ABSTRACT

Al Mira. 24020120120005. **DNA Metabarcoding Approach in Identifying Marine Microbiota Diversity in the Coastal Area of Karimunjawa Island, Jepara.** Under guidance of Sapto Purnomo Putro dan Ni Kadek Dita Cahyani.

Karimunjawa Islands is one of the national parks in Jepara Regency, Central Java, which is famous for its rich underwater natural resources. The high anthropogenic activities such as aquaculture, tourism, capture fisheries, and docks in the area can cause threats to coastal areas including coastal erosion, seawater intrusion, and environmental damage. Therefore, it is necessary to assess the condition of the aquatic environment through the identification of microorganisms with molecular techniques (DNA metabarcoding). This study aims to assess the diversity of marine microbiota and its potential as an indicator of environmental change in the coastal area of the Karimunjawa Islands. eDNA samples were collected from surface waters and filtered using filter paper with a pore size of 0.45 μm, followed by samples extracted using the Zymo Fecal/Soil DNA Kit and DNA purity levels were measured using Nanodrop spectrophotometry. DNA sequencing using 16S rRNA genetic markers in the V3-V4 region and Next Generation Sequencing (NGS) technology Illumina MiSeq platform. Sequencing results were analyzed using QIIME2 and R Studio. The three research sites identified a relatively high diversity of microbiota with a composition of 2 kingdoms, 11 phyla, 11 classes, 11 orders, and 12 families. Most taxa in anthropogenic sites have more potential as pathogenic bacteria. Whereas in non-anthropogenic locations, the majority of taxa have varied ecological roles and tend to be beneficial to the aquatic environment. The presence of marine microbiota from the families Arcobacteraceae (phylum Campilobacterota) and Nitrincolaceae (phylum Proteobacteria) indicates that the aquatic environment at anthropogenic sites (close to aquaculture) is not good for the survival of aquatic biota. While the aquatic environment in non-anthropogenic locations (far from aquaculture areas) has good water quality as evidenced by the presence of taxa from the Cyanobiaceae family (phylum Cyanobacteria).

Keywords: *16S rRNA gene, DNA metabarcoding, microorganism, diversity, anthropogenic*