

Microbial Taxonomy

Traditional taxonomy or the **classification** through **identification** and **nomenclature** of microbes, both "prokaryote" and eukaryote, has been in a mess – we were stuck with it for traditional reasons.

A "natural" taxonomy would be based on evolutionary relatedness: Thus, organisms in same "genus" (a collection of "species") would have similar properties in a fundamental sense.

A natural taxonomy of microbes has long been possible: Large organisms have many easily distinguished features (e.g., body-plans and developmental processes, that can be used to describe hierarchies of relatedness).

Microbes usually have few distinguishing properties that relate them, so a hierarchical taxonomy mainly has not been possible.

Recent advances in **molecular phylogeny** have changed this picture. We now have a relatively quantitative way to view **biodiversity**, in the context of phylogenetic maps or evolutionary trees.

Slowly evolving molecules (e.g., rRNA) used for large-scale structure; "fast- clock" molecules for fine-structure.

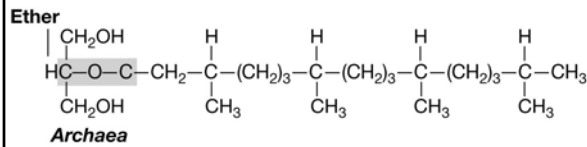
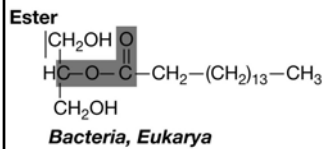
The literature language (e.g., "species") and formal nomenclature, however, remain solidly rooted in the tradition of Linnaeus at this time. (You have to call them something!)

Table 17.1 Hierarchical classification of the bacterium *Spirochaeta plicatilis*

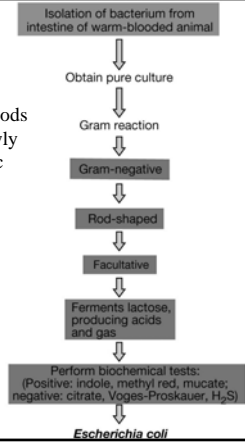
Taxon	Name
Domain	<i>Bacteria</i>
Phylum	<i>Spirochaetes</i> (vernacular name: spirochetes)
Class	<i>Spirochaetes</i>
Order	<i>Spirochaetales</i>
Family	<i>Spirochaetaceae</i>
Genus	<i>Spirochaeta</i>
Species	<i>plicatilis</i>

