



Draft Genome Sequences of Two *Acinetobacter soli* Clinical Isolates from a Tertiary Hospital in Terengganu, Malaysia

Farahiyah Mohd. Rani,^a Nor Iza A. Rahman,^a Salwani Ismail,^a  David W. Cleary,^{b,c}  Stuart C. Clarke,^{b,c,d,e}  Chew Chieng Yeo^a

^aCentre for Research in Infectious Diseases and Biotechnology, Faculty of Medicine, Universiti Sultan Zainal Abidin, Kuala Terengganu, Malaysia

^bFaculty of Medicine and Institute for Life Sciences, University of Southampton, Southampton, United Kingdom

^cNIHR Southampton Biomedical Research Centre, University of Southampton, Southampton, United Kingdom

^dGlobal Health Research Institute, University of Southampton, Southampton, United Kingdom

^eInstitute for Research, Development, and Innovation, International Medical University, Kuala Lumpur, Malaysia

ABSTRACT We report the draft genome sequences of *Acinetobacter soli* AC1511 and AC15148, which were isolated from a tertiary hospital in Terengganu, Malaysia, in 2015. AC1511 was assembled into 43 contigs with a total genome size of 3,320,693 bp, whereas AC15148 was 3,260,687 bp over 47 contigs.

Bacteria of the genus *Acinetobacter* are opportunistic pathogens, and although *A. baumannii* is the most clinically important species due to its multidrug-resistant characteristics, other non-*baumannii* species, such as *A. nosocomialis*, *A. pittii*, and *A. soli*, are known etiologic agents of nosocomial infections (1). Here, we report the draft genome sequences of two *A. soli* isolates, AC1511 and AC15148, from Hospital Sultanah Nur Zahirah (Terengganu, Malaysia). Ethical approval for the collection of isolates was obtained from the Medical Research and Ethics Committee review board of the Malaysian Ministry of Health (protocol number NMRR-14-1650-23625 [IIR]). AC1511 was isolated from the sputum of a 59-year-old female patient with community-acquired pneumonia in 2015, whereas AC15148 was isolated from the blood of a 3-year-old boy with acute tonsillopharyngitis in 2018. AC1511 and AC15148 were identified as *A. soli* by PCR-amplification and sequencing of the *rpoB* gene (2, 3). Antimicrobial susceptibility was determined using CLSI breakpoints (4) by obtaining the MIC values using Etest strips for carbapenems and cephalosporins and broth microdilution for polymyxins, whereas disc diffusion was used for other antimicrobials. Both *A. soli* AC1511 and *A. soli* AC15148 were susceptible to all antibiotics tested—the carbapenem class (i.e., imipenem, meropenem, and doripenem), cephalosporins (cefotaxime, ceftriaxone, ceftazidime, and cefepime), β -lactam/ β -lactamase inhibitor combinations (piperacillin/tazobactam and ampicillin/sulbactam), aminoglycosides (amikacin, gentamicin, and tobramycin), trimethoprim/sulfamethoxazole, fluoroquinolones (ciprofloxacin and levofloxacin), tetracyclines (tetracycline, doxycycline, and minocycline), and polymyxins (polymyxin B and colistin). Genomic DNA was isolated using the Geneaid Presto mini-genomic DNA (gDNA) bacterial kit from a 5-mL overnight culture grown at 37°C in Luria broth. The Nextera XT DNA library preparation kit (Illumina) was used to prepare genomic DNA libraries, which were sequenced on the Illumina HiSeq platform (2 × 150-bp paired-end reads) by a commercial sequencing provider (Novogene) with quality inspection carried out using FastQC v0.11.8 and MultiQC v1.7 (5). The draft genome sequences were assembled using SPAdes v3.11.1 (6). For all software, default parameters were used except where otherwise noted. The genome of *A. soli* AC1511 was assembled into 43 contigs (N_{50} value of 246,341 bp, GC content of 43.1%, genome coverage of 150×) with a total genome size of 3,320,693 bp. The *A. soli* AC15148 genome size was 3,260,687 bp and was assembled into 47 contigs with an N_{50} value of 173,816 bp, GC content of 42.7%, and genome coverage of 150×. In comparison with the reference *A. soli* strain, GFJ2 (GenBank version number [GCF_001953195.1](https://www.ncbi.nlm.nih.gov/nuccore/GCF_001953195.1)), the genome of AC1511 showed an average

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

Copyright © 2022 Mohd. Rani et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Chew Chieng Yeo, chewchieng@gmail.com.

The authors declare no conflict of interest.

