JB Journals.ASM.org

GENOME ANNOUNCEMENT

First Genome Sequence of a *Burkholderia pseudomallei* Isolate in China, Strain BPC006, Obtained from a Melioidosis Patient in Hainan

Yao Fang,[a] Yong Huang,[b] Qian Li,[a] Hai Chen,[c] Zhen Yao,[c] Jin Pan,[d] Jiang Gu,[a] Bin Tang,[a] Hai-guang Wang,[a] Bo Yu,[a] Yi-gang Tong,[b] Quan-ming Zou,[a] and Xu-hu Mao[a]

Department of Clinical Microbiology and Immunology, College of Medical Laboratory, National Engineer Research Center for Immunization Products, Third Military Medical University, Chongqing, China[a]; State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing, China[b]; Sanya People's Hospital of Hainan Province, Sanya, China[c]; and Department of Clinical Hematology, Third Military Medical University, Chongqing, China[d]

Melioidosis, caused by *Burkholderia pseudomallei*, is considered to be endemic to Northern Australia and Southeast Asia, with high mortality and relapse rates, regardless of powerful antibiotic therapy. Here we report the first genome sequence of *Burkholderia pseudomallei* strain BPC006, obtained from a melioidosis patient in Hainan, China. The genome sizes of the 2 chromosomes were determined to be 4,001,777 bp and 3,153,284 bp.

Burkholderia pseudomallei is an opportunistic pathogen which can cause a tropical disease, melioidosis, affecting almost all organs (6). *B. pseudomallei* can be found widespread in water and soil in regions where it is endemic, such as Hainan, Guangdong, and Guangxi in China (3, 5). It was also classified as a category B pathogen by the CDC in 2006. However, little is known about the *B. pseudomallei* strain without molecular epidemiological or clinical data in China. Here we first report the complete genome of *B. pseudomallei* strain BPC006, an isolate from a melioidosis patient in Hainan, China.

B. pseudomallei strain BPC006 was identified and determined as highly pathogenic by the bioMérieux system, with 95% probability. The whole-genome shotgun sequencing was then performed with 454 Titanium. In total, 494,449 reads with a mean length of 325 bp were generated. Newbler 2.3 was carried out to perform the assembly of raw sequencing reads. Next, 480,015 reads (97.1% of the total) were assembled into 8 contigs and 13 contigs, with a length of 3,997,601 bp and 3,138,777 bp in chromosome I (BPC006_1) and chromosome II (BPC006_2), respectively. The order of contigs was determined by alignment with the published genome sequence of *B. pseudomallei* strain 1106a (GenBank accession numbers CP000572 and CP000573). Gaps between contigs were closed by local assembly and sequencing PCR products using an ABI 3730 capillary sequencer.

B. pseudomallei has a large chromosome and a small chromosome. BPC006_1 has 4,001,777 bp, with a 68.0% G+C content, and BPC006_2 has 3,153,284 bp, with a 68.5% G+C content. The annotation was performed using the Xbase annotation server (2) and RAST server (1). BPC006_1 has 4,118 coding sequences (CDSs), including 4,057 protein-coding genes, 52 tRNA genes, 3 16S rRNA genes, 3 23S rRNA genes, and 3 5S rRNA genes, which cover 87.05% of the chromosome. Meanwhile, BPC006_2 has 3,125 coding sequences, including 3,115 protein-coding genes, 7 tRNA genes, 1 16S rRNA gene, 1 23S rRNA gene, and 1 5S rRNA gene, which cover 87.55% of the chromosome.

The comparison analysis revealed the highest homology between *B. pseudomallei* strain 1106a and strain BPC006. Compared with *B. pseudomallei* 1106a, BPC006_1 has a deletion of 14 CDSs between positions 80816 and 81463 and a mutation of 10 CDSs between positions 3800125 and 3819938. In addition, a 47.6-kb lysogenic insertion within 58 CDSs occurs on BPC006_1 and a 59.6-kb lysogenic insertion within 79 CDSs occurs on BPC006_2. Among those CDSs, phage-related products from other *Burkholderia* species (like *B. pseudomallei* strain 1026b, *B. pseudomallei* strain 112, and *B. pseudomallei* strain 9) were largely found, revealing important roles of lysogenic phage-mediated insertion and gene transfer within different species. Such innovation strategy would be helpful for deep analysis of evolution and mutation of the first Chinese *B. pseudomallei* strain and for understanding the origin of the prevalent pathogen.

The complete genome sequencing vividly shows the features of *B. pseudomallei* strain BPC006, which is a key to further research into *B. pseudomallei* in China and enriches its molecular epidemiological documentation. Deep analysis of the complete genome would be helpful for us in understanding the evolution of the bacterium and its adaptation to the environment, such as high temperatures and antibiotics (4).

Nucleotide sequence accession numbers. The genome sequences of *B. pseudomallei* strain BPC006 have been deposited in the GenBank database under the accession numbers CP003781 and CP003782.

ACKNOWLEDGMENTS

This work was supported by the Military Twelfth Five-Year Plan of Major Scientific Research Projects (project no. AWS11J011-04).

We thank Xiaoping An (Beijing Institute of Microbiology and Epidemiology at Beijing) for technical assistance with sequencing.

REFERENCES

1. **Aziz RK, et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9**:75.

Received 29 August 2012 **Accepted** 10 September 2012

Address correspondence to Xu-hu Mao, mxh95xy@tom.com.

doi:10.1128/JB.01577-12

2. **Chaudhuri RR, Pallen MJ.** 2006. xBASE, a collection of online databases for bacterial comparative genomics. Nucleic Acids Res. **34**:D335–D337.
3. **Currie BJ, Dance DA, Cheng AC.** 2008. The global distribution of Burkholderia pseudomallei and melioidosis: an update. Trans. R. Soc. Trop. Med. Hyg. **102**(Suppl 1):S1–S4.
4. **Holden MT, et al.** 2004. Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. Proc. Natl. Acad. Sci. U. S. A. **101**: 14240–14245.
5. **Ma G, et al.** 2010. Prevalence of Burkholderia pseudomallei in Guangxi, China. Epidemiol. Infect. **138**:37–39.
6. **Wiersinga WJ, et al.** 2006. Melioidosis: insights into the pathogenicity of Burkholderia pseudomallei. Nat. Rev. Microbiol. **4**:272–282.