures of a similar age (3,460 million years) have been found in bedded cherts from the Apex Formation of Western Australia[11]. These are most probably fossils of bacteria or archaea, although the evidence for this is still debated. Nevertheless, the existence of these stromatolites and of fossil-bearing cherts, and their moderate enrichment in ^{18}O and ^{30}Si, favour the idea that ancient bacteria lived in hot oceans.

Matching the phylogenetic tree of life to the geological record remains a fundamentally difficult problem, because the tree is built from molecules whose early rates of evolution are unknown. The significance of Gaucher and colleagues' contribution[1] is that it might open up a new way to overcome this problem: using molecular data to provide information about ancient environmental features that could allow ancestral organisms to be dated through the geological record. ■

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DEVICE PHYSICS

Update on 3D displays

Joseph W. Perry

Static three-dimensional images are easy to make using holographic techniques. Moving pictures are more of a problem. A palm-sized, updatable display using a specially designed polymer could be a breakthrough.

Moviegoers who crave that feeling of being 'inside' the action will welcome the news from Tay *et al.* on page 694 of this issue[1]. The authors report a development that brings this dream a step closer to reality — an updatable, three-dimensional display based on cheap, easy-to-process photorefractive polymer materials. The technology still has some way to go to maturity, but ultimately it's not just the cinéastes who could benefit: displays that can provide realistic three-dimensional images with a wide angular viewing range might also be used in military or medical contexts, such as the simulation of field situations or the guidance of keyhole surgery.

Three-dimensional (3D) visualization technologies have a long history[2]. Early 'stereoscopic' approaches — familiar from the 3D movie craze of the early 1950s — used 2D displays and special eye-wear with polarizing lenses or lenses of different colours, so that separate images were seen in each eye. Alternatively, two images were switched rapidly on and off, with viewing glasses shuttered in synchrony to make the display appear continuous.

That kind of eye-wear is cumbersome, and

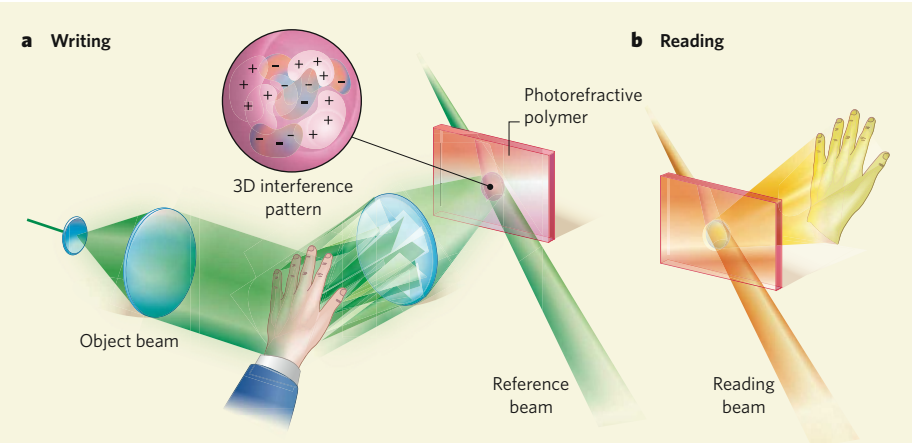

Figure 1 | Handy display. a, The base medium of Tay and colleagues' updatable, three-dimensional holographic display[1] is a photorefractive polymer onto which the 3D interference pattern of light scattered by an object and a reference laser beam can be etched volumetrically. In brighter regions of the interference pattern, mobile charge carriers — electrons (–) and 'holes' (+) left by departed electrons — are generated and the more mobile holes drift into the darker regions. The electric-field distribution, and so the local refractive index, of the medium are thus altered in a way that maps the amplitude and phase information of the light from the imaged object. **b,** When light from a second, reading laser beam illuminates the polymer, it is scattered in the same way as light on the original object, and a 3D image results. As the writing mechanism depends solely on the dynamics of charge carriers in the polymer, which in turn (for a given polymer and applied voltage) depends only on the incident interference pattern, the display is in principle fully updatable.