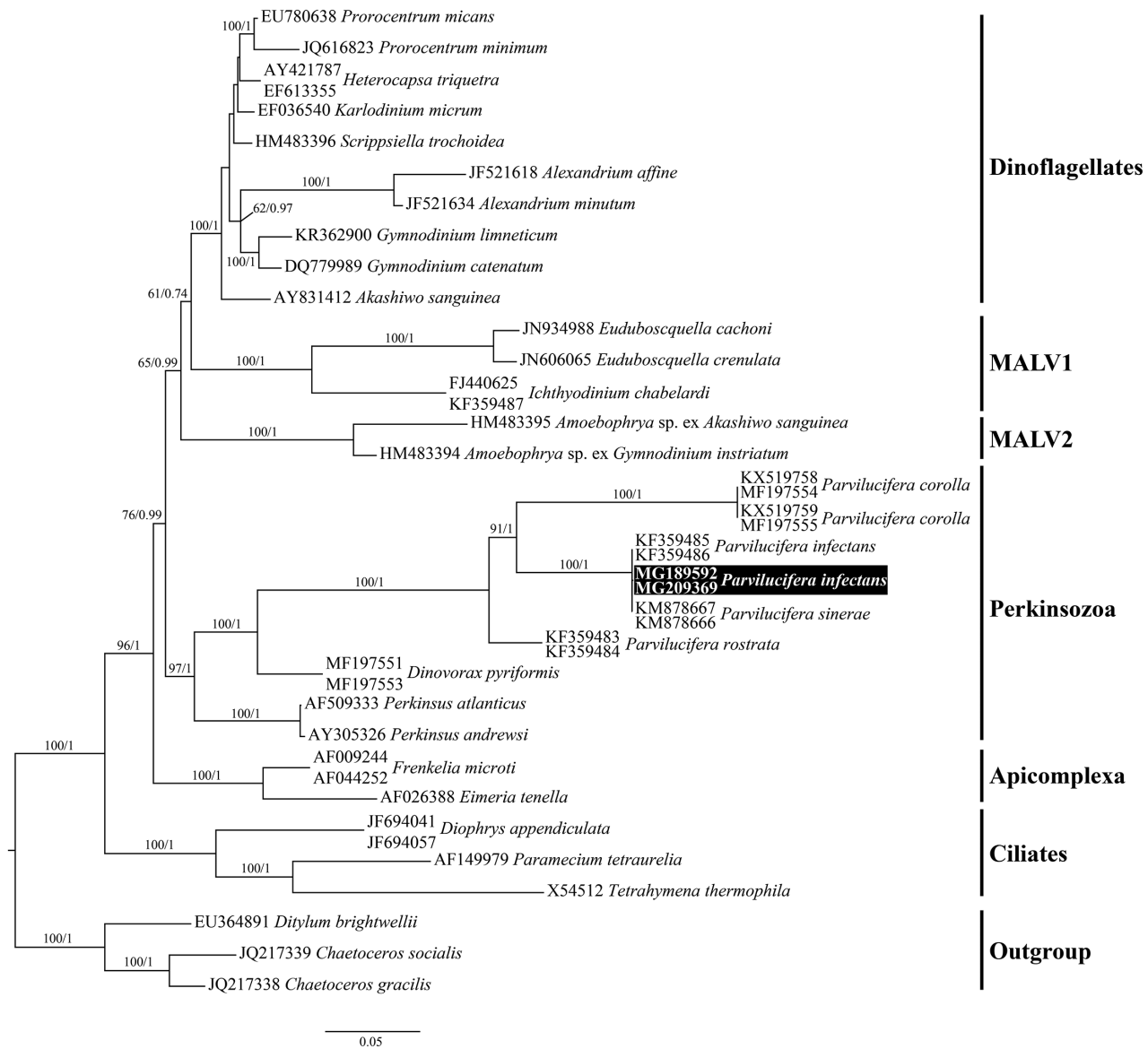


# Supplementary Material

Algae 2018, 33(1): 1-19

<https://doi.org/10.4490/algae.2018.33.3.6>

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**Supplementary Fig. S1.** A RAxML phylogenetic tree inferred from combination of small and large subunit rRNA gene sequences (2,398 bp). Numbers shown on nodes are support values of bootstrap percentages (left) using RAxML fast bootstrapping analysis and Bayesian posterior probabilities (right) higher than 50% and 0.5, respectively. The sequence for *Parvilucifera infectans* in the present study is highlighted in a black box.