عنوان مقاله:

Analysis of Nucleotide Sequences Similarity and Protein Prediction of Some Resistance Genes in Escherichia coli Isolated from Iraqi Patients with Urinary Tract Infections

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خلاصه مقاله:

Antibiotic resistance leads to a dramatic increase in the morbidity and mortality caused by infectious diseases. Even though estimates vary widely, the economic cost of antimicrobial-resistant bacteria is on a rise. The current aimed to identify the antimicrobial resistance of Escherichia coli (E. coli). In fact, this study focused on the recent deep-learning methods (sequencing) to investigate E. coli antibiotic resistance and their protein sequences. To evaluate antibiotic resistance, the sequencing method could be considered the method of choice. The E. coli was identified by either specific biochemical tests or polymerase chain reaction (PCR) using the ۱۶S rRNA gene. The results of aadA۱ gene sequences demonstrated ۱۰ nucleic acid substitutions throughout, as compared to the reference NCBI database (MG۳۸۵۰۶۳). Out of the ۱۰ nucleic acid substitutions, ۹ missense effects were observed. While the dfrA۱ gene sequences illustrated ۲۰ nucleic acid substitutions throughout, compared to the reference NCBI database (KY۷۰۶۰۸۰), out of the ۲۰ nucleic acid substitutions, ۸ missense effects were observed. Furthermore, the sul۱ gene sequences displayed ۲۰ nucleic acid substitutions throughout, in comparison with the reference NCBI database (CP۰۶۹۵۶۱), and out of the ۲۰ nucleic acid substitutions, ۱۲ missense effects were detected. The cat۱ gene sequences showed ۱۴ nucleic acid substitutions throughout, compared to the reference NCBI database (NC۰۱۷۶۶۰), and out of the ۱۴ nucleic acid substitutions, ۸ missense effects were observed. The precise point (Missense) mutation in four genes (aadA۱, dfrA۱, sul۱, and cat۱) in the expected sequence is interpreted to be the target site of a site-specific recombination mechanism that led to antibiotics resistance in E. coli isolates.

کلمات کلیدی:

aadA۱, cat۱, dfrA۱, Escherichia coli, NCBI, Resistance genes, Sequencing, sul۱

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