

Again, the closeness of amphioxus and vertebrates receives support from neuroanatomy (B. Fritsch, Creighton Univ., Omaha), myosin light-chain expression (D. A. Pace and L. Z. Holland, Scripps), DNA hybridization kinetics (G. N. Sideris, New York Univ.) and mitochondrial gene arrangements (W. M. Brown and L. L. Daehler, Univ. of Michigan, Ann Arbor). And scratch out the bit in your textbooks that says how the excretory organs of the amphioxus are like those in flatworms. This has been debunked by some neat histology showing that they are similar to vertebrate glomeruli, with some modifications allowing for their small size (E. E. Ruppert, Clemson Univ., South Carolina). Few of these advances would have been possible without modern technology, yet they lay some weighty problems to rest.

So too, though, does something as simple as a video film, showing how amphioxus larvae actually feed — a problem that had troubled the finest minds for a century (T. H. J. Gilmour, Univ. of Saskatchewan). Likewise, a 'timetable' of amphioxus development compiled from scanning electron micrographs (M. D. Stokes and N. D. Holland, Scripps) showing that the anus originates on the right, swinging over to the left later on (just like Van Wijhe said it did back in the 1890s, only nobody believed him). Submicroscopic detail of the amphioxus nervous system is being revealed through the ability to tag individual neurons with a fluorescent dye and trace their subsequent development (L. S. Demski and J. B. Morrill, Univ. of South Florida).

Yet the amphioxus still has many other old problems with which to challenge us. Still unsolved is the curiously lopsided development of the larva, in which precocious left gill slits appear long before the right-hand series. Whereas left and right somites in vertebrates are locked in phase with each other, amphioxus somites are prone to slippage with respect to one another and the notochord (R. Presley and T. J. Horder, Univ. of Wales, Cardiff, and J. Slipka, Charles Univ., Czech Republic). This could be one example of a tendency towards asymmetry seen in deuterostomes generally (R. P. S. Jefferies, Natural History Museum, London), which modern methods have so far proved powerless to explain. □

Henry Gee is an assistant editor of *Nature*.

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## Oldest rocks in Europe

Stephen J. G. Galer

How did the ancient continents differ from those of today, and how were they formed? These are key questions facing geologists studying the Archaean period, which spanned almost the first half of Earth history, ending 2.5 billion years (Gyr) ago. Answers can in principle be sought by examining old surviving rocks. But unfortunately, the further one looks back in geological time the more fragmentary the rock record becomes. It is for this reason that the discovery of yet older fragments of continental crust excites particular interest. On page 552 of this issue, Burton and colleagues<sup>1</sup> report convincing ages of 3.30 Gyr for two amphibolites — metamorphosed basalts — from the Lewisian complex of northwest Scotland.

From a worldwide perspective these ages, obtained by <sup>147</sup>Sm–<sup>143</sup>Nd and <sup>207</sup>Pb–<sup>206</sup>Pb dating, are not strikingly old: a number of Archaean terrains contain size-

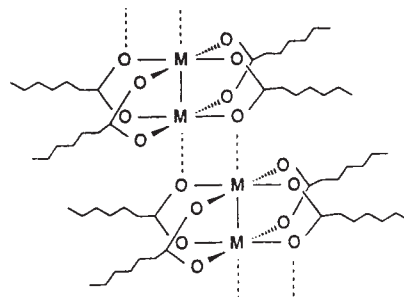
able pieces with ages in excess of 3.3 Gyr, notably in Canada, Greenland, southern Africa and Western Australia. The Acasta gneisses, located in the Slave province of northwestern Canada, contain components clocking in at 3.96 Gyr (ref. 2), making them the world's oldest rocks. Nevertheless, the results of Burton *et al.* are important for a number of reasons. The most trivial of these is that they have identified the oldest known European rocks, provided that Greenland is considered to be part of North America. Isolated pockets of 3.1–3.2-Gyr-old tonalitic gneiss are known from the eastern Baltic Shield<sup>3,4</sup>, and previously held the European age record.

