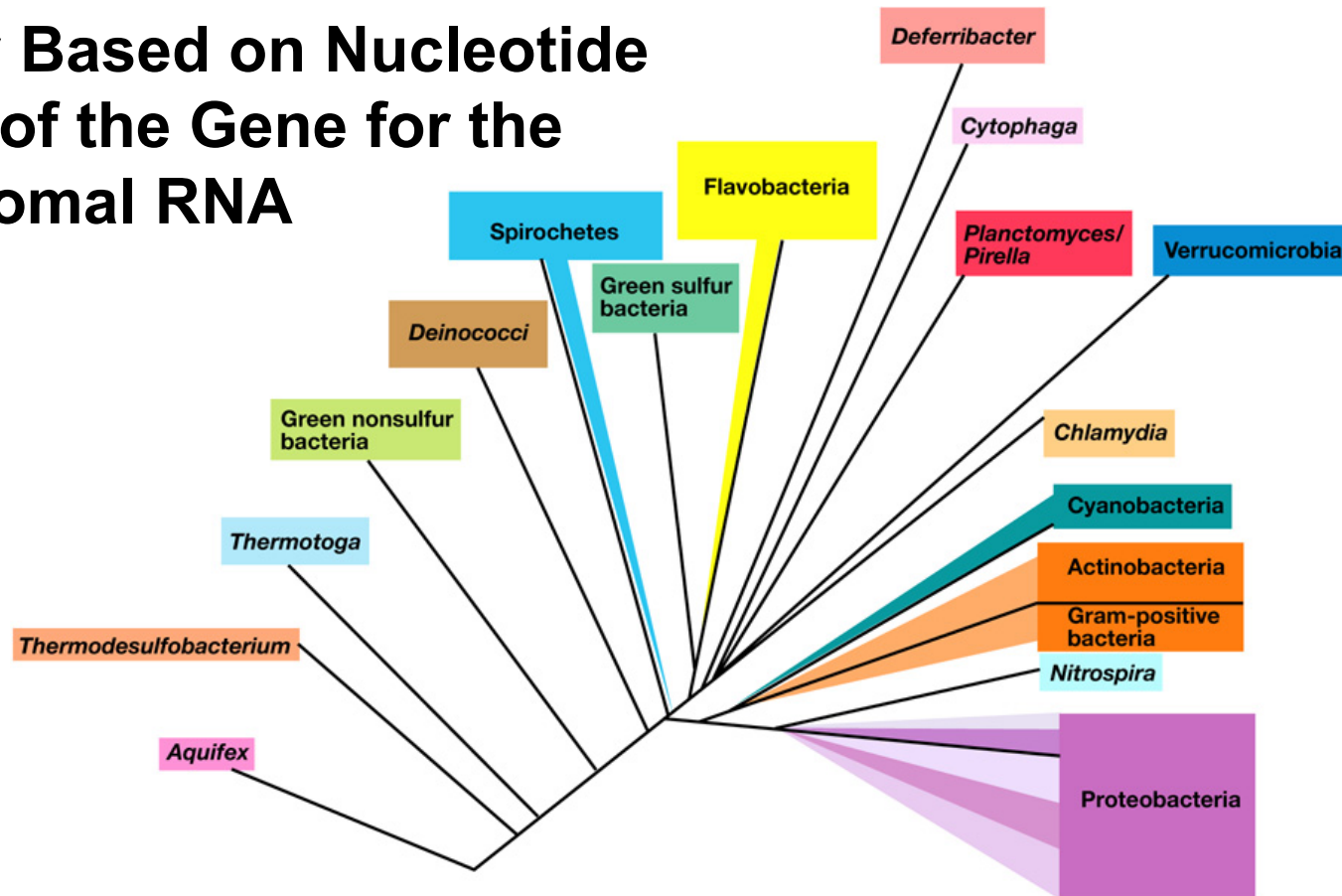


Phylogeny Based on Nucleotide Sequence of the Gene for the 16S Ribosomal RNA



PHYLOGENY BASED ON DNA SEQUENCE HOMOLOGY (OR DEGREE OF SIMILARITY)

From a common ancestor, mutations occurred within genomes, evolution occurred, and biodiversity is the end result. During evolution, the number of mutations within a chromosome (or within a given gene) increases with time. Therefore, relatedness of two organisms can be determined by measuring the degree of nucleotide sequence similarity within their genomes (or within a specific gene). That is, if two organisms share a great degree of homology within their genome, they are closely related and they evolved from a common ancestor relatively recently. There has not been much time for many different mutations to occur. On the other hand, if two organisms have a very low degree of homology within their genome, they are not closely related and they evolved from a common ancestor long ago. Over that long time, many mutations occurred.

One of the gene sequences used to measure homology is the gene for the 16S ribosomal RNA (or 18S RNA in eukaryotes). This gene is advantageous because it is universally conserved (that is, present in all organisms), was likely to be present even in the most ancient organisms, and is neither too short nor too long.