

IDENTIFIKASI GEN RESISTENSI ANTIBIOTIK YANG TERKAIT DENGAN PAPARAN RESIDU ANTIBIOTIK PADA SUNGAI BANJARAN KABUPATEN BANYUMAS DENGAN ANALISIS METAGENOMIK

ABSTRAK

Latar belakang: Penggunaan antibiotik di sektor kesehatan dan agraris dapat menghasilkan limbah residu antibiotik yang mencemari lingkungan sungai. Residu antibiotik pada lingkungan dapat menyebabkan timbulnya gen resistensi antibiotik akibat terjadinya *antibiotic-induced mutagenesis* pada bakteri. **Tujuan:** Mengidentifikasi gen resistensi antibiotik yang terkait dengan paparan residu antibiotik pada air yang mengalir di bagian hulu, tengah, dan hilir Sungai Banjaran. **Metode:** Penelitian ini merupakan penelitian *in silico* dengan pendekatan komputasional dengan sampel air dari Sungai Banjaran yang diambil pada bagian hulu, tengah, dan hilir. Sampel air akan dilakukan ekstraksi DNA menggunakan kit *Quick-DNA™ MagBead Plus Kit* untuk memperoleh DNA murni. Hasil ekstraksi DNA kemudian disekuensing menggunakan *shotgun metagenomic sequencing* untuk mendapatkan sekuens DNA. Sekuens DNA selanjutnya dianalisis menggunakan *Bacterial and Viral Bioinformatics Resource Center 3.33.16* yang di dalamnya terdapat algoritma *Basic Local Alignment Search Tool* (BLAST) untuk mengidentifikasi gen resistensi antibiotik. **Hasil:** Hasil analisis pada bagian hulu ditemukan 101 gen resistensi dengan 76 gen resistensi intrinsik, 22 gen melalui *Horizontal Gene Transfer* (HGT), dan 3 gen hasil mutasi. Sampel dari bagian tengah teridentifikasi 83 gen resistensi dengan 38 gen intrinsik, 35 gen melalui HGT, 4 gen mutasi, serta 6 gen yang terkait dengan paparan residu antibiotik. Sampel dari bagian hilir ditemukan 40 gen resistensi dengan 19 gen intrinsik, 18 gen HGT, 2 gen mutasi, dan 1 gen yang terkait dengan paparan residu antibiotik. **Kesimpulan:** Terdapat 6 gen yang terkait dengan paparan residu antibiotik *phosphonic*, kloramfenikol, dan fluorokuinolon pada sampel air dari bagian tengah sungai, serta 1 gen yang terkait dengan paparan residu antibiotik tetrasiklin pada sampel dari bagian hilir sungai.

Kata kunci: Analisis metagenomik, gen resisten antibiotik, pencemaran residu antibiotik, Sungai Banjaran

IDENTIFICATION OF ANTIBIOTIC RESISTANCE GENES ASSOCIATED WITH EXPOSURE TO ANTIBIOTIC RESIDUES IN THE BANJARAN RIVER, BANYUMAS DISTRICT USING METAGENOMIC ANALYSIS

ABSTRACT

Background: The excessive use of antibiotics in the health and agricultural sectors can produce antibiotic residue waste that pollutes river environments. Antibiotic residues in the environment can lead to the emergence of antibiotic resistance genes through antibiotic-induced mutagenesis in bacteria. **Objective:** Identifying antibiotic resistance genes associated with exposure to antibiotic residues in the upstream, middle, and downstream parts of the Banjaran River. **Methods:** This research is an *in silico* study using a computational approach with water samples from the Banjaran River, taken from the upstream, middle, and downstream parts. DNA extraction was carried out using the Quick-DNA™ MagBead Plus Kit, followed by sequencing with shotgun metagenomic sequencing. Bioinformatics analysis was conducted using the Bacterial and Viral Bioinformatics Resource Center 3.33.16. The identification of antibiotic resistance genes was performed using the Basic Local Alignment Search Tool (BLAST) algorithm. **Results:** The upstream analysis identified 101 resistance genes, including 76 intrinsic resistance genes, 22 genes acquired through Horizontal Gene Transfer (HGT), and 3 genes resulting from mutations. Samples from the middle section revealed 83 resistance genes, comprising 38 intrinsic genes, 35 genes acquired through HGT, 4 mutation genes, and 6 genes related to exposure to antibiotic residues. Samples from the downstream section identified 40 resistance genes, consisting of 19 intrinsic genes, 18 HGT genes, 2 mutation genes, and 1 gene associated with exposure to antibiotic residues. **Conclusion:** There were six genes associated with exposure to residues of phosphonic antibiotics, chloramphenicol, and fluoroquinolones in water samples from the middle part of the river, and one gene associated with exposure to residues of tetracycline antibiotics in samples from the downstream of the river.

Keywords: Antibiotic resistance gene, antibiotic residue pollution, Banjaran River, metagenomic analysis