

## *Genome-level Characters for Phylogeny*

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The first whole genomes to be compared for phylogenetic inference were those of mitochondria and plastids. These constituted model systems for understanding genome evolution and, in addition, provided the first sets of genome-level characters for phylogenetic reconstruction. These characters included such things as the relative arrangements of genes which proved to be very powerful at resolving numerous branch points, including some that had remained recalcitrant even with very large molecular sequence datasets in hand. Now the world is facing a tsunami of complete nuclear genome sequences. In addition to the tremendous amount of DNA sequence that is becoming available for comparison, there is also the potential for many more genome-level characters to be developed, including the relative positions of introns, the domain structures of proteins, gene family membership, presence of particular biochemical pathways, aspects of DNA replication or transcription, and a host of others. These characters can be especially convincing because of their low likelihood of reverting to a primitive condition or occurring independently in separate lineages, so reducing the occurrence of homoplasy. The comparisons of organelle genomes pioneered the way for using such features for phylogenetic reconstructions, and it is almost certainly true that further use of genome-level characters will play a big role in outlining the branches among major animal groups.