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Application of multiple-locus variable number tandem repeat analysis (MLVA) for subtyping of Swedish isolates of *Francisella tularensis*

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Tularaemia is a zoonotic disease caused by the gram-negative coccobacillus *Francisella tularensis*. Its wide distribution in Sweden poses a challenge for understanding the transmission, ecology and epidemiology of the disease. The aim of this study was to evaluate MLVA as a typing system for practical use in epidemiological investigation i.e. the possibility to use molecular epidemiology to predict where patients have been infected. MLVA based on five previously described VNTR:s was applied on *F. tularensis* isolates collected during 1995-2007 from 95 Swedish patients with ulceroglandular tularaemia. MLVA types were compared to detailed epidemiological information including map locations.