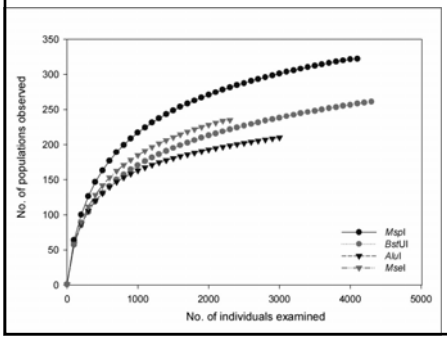
Bacterial & Archaeal Diversity

A Major Paradigm Shift for
ALL of Biology

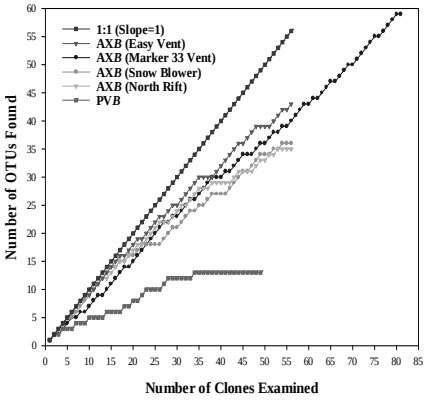
Diversity

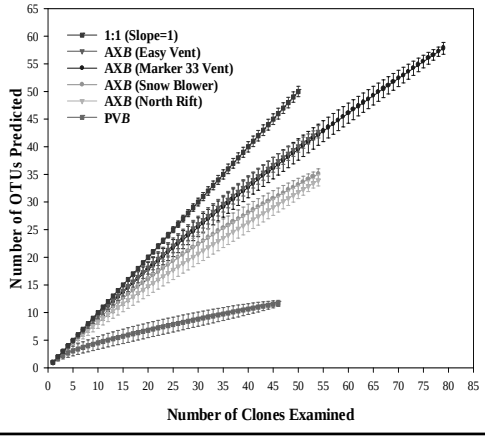
- This concept has duel meanings!!!
- **Richness** or the number of populations within a community.
- **Relatedness** or how closely related one population is to another.

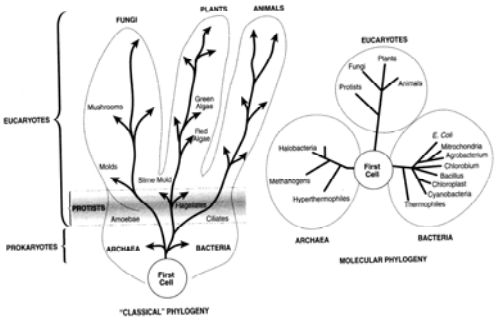
Rarefaction $E(S_n) = \sum_{i=1}^{s}\left[1 - \binom{N - N_i}{n} \Big/ \binom{N}{n}\right]$

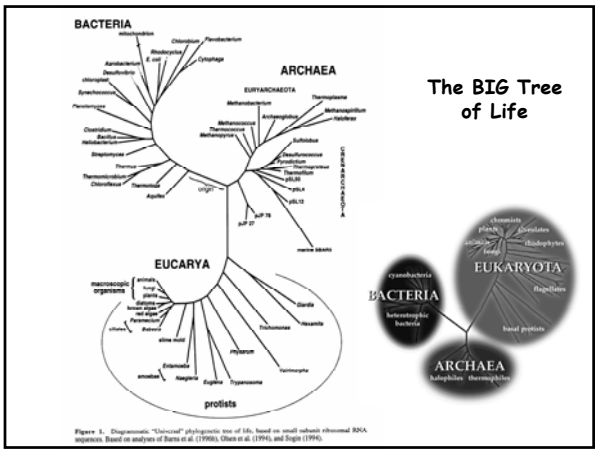


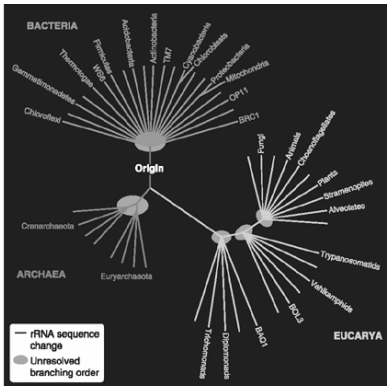
- Abscissa indicates number of peaks between 50-500 bp
- Ordinate indicates resolving ability











Norm Pace, Microbe 2008

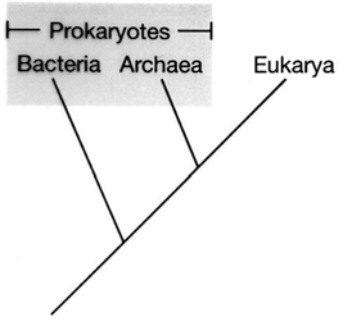
Summary Regarding the use of the term "Prokaryote" (Norm Pace, Microbe 2008)

* Comparisons of gene sequences provide an objective view of evolutionary relationships and the course of evolution, in the context of a molecular tree of life.

