





Draft Genome Sequence of Raoultella ornithinolytica P079F W, Isolated from the Feces of a Preterm Infant

Yuhao Chen,a Thomas C. Brook,b Cristina Alcon-Giner,c Paul Clarke,d Lindsay J. Hall,c Lesley Hoylese

- ^aDepartment of Surgery and Cancer, Imperial College London, London, United Kingdom
- Department of Biomedical Sciences, University of Westminster, London, United Kingdom
- ^cGut Microbes and Health Programme, Quadram Institute Bioscience, Norwich, United Kingdom
- dNeonatal Intensive Care Unit, Norfolk and Norwich University Hospital, Norwich, United Kingdom
- eDepartment of Biosciences, Nottingham Trent University, Nottingham, United Kingdom

ABSTRACT Here, we describe the draft genome sequence of Raoultella ornithinolytica P079F W, isolated from the feces of an infant residing in a neonatal intensive care unit during an ongoing study to characterize the neonate gut microbiota. P079F W will be used in studies investigating the role of the microbiome in neonatal infections.

aoultella ornithinolytica is an inhabitant of aquatic environments, but it is recognized as an emerging and underreported cause of nosocomial infections (1). While its genomic diversity and prevalence in the preterm neonate gut microbiota are poorly understood, R. ornithinolytica has been associated with bacteremia, urinary tract infection, and early-onset sepsis in infants (2-4).

Here, we report the draft genome of an R. ornithinolytica strain, P079F W, isolated from the feces of a 12-day-old male preterm infant who had been delivered by Caesarean section at Norfolk and Norwich University Hospital in the United Kingdom. The fecal sample was collected from the infant under ethical approval obtained from the Ethics Committee of the Faculty of Medical and Health Sciences in the University of East Anglia (Norwich, UK) with informed and written consent obtained from the parents. The protocol for feces collection was laid out by the Norwich Research Park (NRP) Biorepository (Norwich, UK), was in accordance with the terms of the Human Tissue Act 2004, and was approved with license no. 11208 by the Human Tissue Authority. The infant had suspected sepsis against a background of prematurity (gestational age, 30 weeks, days unknown; weight, 1,544 g), premature rupture of membranes, and respiratory distress. Chorioamnionitis and funisitis were confirmed on placental histology. Blood culture and lumbar puncture were unremarkable. The infant had a partial septic screen, and intravenous antibiotics (benzylpenicillin and gentamicin) were commenced during the first week of life. After 5 days of antibiotics, the infant showed no signs of infection.

After storage at -80°C, the fecal sample was diluted 1:10 in buffer and plated onto MacConkey agar no. 3 to isolate lactose-positive (pink) colonies. Strain P079F W was isolated along with strain P079F P (5) from the fecal sample. Both isolates were identified by phenotypic testing as Klebsiella oxytoca [API20E code 524577(3/7)]. DNA was extracted from an overnight culture of P079F W using a phenol-chloroform method described fully by Kiu et al. (6) and sequenced using the 96-plex Illumina HiSeq 2500 platform to generate 1,092,878 125-bp paired-end reads (7). Raw data provided by the sequencing center were checked using FastQC v0.11.4 (https://www.bioinformatics .babraham.ac.uk/projects/fastqc/); no adapter trimming was required, and reads had an average Phred score of >25. MetaPhlAn2.6 (8) was used to identify the closest relative

Citation Chen Y, Brook TC, Alcon-Giner C, Clarke P, Hall LJ, Hoyles L. 2019. Draft genome sequence of Raoultella ornithinolytica P079F W, isolated from the feces of a preterm infant. Microbiol Resour Announc 8:e00493-19. https://doi.org/10.1128/MRA.00493-19.

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

Copyright © 2019 Chen et al. This is an openaccess article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Lindsay J. Hall, Lindsay.Hall@quadram.ac.uk, or Lesley Hoyles, lesley.hoyles@ntu.ac.uk.

Received 14 May 2019 Accepted 22 July 2019 Published 15 August 2019



of P079F W, leading to a reference-based assembly (against Raoultella ornithinolytica 2-156-04_S1_C1; Assembly accession no. GCA_000703465) being produced by Bug-Builder v1.0.3b1 (default settings for Illumina assembly) (9). The genome of P079F W comprised 5,582,297 bp in 47 contigs ($N_{50} = 295,345$), with a G+C content of 55.6% and 5,194 coding sequences (CDS) and 75 tRNAs (NCBI Prokaryotic Genome Annotation Pipeline [10]). It shared 99.59% average nucleotide identity (OrthoANI [11]) with the genome of R. ornithinolytica NBRC 105727^T (Assembly accession no. GCA_001598295), confirming its affiliation to this species (12-14). Genome completeness was estimated to be 99.84% using CheckM v1.0.13 (15). The strain was capsule type K27 (https:// bigsdb.pasteur.fr/klebsiella/) and encodes several virulence factors (yersiniabactin [iron acquisition]; RcsAB [regulation]; type I and type III fimbriae [adherence]) according to a BLASTN search with the draft genome via VFanalyzer (Klebsiella data set) at http://www .mgc.ac.cn/cgi-bin/VFs/v5/main.cgi (16). The genome encodes homologs (strict Comprehensive Antibiotic Resistance Database matches) of antibiotic-resistant determinants associated with efflux pumps and transporters, namely CRP (Antibiotic Resistance Ontology [ARO]:3000518), marA (ARO:3000263), acrB (ARO:3000216), msbA (ARO: 3003950), and PmrF (ARO:3003578; linked to colistin resistance) (17).