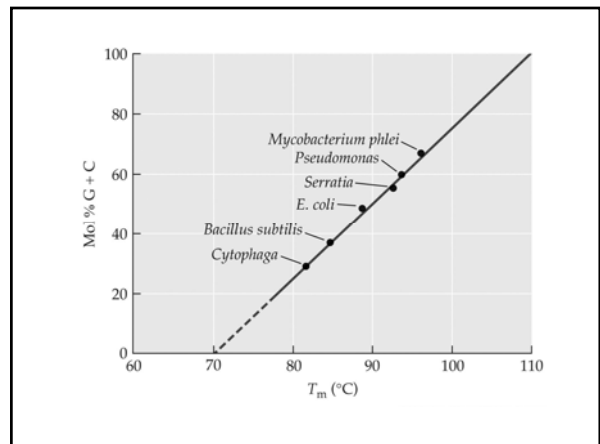
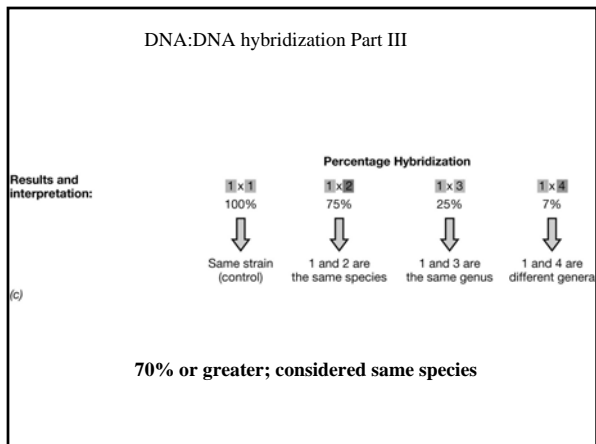
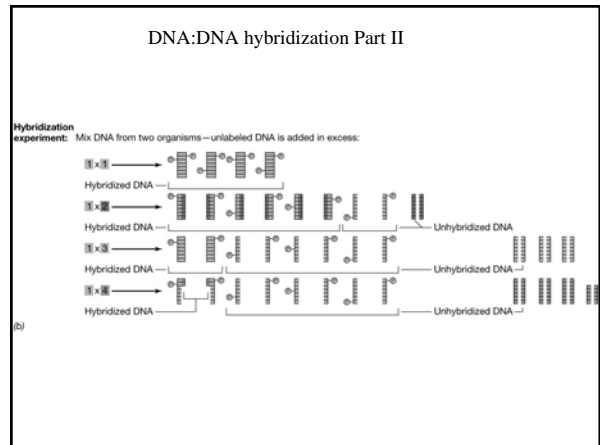
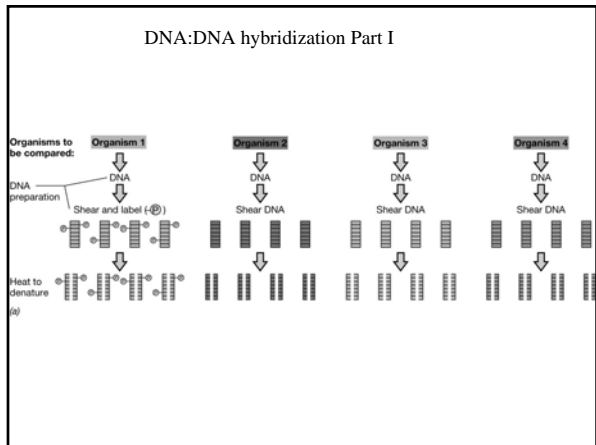
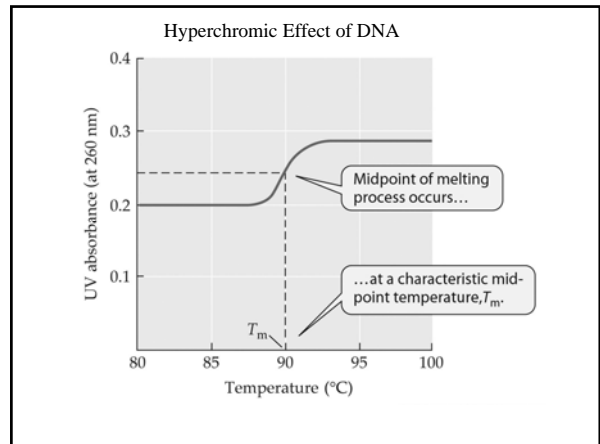
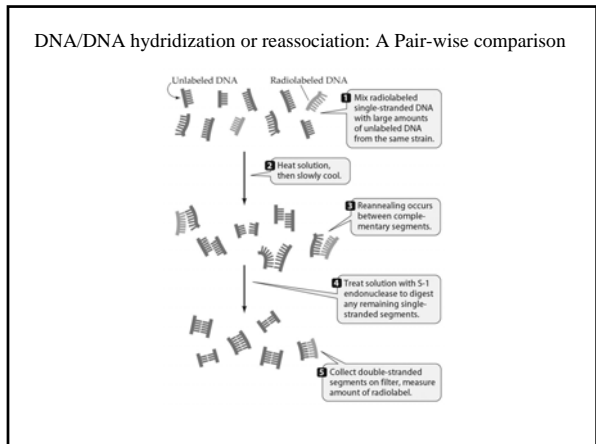
TABLE 11.4 Some phenotypic characteristics of taxonomic value

