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SCREENING AND GENOMIC CHARACTERIZATION OF MULTI-DRUG RESISTANT (MDR) BACTERIA FROM HOSPITAL WASTEWATER

by

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Abstract

Antimicrobial resistance poses an imminent global threat to public health, with multidrug-resistant (MDR) bacteria being particularly worrisome due to their resistance to multiple antibiotics. Hospital wastewater has been identified as a potential source of MDR bacteria and antibiotic-resistant genes (ARGs). This study aimed to investigate the prevalence, diversity and genomic potential of MDR bacteria in hospital wastewater samples collected from three different hospitals in the UAE. Samples were processed for culturing antibiotic-resistant bacteria using different HiCrome™ chromogenic media to screen for ESBL-producing and Vancomycin-, Carbapenem-, colistin-, and Methicillin-resistant bacteria. The isolates were characterized using VITEk2 antibiotic profiling and identified using 16S rRNA sequencing followed by whole genome sequencing (WGS) of selected isolates. The results showed that a total of 63 bacterial isolates were obtained, with 90% being Gram-negative and 10% being Gram-positive bacteria. The phylum Proteobacteria was the most prevalent, with the genus Aeromonas being the most abundant, accounting for 38.09% of the isolates, followed by Escherichia (14.28%), Enterococcus and Serratia (each 9.52%). Phylogenetic analyses displayed two distinct clusters of all the isolates, indicating a close evolutionary relationship of bacteria. The VITEK2 analyses showed that among the Gram-negative bacteria, the highest percentage of resistance was observed for ampicillin (49.12%), followed by fosfomycin (43.85%) and nitrofurantoin (21.05%), whereas Gram-positive bacteria showed resistance against clindamycin, quinupristin/dalfopristin and tetracycline (83.33%). The abundance of MDR bacteria varied among the three hospitals, with Hospital 3 exhibiting a significantly highest prevalence (25.4%) compared to other hospitals. Using WGS analyses, a 98% complete genome (5936 bp) of Escherichia coli was recovered using 131 contigs with 51% GC content. Further analyses revealed the presence of various ARGs, including those conferring resistance to quinolone/fluoroquinolone (gyrA, parC, qnrS1) and macrolides (mph(E), msr(E)). These findings highlight the potential of hospital wastewater as a reservoir for MDR bacteria and ARGs, emphasizing the importance of effective management and control measures to prevent the spread of antibiotic resistance. In conclusion, this study provides valuable insights into the prevalence and diversity of MDR bacteria and ARGs in hospital wastewater of UAE. The findings underscore the need for continued surveillance and intervention efforts to mitigate the emergence and spread of antibiotic resistance in healthcare settings, thus enabling the implementation of appropriate strategies to combat antimicrobial resistance.

Keywords: Antimicrobial resistance (AMR), Antibiotic-Resistance genes, Hospitals, Multidrug-resistant (MDR) bacteria, Wastewater, Whole Genome Sequencing (WGS), 16S rRNA gene