The Genomic Profile of the Antibiotic-Resistant of Predominant Gram-Negative Bacteria in Children Feces with Acute Diarrhea in Jakarta = Profil Genom Bakteri Gram-Negatif predominan yang Resistan terhadap Antibiotik pada Feses Anak dengan Diare Akut di Jakarta

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Abstrak

Diarrhea poses significant health risks in developing countries like Indonesia, especially among children, contributing to high morbidity and mortality rates according to the 2018 World Health Organization report. The escalating antimicrobial resistance among enteric pathogens in these nations is also a critical concern. The aim of this research is to profile Gram-negative bacteria in pediatric patients with diarrheal conditions and analyze the antibacterial gene resistance of Gram-negative bacteria in these patients. Stool samples were cultured and sent to the FKUI Microbiology Laboratory for DNA isolation. Pathogenic Gram-negative bacteria were identified and sequenced at the Bioinformatics Core Facilities at IMERI-FKUI using Next-Generation Sequencing (NGS). Antibiotic resistance to antibiotics such as cefixime, co-trimoxazole, ciprofloxacin, and carbapenem was determined. Eighteen bacterial samples revealed a diverse landscape of Klebsiella pneumoniae and E. coli strains. Klebsiella pneumoniae predominated (56%), with various Sequence Types (STs) and phylotypes identified. Notably, ST-231 and ST-101 were associated with the K1 phylotype, indicating potential virulence. E. coli (44% of samples) showed a spectrum of pathogenicity, including ExPEC as the most prevalent. Virulence gene analysis highlighted complex pathogenic mechanisms and significant antibiotic resistance, especially in E. coli. K. pneumoniae and E. coli isolates showed high resistance to multiple antibiotics, including fluoroquinolones, fosfomycin, aminoglycosides, and beta-lactams. This research enhances the understanding of gastrointestinal health in children and underscores the urgent need for effective antimicrobial stewardship to combat antimicrobial resistance.