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Data in Brief

Draft genome sequence of a multidrug-resistant *Chryseobacterium indologenes* isolate from Malaysia

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ABSTRACT

Chryseobacterium indologenes is an emerging pathogen which poses a threat in clinical healthcare setting due to its multidrug-resistant phenotype and its common association with nosocomial infections. Here, we report the draft genome of a multidrug-resistant *C. indologenes* CI_885 isolated in 2014 from Malaysia. The 908,704-kb genome harbors a repertoire of putative antibiotic resistance determinants which may elucidate the molecular basis and underlying mechanisms of its resistant to various classes of antibiotics. The genome sequence has been deposited in DDBJ/EMBL/GenBank under the accession number LJOD00000000.

Specifications	
Organism/cell line/tissue	*Chryseobacterium indologenes*
Strain(s)	CI_885
Sequencer or array type	Illumina Hi-Seq
Data format	analyzed
Experimental factors	genomic sequence of pure microbial culture
Experimental features	genome sequencing and annotation of multidrug-resistant *Chryseobacterium indologenes*
Consent	not applicable
Sample source location	wound swab, Malaysia

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/PRJNA295461.

2. Experimental design, materials and methods

Chryseobacterium indologenes is a member of the family Flavobacteriaceae and the Gram-negative rod-shaped bacterium can be found in diverse habitats including soils, plants and water [1]. Although *C. indologenes* is not a part of the human microflora, this bacterium is the most commonly encountered flavobacterial species in hospital settings and has been implicated in a myriad of nosocomial infections such as meningitis, bacteremia, sepsis, pneumonia as well as biliary tract and intra-abdominal infections [2–7]. *C. indologenes* has emerged as an important nosocomial pathogen as it causes difficult-to-treat infections due to its resident or chromosomally-encoded IND-type metallo-β-lactamase which confers the species with intrinsic resistance against most β-lactams including carbapenems [8].

In this study, we present the draft genome of a *C. indologenes* strain CI_885 isolated from a wound swab in July 2014. *C. indologenes* CI_885 was found to be resistant to clinically used antibiotics including extended-spectrum penicillins, 1st to 4th generations of cephalosporins, aztreonam, ertapenem, doripenem and meropenem but remained susceptible to imipenem, quinolones, tigecycline and trimethoprim/sulfamethoxazole. High quality genomic DNA was purified from broth culture of *C. indologenes* CI_885 using a MasterPure DNA Purification Kit (Epicentre Biotechnologies, USA) and the whole genome sequencing was performed using an Illumina HiSeq 2000 (Illumina, USA). A total of 4,410,078 paired-end reads were generated, which were subsequently trimmed and assembled using CLC Genomic workbench version 7.5 (CLC Bio, Denmark). The draft genome was annotated with Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) via NCBI and Rapid Annotations using Subsystems Technology (RAST) [9] server.

The assembled draft genome of *C. indologenes* CI_885 comprised of 908,704 bp with a GC content of 38.23% and an average 79.48–fold genome coverage was obtained. The genome contains 3 rRNAs and 62

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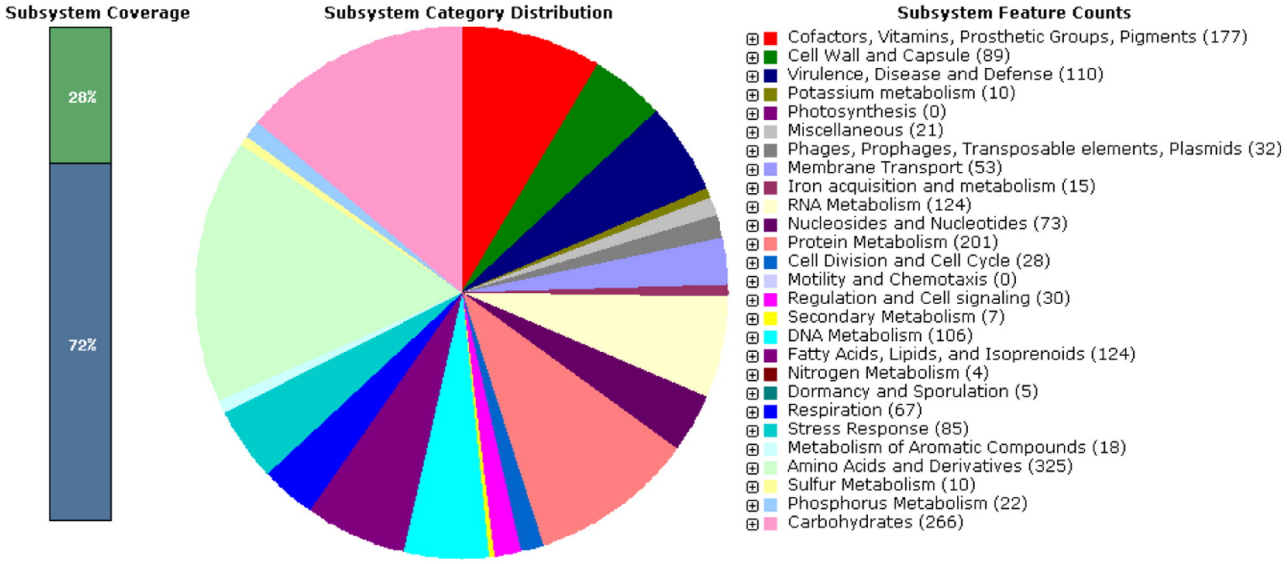

Fig. 1. Subsystem distribution of *C. indologenes* CI_885 (based on RAST annotation server).

tRNAs as predicted by PGAAP. In total, 4644 coding genes in 356 subsystems were functionally annotated by RAST (Fig. 1). Genomic analysis revealed that *C. indologenes* CI_885 possessed a new variant of resident IND-type metallo-β-lactamase gene which shared 78–86% amino acid identity with existing IND-1 to IND-15. In addition to beta-lactamases and aminoglycoside adenylyltransferase, evidences of efflux-pump-mediated resistance to the antibiotics were also found. *C. indologenes* CI_885 is also resistant to toxic compounds due to the presence of determinants encoding resistance to arsenic as well as heavy metals such as copper and zinc. Several iron acquisition genes, *Mycobacterium* derived pathogenesis-related operons and internalin-like protein synthesis genes that may play a role in the pathogenesis of chryseobacterial infections were detected in this strain. Information derived from a deeper analysis of the draft genome will further shed light on the physiology, resistance mechanisms and virulence of this emerging pathogen.

3. Nucleotide sequence accession number

The genome sequence of *C. indologenes* CI_885 has been deposited in DDBJ/EMBL/GenBank under the accession number LJOD00000000. The version described in this paper is the first version, LJOD01000000.

Conflict of interest

The authors declare that there is no conflict of interests on the work published in this paper.

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