

Molecular phylogeny and evolution of Parabasalia with new protein markers

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SUMMARY

The traditional taxonomy within the phylum Parabasalia is based on their morphology, and it is mostly linked to their cytoskeletal structures that range from rudimentary to very complex. Although the SSU rRNA phylogeny suggests the necessity of the reclassification, the resolution remains poor because of extreme divergence of the sequences. This study identified four gene sequences encoding SSU rRNA, GAPDH, actin, and EF-1 α from various parabasalids to obtain more reliable phylogeny. We inferred the phylogenetic relations among parabasalids and examined the root position of parabasalids based on concatenated sequence data of the four genes. The concatenate dataset for 26 diverse taxa provides robust relations of the major groups and the more plausible new root position. The new root position strongly suggests that the ancient, most primitive parabasalids have Trichomonadida-like characteristics. The Parabasalia evolution is complex in terms of their morphology because of a number of independent multiplication and simplification of flagellar and the associated cytoskeletal structures. Probably, their ecology strongly affects the parabasalid evolution through adaptation to their ecological niches associated with the hosts and co-diversification with their hosts.