



Draft Genome Sequences of Two Clinical Isolates of *Burkholderia mallei* Obtained from Nasal Swabs of Glandersous Equines in India

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ABSTRACT *Burkholderia mallei* is a Gram-negative coccobacillus which causes glanders—a fatal disease of equines that may occasionally be transmitted to humans. Several cases of outbreaks have been reported from India since 2006. This paper presents draft genome sequences of two *B. mallei* strains isolated from equines affected by glanders in India.

Glanders is a fatal and contagious disease of equines caused by the bacterium *Burkholderia mallei*. The disease in equines is characterized by chronic suppurative lesions of skin and mucous membrane, pneumonia, and septicemia (http://www.oie.int/index.php?id=169&L=0&htmfile=chapitre_glanders.htm). Asymptomatic carrier horses are the only natural reservoirs of *B. mallei* and the source of infection. It is a notifiable disease to the World Organization of Animal Health (OIE) and the organism is classified as category B select agents by the U.S. Centers for Disease Control and Prevention (1). Unprecedented emergence of glanders in several countries throughout the Middle East, Southern Asia, parts of Africa, and South America were reported in the past decade (2). Following the re-emergence of glanders in northern states of India during 2006, the disease has spread to several states of India over the past decade affecting hundreds of equines (3). Here, we present the draft genome sequences of two *B. mallei* strains 3076HP_India and 3712UP_India, which were isolated from clinical samples (nasal swab) of a mule and a mare in 2013 and 2015, respectively.

Genomic DNA was extracted from stationary phase *B. mallei* culture using the Gene Jet DNA purification kit (Thermo Scientific, USA). The bacterial genome was sequenced on an Illumina HiSeq 2500 using 2 × 125 bp chemistry at Eurofins Genomics (India). The raw reads generated were filtered using Trimmomatic v0.35 with quality value QV > 30. The filtered high-quality reads were assembled using Velvet v1.2.10 (4). Genes were predicted from the assembled sequences using Prodigal v2.6.3 with default parameters (5). Functional annotation of the genes was performed using NCBI BLASTx-2.3.0+ stand alone tool using the nonredundant (NR) protein database (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastx&PAGE_TYPE=BlastSearch&BLAST_SPEC=&LINK_LOC=blasttab&LAST_PAGE=blastn). The assembled genomes were aligned to the *B. mallei* ATCC 23344 reference genome using MUMmer v3.0 with default parameters and a circos plot was generated for graphical representation using Circos v0.69.1 (6, 7).

The high-quality data thus obtained were 2.2 GB with 8,810,805 reads. Genome assembly generated 250 and 257 contigs (215 scaffolds) with an N_{50} of 36,813 bp for the *B. mallei* strains 3076_HP and 3712_UP, respectively. The assembled genome was 5.6 Mb in size with 67.07% G+C content. A total number of 4,713 genes were predicted

Received 23 January 2017 Accepted 24 January 2017 Published 6 April 2017

Citation Singha H, Malik P, Saini S, Khurana SK, Elschner MC, Mertens K, Barth SA, Tripathi BN, Singh RK. 2017. Draft genome sequences of two clinical isolates of *Burkholderia mallei* obtained from nasal swabs of glandersous equines in India. *Genome Announc* 5:e00063-17. <https://doi.org/10.1128/genomeA.00063-17>.

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with an average gene size of 987 bp. In annotation, 4,660 genes found hits while 53 genes were not annotated against the NR database. More genomic data of clinical *B. mallei* isolates from different geographical locations may be useful in providing insight into the molecular evolution and epidemiology.

Accession number(s). This whole-genome shotgun sequencing project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [MDTH00000000](#) and [MDJV00000000](#). The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

We thank the Indian Council of Agricultural Research (ICAR), New Delhi, India and the World Organization of Animal Health (OIE), Paris, France for financial support to carry out this work.

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