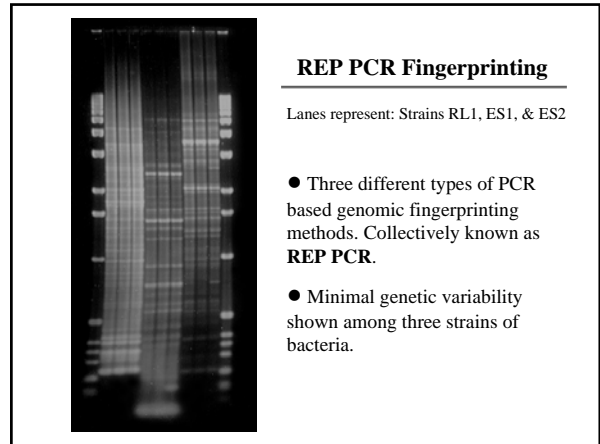
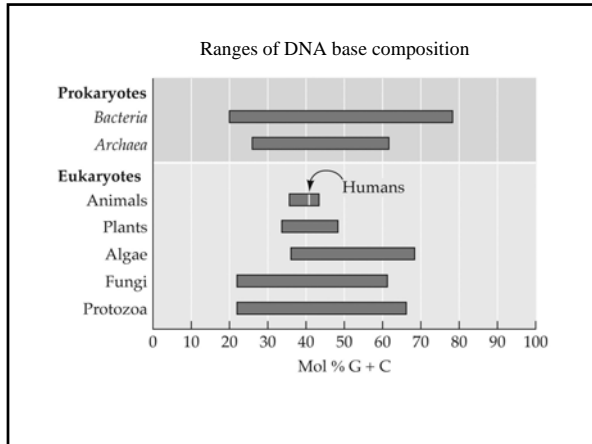
Major category	Components
I. Morphology	Shape; size; Gram reaction
II. Motility	Motile by flagella; motile by gliding; motile by gas vesicles; nonmotile
III. Nutrition and physiology	Mechanism of energy conservation (phototroph, chemoorganotroph, chemolithotroph); relationship to oxygen; temperature, pH, and salt requirements/tolerances; ability to use various carbon, nitrogen, and sulfur sources
IV. Other factors	Pigments; cell inclusions, or surface layers; pathogenicity; antibiotic sensitivity



Example of methods used to ID a newly isolated enteric bacterium



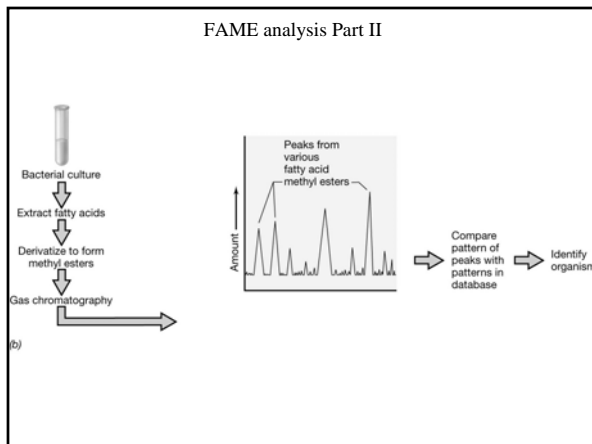
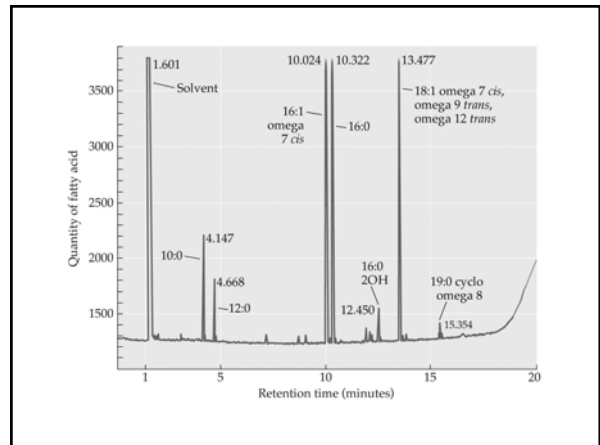




FAME analysis Part I

Classes of Fatty Acids in *Bacteria*

Class	Example	Structure of example
Saturated	tetradecanoic acid	<chem>CCCCCCCCCCCC(=O)O</chem>
Unsaturated	omega-7-cis hexadecanoic acid	<chem>CCCC=CCCCCCCC(=O)O</chem>
Cyclopropane	cis 7-8 methylene hexadecanoic acid	<chem>CCCC1=CC(C1)CCCC(=O)O</chem>
Branched	13-methyltetradecanoic acid	<chem>CCCC(C)CCCCCCCC(=O)O</chem>
Hydroxy	3-hydroxytetradecanoic acid	<chem>CCCC(O)CCCCCCCC(=O)O</chem>



Taxonomy Summary

Classical physiological descriptions of microbes constitute a taxonomy, but do not provide relationships (except as might be inferred subjectively). *Key Words: Classification, Identification & Nomenclature.*

Methods such as FAME, DNA-DNA hybridization, or REP PCR establish relationships, but only if close, i.e., they are not sufficiently general to be broadly applicable.

All these methods require pure-cultivation of organisms for characterization, but we can't cultivate much of what is out there.

