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FROM THE PRIMITIVE SOUP TO CYANOBACTERIA: IT MAY HAVE TAKEN LESS THAN 10 MILLION YEARS

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INTRODUCTION

Most scientific discussions on the likelihood of extraterrestrial life have been constrained by the characteristics of life on our planet and the environmental conditions under which it may have emerged. Although it has been generally assumed that this process must have been extremely slow, involving hundreds of millions or even billions of years (Oparin 1938, Urey 1952, Wald 1954, Huang 1959a, Simpson 1964, Cloud 1968, Dickerson 1978, Schidlowski 1992), a number of recent discoveries have led to a considerable compression of the time believed necessary for life to appear. It is now recognized that during its early history the Earth and other bodies of the inner Solar System went through a stage of intense collisions. Some of these impacts by large asteroids or comets may have raised the terrestrial surface to sterilizing temperatures and may have evaporated the oceans and killed off life as late as 3.8×10^9 years ago (Sagan 1974, Maher and Stevenson 1988, Sleep et al. 1989, Chyba et al. 1990, Oberbeck and Fogleman 1990). However, there is also ample paleontological evidence derived from the 3.5×10^9 year old Warrawoona sediments showing that only 300 million years after the period of intense impacts ended, our planet was populated by phototactic, stromatolite-forming microorganisms (Schopf 1983, 1993). Although these discoveries are now

generally interpreted to imply that the origin and early evolution of life were rapid, no attempts have been made to estimate the actual time required for these processes to occur. As discussed here, all the available evidence derived from (a) the rates of plausible prebiotic chemical reactions, (b) the half-lives of organic compounds in the primitive Earth, and (c) the observed rates of gene amplification in contemporary prokaryotic populations, suggests that the transition from the prebiotic soup to the RNA world, from there to the DNA/protein world, and then to cyanobacteria, may have taken place in less than 10 million years.

THE RATES OF SYNTHESES AND DESTRUCTION OF PREBIOTIC ORGANIC COMPOUNDS

The chemistry of prebiotic reactions is fast and robust. The rates of the prebiotic synthesis of amino acids, almost all of which are the result of the Strecker synthesis, have been worked out in some detail. The rates depend on temperature, pH, and HCN, NH_3 and aldehyde concentrations. At pH 8 and 0°C the slow step in amino acid synthesis, the hydrolysis of the corresponding aminonitrile to the amide, is approximately forty years (Miller and Van Trump 1981). The Murchison meteorite amino acids provide an example of a rapid prebiotic synthesis, since the whole process apparently took place in the meteorite parental body in less than 10^5 years (Peltzer et al. 1984). Adenine synthesis is also rapid from concentrated solutions of NH_4CN, requiring hours at 100°C (Oró 1960), a few weeks at 0°C, and months in dilute aqueous solution frozen at -20°C (Sánchez et al. 1966). Even though it is unlikely that sugars were components of the earliest genetic material (Joyce et al. 1987, Shapiro 1988), their synthesis from formaldehyde is also rapid. This is not to imply that all the monomers were formed in a few years. The formation and buildup of the prebiotic soup took place in very few millions of years, but the individual reactions have short half-lives, and there are no known slow steps.

The accumulation of organic compounds is limited by destructive processes. All organic compounds in aqueous solutions undergo decomposition reactions that are significant even at 0°C (Miller and Orgel 1974). As shown in Table 1, although some compounds such as fatty acids (e.g., acetic acid) and aliphatic amino acids (e.g., alanine) are very stable, sugars and many amino acids decompose in hundreds or tens of thousands of years, as do peptide bonds. Furthermore, the destruction rate that applies to all organic compounds on the Earth is controlled by the pyrolysis of organics in the submarine vents at temperatures of 350°C (Miller and Bada

TABLE 1. *Thermal Decomposition of Organic Compounds at 0°C*

Compound	*Mean Life*
Alanine	10^9 years
Fatty Acids	10^9 years
Serine	10^5 years
Sugars	44 years
Peptides	10^4 years
RNA and DNA	10^3 years

1988). The approximate passage time of the whole ocean through the vents is inversely proportional to the heat flow and to the ocean size, and currently requires about 10 million years (Edmonds et al. 1982), but may have been less than 5 million years on the early Earth because the heat flow was about ten times greater and the oceans may have been smaller. Not all organic compounds on the prebiotic Earth would have been destroyed by the vents, since some of them could survive in inland sediments, salt deposits, evaporites, and in the nonmixed parts of the oceans, but even in these protected environments they would eventually undergo thermal decomposition (Table 1).

