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## GENOME ANNOUNCEMENTS

### High-Redundancy Draft Sequencing of 15 Clinical and Environmental *Burkholderia* Strains<sup>∇</sup>

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**The Gram-negative *Burkholderia* genus includes several species of intracellular bacterial pathogens that pose substantial risk to humans. In this study, we have generated draft genome sequences of 15 strains of *B. oklahomensis*, *B. pseudomallei*, *B. thailandensis*, and *B. ubonensis* to an average sequence read coverage of 25- to 40-fold.**

The Gram-negative *Burkholderia* genus includes several species of intracellular bacterial pathogens that pose substantial risk to humans. The high virulence of the *B. pseudomallei*/*B. mallei* species by the respiratory route and the fact that the bacteria can be aerosolized has caused them to be considered bioterrorists (1); both *B. pseudomallei* and *B. mallei* have been designated category B select agents by the Centers for Disease Control and Prevention (CDC) (18).

Genomes of 15 strains of *B. oklahomensis*, *B. pseudomallei*, *B. thailandensis*, and *B. ubonensis* were sequenced using the Roche/454 Sequencing GS-20 instrument (13). The average read length obtained from the 15 libraries was 97 nucleotides (nt). Raw sequence data assembled into 450 to 1,000 contigs of more than 1,000 nt per genome, with an average redundancy of coverage of 25 to 40 reads per base. The GC contents of the nucleotide sequences of the strains were 63 to 67%.

High-redundancy draft genome sequencing is an economic way of assessing species diversity and is used to screen strains for subsequent genome sequence completion. The data generated in this project have already proved useful in helping to

identify conserved vaccine targets (2), have been incorporated into global comparative genomics analyses of the *Burkholderia* genus (16, 20), and have been used for identification of candidate loci for multilocus variable-number tandem-repeat typing schemes (19).

**Brief strain descriptions.** *B. pseudomallei* strain B7210 is a human isolate from Australia, obtained in a case of empyema infection in 1970 (4, 6). Strain BCC 215 is an isolate obtained in a fatal case of septicemic melioidosis in a family located in rural northeastern Brazil. Three of four affected children, all siblings, died. An indirect hemagglutination assay (IHA) indicated seroconversion subsequent to clinical recovery for the one survivor (17). DM98, a strain with a persistently mucoid phenotype, was isolated in a single case of septicemic melioidosis in tropical northern Australia and was obtained from a blood culture (8). NCTC 13177 (also known as BCC 6) was isolated in an outbreak of fatal septicemic melioidosis cases in northwestern Australia that were linked to a contaminated water supply (9–11). PHLS 9 (CDC2002721637) is a human isolate from Pakistan, obtained in 1988 (4, 6). PHLS 14 was isolated from a monkey liver in the Philippines in 1990 (4, 6). PHLS 91 is a sheep lung isolate from Australia, obtained in 1984 (4, 6). PHLS 112 is a human isolate obtained from north-east Thailand in 1992 (4, 6). Strain 7894 is a human isolate obtained from Ecuador in 1962 (4, 6).

*B. oklahomensis* strain C6786 was isolated from an infected human in Oklahoma (7, 14). E0147 was isolated in a case of human infection in Georgia (7, 15).

*B. thailandensis* Bt4 is an environmental isolate from northern Australia, obtained during an investigation of *Burkholderia* ecology in potable water supply systems (12). MSMB43 is an arabinose-assimilating environmental strain from a borehole near Darwin, Northern Territories, Australia, and falls into an intermediate phylogenetic clade relative to *B. pseudomallei* and

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*B. thailandensis* (3). CDC3015869 (TXDOH) was isolated from the blood of a 2-year-old boy infected after a near-drowning incident (5).

*B. ubonensis* strain Bu was isolated from a rhizosphere sample from a mine site in northern Australia (12).

**Nucleotide sequence accession numbers.** The sequences determined in this study have been deposited in the National Center for Biotechnology Information (NCBI) RefSeq database under the following accession numbers: for *B. pseudomallei* strains B7210, BCC 215, DM98, NCTC 13177, PHLS 9, PHLS 14, PHLS 91, PHLS 112, and 7894, NZ\_ABBN00000000, NZ\_ABBR00000000, NZ\_ABBI00000000, NZ\_ABBQ00000000, NZ\_ABBL00000000, NZ\_ABBJ00000000, NZ\_ABBK00000000, NZ\_ABBP00000000, and NZ\_ABBO00000000, respectively; for *B. oklahomensis* strains C6786 and E0147, NZ\_ABBG00000000 and NZ\_ABBF00000000; for *B. thailandensis* strains Bt4, MSMB43, and CDC3015869, NZ\_ABBH00000000, NZ\_ABBM00000000, and NZ\_ABBD00000000, respectively; and for *B. ubonensis* strain Bu, NZ\_ABBE00000000.

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