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Diversity of virulence genes in *Brucella melitensis* and *Brucella abortus* Detected from Patients with Rheumatoid Arthritis

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Abstract:

The presence of *Brucella melitensis* and *Brucella abortus* genomes were investigated in the synovial fluid (SF) samples from 90 patients with rheumatoid arthritis (RA). DNA extraction and PCR assay were performed for simultaneous identification and discrimination of *B. melitensis* and *B. abortus* from the SF using three specific primers. After gel electrophoresis, the PCR products were confirmed by DNA sequencing. The *cbg*, *omp31*, *manA*, *virB*, and *znuA* virulence genes typing were performed by multiplex-PCR. Of the 90 samples, 14 were positive for *B. melitensis* (n=9; 10%) and *B. abortus* (n=5; 5.5%). The virulotyping of positive samples revealed the presence of all five virulence genes in *B. melitensis*. The *virB*, *cbg*, and *omp31* were detected in all nine samples of *B. melitensis*. In addition, *zhuA* and *manA* were detected in three (60%) and four (80%) samples, respectively, of the *B. abortus*-positive samples. Moreover, a total of 94.2% and 89.2% of the 14 positive samples were also found positive for *manA* and *znuA*, respectively. Our findings revealed that the *Brucella* spp. genomes can be detected in the SF of RA patients by the PCR-based method. We thus suggest that physicians should consider the *Brucella* spp. as indicators of potential RA for the timely diagnosis and treatment of RA.

Key word: *Brucella melitensis*, *Brucella abortus*, Synovial fluid, Rheumatoid arthritis, Virulotyping, PCR

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