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Study of *Mycobacterium bovis* genotypes in human and bovine isolates using spoligotyping, MIRUVNTR and RFLP-PCR

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ABSTRACT

Aims and objectives: The aim of this study is to investigate and detect the prevalence of *Mycobacterium bovis* subtypes (*Mycobacterium bovis* subtype *bovis* and *Mycobacterium bovis* subtype *caprae*) in humans and compare the genetic diversity of *Mycobacterium bovis* in humans and cattle with spoligotyping methods, as well as pyrazinamide susceptibility study of subtypes.

Methods: Examining these subtypes with molecular epidemiology techniques is particularly important due to different treatment of *M. bovis* diverse subtypes in humans. Culture tests were performed on clinical samples that were isolated from Lowenstein-Jensen culture medium. Identification tests were performed to differentiate *Mycobacterium bovis* from *Mycobacterium tuberculosis*. DNA was extracted and spoligotyping (spacer oligonucleotide typing) was performed using the DRb and DRa primers.

Results: The results were analyzed with the SPOLDB4 site. PCR-RFLP method of pncA gene was used to evaluate the resistance to pyrazinamide and pncA gene polymorphism.

Conclusions: *Mycobacterium bovis* subtype *bovis* in the Iranian population was reported with a frequency of 0.6% which was below the average of the previous reviews. In this study, all the strains were *M. bovis* subtype *bovis* resistant to pyrazinamide. No *Mycobacterium bovis* subtype *caprae* was detected. The only shared ST between humans and cattle was ST694. *Mycobacterium bovis* subtype *bovis* with ST 595 was reported as human bovis index.

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