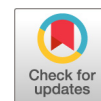


Title	Genome sequence of Paracoccus sp. JM45, a bacterial strain isolated from a marine sponge with a dual quorum sensing inhibition activity
Authors	Gutiérrez-Barranquero, José A.;Parages, María L.;Dobson, Alan D. W.;Reen, F. Jerry;O'Gara, Fergal
Publication date	2019
Original Citation	Gutiérrez-Barranquero, J.A., Parages, M.L., Dobson, A.D., Reen, F.J. and O'Gara, F., 2019. Genome Sequence of Paracoccus sp. JM45, a Bacterial Strain Isolated from a Marine Sponge with a Dual Quorum Sensing Inhibition Activity. Microbiology Resource Announcements, 8(2), e01496-18, (3pp.) DOI: 10.1128/MRA.01496-18
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://mra.asm.org/content/8/2/e01496-18 - 10.1128/MRA.01496-18 https://www.ncbi.nlm.nih.gov/nucleotide/10149618
Rights	© 2019 Gutiérrez-Barranquero 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/
Download date	2024-04-19 19:00:32
Item downloaded from	https://hdl.handle.net/10468/7887



UCC

University College Cork, Ireland
Coláiste na hOllscoile Corcaigh



Genome Sequence of *Paracoccus* sp. JM45, a Bacterial Strain Isolated from a Marine Sponge with a Dual Quorum Sensing Inhibition Activity

José A. Gutiérrez-Barranquero,^{a*} María L. Parages,^{a*} Alan D. W. Dobson,^{b,c} F. Jerry Reen,^{a,b} Fergal O'Gara^{a,d,e}

^aBIOMERIT Research Centre, School of Microbiology, University College Cork, Cork, Ireland

^bSchool of Microbiology, University College Cork, Cork, Ireland

^cEnvironmental Research Institute, University College Cork, Cork, Ireland

^dTelethon Kids Institute, Perth, Western Australia, Australia

^eHuman Microbiome Programme, School of Pharmacy and Biomedical Sciences, Curtin Health Innovation Research Institute, Curtin University, Perth, Western Australia, Australia

ABSTRACT The draft genome sequence of *Paracoccus* sp. strain JM45, isolated from a marine sponge harvested off the west coast of Ireland, is reported here. Quorum sensing and quorum sensing inhibition activities have been reported recently for this bacterium, and genomic analysis supports its potential use for novel therapeutic development.

Paracoccus is a Gram-negative bacterial genus belonging to the *Alphaproteobacteria* class. *Paracoccus denitrificans* is the best-characterized member of this genus, and this is due in part to its broad metabolic diversity (1), capacity for denitrification (2), and ability to degrade organic compounds (3). Recently, the discovery of the cell-cell signaling phenomenon referred to as quorum sensing (QS) in *Paracoccus denitrificans* captured the attention of many researchers, and QS has been reported to be involved in biofilm formation, iron uptake, and denitrification in this organism (4, 5). *Paracoccus* sp. strain JM45 was isolated from a marine sponge sample belonging to the genus *Polymastia* collected off the west coast of Ireland as part of the marine biodiscovery cruise performed in May 2010. To isolate *Paracoccus* sp. strain JM45 from a marine sponge, we followed a protocol previously described with minor modifications in the use of SYP-SW (soluble starch, yeast extract, peptone-seawater) medium and marine agar (Difco) (6). We previously reported QS and quorum sensing inhibition (QSI) properties for this bacterial strain (7). Therefore, here, we announce the genome sequence of *Paracoccus* sp. strain JM45, a promising source of novel QSI compounds with potential for controlling multidrug-resistant pathogens. Total DNA of *Paracoccus* sp. strain JM45 was extracted using the UltraClean microbial DNA isolation kit (Mo Bio Laboratories, Inc., Carlsbad, CA) and was subjected to DNA library preparation using a TruSeq exome library prep kit. The draft genome sequencing project of *Paracoccus* sp. strain JM45 was performed by the Beijing Genomics Institute (BGI, China) using the Illumina HiSeq 4000 sequencing platform involving paired-end reads with a read length of 150 bp. The superfast FASTA/Q file manipulation tool, readfq.v5 (BGI unpublished software [8]), was used for quality trimming. This software removes the paired-end reads with a certain proportion of low-quality bases (default, 40%; parameter setting, 6 bp), reads with a certain proportion of Ns (ambiguous bases; default, 10%; parameter setting, 10 bp), reads with adapter contamination (default, 15 bp overlapped between adapter and reads), and duplicate sequences. Thus, the high-quality-filtered reads were all 150 bp long. A total of 166.66 Mb of data were generated, and high-quality reads were assembled using SOAPdenovo 2.04 with default parameters. The sequencing

