



Species-dependent effects of crustacean plankton on a microbial community, assessed using an enclosure experiment in Lake Taihu, China

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ABSTRACT: A mesocosm experiment was performed to evaluate the species-dependent effects of crustacean plankton on the microbial community in Lake Taihu, a large shallow eutrophic lake in China. Four dominant species of crustacean plankton (*Daphnia galeata*, *Bosmina longirostris*, *Neodiantomus schmackeri*, and *Mesocyclops dissimilis*) in Lake Taihu were selected as predators. Denaturing gradient gel electrophoresis and cloning and sequencing of polymerase chain reaction – amplified ribosomal ribonucleic acid gene fragments were applied to analyze the microbial eukaryotic community composition (MECC) and bacterial community composition (BCC). The changes in the abundance of bacteria, heterotrophic nanoflagellates, ciliates, and phytoplankton were also measured. Crustacean plankton had a significant effect on phytoplankton biomass, the abundance of ciliates and bacteria, and the percentage of filamentous bacteria among total bacteria. Nonmetric multidimensional scaling analysis showed that the MECC and BCC in the treatments involving the same species were generally more similar to each other than to those in treatments with other species on both days 7 and 15. The MECC were clustered into two distinct groups between the cladoceran and copepod treatments on days 7 and 15. A phylogenetic analysis revealed that alveolates, chlorophytes, and fungi were the most important groups in the microbial eukaryotic clone libraries. Crustacean plankton had a significant species-dependent effect on the microbial eukaryotic community and might have both trophic and nontrophic effects on the bacterial community.

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