More important by far is that the history of crustal development in the Lewisian complex will have to be radically rethought. Geochronological investigations of the Lewisian have themselves had

## Liquid crystal fans

THE birefringence of liquid crystals is familiar from digital watch displays, but their possibilities do not end there. Add a transition metal ion, either as a guest within an organic cage or as part of the molecular structure, and a host of magnetic, electronic and redox properties could come to light. So David V. Baxter and co-workers hope, at least. They

have been looking at compounds with the general formula  $M_2(O_2CR)_4$ , where M is one of the group VI metals chromium, molybdenum and tungsten. The molecules are shaped like paddle wheels, and in the crystalline state form 'ladders' loosely held together by oxygen-to-metal intermolecular bonds as shown below (figures reprinted with permission from *J. Am. chem. Soc.* **116**, 4551–



4566; 1994; copyright American Chemical Society). Heat the crystals, and the different metal–oxygen bond strengths make themselves felt: Baxter *et al.* found that the weakly bonded tungsten compounds simply melted to an isotropic liquid, the strongly bonded chromium compounds formed a liquid crystal phase which decomposed on further heating, and many of the molybdenum compounds passed through all three phases in turn. The micrograph above, obtained on cooling isotropic liquid  $Mo_2(O_2C(CF_2)_6CF_3)_4$ , shows the fan-like optical texture of a hexagonal disordered discotic (stacked disk) liquid crystal. The authors conclude from optical, X-ray and NMR evidence that the stacking is retained here, but the intermolecular bonding is readily broken so that molecules can slip sideways or twist about their M–M axes. L. M.

a long history, following the classic study by Moorbath and colleagues<sup>5</sup>. In broad-brush terms, the consensus has been that the Lewisian crust was formed by differentiation of the mantle at about 2.9 Gyr and experienced high-grade granulite facies metamorphism around 2.7 Gyr ago (the grade refers to the severity of metamorphism, reflecting the peak temperatures and pressures reached). The new data from Burton *et al.* extend the geological history of the Lewisian back a further 400 Myr in time, at least in the Gruinard Bay section that they studied. Although Whitehouse<sup>6</sup> reported a whole-rock <sup>207</sup>Pb–<sup>206</sup>Pb isochron of 3.52 Gyr from the Lewisian of the Outer Hebrides, he dismissed this age, probably rightly, as being spurious. So why have previous studies failed to find rocks older than 2.9 Gyr? One answer might simply be that the 2.7-Gyr-old high-grade metamorphism at least partially reset the isotope clocks. The fact that Burton *et al.* find older ages in material metamorphosed under lower-grade conditions is suggestive of this.

Metamorphic resetting can only be part of the story, though, and the younger ages are clearly in most instances primary. Lewisian crustal evolution can now be traced from the Gruinard Bay amphibolites at 3.30 Gyr to the emplacement of the last members of the Scourie mafic dyke swarm 2.00 Gyr ago<sup>7</sup>—a crustal stabilization interval comparable to that of the Kaapvaal craton in South Africa<sup>8</sup>.

Granitoid rocks of the trondhjemite-tonalite–granodiorite (TTG) suite make up much of the Lewisian complex. Burton *et al.* also report much younger ages of 2.40 Gyr for two trondhjemites from Gruinard Bay. But what are the genetic relationships, if any, between the amphibolites, trondhjemites and associated tonalites? Burton *et al.* view the amphibolites as surviving remnants of a once more extensive 3.3-Gyr-old crust of similar composition. Using their own and literature data, they are then able to make a strong case that both the trondhjemites and tonalites were derived by later intracrustal melting of such amphibolitic material, and that new mantle input was minimal. The argument is based on the initial  $\epsilon_{\text{Nd}}$  of the respective isochrons ( $\epsilon_{\text{Nd}}$  is the deviation in <sup>143</sup>Nd/<sup>144</sup>Nd ratio at any time from the corresponding average ratio of the whole Earth, expressed in parts per 10<sup>4</sup>). Initial  $\epsilon_{\text{Nd}}$ -values of the Lewisian rocks apparently decrease monotonically over time, starting from the amphibolite  $\epsilon_{\text{Nd}}$  of +3 at 3.30 Gyr and passing to –4 for the trondhjemites at 2.40 Gyr. A secular change in  $\epsilon_{\text{Nd}}$  like this is most easily explained by closed-system evolution of the crust at a <sup>147</sup>Sm/<sup>144</sup>Nd ratio of about 0.13. As the depleted mantle is expected to have an  $\epsilon_{\text{Nd}}$  of about +4 at 2.4 Gyr, juvenile mantle-derived material cannot have contributed significantly to the tonalites and trondhjemites.

