

A MOLECULAR PERSPECTIVE ON ECOLOGICAL DIFFERENTIATION AND BIOGEOGRAPHY OF CYCLOTRICHIID CILIATES

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Abstract: Cyclotrichiids are of ecological and evolutionary interest by virtue of their importance in red tide formation, their highly divergent small subunit (SSU) ribosomal RNA (rRNA) genes, kleptoplastidy, and utility as indicators of eutrophication. However, only seven strains have had their SSU rRNA genes sequenced and their environmental diversity and distribution are largely unknown. We probed 67 globally dispersed freshwater column/sediment and soil DNA samples (eDNAs) and constructed 24 environmental gene libraries using polymerase chain reaction primers specific to an uncharacterised cyclotrichiid subgroup. We reveal a novel, globally ubiquitous freshwater clade comprising 25 genetically distinct SSU ribosomal DNA (rDNA) sequences (SSU-types). Some identical SSU-types were detected at globally widely distributed sites. The SSU-types form four distinct phylogenetic clusters according to marine or non-marine provenance, suggesting at least one major marine-freshwater evolutionary transition within the cyclotrichiids. We used the same primers to sample intensively 18 sampling points in 13 closely situated lakes, each characterised by 14 environmental variables, and showed that molecular detection or non-detection of cyclotrichiids was most significantly influenced by levels of total phosphorus, dissolved organic carbon, and chlorophyll a. Within the subset of lakes in which cyclotrichiids were detected, closely related SSU-types differed in their ecological preferences to pH, total phosphorus, and sample depth.

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