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ABSTRACT

Detection of Virulence Gene Profiles of Multi-Drug Resistance (MDR) in Pseudomonas aeruginosa Bacteria in Human.

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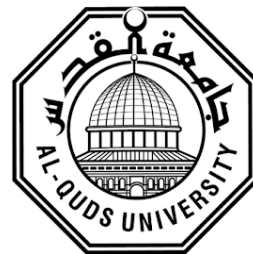
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The spread of opportunistic bacteria *Pseudomonas aeruginosa* in hospitals correlated with several diseases to humans. This bacterium showed high resistance to many antibiotics due to their indiscriminate use, as well as mutations in the pathogenic genes of *Pseudomonas aeruginosa*, which are difficult to treat. *Pseudomonas aeruginosa* is transmitted to humans in hospitals as being special nosocomial bacteria through ventilators, also through food and water contaminated with these bacteria, which causes muscle fatigue, vomiting and nausea. It also weakens the immune system and is more severe in people who suffer from weak immunity, old age and children, and can lead to death. Therefore, scanning virulence genes in *Pseudomonas aeruginosa* helps understand pathogenesis mechanisms.

The main objective of this study was to detect three pathogenic genes in these bacteria: ExoS, Apr, and Pich. Bacteriological samples were collected and detected by the Multiplex PCR mechanism. Results showed that the sizes of genes were: 444bp, 1017bp, and 608bp. The study of the reaction of multiplex polymers to detect genes (ExoS, Apr, Pich) in 32 colonies was provided by Al-Ahli Hospital in Hebron, the percentage of each gene was 95%. In addition to 12 samples provided by the Al-Istishari Hospital in the city of Ramallah, and the percentage of the



presence of each gene in these samples 100%. In the antibiotic examination of *Pseudomonas aeruginosa* of 44 samples, the bacteria had antibiotic resistance, 43% and 31% of the bacterial strains were resistant to Gentamicin and Aztreonam, 27% of which were resistant to Meropenem, Ceftazidime and Ciprofloxacin, 18% of which were resistant to tazobactam and 22.7% of which were resistant to Amikacin.

The minor objective was to identify MDR *Pseudomonas aeruginosa* from clinical isolates. Isolates were evaluated for their antimicrobial susceptibility to seven antibiotics, Meropenem, Ceftazidime, Amikacin, Azteronam, Ciprofloxacin, Gentamicin and Piperacillin-tazobactam. The results also provided a clear picture of bacterial resistance MDR to these antibiotics by 45.45%.

Keywords: *Pseudomonas aeruginosa*, Antibiotic, Resistance, Virulence genes.