

ABSTRAK

Penelitian terkait eksplorasi komunitas bakteri pada suatu sampel lingkungan menjadi *trend* penelitian dalam beberapa dekade terakhir. Sedimen Selat Makassar dan Laut Sawu menjadi sampel lingkungan yang menarik untuk diteliti karena indikasi kontaminasi minyak memengaruhi komposisi taksonomi didalamnya. Tujuan dari penelitian ini adalah mengetahui keanekaragaman komunitas bakteri di sedimen perairan tersebut. Metode metagenomik *amplicon* digunakan dalam penelitian ini dengan menggunakan sampel sedimen dari Selat Makassar (ST45) dan Laut Sawu (ST5). Ekstraksi e-DNA menggunakan kit komersial DNeasy PowerSoil Kit (Qiagen). Selanjutnya, sampel disekuensing di IOCAS (Institute of Oceanology, Chinese Academic of Science). Data hasil sequencing dianalisis menggunakan Rstudio. Hasil dari penelitian ini menunjukkan analisis *alpha diversity* menggunakan indeks Shannon, Simpson, dan Invsimpson menginterpretasikan tingkat keanekaragaman dan dominansi yang tinggi. Berdasarkan hasil analisis *beta diversity* menunjukkan bahwa jarak antar sampel terpaut jauh yang mengindikasikan perbedaan komposisi takson. Hasil analisis komposisi taksonomi menunjukkan sebanyak 49 filum, 84 kelas, 123 ordo, 224 famili, dan 442 genus berhasil diidentifikasi dengan Filum Proteobacteria yang sangat mendominasi hingga mewakili rata-rata kelimpahan relatif sebesar 47,36%. Kesimpulan dari penelitian ini menunjukkan indikasi pengaruh kontaminasi minyak terhadap komposisi taksonomi di ST5 dan ST45 sehingga bisa dijadikan informasi mengenai riset biodegradasi minyak.

Kata kunci: Selat Makassar, Laut Sawu, Metagenomik *amplicon*, *Alpha diversity*, *Beta diversity*, Komunitas bakteri.

ABSTRACT

Research related to the exploration of bacterial communities in an environmental sample has become a research trend in recent decades. Makassar Strait and Sawu Sea sediments are interesting environmental samples to study because indications of oil contamination affect the taxonomic composition therein. The purpose of this study was to determine the diversity of bacterial communities in the sediment of these waters. The amplicon metagenomics method was used in this study using sediment samples from the Makassar Strait (ST45) and Sawu Sea (ST5). The commercial kit DNeasy PowerSoil Kit (Qiagen) was applied to extract the e-DNA. Furthermore, the samples were sequenced at IOCAS (Institute of Oceanology, Chinese Academic of Science). The sequencing data were analyzed using Rstudio. The results of this study showed that alpha diversity analysis using Shannon, Simpson, and Invsimpson indices interpreted a high level of diversity and dominance. Based on the results of beta diversity analysis, it was observed that the distance between samples was far adrift, indicating differences in taxon composition. The results of the taxonomic composition analysis were successfully identified 49 phyla, 84 classes, 123 orders, 224 families, and 442 genera, with the Proteobacteria phylum dominating to represent an average relative abundance of 47.36%. The conclusion of this study indicated the influence of oil contamination on taxonomic composition in ST5 and ST45, which can be used as information on oil biodegradation research.

Keyword: Makassar Strait, Savu Sea, Metagenomic amplicon, *Alpha diversity*, *Beta diversity*, Bacterial community.