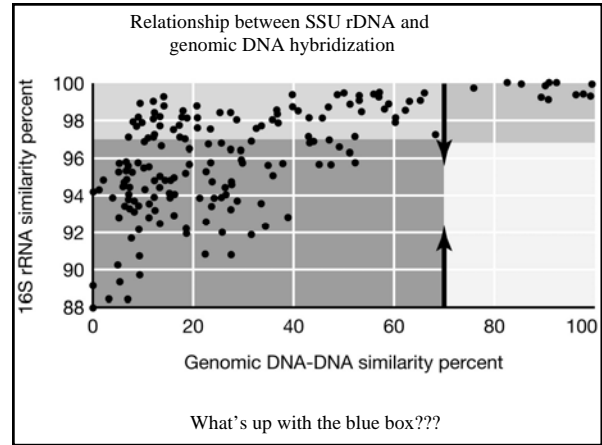
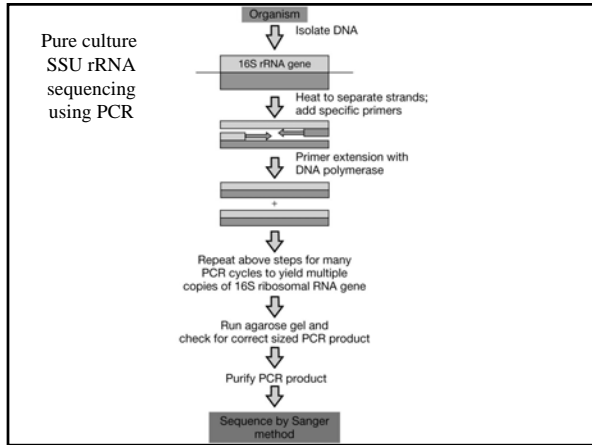
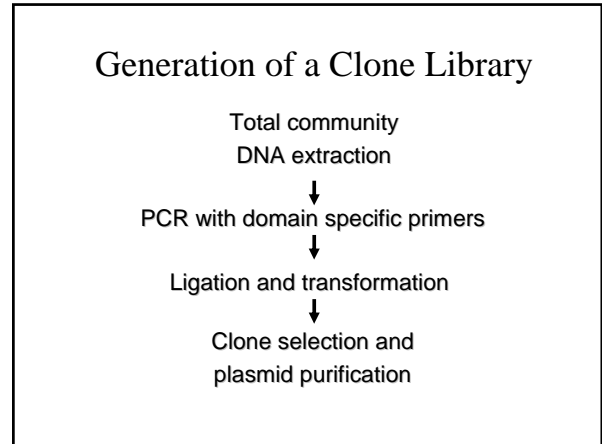
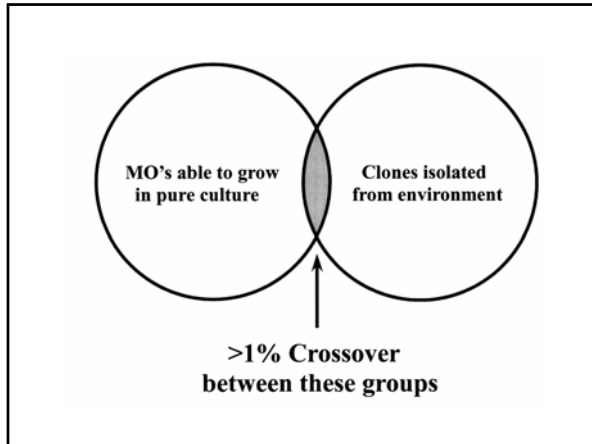


TABLE 11.6 Taxonomic ranks and numbers of known prokaryotic species^a

Rank	Bacteria	Archaea	Total
Domains	1	1	2
Phyla	23	3 ^a	26
Classes	32	8	40
Orders	77	12	89
Families	182	21	203
Genera	871	69	941
Species	5007	217	5224

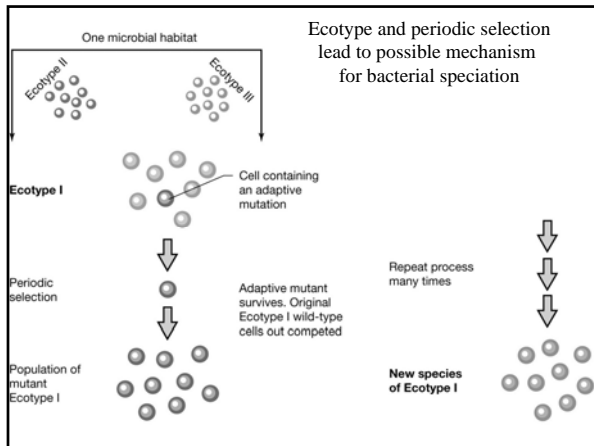
^aNumbers represent validly named genera and species of *Bacteria* and *Archaea* as of 2001. "Korarchaeota" is a provisional phylum.
 Source: Garrity, G.M., Boone, D.R., and R.W. Castenholz (eds.). 2001. *Bergey's Manual of Systematic Bacteriology*, 2d ed., Vol. 1. Springer, New York.

