



Isolation, molecular identification and genomic pattern of *Mycobacterium bovis* isolates collected from tuberculin-positive cattle in infected farms of Shiraz

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Abstract:

Mycobacterium bovis is the main cause of tuberculosis in cattle. At global scale and also in Iran, the most frequent currently-in-use method in detection of infected cattle is tuberculation.

The present study was aimed to improve our genomic knowledge of *Mycobacterium bovis* population structure in cattle farms of Shiraz. Fifty pathological samples from tuberculin-positive cattle collected from two slaughter-houses at Shiraz were subjected to bacterial culture on glycerinated and pyruvated Lowenstein-Jensen media. Genomic material from culture-positive slopes was extracted and used in PCR-16S rRNA, PCR-IS6110, and PCR-RD typing experiments. All the *M. bovis* isolates were further genotyped using *pvu* II-digested PGRS-RFLP strategy. In bacterial culture, a total of 13 (26%) samples proved to carry live mycobacteria where in PCRs their identity was all shown to be *M. bovis*. Genotype profiling by RFLP-PGRS displayed two patterns with 10 isolates shared a single profile identical to that of *M. bovis* BCG (1173 P2) strain and three holding a different genotype. While higher frequency of a BCG-like *M. bovis* in cattle farms of Shiraz is not surprising as this is a typical characteristic of Iranian *M. bovis* population, we assume detection of a highly similar strain found in our work might indicate local evolution of new *M. bovis* strains in the region or infiltration of such strain(s) through cattle farming activities.

Biography:

Nader Mosavari has completed his DVM at the age of 29 years from Shahid Chamran's (Jundishapur) University and PhD studies from Jundishapur University too. He is head of Tuberculosis and Glanders department at Razi Vaccine and Serum Research institute, Iran. He has published more than 59 papers in reputed journals. He could isolate and identify *Burkholderia malle* from tiger at Tehran zoo.



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