

# Draft Genome Sequence of *Catabacter hongkongensis* Type Strain HKU16<sup>T</sup>, Isolated from a Patient with Bacteremia and Intestinal Obstruction

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**We report the draft genome sequence of *Catabacter hongkongensis*, a catalase-positive bacterium which causes bacteremia with high mortality. The 3.2-Mb genome contains 3,161 protein coding sequences, including putative catalase and motility-related proteins, and antibiotic resistance genes, which could be important for its virulence and adaptation to diverse environments.**

Received 20 April 2015 Accepted 27 April 2015 Published 21 May 2015

**Citation** Lau SKP, Teng JLL, Huang Y, Curreem SOT, Tsui SKW, Woo PCY. 2015. Draft genome sequence of *Catabacter hongkongensis* type strain HKU16<sup>T</sup>, isolated from a patient with bacteremia and intestinal obstruction. *Genome Announc* 3(3):e00531-15. doi:10.1128/genomeA.00531-15.

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*Catabacter hongkongensis* was first isolated in 2007 from the blood cultures of four patients from Hong Kong and Canada (1). It is a motile, catalase-positive, strictly anaerobic, nonsporulating, Gram-positive coccobacillus, belonging to the family, *Catabacteriaceae* (1). Several reports of *C. hongkongensis* bacteremia have been subsequently described in Hong Kong, France, and New Zealand (2–4). The source of bacteremia was most likely the gut, since most cases were associated with intestinal or biliary sepsis such as perforated bowel and acute appendicitis. *C. hongkongensis* bacteremia was often associated with complications and high mortality especially in patients with advanced malignancies. In addition to human infections, 16S rDNA sequences related to *C. hongkongensis* have been detected in various environmental samples worldwide, including urban aerosols, mangrove sediment and rice paddy field soil (5–7), as well as fecal microflora of a dugong (*Dugong dugong*) (8). To better understand the biology and pathogenesis of this previously ignored pathogen, we present the draft genome of the type strain, HKU16<sup>T</sup> (= CCUG 54229<sup>T</sup> = JCM 17853<sup>T</sup>), isolated from the blood culture of a patient with intestinal obstruction and secondary sepsis in Hong Kong (1).

The isolate was grown on blood agar at 37°C under anaerobic conditions for 5 days, and genomic DNA was isolated using a genomic DNA purification kit (QIAGEN, Hilden, Germany) as described previously (9, 10). Purified genomic DNA was sequenced by 151-bp paired-end reads with a mean library size of 350 bp. *De novo* assembly was performed using MIRA4 ([http://www.chevreux.org/projects\\_mira.html](http://www.chevreux.org/projects_mira.html)). Prediction of protein coding regions and automatic functional annotation was performed using the Rapid Annotations using Subsystem Technology (RAST) server (11). Antibiotic resistomes were identified using the Antibiotic Resistance Genes Database (12). BLASTn comparisons were run using BLAST+ with an E-value cutoff of 10.0. In addition, manual annotation was performed on putative virulence and

antibiotic resistance genes by protein domain predictions and multiple sequence alignments with orthologous genes.

A total of 1,500,000 reads were produced, resulting in an estimated 40-fold coverage of the genome. The average G+C content was 48.5%. Subsequent assembly resulted in a final draft genome of 3.2 Mb in 142 contigs, of which 70 were >500 bp, representing 99.3% of total sequence information, with the largest contig being 427,854 bp. A total of 3,161 protein coding sequences (CDSs) and 57 RNA genes were predicted. Strikingly, 69 protein features were identified in the category “Virulence, disease and defense.” These include a gene encoding putative catalase protein, which may account for the positive catalase reaction and represent a potential virulence factor. Potential genes encoding bile salt hydrolase and resistance to heavy metals, arsenic, and other toxic compounds were found, which may be important for its survival in the human gut and diverse environments. Antibiotics resistance genes, including  $\beta$ -lactamase, multidrug resistance efflux pumps, and tetracycline resistance proteins, were present, which may explain its variable susceptibility to  $\beta$ -lactams (1, 2). Moreover, 59 proteins were identified in the category “Motility and chemotaxis,” which is consistent with its motile behavior and presence of flagella in flagella stain and electron microscopy of HKU16<sup>T</sup> (1).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [LAYJ000000000](https://www.ncbi.nlm.nih.gov/nuccore/LAYJ000000000). The version described in this paper is version LAYJ01000000.

## ACKNOWLEDGMENTS

We thank members of the Centre for Genomic Sciences, The University of Hong Kong, for their technical support in genome sequencing.

This work was partly supported by the Committee for Research and Conference Grant, and Strategic Research Theme Fund, The University of Hong Kong; Croucher Senior Medical Research Fellowships; and donations from Eunice Lam for the study of emerging infectious diseases.

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