Citation Gutiérrez-Barranquero JA, Parages ML, Dobson ADW, Reen FJ, O'Gara F. 2019. Genome sequence of *Paracoccus* sp. JM45, a bacterial strain isolated from a marine sponge with a dual quorum sensing inhibition activity. Microbiol Resour Announc 8:e01496-18. <https://doi.org/10.1128/MRA.01496-18>.

Editor Steven R. Gill, University of Rochester School of Medicine and Dentistry

Copyright © 2019 Gutiérrez-Barranquero et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

Address correspondence to Fergal O'Gara, f.ogara@ucc.ie.

* Present address: José A. Gutiérrez-Barranquero, Instituto de Hortofruticultura Subtropical y Mediterránea La Mayora (IHSM-UMA-CSIC), Departamento de Microbiología, Facultad de Ciencias, Universidad de Málaga, Málaga, Spain; María L. Parages, Departamento de Ecología, Facultad de Ciencias, Universidad de Málaga, Málaga, Spain.

Received 31 October 2018

Accepted 26 November 2018

Published 10 January 2019

depth provided 45× coverage of the genome. The draft genome assembly comprised 84 contigs with an N_{50} value of 167,336 grouped into 81 scaffolds with a total size of 3,602,847 bp and an overall GC content of 59.1%. Genome sequence annotation and gene identification were carried out by the Rapid Annotations using Subsystems Technology (RAST) server version 2.0 using default parameters and the RAST tool kit (RASTtk) for annotation pipelines (9, 10) and by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) using default parameters. Detection of secondary metabolite gene clusters was performed using antiSMASH bacterial version 3.0 (11). Based on PGAP annotation results, 3,516 coding sequences, 3 ribosomal RNAs, and 45 tRNAs were detected. Two potential acyl homoserine lactone (AHL)-based quorum sensing systems were found in scaffolds 7 and 18. Both systems are related to the production of long-chain AHLs, consistent with our previous finding of AHL-based QS activity in this isolate (7), which was confirmed using the *Agrobacterium tumefaciens* NTL4 biosensor strain (12). In the context of QSI properties, a penicillin amidase enzyme with potential for AHL degradation was encoded in scaffold 1. Finally, antiSMASH predicted several potential gene clusters involved in secondary metabolite production. A gene cluster observed and related to the production of a novel polyketide by type III polyketide synthases was of particular interest. Polyketides are an important class of biologically active compound (13), and while further *in vitro* investigations are required to establish activity profiles, *in silico* identification through antiSMASH supports the bioactive potential of *Paracoccus* sp. strain JM45. Furthermore, an ectoine biosynthetic gene cluster was found in scaffold 1. Based on known activities of ectoine and other compatible solutes, this could be relevant for growth at high concentrations of salt, as previously demonstrated in other bacteria (14).

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [QQVY00000000](https://www.ncbi.nlm.nih.gov/seq/submit/submit.cgi?accession=QQVY00000000). The version described in this paper is version QQVY01000000. The raw reads from this study have been submitted to the NCBI Sequence Read Archive (SRA) under the accession number [SRP166726](https://www.ncbi.nlm.nih.gov/sra/submit/submit.cgi?accession=SRP166726).

ACKNOWLEDGMENTS

This research was supported in part by grants awarded to F.J.R. and F.O. by Enterprise Ireland (CF-2017-0757-P) and to F.O. by Enterprise Ireland (IP-2015-0390), the European Commission (FP7-PEOPLE-2013-ITN, 607786; FP7-KBBE-2012-6, CP-TP-312184; FP7-KBBE-2012-6, 311975; OCEAN 2011-2, 287589; EU2020-634486-2015), Science Foundation Ireland (SSPC-2, 12/RC/2275; 13/TIDA/B2625; 12/TIDA/B2411; 12/TIDA/B2405; 14/TIDA/2438; 15/TIDA/2977; SFI09/RFP/BMT2350), the Department of Agriculture and Food (FIRM 11/F009/MabS; FIRM 13/F/516), the Irish Research Council for Science, Engineering and Technology (GOIPG/2014/647), the Health Research Board/Irish Thoracic Society (MRCG-2014-6), the Department of the Marine (BEAU/BIOD/01), and the Cystic Fibrosis Foundation, USA (OG1710).

