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THE RELATIONSHIP BETWEEN SOME VIRULENCE FACTORS AND ANTIBIOTICS RESISTANCE DETERMINANTS IN PATHOGENIC BACTERIA

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The present study was done to scrutinize the possible relation between virulence genes and antimicrobial resistance in some pathogenic bacteria. Considering the fact that the presence of recognized infective determinants among clinical isolates may promote the emergence of infections and persistence of pathogens. A total of 120 bacterial isolates were obtained from College of Science/ University of Al-Kufa. After the maintenance and subculture of these isolates, some phenotype tests were performed which included plate hemolysis, haemagglutination, serum resistance and biofilm formation. Then genotype study was investigated for some virulence genes (biofilm, *FimH* and *Iss*) and antibiotics resistance genes (bla_{AmpC} , bla_{TEM} , bla_{SHV-5} and bla_{CTX-M}) by using PCR technique. The genotype study investigated for three virulence genes and four antibiotics resistance genes. The results of virulence genes indicated that biofilm gene was the most prevalence gene, where appeared in 95% of bacterial isolates followed by *Iss* gene 86.66% and *FimH* gene 85%. bla_{AmpC} and bla_{TEM} were significantly prevalence in all bacterial isolates compare with bla_{SHV-5} and bla_{CTX-M} at $P \leq 0.05$, the percentage of the prevalence of bla_{AmpC} and bla_{TEM} were 93.33 and 71.66, respectively, while the less percentages were observed in bla_{SHV-5} 20% and bla_{CTX-M} 46.66%. The current study showed a strong significant correlation between virulence and antibiotic resistance profile, where the statistical analysis revealed that the Pearson correlation was 0.957 between virulence and antibiotics determinants. The present study demonstrated a positive relationship, the ability of bacterial isolates to possess antibiotics resistance and the prevalence of virulence genes. The establishment of this correlations between resistance and virulence profiles could provide valuable input about the clinical evolution and recurrence rates of different bacterial infection.

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