BAC042. THE DRAFT GENOME SEQUENCE OF *Burkholderia mallei* BAC 86/19 ISOLATED FROM A HORSE WITH GLANDERS IN BRAZIL

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Burkholderia mallei is a gram-negative bacterium that causes glanders in equids such as horses, mules, and donkeys. Apart from being a significant concern for animal health, it is also a potential bioterrorism agent. Despite the high clonality of the organism, recent studies using whole-genome sequencing have identified genetic markers that can improve strain differentiation and epidemiological studies of *B. mallei* However, the global distribution and genetic diversity of the pathogen have not been extensively characterized. In this context, the objective was obtain the genome sequencing of Brazilian strain *B. mallei* from horse with positive serology for glanders to provide information for better understand the pathogen and its epidemiology. The Brazilian strain *B. mallei* was isolated from trachea tissue cultivation of the a young mare from Tatuí, São Paulo that was found to have a positive result in both the complement fixation screening test (cold procedure) and Western blot, which were performed in an official laboratory according to the Brazilian Equine Health Program. The positive culture obtained was confirmed by biochemical tests, PCR (fliP-IS407) and MALDI-TOF analyzes. The whole genome sequencing of this Brazilian strain *B.mallei* was conducted at the NGS multi-user platform. The WGS revealed a genome size of 5.51 Mb with a GC content of 65.8%, 5,871 genes (including 4 rRNA and 53 tRNA genes), and 5,583 coding DNA sequences (CDSs). Additionally, 227 predicted pseudogenes were detected. In silico analysis of different genomic loci that allow differentiation with Burkholderia pseudomallei confirmed the identity of the isolate as *B. mallei*, in addition to the characteristic genome size. The BAC 86/19 strain was identified as lineage 3, sublineage 2, which includes other strains from Brazil, India, and Iran. The genome sequencing of this strain provides valuable information that can be used to better understand the pathogen and its epidemiology, as well as to develop diagnostic tools for glanders.

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