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Genetic diversity pattern of microeukaryotic communities and its relationship with the environment based on PCR-DGGE and T-RFLP techniques in Dongshan Bay, southeast China

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Abstract

Microeukaryotes play important roles in aquatic ecosystems, and could act as drivers of the biological nutrient cycling processes. However, compared with prokaryotic ones, little is known about the genetic diversity pattern of their community, and the environmental factors affecting their ecological pattern, especially in marine ecosystems. In this study, we used denaturing gradient gel electrophoresis (DGGE) and terminal restriction fragment length polymorphism (T-RFLP) to explore the genetic diversity structure of microeukaryotic communities in Dongshan Bay, southeast China. Our results revealed that microeukaryotic diversity ranged from 31 to 48 phylotypes (on average, 42) using the DGGE approach, while from 22 to 38 phylotypes (on average, 30) based on T-RFLP method, and the Shannon-Wiener diversity (DGGE-based) was relatively higher, suggesting that DGGE displayed a slightly higher resolution than T-RFLP. Surprisingly, the DGGE showed significant horizontal difference among microeukaryotic communities, but was similar with T-RFLP analysis that had no significant influence on microeukaryotic diversity at vertical scales. Further, Redundancy analysis (RDA) indicated that the DGGE-based microeukaryotic communities distribution was significantly correlated with three environmental factors (Chl-a, TP and salinity), whereas microeukaryotic community revealed by T-RFLP was affected by four environmental factors namely salinity, temperature, depth and NO_X-N. Compared with RDA, Biota-Environment (BIO-ENV) analysis showed that NO_X-N was the only significant environmental variable influencing microeukaryotic communities in both methods. These differences may be attributed to the noisy effects caused by the relatively large number of environmental variables. Generally speaking, despite differences in beta-diversity ordination for both DGGE and T-RFLP methods, there exists some consistency in the results of both techniques in terms of microeukaryotes responses