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EARLY EVOLUTION OF EUKARYOTA AS INFERRED FROM
THE COMBINED PHYLOGENY OF
MULTIPLE MOLECULAR SEQUENCE DATA

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Extensive studies aiming to establish the structure and root of the Eukaryota tree by phylogenetic analyses of molecular sequences resulted in no generally accepted tree so far. In order to re-examine the eukaryotic phylogeny using alternative genes, and to obtain a more robust inference for the root of the tree as well as the relationship among major eukaryotic groups, we have sequenced several protein coding genes from various protists. Combined maximum-likelihood analyses of 22 protein coding genes including the ones of which sequence data were newly obtained from several protists demonstrated clearly that two amitochondriate lineages, Diplomonadida and Parabasalia, shared a common ancestor in the rooted tree of Eukaryota, but only when the fast-evolving and thus the 'noise-containing' sites were excluded from the original data sets. The combined analyses, together with recent findings by Stechmann and Cavalier-Smith (Science 297:89-91, 2002; Curr. Biol. 13:R665-666, 2003) on the distribution of a fused dihydrofolate reductase (DHFR) - thymidylate synthetase (TS) gene, narrowed the possible position of the root of the Eukaryota tree on the branch leading to Opisthokonta or to the common ancestor of Diplomonadida/Parabasalia (Arisue et al. MBE 22:409-420, 2005). Although the branching order of major eukaryotic groups and the position of the root of the tree are still obscure, the combined protein phylogeny strongly suggested that the 'classical', small subunit rRNA based tree of Eukaryota, in which three amitochondriate lineages, Microsporidia, Diplomonadida, and Parabasalia, emerge at the basal position, was misleading. The rRNA tree may have been seriously affected by the long branch attraction attributed to the data set including the rRNAs of amitochondriate lineages with extremely accelerated evolutionary rates.