

A metagenome for lacustrine Cladophora (Cladophorales) reveals remarkable diversity of eukaryotic epibionts and genes relevant to materials cycling

ABSTRACT

Periphyton dominated by the cellulose-rich filamentous green alga *Cladophora* forms conspicuous growths along rocky marine and freshwater shorelines worldwide, providing habitat for diverse epibionts. Bacterial epibionts have been inferred to display diverse functions of biogeochemical significance: N-fixation and other redox reactions, phosphorus accumulation, and organic degradation. Here, we report taxonomic diversity of eukaryotic and prokaryotic epibionts and diversity of genes associated with materials cycling in a *Cladophora* metagenome sampled from Lake Mendota, Dane Co., WI, USA, during the growing season of 2012. A total of 1,060 distinct 16S, 173 18S, and 351 28S rRNA operational taxonomic units, from which >220 genera or species of bacteria (~60), protists (~80), fungi (6), and microscopic metazoa (~80), were distinguished with the use of reference databases. We inferred the presence of several algal taxa generally associated with marine systems and detected *Jaoa*, a freshwater periphytic ulvophyte previously thought endemic to China. We identified six distinct *nifH* gene sequences marking nitrogen fixation, >25 bacterial and eukaryotic cellulases relevant to sedimentary C-cycling and technological applications, and genes encoding enzymes in aerobic and anaerobic pathways for vitamin B12 biosynthesis. These results emphasize the importance of *Cladophora* in providing habitat for microscopic metazoa, fungi, protists, and bacteria that are often inconspicuous, yet play important roles in ecosystem biogeochemistry.

Keyword: Cellulases; *Cladophora*; Metagenome; Microbiome; Periphyton