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BIODIVERSITY AND FUNCTIONAL METAGENOMIC PROFILING

OF MICROBIAL COMMUNITIES IN TASIK KENYIR,

TERENGGANU

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ABSTRACT

Tasik Kenyir located in the state of Terengganu is the largest artificial lake in Southeast Asia with mean-depth of 37 m. This lake plays an important role in maintaining the biodiversity in the surrounding environment. Microbial communities in the lake are important, as most of the nutrients are recycled through the “microbial loop”. Thus, understanding the connection between the diversity composition and functional role of aquatic microbial community is crucial for proper lake management.

This study aims to determine the diversity and functions of microbial assemblages in Tasik Kenyir by means of shotgun metagenomics analysis. Briefly, water samples were collected from pristine and disturbed areas. Metagenome DNA were then extracted directly and subjected to clone-independent sequencing. Data sequences of all samples were analyzed and functional annotated using bioinformatics software MEGAN6. Analysis showed up to 41 phyla that had been detected from the water samples with the presence of dominant bacterial populations of more than 90% in all samples. Proteobacteria was the most dominant phylum, representing more than 70% of the microbiome in all samples. Other taxa such as Bacteroidetes, Terrabacteria group, Verrucomicrobia, Planctomycetes and Chloroflexi were also found as part of the microbial communities.

The first sample from the disturbed area, TKSA1 had 3% of total contigs read assigned to genera

Pseudomonas

while the

other samples appeared to be more homogeneous. The lake also appeared to contain a mixture of autotrophs and heterotrophs

capable of performing main biogeochemical cycles. Findings of the present study has provided us valuable information on

the microbial diversity structures and their functions in the nutrient processing pathways that occurred in the Tasik Kenyir

environment and thus sheds light on the importance of freshwater microbial communities for ecosystem and human health.

Key words: Metagenomic, biodiversity, functional profiling, microbial communities, tasik Kenyir