ABSTRACT

Laurensius Mika Jackie. 24020118130112. Microbial Community Diversity and Potential Pollutant Degradation Genes from Freshwater Sponge Samples of *Eunapius carteri* and *Oncosclera asiatica* of Porong River Based on Metagenomics. Under the guidance of Hermin Pancasakti Kusumaningrum and Sri Pujiyanto.

Freshwater microbial communities such as rivers or streams are still not widely explored. Microbes form symbionts with sponges to defend themselves against foreign organisms such as prokaryotic, eukaryotic, or viruses by producing secondary metabolites. *Eunapius carteri* and *Oncosclera asiatica* are freshwater sponges that live in the Porong River and have the potential to be studied. The Porong River is a dumping ground for industrial waste, domestic waste, agricultural pesticide residues, and mud from mud volcanoes, creating a unique habitat for the biodiversity of living things, especially microbial communities. The challenge of examining microbial community structure in a particular niche is that not all microbes can be cultured, which can be solved by metagenomics. This research focuses on reviewing microbial community structure, abundance, diversity, and potential for metagenomics-based pollutant degradation genes. The methods include sequence preparation, bioinformatics analysis to see diversity and abundance with alpha and beta diversity analysis, and prediction of genes encoding pollutant degradation enzymes. The results showed that the diversity analysis showed that the SS sample was low diversity while the EC sample was high diversity. Genus such as *Pseudomona*s was found to dominate the SS1 and SS2 samples, while *Aeromonas* genus dominated the EC1 and EC2 samples. The genus found has the ability to degrade pollutants based on references. Freshwater sponges has a high potential for pollutant degradation genes. The prediction obtained is that benzoate degradation seems to be the main pathway for catabolism of most aromatic compounds, which is supported by key genes.

Keywords: microbial community, biodegradation, metagenomics, gene prediction, Porong River