AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence and Annotation of *Acinetobacter junii* MHI21018, Isolated from Bovine Colostrum

Carsten Kröger,[a] Kristina Schauer,[b] Seán R. Clerkin,[a] Erwin Märtlbauer,[b] Alastair B. Fleming[a]

[a]Department of Microbiology, School of Genetics and Microbiology, Moyne Institute of Preventive Medicine, Trinity College Dublin, Dublin, Ireland
[b]Department of Veterinary Science, Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität München, Oberschleißheim, Germany

ABSTRACT We report here the draft genome sequence of *Acinetobacter junii* MHI21018, isolated in 2009 from bovine colostrum. The draft genome sequence is composed of 3,267,995 bp, has a GC content of 38.54%, and was assembled into 114 contigs (contig size, >500 bp) with an N_{50} value of 72,566 bp.

Members of the genus *Acinetobacter* are versatile Gram-negative bacteria. Most notably, multidrug-resistant *Acinetobacter baumannii* has emerged as a major opportunistic nosocomial pathogen (1, 2). *Acinetobacter junii* species are rarely associated with human disease, but cases of septicemia caused by *A. junii* have been reported (3), as well as strains carrying New Delhi metallo-β-lactamase (4, 5) or the carbapenemase-encoding gene bla_{IMP-1} (6). To date, 23 *A. junii* genome sequences are available in GenBank, and only 3 strains are fully sequenced. Due to the rapidly evolving *Acinetobacter* species, this newly sequenced isolate from an animal source will provide additional information for comparative genomic and evolutionary studies.

Here, we report the draft genome sequence of *A. junii* MHI21018 isolated in 2009 from the colostrum of a cow which gave birth to a calf that developed bovine neonatal pancytopenia (bleeding calf syndrome). *Acinetobacter* spp. were selected by colony morphology, a negative oxidase reaction, and by forming red colonies on chromogenic agar (CHROMagar Acinetobacter). The bacteria form round, smooth, opaque, and convex colonies of 2 to 3 mm in diameter when grown on sheep blood agar plates at 37°C for 24 h. After growth of *A. junii* MHI21018 overnight in 5 ml lysogeny broth (Lennox) at 37°C, genomic DNA was isolated using the Quick-DNA universal kit (Zymo Research). Preparation of the DNA library was carried out using Nextera XT library prep kit (Illumina) following the manufacturer's protocol. The library was sequenced on the Illumina HiSeq 2500 machine (2 × 250-bp paired-end-reads; total number of reads, 424,136; 30× coverage). Reads were trimmed using Trimmomatic version 0.30 with a sliding window quality cutoff of Q15 (7). Library preparation, sequencing, and read trimming were performed by microbesNG (Birmingham, UK). The draft sequence *de novo* assembly was performed using SPAdes version 3.13.0 in default mode (8), and the properties and quality of the assembly (e.g., N_{50}, number of contigs, and GC content) were assessed using QUAST version 5.0.2 in default mode (9). Sequences shorter than 200 bp were removed from the final fasta-formatted sequence prior to genome annotation.

The published assembly is composed of 114 contigs (N_{50}, 72,566 bp), the draft genome size is 3,267,995 bp, and it has a GC content of 38.54%. Species identification was carried out using BLASTn and JSpeciesWS (10). The average nucleotide identity using BLAST (ANIb) returned >97.6% sequence identity with reference *A. junii* strain 65 (>84% aligned nucleotides); therefore, the sequenced strain was assigned to the *A. junii* species. Genome annotation was carried out during sequence submission to the NCBI using the Prokaryotic Genome Annotation Pipeline (11), which predicted the presence

Citation Kröger C, Schauer K, Clerkin SR, Märtlbauer E, Fleming AB. 2019. Draft genome sequence and annotation of *Acinetobacter junii* MHI21018, isolated from bovine colostrum. Microbiol Resour Announc 8:e01700-18. https://doi.org/10.1128/MRA.01700-18.

Editor J. Cameron Thrash, University of Southern California

Address correspondence to Carsten Kröger, Carsten.Kroeger@tcd.ie, or Alastair B. Fleming, Alastair.Fleming@tcd.ie.

