

ABSTRACT

Ais Syafira Agustin 24020121130093. ***Profiling of Bacterial Communities Dependently and Independently from Agricultural, Domestic, and Industrial Pollutant Sources in the Cimande Sub-River Basin, Upstream Citarum River Basin.*** Under guidance of Arina Tri Lunggani and Rini Riffiani.

Water is a compound that plays an important role in life. However, river water is often used as a waste disposal site. The Citarum Basin is an important river system that covers the Bandung Metropolitan Area (BMA) which includes several cities/regencies. This area is developing rapidly in the Upper Citarum Sub-Basin. The area that is developing uncontrollably causes a decline in environmental quality and water resource conservation. Therefore, research is needed to determine the structure of bacterial communities that have the potential to remediate pollutants and can evaluate the health and stability of the ecosystem. The purpose of this study was to identify bacteria, determine the abundance and diversity of bacteria, and determine the relationship between the abundance and diversity of bacteria from agricultural, domestic, and industrial pollutant sources in the Cimande Sub-Basin, Upper Citarum Basin. This study was conducted using the culture dependent and culture independent methods. Bacterial isolation was carried out, the total number of bacteria was calculated using the Total Plate Count (TPC), and extracted using the gSYNC DNA Extraction Kit and then identified molecularly using 16S rRNA sequencing. Culture Independent was conducted with metagenomic tests using the PowerSoil DNA Isolation Kit and sequencing was performed with NGS (Next Generation Sequencing). The results showed that dependent culture could only identify 16 species of bacteria. Independent culture was proven to be able to identify more bacteria with a total of 2046 OTUs in Group 2, while Groups 1 and 3 were 1520 and 1262. The abundance and diversity of bacteria varied with the number of bacteria identified being the highest in industrial areas. This is related to the influence of the complexity of compounds contained in industrial pollutants, microorganisms in this area have special metabolic pathways so that they can adapt and create unique and diverse microbial communities.

Keywords: abundance, basin, culture dependent, culture independent.