more detail, the transfer of information from nucleic acid to nucleic acid, or from nucleic acid to protein may be possible, but transfer from protein to protein, or from protein to nucleic acid is impossible." By 'information', Crick meant a precise sequence, either of bases in a nucleic acid or of amino-acid residues in a protein. So, a fundamental tenet of molecular biology is that a protein constitutes an informational dead-end to the cell.

Put another way, a protein is unable to replicate itself, not because it lacks catalytic capabilities but because its information is irretrievable. So, one of the main aims of those investigating prebiotic molecular evolution is to discover (or re-invent) a molecule with the catalytic prowess of a protein, but the accessible information content of a nucleic acid[1].

For several reasons, RNA is the target of this search. RNA polymerization — which involves the reading of a DNA or RNA template and production of a complementary RNA strand — is likely to have been the responsibility of protein-based enzymes since cellular life began. But enough catalytic RNAs exist to infer that RNA might once have been its own replicating enzyme. Natural catalytic RNAs (ribozymes) have been discovered that enhance reactions similar to those required for replication[4]. Furthermore, ribosomal RNA acts as the catalyst of protein synthesis, so polymerase activity per se (in this case, protein polymerization) is not beyond the scope of RNA[5]. Nevertheless, a possible 'founder' polymerase is either long extinct or as yet undiscovered, leaving biochemists to conjure up proof-of-principle schemes for repopulating a presumptive RNA world.

The reconstruction of an RNA-replicating ribozyme began with experimental modifications of a naturally occurring, self-splicing RNA molecule known as a group I intron[6]. The modified molecules could covalently join several RNA sequences, aligned along an RNA template, efficiently enough to generate a few full-length RNA strands up to 200 nucleotides long[7] (Fig. 1a). Unfortunately, the RNA sequences to be joined had to be about ten nucleotides in size before any appreciable activity was seen, and a 5'-terminal guanosine, instead of the more common pyrophosphate, was the leaving group in the joining reaction. A true RNA polymerase, as we would now define it, must be able to use single nucleotides and join them accurately in the order specified by an RNA template.

The next step came in the form of RNAs that could join two RNA fragments aligned along an RNA template; but they use pyrophosphate as the leaving group[8] (Fig. 1b). These RNAs are still 'ligases' — they do not copy RNA but merely join two RNA molecules — but they promote the same chemical joining reaction as that performed by protein-based polymerases. The RNA enzymes here[8] were obtained not from the group I intron, but by *in vitro* amplification and darwinian selection from an enormous pool of random RNA sequences, each of which was more than 100 nucleotides long. Among the active sequences selected from this morass was one with an unusually complex knot-like structure, which had particularly robust efficiency[9]. This core ligase provided Bartel and co-workers with the fundamental catalytic capability needed to identify a simple polymerase[10].

Starting from the core ligase[9], and performing several iterations of mutation and selection, Bartel and colleagues[2] have developed a new variant that comes even closer to the properties expected of a true RNA-templated, RNA-catalysed, RNA polymerase. Unlike its predecessors, this polymerase has no restrictions on the sequence it replicates. It can synthesize more than a full turn of an RNA helix (up to 14 nucleotides), adding single nucleotide triphosphates to a short primer sequence that is complementary to the RNA template (Fig. 1c). The polymerase can distinguish correct from incorrect primers, and it preferentially extends matched primers with an accuracy of 96–99%, a fidelity on a par with some protein-based polymerases[11].

Yet this polymerase still lacks at least two properties expected of the prebiotic RNA-replicating enzyme: it cannot copy longer templates fully, and its polymerization is not efficient enough to produce progeny RNA molecules at a rate exceeding the rate of decomposition of parental RNAs. Furthermore, given the slow rates of template copying, the polymerase does not appear to be 'processive' — after adding the first nucleotide, the polymerase is more likely to dissociate from the template than to remain associated and add a second nucleotide. Self-complementary regions of the template could form structures that block access by the polymerase. A more processive polymerase, or an enzyme with a companion 'unwinding' activity, may be needed to achieve efficient polymerization. In fact, an unwinding activity might be particularly important because self-replication is actually a two-step process: synthesis of the first strand results in an extended duplex, which must be peeled apart before the new strand can be copied to regenerate the original sequence.

Bartel and colleagues' latest polymerase is relatively large (189 nucleotides) and structurally complex, so the question remains as to how such an RNA could have evolved in the first place. This becomes a matter of the wildest speculation, but the general path from ligase to polymerase used in the *in vitro* selection strategy[2] might provide clues. The

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Geophysics

Martian motion

At some time in the past, an object hit Mars near its south pole. The result was a crater, 45 km in diameter, part of which is evident as the green crescent at the left (west) of this image compiled from Mars Orbiter Laser Altimeter data. But why a crescent? As he describes in the *Journal of Geophysical Research* (**106**, 10075–10085; 2001), James W. Head concludes that the crescent shape resulted from considerable movement of the martian polar cap within the past few million years. Head

constructed profiles of the crater and neighbouring areas, and took especial account of the pattern of an 'ejecta lobe' and secondary ejecta craters seen on higher-resolution pictures.

The south pole of Mars is thought to be covered by seasonally shifting deposits of water-ice, usually with a layer of CO_2 on top. These deposits overlie a much more stable 'polar layered terrain' of ice and dust. Head's thesis is that, in the comparatively recent past, polar layered terrain swept from the

south of the crater to occupy a large part of it, leaving only the original crater floor, seen here in green. This conclusion is largely based on the pattern of surviving secondary craters — those on the ground underlying the layered terrain (brown) close to the impact, or in the path of the part of the polar cap that moved, being obliterated. From features known as mantled deposits — residues of polar layered terrain activity — to the north and east of the crater, Head also surmises that the layered terrain later retreated partially.

The other large impact crater, seen on the right of this picture, lies 300 km from that painstakingly investigated by Head. Its western part likewise contains a lobe of polar layered terrain, a further indication of the possible occurrence of dynamic processes at the martian south pole. **Tim Lincoln**