news and views

scaled down to nearer 670 million years\(^5\), bringing the figures more into line with the fossil record. A ‘late arrival’ model would also imply that the evolution of the main animal groups took place both late in Earth’s history, and rapidly — perhaps in response to the evolution of Hox genes\(^6\) or to the lifting of some external constraint such as insufficient atmospheric oxygen\(^7\).

So should these supposedly ancient markings be accepted as new evidence for the ‘deep time’ model? When a respected researcher such as Seilacher, who has a good track record in the field of trace fossils, makes such a claim as this, it has to be taken seriously. But extraordinary claims, of course, require extraordinary evidence.

The first claim\(^1\) is that these are the traces of ‘triploblastic’ animals. This means that the trace-makers had a gut and a fluid-filled coelom. Such an organization is found only in complex animals from worms to chordates. Seilacher and co-authors’ argument is that, at 5 mm, the burrow diameters are too large to have been made by single-celled protists; but unicellular protists, including early Cambrian forms, can be that large and can make burrows. Moreover, at 5 mm diameter, how could such organisms have remained hidden from the fossil record for over 500 million years? Finally, how come the tunnels are branched? Branching implies a behavioural sophistication which is thought to have appeared about 560 million years ago\(^8\).

These seeming paradoxes may yet be explained by a fresh look at the age of the lower Vindhyan rocks (Fig. 1). Until now, they have broadly been taken to be 1,100 million years old on the basis of potassium-argon and fission-track dates. But these dates were mostly obtained in the 1960s, and no further particulars are given by the authors\(^9\). Unfortunately, the data they cite must now be regarded as a very doubtful guide to the age of the Vindhyan rocks\(^9,10\), for which modern studies of geochronology are urgently required.

In fact, we may be in for a big surprise regarding the age of the Vindhyan supergroup, including, of course, the Chorhat sandstone. Acid digestion of the immediately overlying Rohtasgar limestones, undertaken in India by R.J. Azmi, has yielded a rich, well-preserved and typical early Cambrian skeletal fauna, including certain types of brachiopod\(^11\). This astounding discovery means that supposed trace-fossil markings from the Chorhat sandstone may be little more than 540 million years old, close to the beginning of the Cambrian ‘explosion’. Branched burrow systems up to 5 mm wide are certainly well known from the Ediacaran and Cambrian\(^8\). Unless there is a major break between the Chorhat sandstone and the Rohtasgar limestone, this new interpretation\(^9\) would mean that there is still no reliable fossil evidence to support the ‘deep time’ view of the emergence of animals.

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RNA structure

Ribozyme crevices and catalysis

Daniel Herschlag

Since the X-ray crystallographic structure of the hammerhead ribozyme — a catalytic RNA molecule — was solved\(^1\) in 1994, the RNA community has been waiting for a view of a second RNA enzyme. We are now rewarded for our patience by not one but two ribozyme structures: a 2.3Å structure of the ribozyme from the hepatitis delta helper virus (HDV), reported by Ferré-D’Amare et al.\(^2\) on page 567 of this issue; and a 5Å structure of the group I intron from Tetrahymena thermophila, published by Golden et al.\(^3\) in this week’s Science. The most striking feature of these RNAs is that they look like enzymes — that is, both have active sites that seem to be preorganized and located in crevices, as we are accustomed to seeing in protein enzymes. This is in marked contrast to the hammerhead ribozyme, which exposes the cleavage site in solution, rather than sequestering it in a cavity, and seems to require a substantial conformational rearrangement to perform its catalytic function\(^1,4,5\).

Despite their general similarities, the HDV and Tetrahymena ribozymes are preorganized very differently. The HDV ribozyme is only about one-fifth the size of the Tetrahymena ribozyme, owing to a remarkable intertwining of secondary structural elements in what can be referred to a ‘double pseudoknot’. The positioning of secondary structure (that is, base-pairing) — which accounts for three-quarters of the HDV residues — within the double pseudoknot establishes the overall position of the helices with respect to each other. This allows a complex, three-dimensional architecture. Several tertiary connections then establish the precise tertiary fold, positioning the functional groups that are required for catalysis, despite the ribozyme’s modest size.

In contrast, group I ribozymes are constructed from domains, some of which constitute independent folding units. The structure of one of these domains, the P4-P6 domain, has already been solved to high resolution\(^6\), and this domain is largely unperturbed in Golden and colleagues’ structure. The second domain, P3–P9, was not present in the previous structure, but it can now be seen to wrap around the P4–P6 domain. This observation provides a structural explanation for kinetic-folding results\(^7,8\), which show that the P4–P6 domain forms earlier than the P3–P9 domain.

This structure, along with the many functional data for the Tetrahymena ribozyme, shows how the coming together of these domains is critical for forming the substrate binding sites. The binding site for one substrate, guanosine, was previously localized biochemically\(^9\) to the P7 helix, which is found within the P3–P9 domain. The structure reveals that the P7 helix is distorted when P3–P9 interacts with the P4–P6 interface, presumably allowing P7 to bind guanosine. Distortion of the P7 helix explains an observation from my own laboratory (M. Engelhardt and D. H., unpublished) that removal of the P5abc subdomain of P4–P6 weakens guanosine binding, even though P5abc and P7 are not in direct contact. The intersection of the P4–P6 and P3–P9 domains also creates a shallow crevice. This is lined with residues that have been implicated in binding of the substrate domain P1–P2, which is absent from the molecule crystallized by Golden et al.\(^8\). Further experiments will reveal whether the 5Å limit to resolution comes from limits that are specific to this crystal, or whether it is due to inherent flexibility in the absence of the P1–P2 substrate domain.

The two new structures provide an opportunity to evaluate what works in structural prediction, what doesn’t work, and why. Because RNA secondary structure is determined locally, most secondary-structure elements can be identified through evolutionary relationships and mutagenic tests involving compensatory changes of putative pairing partners. A remarkably accurate three-dimensional model of the group I intron was derived from such analysis\(^10\). Similarly, secondary-structure prediction turns out to have been very good for

10. Azmi, R. J. Geol. Soc. Ind. (in the press).

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