

## Genetic diversity of Iranian isolates of *Burkholderia mallei* by PFGE and PCR-MLVA

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Glanders is a contagious and fatal zoonotic disease seen more often in equines. Causative agent of the disease is *Burkholderia mallei*. In last couple of years, researchers have been looking for raising awareness of the epidemiology of the disease by using modern and sophisticated molecular biology techniques. In order to analyze genetic diversity in Iranian isolates of *B. mallei*, five wild isolates (Tiger, Semirum, Kordan, Oshnavieh and Tehran) and one product strain (*B. mallei* 325) were comparatively examined by PFGE and PCR-MLVA. For MLVA two variable number of tandem repeats (VNTR) loci of VNTR1217 and VNTR13 were employed. The amplification products of MLVA PCRs were sequenced to guaranty accuracy of sizing and nucleotide structure. Consequently, in PFGE three profiles were detected with the

first specific to *B. mallei* 325 and the second represented by *B. mallei* Semirum. The other three strains shared the third type. The PFGE pattern of the 325 strain was characteristically different from those of the Iranian isolates. In MLVA, at VNTR13 three alleles were detected where *B. mallei* 325 appeared to be clearly different from other four examined strains. Furthermore, at VNTR1217 two alleles were observed leading to a total of four combinational VNTR profiles between the five strains. Findings of this study back the assumption that if an appropriate panel of VNTR loci are selected, MLVA typing can provide the capability required for epidemiologic investigations. This is a much needed requirement specifically in the Iranian environment where mini outbreaks of glanders take place every year.