

Shaky tree of life

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Ribosomes are vital components of all cells, because they are a major part of the cell's protein synthesis machinery. They contain their own nucleic acid, ribosomal RNA (rRNA), distinct from the cell's chromosomal DNA (which codes for the rRNA). The fact that rRNA sequences are very similar in all organisms has convinced molecular evolutionists that ribosomes are a good record of life's evolutionary history.

For over two decades, rRNA sequence analysis has provided molecular evolutionists with the basic tool for the construction of phylogenetic or family trees, with all life now generally classified into three kingdoms, the archaea (or archaeobacteria), the true bacteria (eubacteria), and the eukarya (or eukaryotes), which include animals, plants, fungi and protists such as protozoa and slime molds.¹ According to evolutionary theory, the eukarya developed from the archaea, and are represented as a sub-branch in the current evolutionary tree of life (Figure 1). Both archaea and eubacteria lack a nucleus and are grouped as prokaryotes, whereas cells from eukaryotes have a defined nucleus.

Until recently, it was believed that rRNA changes originate from single base substitutions, small deletions and insertions throughout the span of billions of years, to give a linear sequence of molecular descendents. Genes are believed to have been passed on throughout generations, mutant genes giving rise to novel organisms and speciation. Sequence similarity supposedly then shows the closeness in evolutionary relationship between organisms. This is also known as the clonal theory of evolution.

Recently, however, complete chromosomal DNA sequences from prokaryotes and a yeast (a eukaryote), are revealing connections between

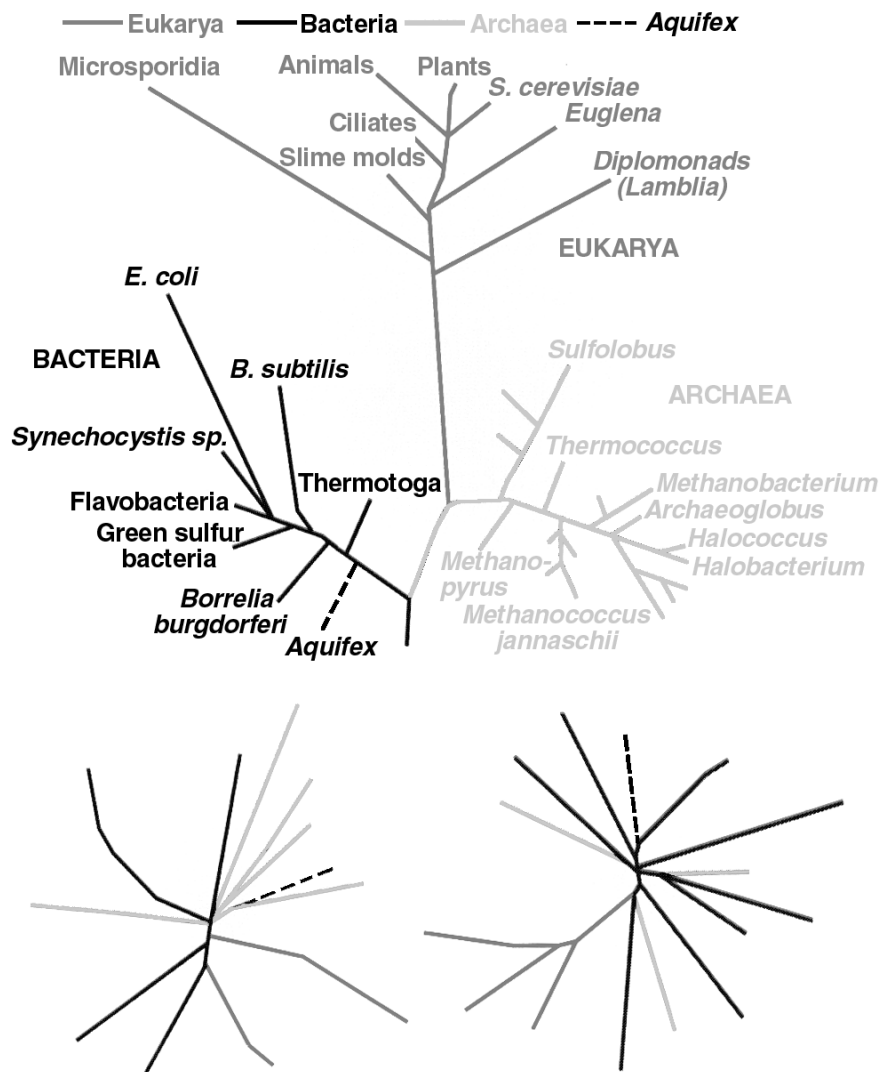


Figure 1. r-RNA tree of life (top). Phylogenetic placement of *Aquifex* based on analyses of two different *Aquifex* genes (left and right) (after Pennisi).³

organisms believed to have diverged millions of years ago, and they are now raising doubts about the validity of this tree for the evolutionary classification of life. Apparently, aminoacyl-tRNA synthetases, enzymes that link amino acids together in chains to form proteins, display an inconsistent pattern of relatedness among the three cell types, archaea, bacteria and eukarya. Also, enzymes that synthesize amino acids, such as isoleucine synthetase are more similar between archaeans and eukaryotes, the branches believed to be more related, whereas valine synthetases are more similar between bacteria and eukaryotes.²