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. QFTY00000000. Raw sequence reads have been deposited at DDBJ/EMBL/GenBank under accession no. SRR9048023. The version described in this paper is the first version, QFTY01000000.

ACKNOWLEDGMENTS

Chen et al.

This work used the computing resources of the UK MEDical BlOinformatics partner-ship (UK Med-Bio), which was supported by the Medical Research Council (grant MR/L01632X/1). T.C.B. was funded by a University of Westminster Ph.D. studentship and by a Research Visit Grant from the Microbiology Society (grant RVG16/3). This work was funded via a Wellcome Trust Investigator Award to L.J.H. (100/974/C/13/Z), an Institute Strategic Programme grant for Gut Health and Food Safety (BB/J004529/1), BBSRC Institute Strategic Program Gut Microbes and Health (BB/R012490/1) and its constituent project (BBS/E/F/000PR10353) (to L.J.H.), and by a BBSRC Norwich Research Park Bioscience Doctoral Training Grant (BB/M011216/1; supervisor, L.J.H.; student, C.A.-G.).

L.H. is a member of the ESCMID Study Group for Host and Microbiota Interaction (https://www.escmid.org/research_projects/study_groups/host_and_microbiota_interaction/).

REFERENCES

- Seng P, Boushab BM, Romain F, Gouriet F, Bruder N, Martin C, Paganelli F, Bernit E, Le Treut YP, Thomas P, Papazian L, Raoult D, Stein A. 2016. Emerging role of *Raoultella ornithinolytica* in human infections: a series of cases and review of the literature. Int J Infect Dis 45:65–71. https://doi.org/10.1016/j.ijid.2016.02.014.
- Abbas A, Ahmad I. 2018. First report of neonatal early-onset sepsis caused by multi-drug-resistant *Raoultella ornithinolytica*. Infection 46: 275–277. https://doi.org/10.1007/s15010-017-1098-9.
- De Petris L, Ruffini E. 2018. Raoultella ornithinolytica infection in infancy: a case of febrile urinary tract infection. CEN Case Rep 7:234–236. https://doi.org/10.1007/s13730-018-0333-2.
- Mau N, Ross LA. 2010. Raoultella ornithinolytica bacteremia in an infant with visceral heterotaxy. Pediatr Infect Dis J 29:477–478. https://doi.org/ 10.1097/INF.0b013e3181ce9227.
- Chen Y. 2018. Genome analysis of Gram-negative bacteria isolated from preterm baby faeces and whole-genome analysis of Klebsiella oxytoca. MSc thesis. Imperial College London, London, United Kingdom.
- Kiu R, Caim S, Alcon-Giner C, Belteki G, Clarke P, Pickard D, Dougan G, Hall LJ. 2017. Preterm infant-associated *Clostridium tertium, Clostridium cadaveris*, and *Clostridium paraputrificum* strains: genomic and evolutionary insights. Genome Biol Evol 9:2707–2714. https://doi.org/10.1093/gbe/evx210.
- 7. Harris SR, Feil EJ, Holden MT, Quail MA, Nickerson EK, Chantratita N,

- Gardete S, Tavares A, Day N, Lindsay JA, Edgeworth JD, de Lencastre H, Parkhill J, Peacock SJ, Bentley SD. 2010. Evolution of MRSA during hospital transmission and intercontinental spread. Science 327:469–474. https://doi.org/10.1126/science.1182395.
- Segata N, Waldron L, Ballarini A, Narasimhan V, Jousson O, Huttenhower C. 2012. Metagenomic microbial community profiling using unique clade-specific marker genes. Nat Methods 9:811–814. https://doi.org/10 .1038/nmeth.2066.
- 9. Abbott JC. 2017. BugBuilder—an automated microbial genome assembly and analysis pipeline. bioRxiv. https://doi.org/10.1101/148783.
- 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.
- Lee I, Ouk Kim Y, Park S-C, Chun J. 2016. OrthoANI: an improved algorithm and software for calculating average nucleotide identity. Int J Syst Evol Microbiol 66:1100–1103. https://doi.org/10.1099/ijsem.0.000760.
- Chun J, Oren A, Ventosa A, Christensen H, Arahal DR, da Costa MS, Rooney AP, Yi H, Xu XW, De Meyer S, Trujillo ME. 2018. Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. Int J Syst Evol Microbiol 68:461–466. https://doi.org/10.1099/ijsem.0.002516.
- Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to

Volume 8 Issue 33 e00493-19 mra.asm.org **2**

- whole-genome sequence similarities. Int J Syst Evol Microbiol 57:81–91. https://doi.org/10.1099/ijs.0.64483-0.
- 14. Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci U S A 106: 19126-19131. https://doi.org/10.1073/pnas.0906412106.
- 15. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 25:1043-1055. https://doi.org/10.1101/gr.186072.114.
- 16. Liu B, Zheng D, Jin Q, Chen L, Yang J. 2019. VFDB 2019: a comparative pathogenomic platform with an interactive Web interface. Nucleic Acids Res 47:D687-D692. https://doi.org/10.1093/nar/gky1080.
- 17. 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 FS, 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.

Volume 8 Issue 33 e00493-19