

Original Paper

## Genomic structure of *Burkholderia mallei* Razi 325, the strain used for industrial production of Mallein in Iran

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### Abstract

**Background and Objective:** Iran remains a major stronghold for glanders in the Middle East. In Iran, the non-indigenous *Burkholderia mallei* Razi 325 strain is used in manufacturing of the mallein, required for malleination of animals. Multi Locus Variable number tandem repeat analysis is currently the standard globally accepted genotyping system for *Burkholderia mallei*. This study was done to survey the genomic structure of *Burkholderia mallei* Razi 325, the strain used for industrial production of Mallein.

**Methods:** In this descriptive study, a MLVA genotyping system with 4 previously-characterized loci VNTR140, VNTR1367, VNTR2065, VNTR2971 along with two new loci of VNTR24, VNTR41 was used.

**Results:** Optimization of PCRs resulted in a single protocol that enabled simultaneous amplification of all the six loci. Sequencing of PCR products revealed there were 2, 3, 12, 6, 1 and 2 copies of the unit repeat hold in the genome of the *Burkholderia mallei* Razi 325 strain. This observation was extended to include the already-whole genome sequenced Chinese *Burkholderia mallei* ATCC 23344 and *Burkholderia mallei* BMQ and also *Burkholderia mallei* SAVP1 strains.

**Conclusion:** The *Burkholderia mallei* Razi 325 strain is distinguishable from the other three strains through MLVA genotyping method.

**Keywords:** Glanders, Mallein, *Burkholderia mallei* Razi 325, MLVA genotyping, VNTR

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