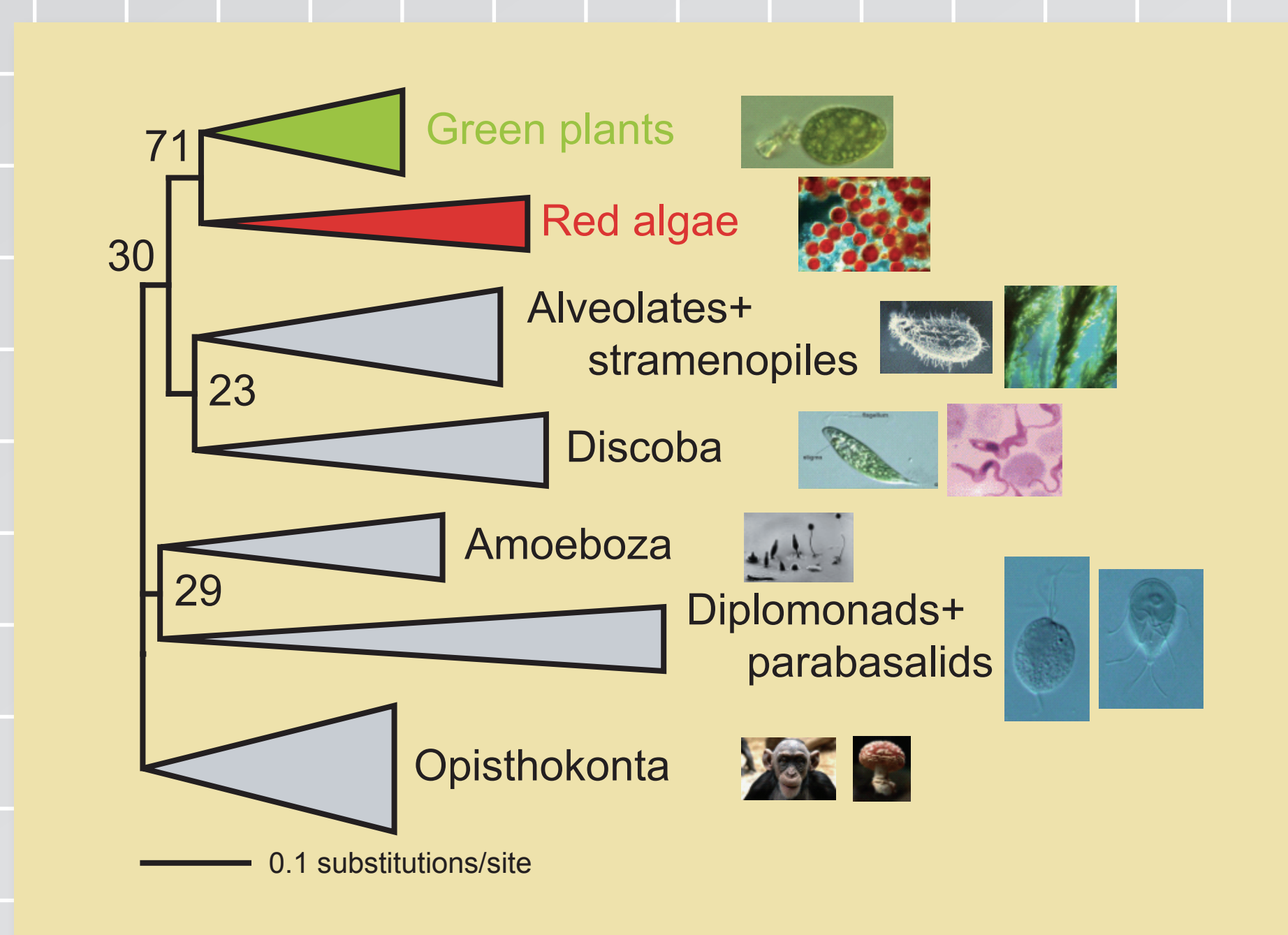




# Division of Biological Sciences

## Phylogenetic Inference on the Universal Tree of Life

The central focus of our research is to gain insight into origin and early evolution of eukaryotes, one of the most important questions in evolutionary biology. One of the goal of this research is to reconstruct the Universal Tree of Life including diverse organisms on the Earth, based on molecular phylogenetic approach. Since a reliable phylogenetic inference simultaneously requires numerous genes and species, a large scale data analysis using high performance computers plays a key role in our study.

