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Search for a 'Tree of Life' in the thicket of the phylogenetic forest. Pere Puigbo, Yuri I Wolf and Eugene V Koonin. 2009 July; 13

The concept of the tree of life is being undermined due to new discoveries. The concept that shows how life have evolved or formed and that essentially different species have gone from a central branch and have then evolved from one form to another. Genomics has revealed that there is extensive horizontal gene transfer in prokaryotes. They studied 6,901 phylogenetic trees and found that in certain areas like shallow tree depths. They also stated that consistency in the topology dropped at the levels of radiation and where there were bacterial phyla.

Most trees contained only a small number of species and often less than 20. Trees consist of different sets of species in general. Thus they stated, "Suggesting that early phases of evolution could be non tree like." The research that they did stated to not represent all forest areas but brought them to the idea that instead of the tree of life theory in evolution that due to horizontal gene transfer, life itself could potentially evolve at early stages as a big bang theory of evolution. Analysis of a forest containing roughly around 6901 phylogenetic trees for prokaryotic genes Very few genes are consistent among the trees that were studied.

They analyzed dataset consisted of representatives of 6,901 clusters. They used 59 bacteria and 41 archaea of which were selected to represent all major divisions throughout the phylogenetic forest of trees. Protein sequence alignment using the Muscle program [62] to understand the traits and the gene transfer of the trees to figure out part of the genetic gene transfer that was occurring. Super network construction and analysis was used following the methods developed by Hudson et al. They also obtained the topology of the ultra metric tree from the super tree of the 102 NUT's causing the CLANN program. They also used the CMDS procedure to show the dimensions in similarities amongst the trees.

NUTs (or subset of nearly universal trees) contained a strong consistent phylogenetic signal and Typologies of the NUT trees were generally highly coherent with connectivity at 50% similarity. 56% of NUT's had archaea and bacteria perfectly separated. Resulting in the possibility of a biological Big Bang Theory or as stated the "compressed cladogenisi model."

When they compared the dependence of the inconsistency on phylogenetic depth for the 102 NUT's and the complete FOL, Nuts showed comparable levels of inconsistency. The important issue that came about that they mentioned could affect the status of the NUT's was the dependence of tree inconsistency when it came to phylogenetic depth. Sharply increasing inconsistencies at deep levels of the forest of life suggested the possibility of the biological big bang theory. They simulated the evolutionary processes that produced the forest of life

After the recent developments in prokaryotic genomics they revealed omnipresence of HGT. They found that when they studied the topology of the trees instead of the trees being clustered as expected, they were scattered in different patterns. The patterns were that of a cloudy nature where some of the trees had similarities at different points. This was accomplished using IS and CMDS procedures. There were many inconsistencies with the tree of life that led them to the theory of Biological big bang theory. They then determined that NUT's could not represent the forest entirely due to transfer events where they observed that HGT was distributed at random. Thus they concluded that horizontal gene transfer occurred with some inconsistencies and was pervasive among prokaryotic cells.