The case for closed-system evolution is made far more compelling by the fact that the measured whole-rock <sup>147</sup>Sm/<sup>144</sup>Nd ratios of the amphibolites themselves are around 0.13. A similar, albeit more complicated, story can be woven around the initial lead isotope ratios.

The TTG-suite rocks seem, then, to be genetically related to the amphibolites, presumably by melting. Support for this view comes from two other sources. First, it has long been supposed that the TTG-suite rocks in Archaean terrains require the presence of amphibole and garnet in their sources, on the grounds of their abundance patterns of rare earth elements<sup>9,10</sup>. Second, experimental studies have shown that trondhjemitic and tonalitic magmas can indeed be produced by melting amphibolite<sup>11–13</sup>.

Burton *et al.* have as yet identified only one isolated enclave of older mafic material in the Lewisian; with luck, more will be found in future studies. No doubt even older European rocks wait to be discovered as well. Nonetheless, a relatively complete and consistent picture of Lewisian geological history seems to be emerging: intracrustal melting of mafic precursors occurred over a protracted period and was extremely important in stabilizing the Lewisian crust and establishing its overall tonalitic composition. □

Stephen J. G. Galer is in the Abteilung Geochemie, Max-Planck-Institut für Chemie, Postfach 3060, 55020 Mainz, Germany.

Stephen J. G. Galer is in the Abteilung Geochemie, Max-Planck-Institut für Chemie, Postfach 3060, 55020 Mainz, Germany.

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## ENZYME STRUCTURE

# Cracking tyrosine phosphatases

John Tainer and Paul Russell

THE structure of a secret biological weapon responsible for the deaths of millions has been revealed. At the molecular level, this revelation should enable us to find out more about how phosphotyrosine signal transduction pathways are controlled. Of the two new protein tyrosine phosphatase (PTP) structures reported on pages 571 and 575 of this issue<sup>1,2</sup>, one is a virulence factor for the bacterium of the genus *Yersinia* that is responsible for bubonic plague<sup>1</sup>, infamous as the Black Death which killed one-third of Europe's population in the fourteenth century; the other is one of the first representatives from a class of low-molecular-weight PTPs ubiquitously expressed in mammalian tissues, but unrelated in sequence to the *Yersinia* PTP (ref. 2). These two new structures help solve the puzzle of how PTPs can have widely varying sequences and protein substrates, yet remain selective for phosphotyrosine and not phosphothreonine or phosphoserine.

These different PTP structures are striking examples of convergent evolution achieving highly similar active-site clefts. Both structures, as well as human PTP1B (ref. 3), which shares about 20 per cent sequence identity with the *Yersinia* PTP, have a common central structural core consisting of four parallel  $\beta$ -strands with surrounding  $\alpha$ -helices. All three PTP

structures share a conserved phosphate-recognition loop (P-loop) structure which is formed by the signature sequence H/V-C-(X)<sub>5</sub>-R-S/T-G/A/P (single-letter amino-acid code; X is any amino acid) common to more than 40 PTPs. Based upon crystal structures with bound tungstate<sup>1</sup> and sulphate<sup>2</sup>, the P-loop provides a circular array of amino-nitrogen hydrogen bonds plus a critical arginine side-chain interaction which activate the catalytic cysteine thiolate and stabilize the subsequent bound phosphate anion. This P-loop lies at the carboxyl end of the parallel  $\beta$ -strands, forms the base of the catalytic cleft, and aligns the bound phosphate anion at the positive dipole of an  $\alpha$ -helix. The surrounding loops are believed to confer the phosphotyrosine specificity of PTPs by producing a deep phosphate-binding site that prohibits tight binding by the shorter phosphoserine and phosphothreonine side chains.

Although the phosphate-binding P-loop structure is conserved, the  $\beta$ -sheet and  $\alpha$ -helices in the protein core have distinct topologies. In the bovine low-molecular-weight PTP, the four  $\beta$ -stranded core region is formed by two  $\beta$ - $\alpha$ - $\beta$  Rossmann motifs. In the *Yersinia* PTP structure, what would be the equivalent two  $\beta$ - $\alpha$ - $\beta$  motifs are split by their  $\beta$ -strand interdigitation. Outside this core region, these structures vary greatly.