FROM THE RNA WORLD TO THE DNA/PROTEIN WORLD

Perhaps the major uncertainty in the understanding of the origin of life currently lies in our inability to explain the emergence of a self-replicating system capable of undergoing Darwinian selection. Although it is not possible to estimate the time period for this system to emerge, there are some constraints that may be recognized. An informational polymer must have a lifetime comparable to that of the organism (Westheimer 1987) or, at least, to the time required for its replication. If a slow addition of monomers to polymers is assumed, the rate of polymer formation must nonetheless be rapid compared with hydrolysis rates, especially if a considerable amount of genetic information is to be contained in the polymer. Thus, a 100-base-long RNA molecule needs to be synthesized 100 times faster than the hydrolysis rate of a single phosphodiester bond.

The second major bottleneck in this process is represented by the origin of protein biosynthesis. How this process actually began is unknown, but it is generally assumed that it resulted from the interaction of RNA molecules (or their precursors in a pre-RNA world) with amino acids of prebiotic origin that may have been

available. Thus, protein biosynthesis must have begun to take place when suitable concentrations of amino acids were still available, and had not yet diminished by decomposition or destruction by the vents.

We assume that life arose in a prebiotic soup containing most, if not all, of the necessary small molecules, and that the evolution of the basic biosynthetic pathways occurred in a stepwise fashion (Horowitz 1945) or through a related mechanism. It is clear that this provides both for the growth and the energy supply of a large number of organisms, but it would quickly result in the depletion of the available nutrients. There was a potential considerable energy supply from different fermentations of the prebiotic synthesized organic compounds. The usual example cited is the fermentation of glucose, but it is unlikely that large quantities of this sugar were available because of its instability. A more likely early fermentation reaction is that suggested by Clarke and Elsden (1980):

$$\text{glycine} + \text{NADH} + \text{ADP} + P_i = \text{acetate} + NH_4^+ + NAD^+ + \text{ATP}$$

An ocean with a volume $V_{ocean} = 1.5 \times 10^{21}$ liters with a 1×10^{-4} M concentration of glycine would have contained 1.5×10^{17} moles of glycine. At one mole ATP per mole of glycine, this would be equivalent to 8.4×10^{28} cells, which corresponds to 7×10^4 cells/cm^3 of ocean. A glycine concentration of 10^{-4} M is a rich prebiotic soup, but producible under reducing conditions (Stribling and Miller 1987). The concentration may have been much lower—10^{-8} M of glycine—if the organic compounds were only of extraterrestrial origin (Anders 1989, Chyba et al. 1990), but it would still correspond to 10^{25} cells. As the primitive populations of heterotrophs thrived in the soup, there would have been an exponential decrease in the concentration of the available fermentable organic compounds of prebiotic origin. Such a decrease would have rapidly led to a metabolic energy crisis; that is, there would be strong selection pressure for the development of photosynthesis, as the only really abundant energy source was visible light.

FROM THE PRIMITIVE HETEROTROPHS TO FILAMENTOUS CYANOBACTERIA

It is generally accepted that the first oxygen-releasing photosynthetic prokaryotes were the ancestors of contemporary cyanobacteria. The sheathed filamentous cyanobacteria *Oscillatoria* spp. and *Nostoc* spp., which appear to be morphologically similar to the Warrawoona microfossils, have genomes of approximately 7×10^9 base pairs (Herdman 1985). Thus, if we assume that

the first DNA/protein organism had about 100 enzymes with ~ 1000 base pairs/gene, we need to estimate the time needed to go from a primordial organism with 100 genes to an oscillatorian-like cyanobacteria with approximately 7000 enzymes.