Bacterial species more like animal genus, order or family.

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

Property	<i>E. coli</i>	<i>Homo sapiens</i>	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

^aAdapted from J. T. Staley, *ASM News*, 1999.
^bValue for all primates.
^cMouse 18S rRNA differs from humans by 16 bases.
^dComparison between *Homo sapiens* and chimpanzee.
^eComparison between *Homo sapiens* and lemurs.



Why ribosomal RNAs?

- Found among all living organisms (for 3.8 of the last 4.5 billion years). Integral part of protein synthesis machinery.
- Cell component analyses provide culture-independent means of investigating questions in microbial ecology (lack of morphology).
- rRNAs offer a type of sequence information that makes them excellent descriptors of an organism's evolutionary history.
- No detectable horizontal gene transfer, especially important for the prokaryotes.
- Large and growing database; RDP contains >100K SSU rRNAs.

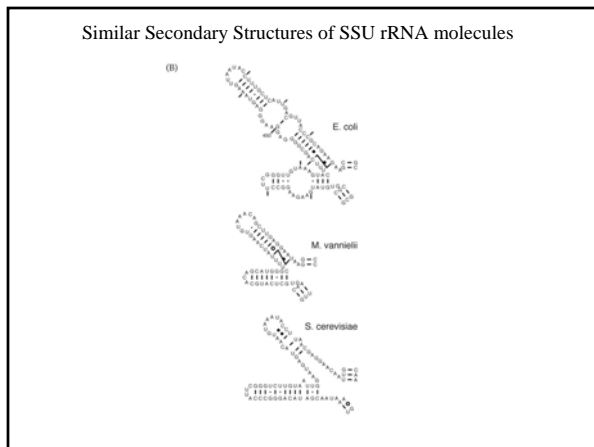
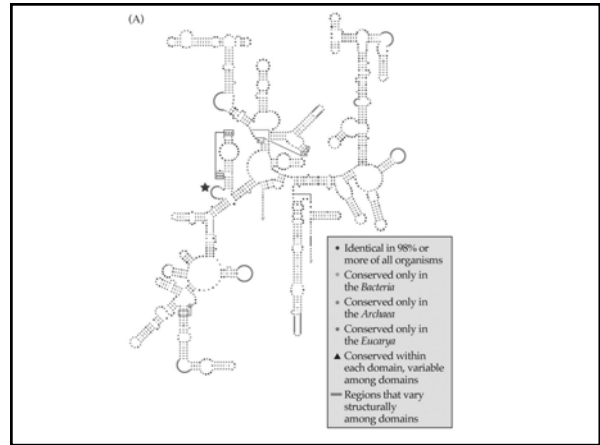
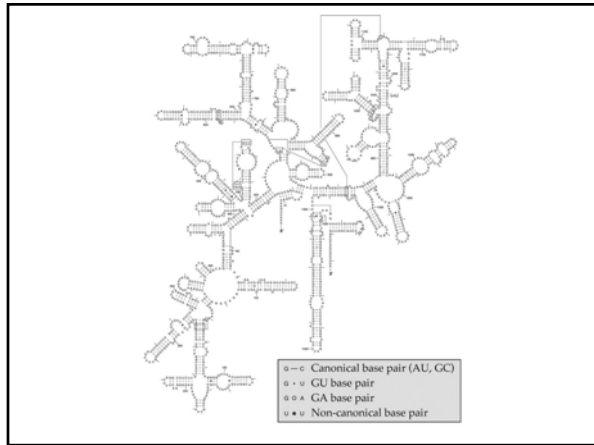
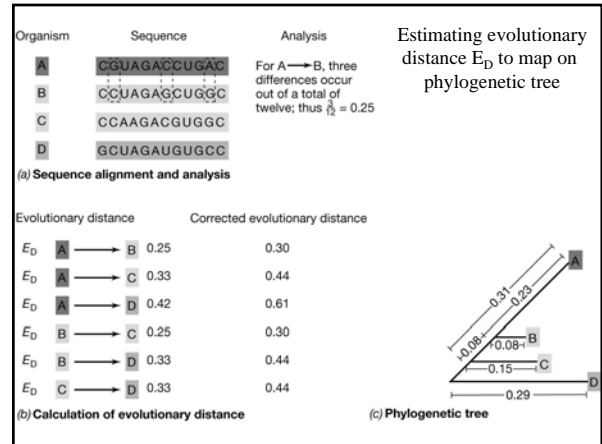
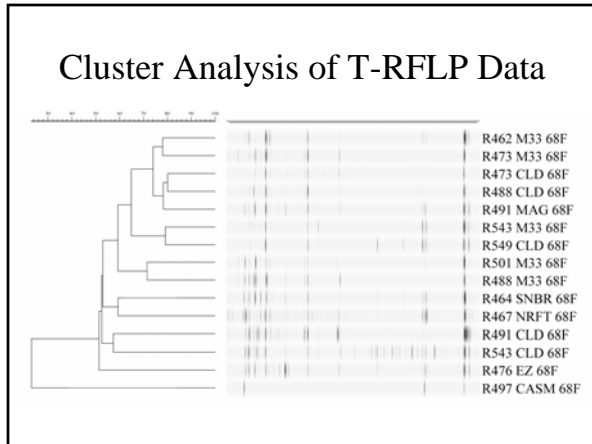
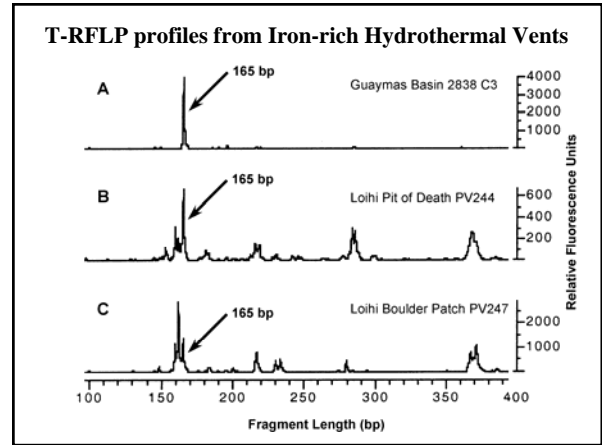
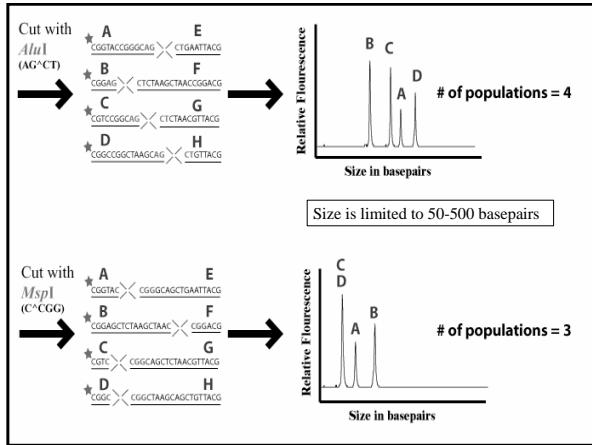
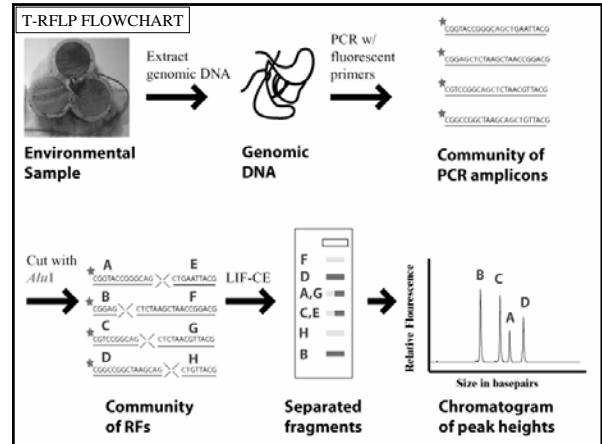
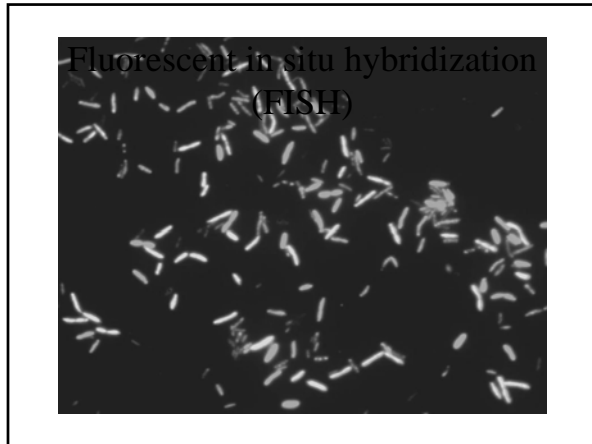


