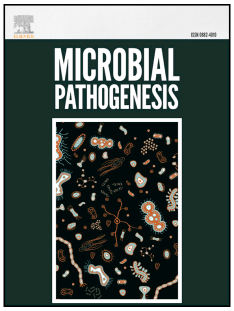

Diversity of virulence genes in *Brucella melitensis* and *Brucella abortus* detected from patients with rheumatoid arthritis

Hossin Ali Rahdar, Reza Golmohammadi, Reza Mirnejad, Ramezan Ali Ataee, Gholam Hossein Alishiri, Hossein kazemian

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

Hossin Ali Rahdar[a, d], Reza Golmohammadi[a*], Reza Mirnejad[a], Ramezan Ali Ataee[b], Gholam Hossein Alishiri[c], Hossein kazemian[d].

[a] Molecular Biology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran
[b] Department of Medical Microbiology, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran.
[c] Department of Rheumatology, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran.
[d] Department of Medical Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.

[*] Corresponding author.
Email: rsr.golmohammadi@bmsu.ac.ir (R. Golmohammadi)

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, man*A, *vir*B, *and znu*A 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 *vir*B, *cbg*, and *om31* were detected in all nine samples of *B. melitensis*. In addition, *zhu*A and *man*A 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