

The Tree of Life

How do we select a gene sequence for comparison?

(source: outreach.mcb.harvard.edu, Summer08)

Criteria For Choosing a Sequence to Construct the Tree of Life

- The gene sequence must be found in all organisms
- As in *Goldilocks and the Three Bears*, the mutation rate must be “just right”:
 - It must show variation among the different organisms to be compared
 - The sequence must be highly conserved so that it is recognizable by the computer programs that will do the comparisons.

Why rRNA Fits the Bill for Constructing the Tree of Life

Ribosomes

- The protein - making machinery of all organisms
- Made up primarily of ribosomal RNA (rRNA)
- Ribosomal RNA is copied (transcribed) from the DNA (genome) of an organism

16S* Ribosomal RNA (rRNA) is “Just Right” for Constructing a Tree of Life

- Found in of all living organisms
 - Performs a common and necessary function
- rRNA sequences vary from one group of organisms to another
- rRNA sequences are recognizable in all groups of organisms
 - The 16s rRNA sequences are highly conserved

* In prokaryotes the small subunit of the ribosome (SSU) contains 16S (r)RNA; in eukaryotes the homologous rRNA is termed 18S RNA