

عنوان مقاله:

Genetic Diversity of ctxB Gene Among Classical O1 and El Tor Strains of *Vibrio cholerae* using High-Resolution Melting Curve Analysis

محل انتشار:

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خلاصه مقاله:

Background & Objective: *Vibrio cholerae* is a natural inhabitant of the environment and causes severe diarrhea ailments (cholera) that affects thousands of people each year worldwide. The most important virulence factors of this pathogen are cholera toxin (cholera toxin CT) and Type IV pili (toxin co-regulated pili TCP), which are encoded within the genome of the filamentous bacteriophage CTX ϕ . In the present study, according to researchers' report on genotypic variations of cholera toxin, we evaluated the sequence of ctxB subunit obtained from 100 strains of patients infected with cholera in Iran. **Methods:** The evaluation of genotype variations of cholera toxin was made by high-resolution melting curve analysis illustrating a single nucleotide change. Then, ctxB gene sequencing was performed. Through this analysis and the sequencing process, two standard samples were studied. **Results:** Using serologic tests, all the strains analyzed in this study were identified to be in O1 serotype. However, there have been differences in sequences of ctxB as some were similar to *V. cholerae* O1 biovar El Tor str. N16961 while others were similar to the genotype of *V. cholerae* ATCC 14035. We did not observe any particular pattern within the process of mutation. **Conclusion:** The analysis of the new samples of ctxB showed that they were potentially different. It seems that these complicated species were affected by a new genetic exchange of El Tor and classic genotypes.

کلمات کلیدی:

ctxB, *Vibrio cholerae*, High-resolution melt analysis, Genotyping Techniques

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