

عنوان مقاله:

Determination Brucella vaccine strains of genetic typing with use VNTR-PCR HOOF PRINT

محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

تعداد صفحات اصل مقاله: 1

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خلاصه مقاله:

Introduction and Objectives: The assessment of the genetic stability is one of the essential elements to guarantee the biological quality of the live anti-bacteria vaccines. In this study, genetic patterns in Brucella vaccinal strains were evaluated using VNTR method. **Materials and Methods:** 410 bacterial strains were investigated in this study included B. melitensis Rev. 1, B. abortus S.19 (respectively, 92 & 100 commercially prepared vaccine production lots) and field strains of B. melitensis, B. abortus & B. suis (respectively, I II, 95 & II strains from RVSRIIm culture collection). A reproducibility evaluation was integrated into the protocol by analyzing every sample twice in independent assays (16 parallel PCR reaction for individual sample). The genotypic fingerprints for each isolate was generated from the allelic profile and evaluated by the program ESGEM and all eight loci of that isolate were measured. HOOF Prints based on multi-locus characterization of a variable number, eight base pair, tandem repeat in 8 microsatellite loci which has been named VNTRsII, introduce a survey method for assessment of genetic variation in Brucella strains. **Results:** Vaccinal strains were genetically more homogenous, as Rev. I & S.19 vaccine strains, respectively, clustered 15 & 8 HOOF Prints genotypes. Field strains of B. melitensis and B. abortus, respectively, divided into 88 & 65 genotypes. But they showed less variation in fingerprinting patterns. It seems that HOOF Prints can significantly contribute to epidemiological trace-back analysis of Brucella infections and may advance surveillance and control of human brucellosis. **Conclusion:** The outcome of the present study indicates that genetic patterns could be an essential assay to guarantee the quality and stability Brucella vaccinal strains. The validity of biovars established by classical microbiological methods could not be confirmed by microsatellites loci in assays. It seems that assay can significantly contribute to epidemiological trace-back analysis of Brucella infections and may advance surveillance and control of human brucellosis.

کلمات کلیدی:

VNTR-PCR, Brucella, Genetic pattern, vaccinal strains, IRAN