There are several sources that may increase the cellular DNA dosage (Fig. 1), but it is likely that in early Archean times the most significant one was gene duplication. It has been observed in some directed evolution experiments that populations of haploid microorganisms undergo duplications of large segments covering several genes to provide more enzymes to overcome the lowered concentrations of nutrients (Sonti and Roth 1989) and, at least in some cases, the duplicated copies became fixed in a few weeks (Hartley 1974, Hansche 1975).

We can estimate the rate of increase of genomes by gene duplication by assuming that the latter are neutral events (Kimura 1968, Li 1982). Accordingly, at any given time in a population there should be numerous duplicates on their way to fixation or loss, and the number of neutral duplicate genes that will become established per generation in a given population will be equal to their rate of occurrence (Doolittle 1979, Li 1982). The observed rates of spontaneous duplication of bacterial genes have values of 10^{-5} to 10^{-3} gene duplications per gene per cell generation (Anderson and Roth 1977, Tlsty et al. 1984). If we use the most conservative value of 10^{-5}, and for the sake of simplicity assume that during the early Archean there were ten generations of cells per year, the rate of accumulation of duplicons in a primordial genome encoding 100 enzymes

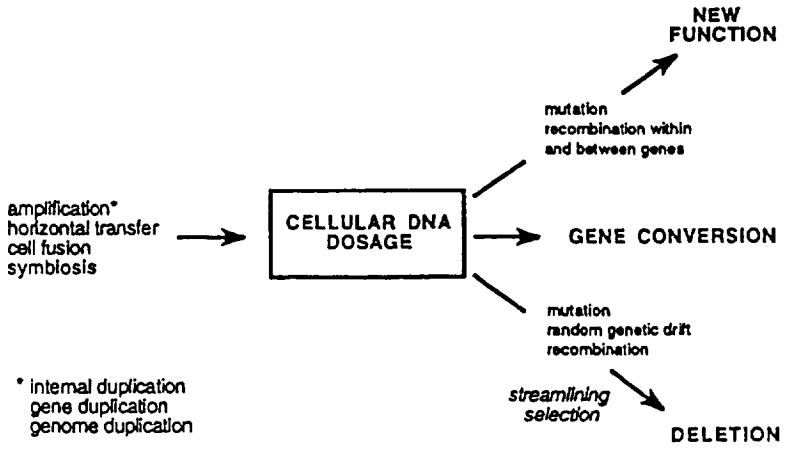

FIG. 1. *Mechanisms that may increase cellular DNA content and their possible evolutionary fate.*

would be 100 genes × 10 cell generations per year × 10^{-5} gene duplications per gene per cell generation, which equals 0.01 gene duplications per year. If we assume that only 10% of the duplications are neutral (Li 1982), the rate of accretion of duplicons would be 0.001 gene per year, which implies that the genomes would be increasing their DNA content at a rate of one nucleotide pair per year. Thus, under the assumptions discussed here, the time required to go from the 100-gene DNA/protein organisms to a 7000-gene filamentous cyanobacteria would be 7×10^6 years, but it may have been much less.

The situation under strong positive selection should be much faster. If the fixation of new duplicates increases the overall fitness of the population, then the rate of accretion of new genes may be expected to increase significantly. If one of the duplicate gene copies undergoes favorable mutations or internal recombinations (Fig. 1), then it will spread rapidly throughout the population. The rapid divergence of a fixed duplicate is exactly what we envision in the primitive Earth, as the prebiotic soup became exhausted compound by compound. The heterotrophs that developed abilities to metabolize the remaining compounds would have been strongly selected over others, and those bacteria that had developed an enzymatic apparatus allowing the use of photochemical energy sources would be rapidly favored.

