

TITLE: USE OF GEOGRAPHIC INFORMATION SYSTEMS TO MONITOR AND PREDICT NON-NATIVE AQUATIC PLANT DISPERSAL THROUGH NORTH-EASTERN NORTH AMERICA

Authors: Boylen C. W.; Eichler L. W.; Bartkowski J. S.; et al.

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Abstract: The recent discovery of a diverse phylogenetic assemblage of picoeukaryotes from environments such as oceans, salt marshes and acidic habitats, has expanded the debates about the extent and origin of microbial eukaryotes. However, the diversity of these eukaryote microorganisms, that overlap bacteria in size, and their environmental and biogeographical ubiquity remains poorly understood. Here we survey picoeukaryotes (microbial eukaryotes of 0.2-5 μm in size) from an oligotrophic (nutrient deficient) freshwater habitat using ribosomal RNA gene sequences. Three taxonomic groups the Heterokonta, Cryptomonads and the Alveolata dominated the detected diversity. Most sequences represented previously unsampled species, with several being unassignable to known taxonomic groups and plausibly represent new or unsampled phyla. Many freshwater phylogenetic groups identified in this study appeared unrelated to picoeukaryotic sequences identified in marine ecosystems, suggesting that aspects of eukaryote microbial diversity are specific to certain aquatic environments. Conversely, at least five phylogenetic clusters comprised sequences from freshwater and globally dispersed and often contrasting environments, supporting the concept that a number of picoeukaryotic lineages are widely distributed.

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