Received 8 January 2019
Accepted 6 February 2019
Published 7 March 2019

of 3,341 genes, including 3,086 coding sequences, 68 tRNA genes, 172 pseudogenes, and 1 CRISPR array. Comprehensive Antibiotic Resistance Database (CARD) Resistance Gene Identifier (RGI) analysis predicted the presence of a nitroimidazole antibiotic efflux pump gene (*msbA*) and an ANT(3″)-IIb locus conferring resistance to aminoglycosides (12). PHASTER predicted the presence of one intact prophage (13) with great sequence identity to *Psychrobacter* phage pOW20-A (NCBI RefSeq accession number NC_020841) and one incomplete prophage, *Salmonella* phage vB_SosS_Oslo (NCBI RefSeq accession number NC_018279), that are in adjacent chromosomal loci and predicted to partially overlap.

Data availability. The raw reads used for the draft genome sequence assembly were deposited in the Sequence Read Archive (SRA) under BioProject number PRJNA509118. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under accession number RWKP00000000. The version described in this paper is version RWKP01000000.

ACKNOWLEDGMENTS

Work in the Fleming lab was supported by a Science Foundation Ireland grant (10/RFP/GEN2761). Genome sequencing was provided by microbesNG (http://www.microbesng.uk), which is supported by the BBSRC (grant number BB/L024209/1).

REFERENCES

1. Kröger C, Kary SC, Schauer K, Cameron ADS. 2016. Genetic regulation of virulence and antibiotic resistance in Acinetobacter baumannii. Genes 8:12. https://doi.org/10.3390/genes8010012.
2. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, Pulcini C, Kahlmeter G, Kluytmans J, Carmeli Y, Ouellette M, Outterson K, Patel J, Cavaleri M, Cox EM, Houchens CR, Grayson ML, Hansen P, Singh N, Theuretzbacher U, Magrini N, Aboderin AO, Al-Abri SS, Awang Jalil N, Benzonana N, Bhattacharya S, Brink AJ, Burkert FR, Cars O, Cornaglia G, Dyar OJ, Friedrich AW, Gales AC, Gandra S, Giske CG, Goff DA, Goossens H, Gottlieb T, Guzman Blanco M, Hryniewicz W, Kattula D, Jinks T, Kanj SS, Kerr L, Kieny M-P, Kim YS, Kozlov RS, Labarca J, Laxminarayan R, Leder K, et al. 2018. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. Lancet Infect Dis 18:318–327. https://doi.org/10.1016/S1473-3099(17)30753-3.
3. Linde H-J, Hahn J, Holler E, Reischl U, Lehn N. 2002. Septicemia due to *Acinetobacter junii*. J Clin Microbiol 40:2696–2697. https://doi.org/10.1128/JCM.40.7.2696-2697.2002.
4. Montaña S, Cittadini R, del Castillo M, Uong S, Lazzaro T, Almuzara M, Barberis C, Vay C, Ramírez MS. 2016. Presence of New Delhi metallo-β-lactamase gene (NDM-1) in a clinical isolate of *Acinetobacter junii* in Argentina. New Microbes New Infect 11:43–44. https://doi.org/10.1016/j.nmni.2016.02.008.
5. Zhou Z, Guan R, Yang Y, Chen L, Fu J, Deng Q, Xie Y, Huang Y, Wang J, Wang D, Liao C, Gong S, Xia H. 2012. Identification of New Delhi metallo-β-lactamase gene (NDM-1) from a clinical isolate of *Acinetobacter junii* in China. Can J Microbiol 58:112–115. https://doi.org/10.1139/w11-112.
6. Cayô R, Streling AP, Nodari CS, Matos AP, de Paula Luz A, Dijkshoorn L, Pignatari ACC, Gales AC. 2018. Occurrence of IMP-1 in non-*baumannii Acinetobacter* clinical isolates from Brazil. J Med Microbiol 67:628–630. https://doi.org/10.1099/jmm.0.000732.
7. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.
8. 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.
9. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
10. 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.
11. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
12. Jia B, Raphenya AR, Alcock B, Waglechner N, Guo P, Tsang KK, Lago BA, Dave BM, Pereira S, Sharma AN, Doshi S, Courtot M, Lo R, Williams LE, Frye JG, Elsayegh T, Sardar D, Westman EL, Pawlowski AC, Johnson TA, Brinkman FSL, Wright GD, McArthur AG. 2017. CARD 2017: expansion and model-centric curation of the comprehensive antibiotic resistance database. Nucleic Acids Res 45:D566–D573. https://doi.org/10.1093/nar/gkw1004.
13. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res 44:W16–W21. https://doi.org/10.1093/nar/gkw387.