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Application of MLVA-15 genotyping for typing of *Brucella abortus* isolates from India

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Brucellosis is considered as one of the most widespread zoonosis in the world. For complete eradication of infection from herds, strain-specific identification is essential to know the source of infection. In the present study, MLVA-15 genotyping scheme was applied to differentiate the field strains of *B. abortus*. A total of 13 *B. abortus* strains along with 4 representative reference strains (*B. abortus* 544 (ATCC 23448), *B. abortus* strains S19, S99 and 1119-R) were taken from the repository of the Brucella Laboratory, Div. of VPH, IVRI, Izatnagar. For MLVA-15 genotyping, 15 sets of primers (8 minisatellites and 7 microsatellites markers) were used for the amplification of 15 VNTR loci in all the strains that resulted in 13 different genotypes. Of these, 10 profiles were unique while remaining 3 profiles were shared by at least 2 strains. In *B. abortus*, Bruce 6, 8, 11, 21, 42, 43, 45 and 55 were found to be most conserved with no length polymorphism. Bruce 4, 9, 12, 16 and 18 showed moderate length polymorphism. Bruce 7 showed significant length polymorphism whereas highest length polymorphism was seen at locus Bruce 30. The dendrogram based on MLVA data was generated using the UPGMA clustering method implemented by START vs. 1.0.5 software. Through clustering analysis using UPGMA, the *B. abortus* isolates were grouped in 6 clusters showing a 90% similarity. Allelic diversity for each of the locus was calculated using HGD index. In the present study, the MLVA-15 genotyping clearly discriminated Indian field isolates of *Brucella abortus*.

Biography

Gita Kumari has completed her PhD from Division of Veterinary Public Health, Indian Veterinary Research Institute, India. She has published 11 papers in reputed journals. Presently she is working as Touring Veterinary Officer in Govt. of Animal and Fisheries Resources, Bihar, India.

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