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Genetic characterization of *Brucella melitensis* and *Brucella abortus* geographical clusters in Italy

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Abstract

The genetic diversity of *Brucellamelitensis* and *Brucellaabortus* genotypes isolated from 201cattle and sheep in 8 regions of Southern Italy in 2011 was determined using 16 VNTR loci in a MLVA-16 methodology. The existence of possible genetic clusters was verified through a hierarchical cluster analysis based on 'single link' which is closely related to the minimal spanning tree. The Hammington weighted distance matrix was adopted in the analysis. All calculations were performed using R and the additional lybrariesphangorn.For a number of clusters ranging from 2 to 15 the average silhouette width has been calculated. The number of clusters adopted was identified according to the maximum average silhouette width. For *Brucellaabortus* and *Brucellamelitensis* 6 and 11 genetic clusters were respectively identified. Three out of six *B. abortus* clusters include 96.7% of all *B. abortus* isolates and they are clearly geographically separated, highlighting known epidemiological links among them. *B. melitensis* genotypes resulted more heterogeneous and the three more representative genetic clusters include 79.7% of all *B. melitensis* isolates. A clear geographical clusterization of genotypes is recognizable only for one cluster, whereas the others are more widespread across Southern Italy. The genetic characterization of *Brucella* strains isolated from animals may be a useful tool for better understanding the epidemiology and dissemination patterns of this pathogen through host populations.

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