

## Molecular Identification of Virulence Factors Genes (bvfA, VirB ,and Ure) of *Brucella* Isolates in Fars Province, Iran

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**Background & Objectives:** *Brucella*, causative of brucellosis, has some potential virulence factors involved in brucella replication, and brucella's strategies to circumvent the immune response. One of them is the virB gene that encode the type IV secretion system proteins, and that are involved in intracellular replication of organism. *Brucella* virulence factor A (bvfA), and urease (ure) has also been described as being implicated in brucella survival, and virulence in the hosts. The aim of this study was to investigate the frequency of brucella virulence factor genes among brucella isolates from aborted fetuses of sheep, and goats, in Fars province, Iran.

**Methods:** A total of 42 isolates of *Brucella spp.*, isolated from aborted fetuses between 2005-2011 was used in this study. PCR assay was performed in order to detect of virB, bvfA, and ure genes of *Brucella spp.* using specific primers.

**Results:** The frequency of bvfA, virB, and ure genes was 78.50%, 73.80%, and 88.09% among all isolates respectively.

**Conclusion:** The pathogenicity of brucellae is due to its amazing ability to adapt to the environmental conditions encountered intracellularly, and this refer to the existence of virulence factors genes in their genome. The results of the present study showed that most brucella isolates from Iran have virulence factors genes (virB, bvfA, ure ) in their genome, and most *Brucella* isolates had ure genes that has been hypothesized to play a role in the pathogenesis of disease.

**Keywords:** *Brucella*; Virulence Factors; bvfA; VirB; Ure