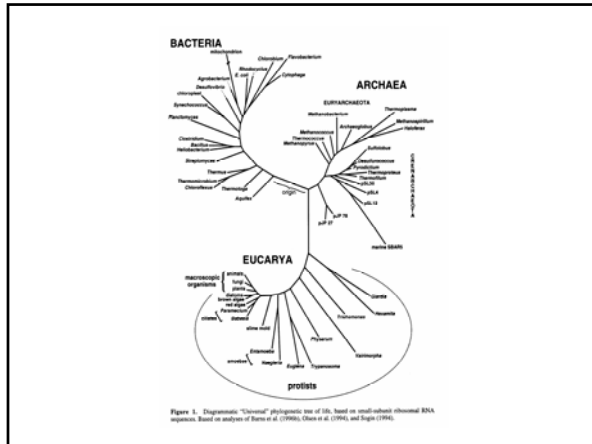
TABLE 11.1 Signature sequences from 16S or 18S rRNA defining the three domains of life

Oligonucleotide signatures ^a	Approximate position ^b	Occurrence among ^c		
		Archaea	Bacteria	Eukarya
CACYYG	315	0	> 95	0
AAACUCAAA	910	3	100	0
AAACUUAAG	910	100	0	0
YUYAAUUG	960	100	< 1	100
CAACCYCR	1110	0	> 95	0
UCCUCG	1380	> 95	0	100
UACACACCG	1400	0	> 99	100
CACACACCG	1400	100	0	0

^aY, any pyrimidine; R, any purine.
^bRefer to Figure 11.8c for numbering scheme of 16S rRNA.
^cOccurrence refers to percentage of organisms examined in any domain that contain that sequence.

Signature sequences can be obtained at any level of taxonomic hierarchy

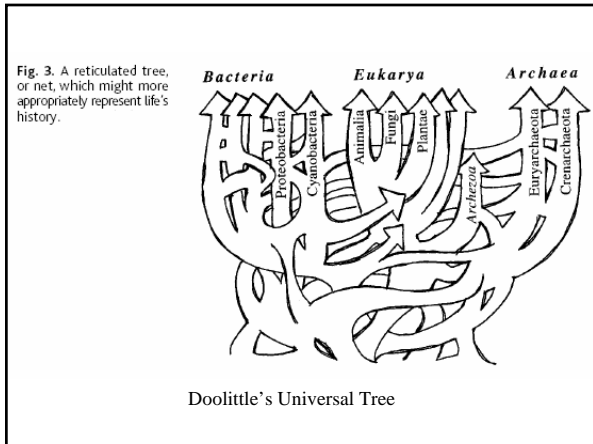
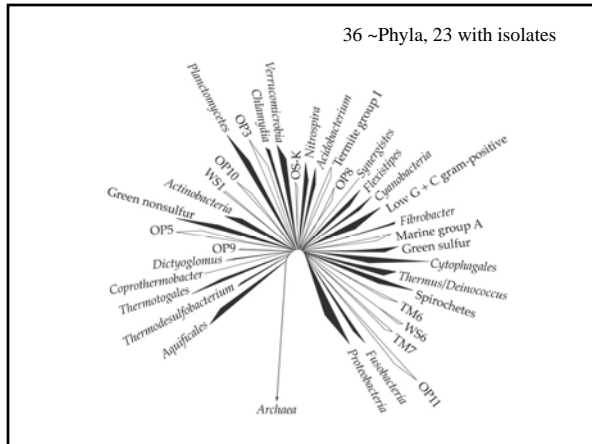
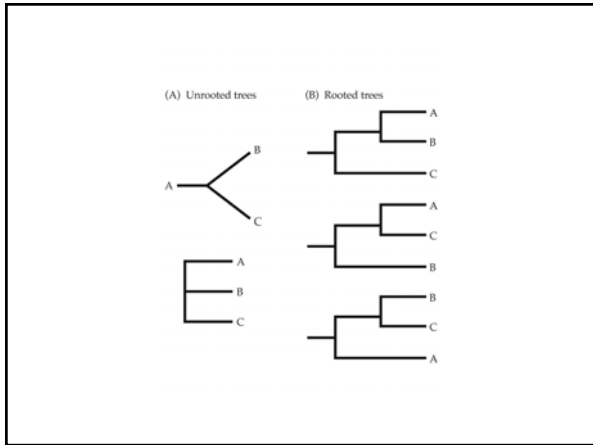
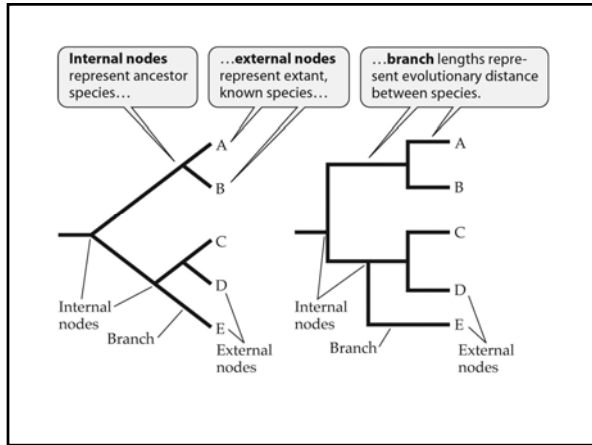




