ANALISIS PROFIL BAKTERI PATOGEN DAN GEN RESISTENSI ANTIBIOTIK MENGGUNAKAN *SHOTGUN METAGENOMIC SEQUENCING* PADA ALIRAN SUNGAI BANJARAN

ABSTRAK

Latar belakang: Kontaminasi antibiotik di lingkungan akibat penggunaan berlebih dan penyalahgunaan antibiotik dapat menciptakan fenomena adaptasi bakteri terhadap antibiotik. Sungai dianggap sebagai salah satu reservoir bakteri patogen dan gen resistensi antibiotik yang paling penting, yang berperan dalam penyebaran terjadinya resistensi antibiotik. **Tujuan:** Penelitian ini bertujuan untuk mengetahui profil bakteri patogen dan gen resistensi antibiotik di aliran Sungai Banjaran. **Metodologi:** Penelitian ini menggunakan metode eksperimental *in-silico* dengan sampel air yang diambil di bagian hulu dan hilir Sungai Banjaran. Sampel air di filtrasi menggunakan membran filter dan *DNeasy PowerWater* digunakan untuk ekstraksi DNA kemudian sekuensing DNA dilakukan dengan *Shotgun Metagenomic Sequencing*. Data kemudian di analisis menggunakan *Bacterial and Viral Bioinformatics Resource Center*. **Hasil:** Terdapat 103 gen resisten antibiotik dan 28 spesies bakteri patogen yang terdeteksi pada Aliran Sungai Banjaran. 18 spesies dan 90 gen terdeteksi di bagian hulu , sedangkan di bagian hilir terdeteksi 23 spesies dan 32 gen. Kelimpahan spesies dan gen yang ditemukan cenderung mengalami penurunan di bagian hilir. **Kesimpulan:** Terdapat perbedaan profil bakteri patogen dan gen resistensi antibiotik pada aliran Sungai Banjaran, karena terjadinya proses *self purification* sungai.

Kata kunci: Bakteri patogen, gen resisten antibiotik, resistensi antibiotik, *shotgun metagenomic sequencing*, sungai

ANALYSIS OF PROFILES OF PATHOGEN BACTERIA AND ANTIBIOTIC RESISTANCE GENES USING SHOTGUN METAGENOMIC SEQUENCING IN THE BANJARAN RIVER STREAM

ABSTRACT

Background: *Antibiotic contamination in the environment due to overuse and misuse of antibiotics can create bacterial adaptation to antibiotics. Rivers are considered one of the most important reservoirs of pathogenic bacteria and antibiotic-resistance genes, which play a role in the spread of antibiotic resistance.* **Objective**: *This research aims to determine the profile of pathogenic bacteria and antibiotic-resistance genes in the Banjaran River.* **Methodology**: *This study employs in-silico experimental methods with water samples taken in the upstream and downstream parts of the Banjaran River. Water samples are filtered using membrane filters, and DNA extraction is performed using DNeasy PowerWater, followed by DNA sequencing using Shotgun Metagenomic Sequencing. The data analysis uses the Bacterial and Viral Bioinformatics Resource Center.* **Results**: *103 antibiotic resistance genes and 28 species of pathogenic bacteria were detected in the Banjaran River. 18 species and 90 genes were detected in the upstream section, while 23 species and 32 genes were detected in the downstream section. The abundance of species and genes found tends to decrease downstream.* **Conclusion**: *Due to the river self-purification process, there are differences in the profile of pathogenic bacteria and antibiotic resistance genes in the Banjaran River.*