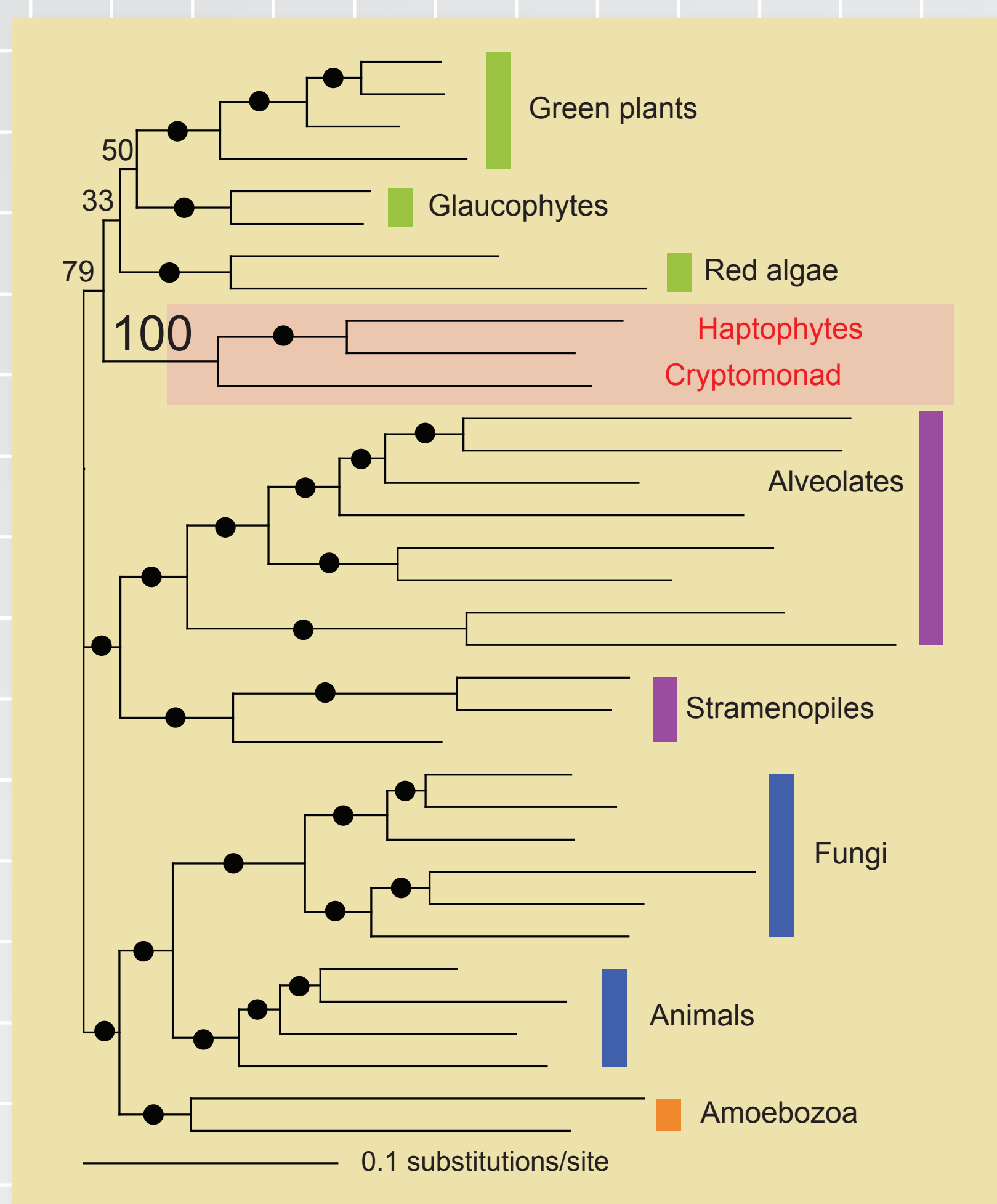


Maximum-likelihood (ML) phylogenetic analyses of a “27-gene” data set supported the sisterhood between green plants and red algae.

Phylogenetic analyses was performed by using 27 protein-coding genes with  $\geq 10,000$  amino acid positions. The tree was selected from 945 possible pre-defined trees for 7 taxonomic groups. The numbers on nodes indicate bootstrap percent support values.

An investigation of phylogenetic signal in each gene suggested the signals of translation elongation factor 2 (EF2) and and alpha-tubulin were diverged from those of other genes (Data not shown). Nevertheless,

exclusion of the two genes from multi-gene analyses had no substantial impact on the sister relationship between green plants and red algae.



ML phylogenetic analyses of a 102-gene data set revealed the monophyly of haptophyte and cryptomonad host lineages.

### Cryptomonad



### Haptophytes



Phylogenetic analyses was performed by using 102 protein-coding genes with  $\geq 18,000$  amino acid positions. The numbers on nodes indicate bootstrap percent support values. Filled circles indicate bootstrap support greater than 95%.

The 102-gene analysis successfully recovered the monophyly of two major algal groups, haptophytes and cryptpmonads, with bootstrap support with 100%. The haptphytes/cryptomonads monophyly was not changed by taxon sampling, substitution models for tree reconstruction, or alignment sites used (data not shown). Our analysis was the first result revealed this novel relationship in global eukaryotic phylogeny.