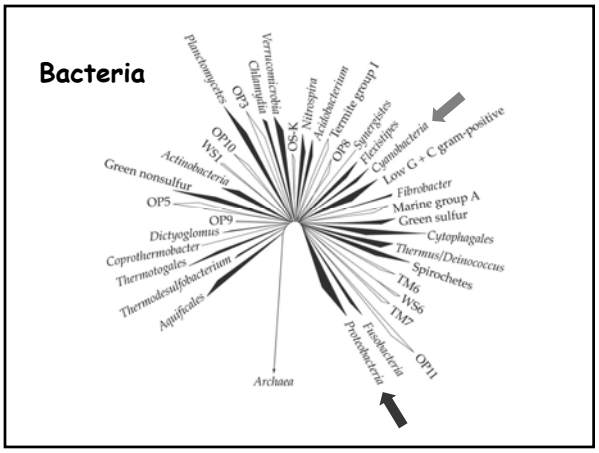
* Culture-independent, sequence-based identifications of microbes in the environment are dramatically expanding our knowledge of microbial diversity.

* The results of environmental surveys affirm the three-domain model for phylogenetic organization and the course of evolution.

* Experimental results represented by the molecular tree render the concept of "procaryote" obsolete, making it a misleading term, particularly when used in teaching.



Paraphyletic Grouping !!!



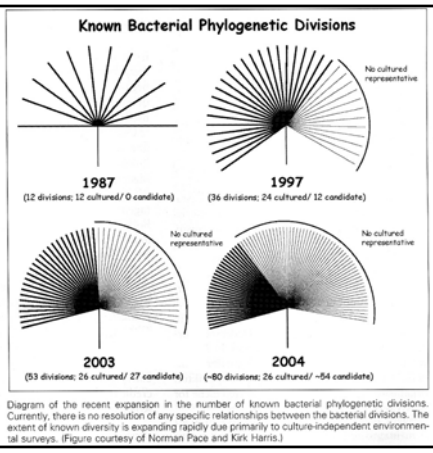
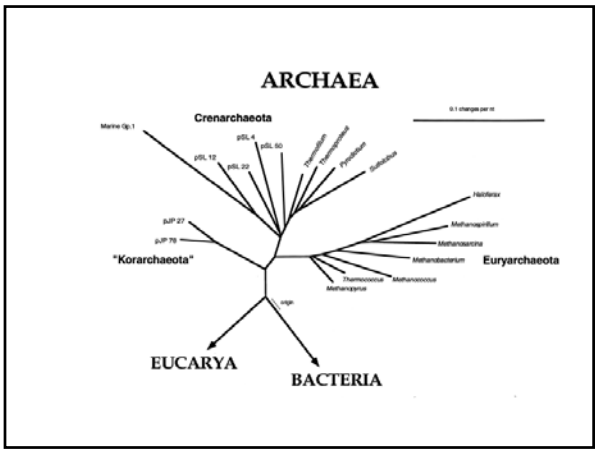
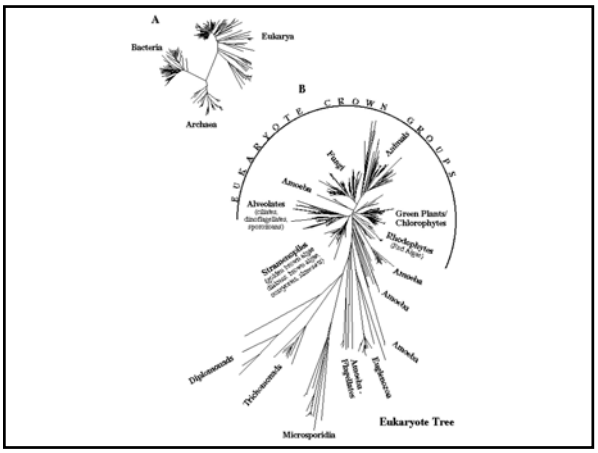
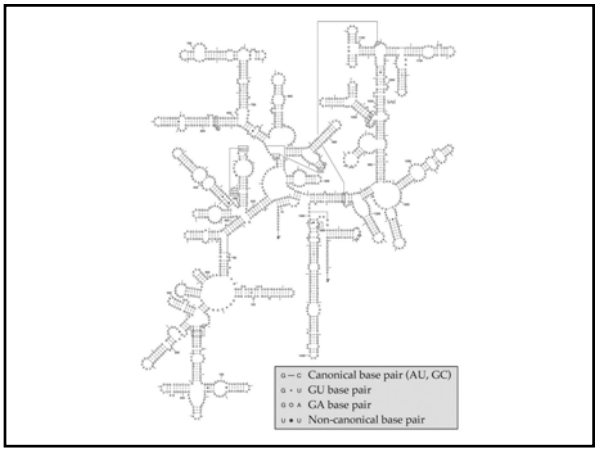
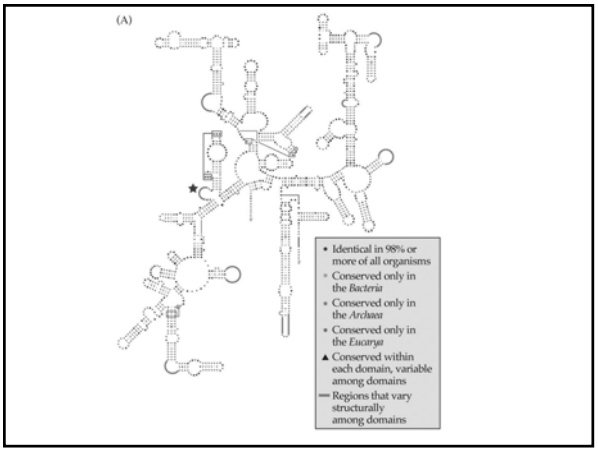


