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**Development of a Multiple-Locus Variable number of tandem repeat Analysis (MLVA) for Chinese *Francisella tularensis* and its application to some strains**

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**Objective:** To develop Multiple-Locus Variable number of tandem repeat Analysis for Chinese *Francisella tularensis* (*F. tularensis*) and study the genotypes of some Chinese strains.

**Methods:** Primers sequences of 25 loci obtained from GPMS (Genomes, Polymorphism and Mini-satellites) database, the method was optimized and evaluated. Using established method to explore the genetic diversity within Chinese strains.

**Results:** 20 strains used for the development of the method showed good results. The 25 loci displayed repeat sizes from 2 bp (M-25) to 23 bp (M-23) in length. 6 loci showed some genetic diversity, among which M-3 locus containing seven genotypes had highest diversity value (0.91). Based on the results from MLVA, phylogenetic analysis was done. It revealed 5 groups among Chinese strains, i.e. the group of Tibet, Xinjiang, Heilongjiang, Inner Mongolia and vaccine, which was concordant with the distribution pattern of tularemia in China.

**Conclusion:** The MLVA described in this report was proved to be a powerful tool for Chinese *F. tularensis*, the strains used in the study showed high genetic diversity and conservation among different loci.