

# PROFIL DIVERSITAS GEN RESISTEN ANTIBIOTIK PADA ALIRAN SUNGAI BANJARAN DI HULU DAN KAWASAN PETERNAKAN

## ABSTRAK

**Latar Belakang:** Penggunaan antibiotik berlebihan di peternakan dapat menyebabkan penambahan gen resisten antibiotik melalui residu antibiotik yang mencemari lingkungan sehingga berpotensi menyebabkan penyebaran resistensi antibiotik pada bakteri melalui air termasuk di aliran Sungai Banjaran. **Tujuan:** Untuk mengetahui kelimpahan gen resisten antibiotik yang berasal dari kegiatan peternakan di sekitar Sungai Banjaran. **Metode:** Penelitian ini menggunakan metode eksperimental *in silico* dengan sampel air dari hulu sungai dan kawasan peternakan dengan metode *grab sampling*. Analisis sekuensing menggunakan *Shotgun Metagenomic Next-Generation Sequencing*. Analisis bioinformatika dengan *Bacterial and Viral Bioinformatics Resource Center* seri 3.32.13a dan seri 3.33. Analisis identifikasi bakteri berdasarkan 16s rRNA dan pensejajaran (BLAST) untuk identifikasi gen resisten bakteri. **Hasil:** Terdapat 29 gen resisten antibiotik yang berasal dari kegiatan peternakan di sekitar Sungai Banjaran teridentifikasi pada bakteri *Enterobacter cloacae*, *Escherichia coli*, *Moraxella catarrhalis*, *Pasteurella multocida*, dan *Salmonella enterica*. 9 gen muncul akibat paparan antibiotik dari kegiatan peternakan, 6 gen muncul akibat resistensi intrinsik, 4 gen muncul karena stress lingkungan, dan 10 gen muncul karena transfer gen horizontal. **Kesimpulan:** Terdapat peningkatan kelimpahan gen resisten antibiotik di Sungai Banjaran pada daerah sekitar peternakan.

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**Kata kunci:** Resistensi antibiotik, gen resisten antibiotik, peternakan, Sungai Banjaran, *Shotgun Metagenomic Next-Generation Sequencing*

## **PROFILE OF ANTIBIOTIC RESISTANCE GENE DIVERSITY IN THE BANJARAN RIVER UPSTREAM AND LIVESTOCK AREAS**

### **ABSTRACT**

**Background:** The excessive use of antibiotics in livestock can lead to an increase in antibiotic-resistant genes through the contamination of the environment with antibiotic residues causing the spread of antibiotic resistance bacteria through water, including in the Banjaran River. **Objective:** To determine the abundance of antibiotic-resistant genes originating from livestock activities around the Banjaran River. **Methods:** This study employed an *in silico* experimental method with water samples collected from the river's upstream and livestock farming areas using grab sampling. Sequencing analysis was conducted utilizing Shotgun Metagenomic Next-Generation Sequencing. Bioinformatics analysis was performed using Bacterial and Viral Bioinformatics Resource Center series 3.32.13a and series 3.33. Bacterial identification based on 16s rRNA and alignment (BLAST) were employed for the identification of antibiotic-resistant bacterial genes. **Results:** 29 antibiotic-resistant genes originating from livestock activities around the Banjaran River were identified in bacteria such as *Enterobacter cloacae*, *Escherichia coli*, *Moraxella catarrhalis*, *Pasteurella multocida*, and *Salmonella enterica*. Among these, 9 genes emerged due to antibiotic exposure from livestock activities, 6 genes emerged due to intrinsic resistance, 4 genes emerged due to environmental stress, and 10 genes emerged due to horizontal gene transfer. **Conclusion:** There is an increase in the abundance of antibiotic-resistant genes in the Banjaran River in the areas surrounding livestock activities.

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**Keywords:** Antibiotic resistance, antibiotic-resistant genes, livestock, Banjaran River, Shotgun Metagenomic Next-Generation Sequencing