Diagram of the recent expansion in the number of known bacterial phylogenetic divisions. Currently, there is no resolution of any specific relationships between the bacterial divisions. The extent of known diversity is expanding rapidly due primarily to culture-independent environmental surveys. (Figure courtesy of Norman Pace and Kirk Harris.)

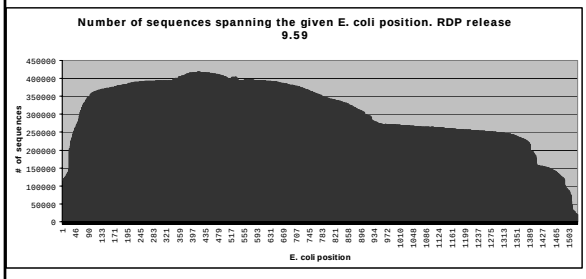






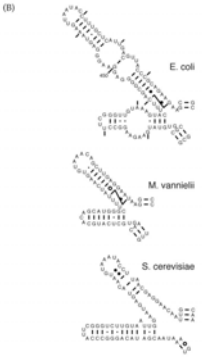


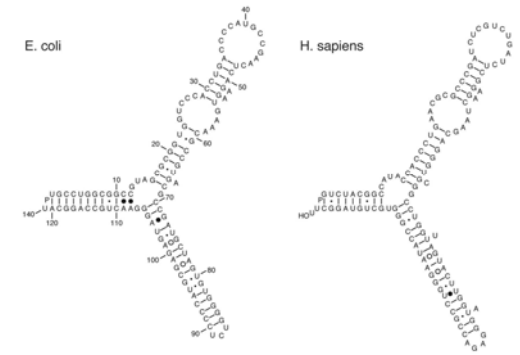
RDP Database



As of Mar 5, 2008 :: 489,840 SSU rRNAs

Secondary Structures of SSU rRNA show homology





Secondary Structures of rRNAs show homology

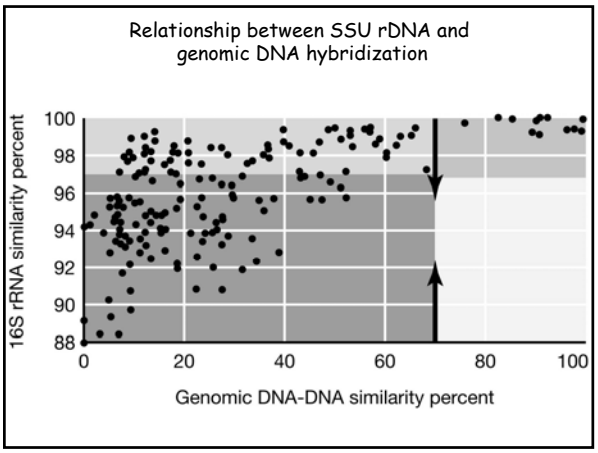


Table 17.2 Comparison of *E. coli* and its primate host species[a]

Property	*E. coli*	*Homo sapiens*	Primates
Mol % G + C	48–52	42	42[b]
16S–18S rRNA variability	>15 bases	?	<16[c]
DNA/DNA reassociation	>70%	98.6%[d]	>70%[e]

[a]Adapted from J. T. Staley, *ASM News*, 1999.
[b]Value for all primates.
[c]Mouse 18S rRNA differs from humans by 16 bases.
[d]Comparison between *Homo sapiens* and chimpanzee.
[e]Comparison between *Homo sapiens* and lemurs.