REFERENCES

- Baker SC, Ferguson SJ, Ludwig B, Page MD, Richter OM, van Spanning RJ. 1998. Molecular genetics of the genus *Paracoccus*: metabolically versatile bacteria with bioenergetic flexibility. *Microbiol Mol Biol Rev* 62: 1046–1078.
- Giannopoulos G, Sullivan MJ, Hartop KR, Rowley G, Gates AJ, Watmough NJ, Richardson DJ. 2017. Tuning the modular *Paracoccus denitrificans* respirome to adapt from aerobic respiration to anaerobic denitrification. *Environ Microbiol* 19:4953–4964. <https://doi.org/10.1111/1462-2920.13974>.
- Siddavattam D, Karegoudar TB, Mudde SK, Kumar N, Baddam R, Avasthi TS, Ahmed N. 2011. Genome of a novel isolate of *Paracoccus denitrificans* capable of degrading N,N-dimethylformamide. *J Bacteriol* 193: 5598–5599. <https://doi.org/10.1128/JB.05667-11>.
- Kumar S, Spiro S. 2017. Environmental and genetic determinants of biofilm formation in *Paracoccus denitrificans*. *mSphere* 2:e00350-17. <https://doi.org/10.1128/mSphereDirect.00350-17>.
- Zhang Y, Gao J, Wang L, Liu S, Bai Z, Zhuang X, Zhuang G. 18 May 2018. Environmental adaptability for quorum sensing: regulating iron uptake during biofilm formation in *Paracoccus denitrificans*. *Appl Environ Microbiol* <https://doi.org/10.1128/AEM.00865-18>.
- Margassery LM, Kennedy J, O’Gara F, Dobson AD, Morrissey JP. 2012. Diversity and antibacterial activity of bacteria isolated from the coastal marine sponges *Amphilectus fucorum* and *Eurypon major*. *Lett Appl Microbiol* 55:2–8. <https://doi.org/10.1111/j.1472-765X.2012.03256.x>.
- Gutiérrez-Barranquero JA, Reen FJ, Parages ML, McCarthy R, Dobson ADW, O’Gara F. 2017. Disruption of *N*-acyl-homoserine lactone specific signalling and virulence in clinical pathogens by marine sponge bacteria. *Microbiol Biotechnol*. <https://doi.org/10.1111/1751-7915.12867>.
- Tong C, Wu Z, Zhao X, Xue H. 2018. Arginine catabolic mobile elements in livestock-associated methicillin-resistant staphylococcal isolates from

- bovine mastitic milk in China. *Front Microbiol* 9:1031. <https://doi.org/10.3389/fmicb.2018.01031>.
9. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
 10. Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parello B, Pusch GD, Shukla M, Thomason JA III, Stevens R, Vonstein V, Wattman AR, Xia F. 2015. RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep* 5:8365. <https://doi.org/10.1038/srep08365>.
 11. Weber T, Blin K, Duddela S, Duddela S, Krug D, Kim HU, Brucoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res* 43:W237–W243. <https://doi.org/10.1093/nar/gkv437>.
 12. Yin WF, Purmal K, Chin S, Chan XY, Chan KG. 2012. Long chain *N*-acyl homoserine lactone production by *Enterobacter* sp. isolated from human tongue surfaces. *Sensors* 12:14307–14314. <https://doi.org/10.3390/s121114307>.
 13. Yu D, Xu F, Zeng J, Zhan J. 2012. Type III polyketide synthases in natural product biosynthesis. *IUBMB Life* 64:285–295. <https://doi.org/10.1002/iub.1005>.
 14. Sadeghi A, Soltani BM, Nekouei MK, Jouzani GS, Mirzaei HH, Sadeghizadeh M. 2014. Diversity of the ectoines biosynthesis genes in the salt tolerant *Streptomyces* and evidence for inductive effect of ectoines on their accumulation. *Microbiol Res* 169:699–708. <https://doi.org/10.1016/j.micres.2014.02.005>.