The calculations presented here would seem to ignore not only the possibility that some duplicons may be lost by streamlining selection or by chance events (Fig. 1), but also the complexity of some basic metabolic processes, and of photosynthesis in particular. However complex, the enzymes involved in these processes are mostly the result of multiple gene duplications. As shown in Table 2, examples of gene duplication events that took place before the divergence of eubacteria, archaebacteria, and eukaryotes from their last common ancestor include those encoding enzymes involved in protein biosynthesis, DNA replication, ATP production, and basic metabolic pathways. Evidence of duplication and double-

TABLE 2. *Products of Gene Duplication Events that Are Known to Have Taken Place Before the Divergence of Eubacteria, Archaebacteria and Eukaryotes**

Elongator and Initiator ^{met}tRNA	DNA topoisomerases
Ribosomal Proteins	A and B DNA polymerases
Amino Acyl tRNA Synthetases	Ferredoxins
Elongation Factors	Glutamine synthases
α and β ATPase Subunits	Heat shock proteins
Carbamoyl Phosphate Synthetase	

* *Based on Forterre et al. 1993 and García-Meza et al. 1994.*

duplication events that paved the way to oxygen-releasing cyanobacterial photosynthesis has been preserved in the sequences of ferredoxins (Otaka and Ooi 1989), F-type ATPases (Gogarten et al. 1989), the reductases involved in chlorophyll and bacteriochlorophyll biosynthesis (Burke et al. 1993), the bacterial photosynthetic reaction center (Feher et al. 1989, Blankenship 1992), the two sets of light-harvesting antennae (Youvan and Ismail 1985), and photosystems I and II (Youvan and Marrs 1984, Blankenship 1992). As noted by Chapman and Schopf (1983), a gene duplication of photosystem I and the subsequent development of oxygen-producing photosynthesis still requires the linkage via electron flow of the two photosystems, but this could involve a surprisingly small number of modifications. There is evidence that the photosystems I and II developed in different organisms and combined by horizontal transfer or a fusion event (Büttner et al. 1992, Blankenship 1992), but this would only have accelerated the sequence of evolutionary events.

The rates of microbial evolution may have been accelerated during early Archean times by additional mechanisms, such as intragenic recombination, the modular assembly of new proteins, horizontal transfer, and duplication of the entire primitive genome, as well as by higher mutation rates. Recent measurements have shown that the mutation rate per base pair is inversely proportional to the genome size for DNA viruses, bacteria, and ascomycetes (Drake 1991). Based on this combined evidence, it is reasonable to assume that the rate of evolution during the early Archean would have been considerably faster than that of present day microorganisms, and that evolution to cyanobacteria may have been much faster than the 7×10^6 years calculated here based on genome size growth under neutral conditions.

CONCLUSIONS

We would like to emphasize the uncertainties of some of the figures discussed here. At the present time it is not possible to reconstruct in detail either the sequence of the evolutionary events described here, or the pace at which they took place. In spite of the many uncertainties in the current descriptions of the origin and early evolution of life, the data summarized here suggest that the most important bottlenecks in the process leading from the prebiotic soup to the RNA world, and then to DNA/protein organisms and eventually to cyanobacteria, may correspond to (1) the origin of replicating systems, (2) the emergence of protein biosynthesis, and (3) the evolutionary development of the starter types from which later proteins evolved through gene duplication and divergence. It

is possible, of course, to imagine a process in which periods of rapid evolution such as those described here alternated with stages of slower evolution. In fact, such episodic schemes are known to have taken place during the evolution of some metazoan lineages. However, because of constraints placed by the rapid exhaustion of prebiotically synthesized compounds, it is extremely unlikely that intermediate stages of slow evolution could have persisted for millions and millions of years. We thus see no compelling reason to assume that the origin and early evolution of life took more than 10 million years, and it may have taken considerably less.

The time scales discussed here also suggest that if the early environmental conditions on Mars were comparable to those of the primitive Earth, life may also have started there. If significant amounts of water and organic compounds were present in the Martian environment at the end of the early bombardment, then life could have arisen if the period of time required was as small as estimated here, but perhaps it could not have survived, as the subsequent geological conditions became very unfavorable. In other words, the development of life on Mars would have been constrained not by time, but rather by geological conditions.

Finally, O, B, and A stars, which are usually omitted in calculations of the abundance of life (Huang 1959a,b) because of their short main sequence lifetimes of approximately 1.5 million, 15 million, and 500 million years, respectively (Limber 1960), may have life on planets surrounding them. Double stars, which had previously been omitted from SETI calculations because they were not believed to have long-term stable orbits (Huang 1960), may also have microbial life on their planets.

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