A comparison of genes from the recently completed sequence of the thermophilic ('heat-loving') bacterium *Aquifex aeolicus* led the researchers to comment, 'you get different phylogenetic placements based on what genes are used.'³ Apparently a gene for the synthesis of the amino acid tryptophan places *Aquifex* with the archaea (Figure 1). The researchers also compared the gene for an enzyme involved in the synthesis of the building blocks of DNA, and found that it placed the tested archaea *Aquifex* outside the archaea branch, among the bacteria and the eukaryotes. They concluded that, 'It points to caution in terms of interpreting the 16s [rRNA].'⁴

The above spread of genes across branches has been attributed to **horizontal gene transfer**, a mechanism used by microorganisms to pick up new genes in their environment from other kinds of organisms, supposedly giving rise to new species and kinds. Prior to the above studies, this type of transfer was only used as ‘a last’ resort to excuse phylogenetic inconsistencies. But horizontal transfer has now become an accepted evolutionary process to compensate for the RNA tree’s shortcomings and is believed to be the key mechanism in what has now been termed the chimeric theory for the evolution of genomes .

Further apparent support for the chimeric evolution of whole genomes is now being obtained from the comparison of groups of hundreds of genes instead of just single genes. From a comparison of the entire genomes of two eubacteria, *E. coli* and *Synechocystis* (a cyanobacterium), *Methanococcus* (an archaeobacterium) and *Saccharomyces* (a yeast eukaryote), genes have been grouped into those involved in processes such as transcription and translation (informational genes) and those needed for cellular ‘housekeeping’ (operational genes).⁵ It was found that eukaryotic operational genes are most related

to *E. coli*, while informational genes were most similar to *Methanococcus*. But it must be noted that this grouping is a result of the comparison of only a few genomes and only one from a eukaryote, and may change when other genomes are elucidated.

Has horizontal transfer then salvaged some evolutionary credibility? To the evolutionist, ‘*The absence of gradual intergradations and phylogeny have always been a mortifying embarrassment.*’⁶ The diversity in design observable in the wealth of life forms has always resisted the lineage, or ‘*recognisable line of ancestry with identifiable ancestors and descendants,*’⁷ sought for by evolutionists to construct their phylogenies. Diversity, and thus, lack of lineage, is now also evident at the gene level. With this obvious breakdown of phylogeny, horizontal gene transfer — the opposite of evolution, or common ancestry — has been openly embraced. Thus phylogeny was never a *bona fide* prediction of evolution.

References

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Another threat to the Milankovitch theory quelled?

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Two major paradigm changes have transformed geology during the past 75 years: 1) plate tectonics and 2) the Milankovitch theory of the ice age.¹ Geoffrey Boulton, writing of progress in glacial geology during a 50-year period ending in 1987, remarked:

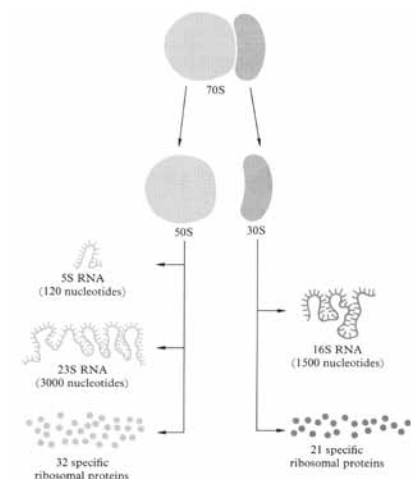
*‘The demonstration of an insistent pulse of environmental change with frequencies of 40,000 and 100,000 years has been one of the two most important geological discoveries of the last 50 years, the other being the plate-tectonic synthesis of Earth’s structural evolution.’*²

Neither theory was new, and both were once believed impossible. Both were quickly ‘verified’ by several key pieces of research and are now widely accepted. Since then, in a band-wagon effect, new research must be explained within the context of the paradigm.

For the Milankovitch paradigm, the watershed paper was published in 1976, purporting to correlate mainly oxygen isotopes in deep sea cores with changes in the earth’s orbital geometry.³ Many geological variables have since been correlated to the Milankovitch cycles, in seemingly consistent agreement. William Ruddiman expounds:

*‘Everything fits together so well that it would have to be a preposterously cruel joke if we were wrong.’*⁴

Therefore, it is understandable that a challenge to the Milankovitch theory would be met with great resistance. One such challenge came in 1988 when Isaac Winograd and co-workers reported a supposed global climate chronology for the latest Quaternary Period.⁵ Their results were based on uranium-series dating and oxygen isotope analysis of a thick calcite coating on the walls of a water-filled fault crack.



Schematic representation of the E. coli ribosome and breakdown of its components. The ribosome is made up of approximately 65 % RNA and 35 % protein (from Stent & Calendar).⁸