Received 28 January 2022

Accepted 18 March 2022

Published 4 April 2022

nucleotide identity (ANI) of 98.47% using the BLAST algorithm (ANiB) and 98.7% using the MUMmer alignment tool (ANIm) at JSpeciesWS (7). AC15148 gave an ANiB value of 98.43% and an ANIm value of 98.69% compared with *A. soli* GFJ2, thus validating the identities of AC1511 and AC15148 as *A. soli*. Genome annotation was performed using the Prokaryotic Genome Annotation Pipeline v5.1 during sequence submission to NCBI (8). No resistance genes were detected from the genomes of AC1511 and AC15148 using ResFinder (9) and the Comprehensive Antimicrobial Resistance Database (CARD) (10), which confirmed their observed susceptible phenotypes.

Data availability. The raw reads used for the draft genome sequence assemblies were deposited in the Sequence Read Archive under accession numbers [SRR18110793](https://www.ncbi.nlm.nih.gov/sra/SRR18110793) (for *Acinetobacter soli* AC1511) and [SRR18120237](https://www.ncbi.nlm.nih.gov/sra/SRR18120237) (for *A. soli* AC15148). The draft genome sequences of the strains obtained in this study were deposited under BioProject number [PRJNA576555](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA576555) with the assembled genomes under the accession numbers [JAGFOS000000000](https://www.ncbi.nlm.nih.gov/assembly/JAGFOS000000000) (*A. soli* AC1511) and [JAGFOR000000000](https://www.ncbi.nlm.nih.gov/assembly/JAGFOR000000000) (*A. soli* AC15148).

ACKNOWLEDGMENTS

Our thanks go to Fatimah Haslina Abdullah and Norlela Othman of Hospital Sultanah Nur Zahirah for the isolates described in this work.

This project was financially supported by the Malaysian Ministry of Higher Education through a fundamental research grant scheme (grant number FRGS/2017/01/SKK/11/04).

REFERENCES

- Baraka A, Traglia GM, Montaña S, Tolmasky ME, Ramirez MS. 2020. An *Acinetobacter non-baumannii* population study: antimicrobial resistance genes (ARGs). *Antibiotics* 10:16. <https://doi.org/10.3390/antibiotics10010016>.
- La Scola B, Gundi VAKB, Khamis A, Raoult D. 2006. Sequencing of the *rpoB* gene and flanking spacers for molecular identification of *Acinetobacter* species. *J Clin Microbiol* 44:827–832. <https://doi.org/10.1128/JCM.44.3.827-832.2006>.
- Gundi VAKB, Dijkshoorn L, Burignat S, Raoult D, La Scola B. 2009. Validation of partial *rpoB* gene sequence analysis for the identification of clinically important and emerging *Acinetobacter* species. *Microbiology (Reading)* 155:2333–2341. <https://doi.org/10.1099/mic.0.026054-0>.
- CLSI. 2020. M100 performance standards for antimicrobial susceptibility testing; 30th informational supplement, 30th ed. Clinical and Laboratory Standards Institute, Wayne, PA.
- Ewels P, Magnusson M, Lundin S, Käller M. 2016. MultiQC: summarize analysis results for multiple tools and samples in a single report. *Bioinformatics* 32:3047–3048. <https://doi.org/10.1093/bioinformatics/btw354>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. *Bioinformatics* 32:929–931. <https://doi.org/10.1093/bioinformatics/btv681>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EPP, Zaslavsky L, Lomsadze A, Pruitt KDD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Bortolaia V, Kaas RS, Ruppe E, Roberts MC, Schwarz S, Cattoir V, Philippon A, Allesoe RL, Rebelo AR, Florensa AF, Fagelhauer L, Chakraborty T, Neumann B, Werner G, Bender JK, Stingl K, Nguyen M, Coppens J, Xavier BB, Malhotra-Kumar S, Westh H, Pinholt M, Anjum MF, Duggett NA, Kempf I, Nykäsenoja S, Olkkola S, Wiczorek K, Amaro A, Clemente L, Mossong J, Losch S, Ragimbeau C, Lund O, Aarestrup FM. 2020. ResFinder 4.0 for predictions of phenotypes from genotypes. *J Antimicrob Chemother* 67:2640–2644. <https://doi.org/10.1093/jac/dkaa345>.
- Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, Huynh W, Nguyen AV, Cheng AA, Liu S, Min SY, Miroshnichenko A, Tran HK, Werfalli RE, Nasir JA, Oloni M, Speicher DJ, Florescu A, Singh B, Faltyn M, Hernandez-Koutoucheva A, Sharma AN, Bordeleau E, Pawlowski AC, Zubyk HL, Dooley D, Griffiths E, Maguire F, Winsor GL, Beiko RG, Brinkman FSL, Hsiao WWL, Domselaar GV, McArthur AG. 2020. CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Res* 48:D517–D525.