ABSTRACT

Bacterial Community Profile of Biofouling on Ship Material Surfaces at Tanjung Mas Semarang Dock Using eDNA Metabarcoding Approach. Naufal Sebastian Anggoro. 24020121420018.

Bacterial communities play a crucial role in the formation of biofouling on marine vessels. These biofouling-forming bacterial communities can reduce operational efficiency, increase fuel costs, slow down the vessel's speed, and cause damage, especially to ships with fiber and aluminum surfaces. This study aims to analyze the bacterial community profile responsible for biofouling formation on fiber and aluminum ship surfaces. The research used the eDNA metabarcoding method with 16S rRNA amplicon samples and HTS DNBSeq-400 technology on biofilm biofouling samples from fiberglass and aluminum ship materials, with three replicates for each material collected from the Tanjung Emas Port area. Data were analyzed using the bioinformatics software QIIME2 with the SILVA v138 SSU RefNR99 database as a reference for taxonomic classification, PICRUSt2, RStudio (ANOVA and PERMANOVA statistical analysis), and the Phyloseq package. The bacterial community profile results on fiber and aluminum ship surfaces showed that the Shannon diversity index indicated higher diversity on aluminum surfaces, while the Inverse Simpson index showed higher results on fiber surfaces. Genus identification revealed 11 genera and 6 species on the fiber surface, and 8 genera with one species, *Thalassotalea ponticola*, contributing 1.63% on the aluminum surface. Aerobic respiration pathways were the dominant metabolism on both fiber and aluminum materials. Descriptive differences were observed from the analysis results, including the number of unique taxa, relative abundance at the family and genus levels, LEfSe, and predicted functional metabolic pathways of the bacterial biofilm communities on both materials.

Keywords: *fiberglass, aluminum, NGS, Amplicon, DNBSeq*