Abstract 871

WHOLE GENOME SEQUENCE ANALYSIS OF TWO ACINETOBACTER OLEIVORANS CLINICAL ISOLATES FROM TERENGGANU, MALAYSIA, REVEALED THE CARRIAGE OF SEVERAL VIRULENCE FACTORS

Type: Abstract Submission

Topic: AS08 Big Data, Genomics and Infectious Diseases

Authors: F. Mohd. Rani¹, N.I. A. Rahman¹, S. Ismail¹, N. Othman², D. Cleary³, F.H. Abdullah², S. Clarke³, <u>C.C.</u> <u>Yeo¹</u>; ¹Universiti Sultan Zainal Abidin, Centre for Research in Infectious Diseases and Biotechnology, Faculty of Medicine, Kuala Terengganu, Malaysia, ²Hospital Sultanah Nur Zahirah, Department of Pathology, Kuala Terengganu, Malaysia, ³University of Southampton, Institute for Life Sciences and Faculty of Medicine, Southampton, United Kingdom

Intro

Acinetobacter oleivorans is an environmental isolate that has rarely been reported to cause human infections, unlike the more notorious nosocomial pathogen, Acinetobacter baumannii. In this study, two clinical isolates of A. oleivorans from Hospital Sultanah Nur Zahirah in Terengganu were subjected to whole genome sequencing and the resulting sequences analysed.

Methods

A. oleivorans AC1583 and AC1885 were both isolated from the sputum of infected patients with pneumonia in 2015 and 2018, respectively. The isolates were initially identified as *A. oleivorans* by *rpoB* gene sequencing. Antimicrobial susceptibility was tested using a panel of 21 antibiotics encompassing 8 antimicrobial classes. Genome sequencing was performed on the Illumina HiSeq platform and assembled using Unicycler v.0.4.8.

Findings

AC1583 was susceptible to all tested antibiotics whereas AC1885 only displayed resistance to trimethoprim/sulfamethoxazole. The assembled genome size for AC1583 was 4,200,796 bp and 4,287,299 bp for AC1885. Multilocus sequence typing (MLST) using the Pasteur scheme indicated that AC1583 and AC1885 were typed as ST1616 and ST1617, respectively. Phylogenetic analysis showed that AC1583 and AC1885 were closely related to clinical isolates from Japan (*A. oleivorans* TUM15450) and the United States (*A. oleivorans* ACIN00177), respectively. Several virulence-associated genes were identified from the genome sequences of AC1583 and AC1885, and these include exotoxin genes such as phospholipase C and catalase, various genes for biofilm formation, immune modulation, and heme utilisation. AC1583 also harboured a small 8,731 bp plasmid, pAC1583-1, that was identical with a putative virulence-associated plasmid initially found in *A. baumannii* which harboured genes encoding a *tonB*-dependent receptor and *sel1* repeat protein. This plasmid was absent in AC1885, which harboured a 11,715 bp cryptic plasmid designated pAC1885-1 instead.

Discussion

Conclusion

Despite its susceptibility to most antimicrobials, *A. oleivorans* was still capable of causing infections due likely to its carriage of several virulence factors and thus warrants vigilance.

Funding: FRGS/1/2018/SKK11/UNISZA/01/1