Some Lessons from the BIG TREE: Map of the Biological Record

Evolutionary "clock" is NOT constant between different lineages

- Terminal nodes NOT all the same length, so not constant for all organisms either!
- Endosymbionts sped up very fast (semi-autonomous organelles).
- Eucarya – Fast clocks
- Archaea – Slow clocks
- Bacteria – Intermediate



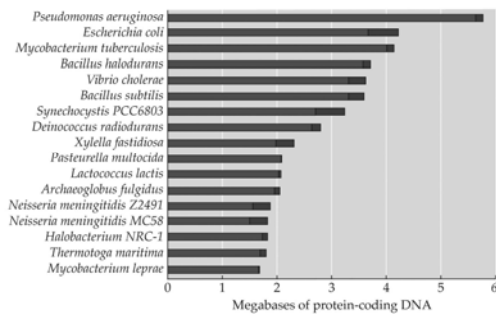
... the general course of evolution [for bacteria] will probably never be known, and there is simply not enough objective evidence to base their classification on phylogenetic grounds... For these and other reasons, most modern taxonomists have explicitly abandoned the phylogenetic approach.

(Stanier et al., 1976)

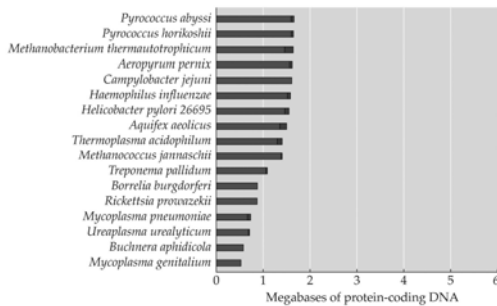
Molecular phylogeneticists will have failed to find the "true tree," not because their methods are inadequate or because they have chosen the wrong genes, but because the history of life cannot properly be represented as a tree."

(W. F. Doolittle, 1999)

Relative importance of horizontal gene transfer



Relative importance of horizontal gene transfer



Some Lessons from the BIG TREE: Map of the Biological Record

What does genome sequencing and study of functional genomics add to our perspective?

- The central information processing machinery encompasses core genome.
- Metabolic functions, that's when relationships get murky.
- Endosymbiosis involved more than organelles, i.e., two-way transfer of genes with most going to the nucleus.
- Mitochondria have been at it much longer than chloroplasts.

A Bit on the Evolution of Evolutionary Thought

A. Prior to the late 19th century, the concept of evolution was on the **evolutionary ladder**. Thus, we still deal in "higher and lower" eucaryotes (I try not to use these terms – they are dumb), "missing links," and "primitive" organisms.

B. In its milieu, *E. coli* is as highly evolved as are we. *E. coli* is **simple** (~5 x 10⁶ bp genome), we are **complex** (~3 x 10⁹ bps); complexity has nothing to do with *evolutionary advancement*.

C. Lineages evolve by diversification, not *progression*. !!!

D. There is no such thing as a *primitive* organism alive today. **Simple**, yes, but still a finely honed product of ~ 4 billion years under the selective hammer of the niches that it and its progenitors have occupied.

Take Home Message

- Phylogeny is right or wrong, we try to infer it the best we can.
- Taxonomy is useful or not, depending upon your point of view.
- Phylogeny allows us to ask testable questions, e.g., hypothesis testing.