

عنوان مقاله:

Genome Investigation of Brucella melitensis Strains Isolated From Brucellosis Patients in Kuwait

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خلاصه مقاله:

Background: Human brucellosis is present on all inhabited continents with high prevalence in many areas of the world, including Kuwait and the Middle East. To implement proper control measures, the identification and characterization of Brucella species and genotypes are required through a reliable and rapid subtyping method. In previous studies, whole-genome sequencing (WGS) has shown its potential as an epidemiological typing tool. Using WGS data, this study aimed to identify the species, phage sequences, putative antibiotic resistance genes, virulence factors, and genotypes of Brucella melitensis strains isolated from patients in Kuwait and other countries. Methods: Five B. melitensis isolates of Kuwaiti origin and ۳۱ other isolates of B. melitensis originating from ۲۸ countries were analyzed using whole genome-based approaches for genotypic identification and typing. In-silico techniques were used to identify the sequences for phages, antibiotic resistance genes, virulence factors, and genotypes using multilocus sequence typing (MLST) and whole-genome single-nucleotide polymorphism (wgSNP). Results: The analysis of WGS data demonstrated that all five Kuwaiti isolates belonged to the non-vaccine strains of B. melitensis. Furthermore, the data represented the presence of two phage sequences, two antibiotic resistance genes, and ۵۱ virulence factors in Kuwaiti isolates. Eventually, the genotypes of all isolates were identified based on MLST and wgSNP analysis, and wgSNP analysis suggested the possible areas/countries of origin of Kuwaiti isolates. Conclusion: WGS data can be used to characterize Brucella isolates, and molecular techniques can be applied in-silico to rapidly identify and classify Brucella into species and genotypes and trace the possible origin of the isolates.

کلمات کلیدی:

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