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Evolutionary Questions: The "Progenote"

M. Mitchell Waldrop, in his Research News article "How do you read from the palimpsest of life?" (3 Nov., p. 578), states that Steven A. Benner *et al.* (1) "try to reconstruct the 'progenote,' which is their name for the last common ancestor of modern forms of life."

Although the name "progenote" was introduced about 10 years ago (2), the underlying concept goes back another decade, to

"the recognition that at sufficiently early stages in evolution the fundamental information-transferring processes . . . must have been error-ridden . . ." (3). This necessarily follows from the fact that the translation apparatus is very complex, far too complex to have evolved in one step. Therefore, in its rudimentary stages it almost certainly translated genetic information in an imprecise, perhaps even ambiguous, fashion (2-4).

As a result of their having rudimentary translation mechanisms, the ancestors of modern cells (which have existed for the last three or so billion years) were by comparison limited in almost every way (2-5): Their proteins had to be smaller or less precisely defined than modern proteins, or both, which meant that primitive enzymes were typically quite different from modern enzymes. As nucleic acid replication was a less accurate process than it now is, the number of different genes the ancestral cell could carry was severely limited. And the states of the cell were simpler and less precisely defined than they are in modern cells. To designate entities that were in various stages of evolving a translation apparatus, whose linkage between their genotype and phenotype was not yet as precise as that seen in

modern cells, we coined the term "progenote" (the modern cell being considered a "genote").

The article by Benner *et al.*, and consequently Waldrop's article, appear to use "progenote" incorrectly, to mean "the most recent common ancestor of all modern forms of life" (1). Whether or not this most recent common ancestor was a progenote (as opposed to being a full-fledged genote) is not a fact, but one of the key unanswered evolutionary questions (5). One hopes that it will some day be answered through the sequencing of the appropriate prokaryotic genomes.

CARL R. WOESE
Department of Microbiology,
University of Illinois,
Urbana, IL 61801

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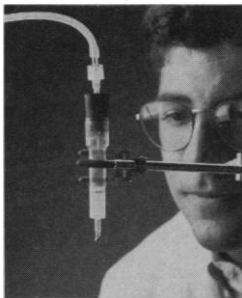
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