Genetic information on OXA-23-producing *Acinetobacter baumannii* strain CCBH15815, belonging to ST730/ST783, isolated from Brazil

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Received: 11 June 2018 / Accepted: 31 March 2019 / Published online: 27 May 2019

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Abstract

In Brazil, *A. baumannii* has been described as nosocomial pathogens causing hospital-acquired infections. Current WGS technologies have been useful in identifying of genetic features between *Acinetobacter* isolates. Here, we report the draft genome sequence of OXA-23 producing *A. baumannii* CCBH15815 clinical isolate, belonging to ST730/ST783, recovered from a 21-year-old hospitalised patient. We observed important resistance determinant genes, especially beta-lactamases-encoding genes, in an estimated genome size of 4,058,633 bp with 3839 predicted coding regions.

Keywords *A. baumannii* · OXA-23 · Multidrug resistance · Bioinformatics analysis · Brazil

Acinetobacter baumannii has reported as an important Gram-negative pathogen increasingly affecting severely ill patients. In the last years, multidrug-resistant *A. baumannii* isolates have been reported around the world and they are often associated with infections with high morbidity and mortality rates [1]. In Brazil, *A. baumannii* has been described as nosocomial pathogens causing hospital-acquired infections with numerous outbreaks [2], due to its prevalence and the carbapenems resistance, usually related to OXA-23 carbapenemase [1].

The apparent predominance of successful carbapenem-resistant *Acinetobacter* strains in Brazilian hospitals underlines the importance of studies that give insight into their molecular features. In this context, current WGS technologies can be useful. This report announces the draft genome sequence of OXA-23 producing *A. baumannii* CCBH15815

recovered from a tracheal aspirate of a 21-year-old hospitalised patient in Santa Catarina State (South Brazil) in March 2014. At the Hospital Infection Research Laboratory (Oswaldo Cruz Institute/Oswaldo Cruz Foundation), CCBH15815 strain was identified according to conventional biochemical [3] and molecular (16S rRNA gene and *rpoB* gene sequencing analysis) tests, and then, it was deposited in the Culture Collection of Hospital-Acquired Bacteria (CCBH).

According to susceptibility tests conducted using the agar diffusion method and interpreted according to Clinical and Laboratory Standards Institute (CLSI) guideline [4], this strain displayed a multidrug resistance profile, which included resistance to amikacin, ciprofloxacin, piperacillin/tazobactam, ceftazidime, cefepime, sulfamethoxazole-trimethoprim, imipenem and meropenem.

Genomic DNA was extracted using QIAamp DNA Blood Mini Kit (Qiagen, Germany) and the DNA library was prepared with Nextera XT (Illumina, San Diego, CA). The DNA sequencing was performed using an Illumina HiSeq sequencing platform (Illumina Inc., USA) generating 100 bp paired-end reads. Then, the sequence data were processed using Trimmomatic (v0.35) and paired-end reads were merged using FLASH (v1.2.11). De novo assembly was performed using SPAdes (v3.7.1). For reference-assisted scaffolding of contigs, Ragout (v1.2) was utilized. Sealer (v1.9.0) and Pilon (v1.16) were used for gap filling and polishing respectively.

Responsible Editor: Elizabeth Marques.

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The resulting assembly was evaluated using REAPR (v1.0.18).

For genome annotation, Rapid Annotation using System Technology (RAST) v.2.0 (available from rast.nmpdr.org/) was performed. By RAST, 3839 coding sequences were annotated from the genome with an estimated size of 4,058,633 bp. The overall G + C content of this isolate amounted to 39%. Other genome assembly statistics included the following: N50 (bp) = 75,960; L50 (bp) = 16; number of contigs (with PEGs) = 179; number of subsystems = 462. Into 462 subsystems, the maximum number of genes was associated with amino acids and derivatives (15.8%), followed by carbohydrates (11.4%), cofactors, vitamins, prosthetic groups and pigments (9.5%) and protein metabolism (8.8%). According to tRNAscan-SE (available from lowelab.ucsc.edu/tRNAscan-SE/) and RNAmmer (available from cbs.dtu.dk/services/RNAmmer/) analysis, we identified 62 tRNAs and three rRNAs, respectively.

Resistance-related genes were analysed using ResFinder 2.1 (available from cge.cbs.dtu.dk/services/ResFinder/) and KmerResistance 2.2 (available from <https://cge.cbs.dtu.dk/services/KmerResistance/>) which identifies acquired antimicrobial resistance genes in total or partial sequenced isolates of bacteria. Using these approaches, we observed resistance genes to beta lactams [*bla*_{OXA-65}, *bla*_{OXA-23}, *bla*_{ADC-25} and *bla*_{TEM-1}], to aminoglycosides [*aadA1*, *aacA4*, *strA*, *strB* and *aph*(3')-VIa], to phenicol [*floR*], to trimethoprim [*dhfrA1*] and to sulphonamide [*sul2*]. These results also could significantly help to explain multidrug resistance profile exhibited by our OXA-23-producing *A. baumannii* strain.

A search for clustered regularly interspaced short palindromic repeats (CRISPRs) and spacers (DR region) was performed using CRISPRFinder (available from <http://crispr.i2bc.paris-saclay.fr>). This approach detected a small possible CRISPR (CRISPR length 156; DR length 55).

For molecular typing, *A. baumannii* contigs were analysed by MLST 1.7 server of Center for Genetic Epidemiology (available from cge.cbs.dtu.dk/services/MLST/). This in silico analysis revealed that CCBH15815 belongs to ST730/clonal complex (CC) 79 (MLST scheme developed by Pasteur Institute) and ST783 (MLST scheme developed by University of Oxford). According to previous studies, this CC79 is one of the major clusters of multidrug-resistant *A. baumannii* widely disseminated in Brazil [1, 5]. The CC79 *A. baumannii* isolates were described in nine Brazilian states (Alagoas, Distrito Federal, Espírito Santo, Goiás, Minas Gerais, Rio de Janeiro, Rio Grande do Norte, Santa Catarina and Mato Grosso do Sul) belonging to the 4 different geographical regions of the country [1]. *A. baumannii* belonging to CC79 usually exhibit multidrug-resistant phenotypes, which could have facilitated its rapid clonal expansion. The CC79 may be responsible for the spread of *bla*_{OXA-23} in South America, since the same ST was also frequently observed among Argentine isolates [5, 6].

This announcement reported whole-genome sequencing of the *A. baumannii* ST730 (CC79) harbouring *bla*_{OXA-23} gene and other gene sequences associated with antibiotic resistance. This CC79 has been described as prosperous complex clonal in Latin America, especially in the Brazilian territory. We suggested that a complementary genomic analysis will be necessary for future studies and would help to identify the other specific features and genetic changes between successful *Acinetobacter* strains in the country.

This Whole Genome Shotgun project has been deposited at DBJ/ENA/GenBank under the accession NLCO00000000. The version described in this paper is version NLCO01000000.

Acknowledgements The authors thank high-throughput platform (Oswaldo Cruz Institute, Fiocruz) for DNA sequencing.

Funding This work was financially supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ) and Oswaldo Cruz Institute (PAPES-FIOCRUZ).

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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