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Genotyping of the Health Protection Agency *Francisella* strain collection

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Aim: The Health Protection Agency (HPA) *Francisella* strain collection consists of 17 *Francisella* isolates collected from North America and Europe over the last 56 years. The aim of this study was to investigate the genotype of the isolates in the *Francisella* strain collection.

Methods: DNA was extracted from the 17 isolates in the *Francisella* strain collection. RD1 analysis was carried out as described by Broekhuijsen *et al*, 2003 to discriminate between the four subspecies. Multi-locus variable-number tandem repeat analysis (MLVA) has been used to further investigate their phylogeny in relation to other isolated strains.

Results: The isolates have been identified to subspecies level using RD1 analysis. MLVA analysis has allowed the genetic relationships to be further broken down, and a comparison to be made with other known characterized strains.

Conclusions: The collection contains isolates belonging to *F. tularensis* subspecies *tularensis*, *F. tularensis* subspecies *holarctica* and *F. tularensis* subspecies *novicida*. The identified subspecies and the locations they were isolated from are in agreement with the current geographical distribution models of *Francisella tularensis*.