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Genome Announcements

Draft genome sequence of a multidrug-resistant beta-lactamase OXA-357-producing *Acinetobacter pittii* ST865 clinical isolate from China

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ABSTRACT

Worldwide increasing emergence of carbapenem-resistant *Acinetobacter* spp. has rendered the limited availability of effective antimicrobial agents and has become a major public health concern. In this study, we report the draft genome sequence of *A. pittii* TCM156, a multidrug-resistant isolate that harbored the $bla_{OXA-357}$ gene. The genome sequence was further analyzed by various bioinformatics methods. The genome size was estimated to be 3,807,313 bp with 3508 predicted coding regions and G + C content is 38.7%. These findings have raised awareness of the possible emergence of OXA-type enzyme-producing *A. pittii* isolate in China.

Acinetobacter pittii, formerly named *Acinetobacter genomic species* (*gen. sp.*) 3, is frequently associated with hospital-acquired infections and outbreaks that poses a particular concern due to its ability to acquire multidrug resistance to a wide range of antibiotics.[1] Carbapenems resistant *Acinetobacter* spp. isolates have been widely implicated in nosocomial infections and have also become an ongoing public health threat of global dimensions.[2] The resistance rates to carbapenems among *Acinetobacter* spp., mainly caused by carbapenem-hydrolyzing class D-lactamases (CHDLs), have increased dramatically in the last decade.[3]

In this study, the strain *A. pittii* TCM156 was recovered from a blood sample of a male hospitalised patient with pneumonia at Hangzhou, Zhejiang province, China, in 2013. It was identified according to both 16S rRNA and *rpoB* gene sequencing. Genomic DNA was extracted using a QIAamp DNA minikit (Qiagen, Valencia, CA). The TruSeq DNA sample preparation kit (Illumina, USA) was used to create the libraries for genome sequencing. The genome of TCM156 was sequenced via the Illumina Hiseq 2500 platform using a TruSeq Rapid SBS Kit and a TruSeq PE (Paired-End) Cluster Kit v3. The draft genome sequence was assembled using CLC Genomics Workbench 9.0 and automatically annotated by the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) server. Resistance-related genes were analyzed using ResFinder 2.1.[4] The multilocus sequence typing (MLST) analysis from the

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assembled genome was performed by BacWGSTdb.[5] Further bioinformatics analysis, such as identification of genomic islands, insertion elements (IS), prophage sequences, clustered regularly interspaced short palindromic repeat (CRISPR) sequences and secondary metabolite gene clusters, were predicted by application of IslandViewer, ISfinder, PHASTER, CRISPRFinder and antiSMASH tools, respectively.[6–10]

The draft genome sequence of *A. pittii* TCM156 consisted of 16 contigs with an average sequencing coverage of 100-fold, which comprised 3,807,313 bases, and PGAP server predicted a total of 3508 protein-coding sequences. The overall G+C content of this strain amounted to 38.7%. In total, 63 tRNA genes and 4 rRNA operons were identified, respectively. We also identified the aminoglycoside resistance genes *strA*, *strB* and *aph(3′)-VIa*, beta-lactam resistance gene bla_{ADC-25} and $bla_{OXA-357}$, macrolide resistance genes *msr(E)* and *mph(E)*, and tetracycline resistance gene *tet(39)*. The genome also contains at least 18 genomic islands and several IS elements: the majority belonging to the IS*3*, IS*5*, and IS*110* families. The presence of three putative secondary metabolite gene clusters, including the arylpolyne, bacteriocin and siderophore biosynthetic gene clusters can also be predicted. The MLST analysis showed that TCM156 belongs to sequence type (ST) 865, according to the MLST scheme of *A. baumannii*.

In summary, these findings have raised awareness of the emergence of a multidrug-resistant OXA-357-producing *A. pittii* isolate in China. The possible emergence of a novel OXA-type enzyme is worrying and must be monitored to avoid their major spread to more clinically relevant bacterial species. To our knowledge, this is the first draft genome sequence of a multidrug-resistant OXA-357-producing clinical *A. pittii* isolate in China.

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LSAL00000000. The version described in this paper is the first version, LSAL01000000.

Declarations

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Conflict of interest

None.

Ethical approval

Not required.

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