

UC Irvine

UC Irvine Previously Published Works

Title

Genome Sequence of Pigmented Siderophore-Producing Strain *Serratia marcescens* SM6.

Permalink

<https://escholarship.org/uc/item/6q02580m>

Journal

Microbiology resource announcements, 8(18)

ISSN

2576-098X

Authors

Khilyas, Irina V
Tursunov, Kanat A
Shirshikova, Tatiana V
et al.

Publication Date

2019-05-02

DOI

10.1128/mra.00247-19

Peer reviewed



Genome Sequence of Pigmented Siderophore-Producing Strain *Serratia marcescens* SM6

Irina V. Khilyas,^a Kanat A. Tursunov,^b Tatiana V. Shirshikova,^a Leysan K. Kamaletdinova,^a Lilia E. Matrosova,^a Prerak T. Desai,^{c*} Michael McClelland,^c  Lydia M. Bogomolnaya^{a,d}

^aInstitute of Fundamental Medicine and Biology, Kazan Federal University, Kazan, Russia

^bLaboratory of Immunochemistry and Immunobiotechnology, National Center for Biotechnology, Astana, Kazakhstan

^cDepartment of Microbiology and Molecular Genetics, University of California Irvine, Irvine, California, USA

^dDepartment of Microbial Pathogenesis and Immunology, College of Medicine, Texas A&M University Health Science Center, Bryan, Texas, USA

ABSTRACT Here we present a draft genome sequence of laboratory strain *Serratia marcescens* SM6. Using the antiSMASH 5.0 prediction tool, we identified five biosynthetic gene clusters involved in secondary metabolite production (two siderophores and a biosurfactant serratamolide, a glucosamine derivative, and a thiopeptide). Whole-genome sequencing information will be useful for the detailed study of metabolites produced by *Serratia marcescens*.

Serratia marcescens is a Gram-negative bacterium from the family *Enterobacteriaceae* that can successfully adapt to different ecological niches and colonize various surfaces. It can also colonize human tissue and cause nosocomial infection of the urinary tract, respiratory tract, bloodstream, and surgical wounds (1). *S. marcescens* has been reported to produce an array of extracellular enzymes, including chitinases, lecithinases, lipases, proteases, and nucleases (2). It can also produce a number of secondary metabolites (3, 4). Among those, siderophores, low-molecular-weight molecules with a high affinity for iron, support the growth of bacteria when the iron supply is limited. Siderophores participate in iron chelating, transport of metals other than iron, protection against oxidative stress, and molecular signaling (5). We present the draft genome sequence and annotation of the laboratory strain *S. marcescens* SM6, which has been widely used in research for the past 50 years (2, 6–8) and was a gift from Michael Benedik, Texas A&M University (College Station, TX). The production of siderophores by this strain was previously reported (9); however, genetic determinants for siderophore production were not previously described.

Genomic DNA from *S. marcescens* SM6 was extracted from an overnight LB-grown culture with a genomic DNA isolation kit (Sigma-Aldrich). The quantity and quality of isolated DNA were determined with a NanoDrop spectrophotometer (Thermo Scientific). A paired-end sequencing library was prepared with the TruSeq DNA kit (Illumina), with an average fragment size of 600 bp, and sequenced with a 300 × 2-bp paired-end sequencing run on the MiSeq sequencing platform (Illumina). This procedure generated 2,895,172 paired-end reads. All reads were trimmed with Cutadapt version 1.5 for the Illumina universal adapter and low-quality bases with a cutoff of 20, and they were assembled with CLC Genomics Workbench version 7.5 (Qiagen) with default parameter settings, which indicated 300× coverage. Annotation was performed with the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) version 4.7. The assembly comprised 5,102,203 bp with 28 contigs in 24 scaffolds, an N_{50} value equal to 1,527,894, and a G+C content of 59.8%. The strain SM6 genome sequence contained 4,890 total genes, 4,736 coding sequence genes (CDS), 42 pseudogenes, and 112 RNA genes, including 82 tRNAs and 17 noncoding RNAs (ncRNAs). A search for the genetic loci required for

Citation Khilyas IV, Tursunov KA, Shirshikova TV, Kamaletdinova LK, Matrosova LE, Desai PT, McClelland M, Bogomolnaya LM. 2019. Genome sequence of pigmented siderophore-producing strain *Serratia marcescens* SM6. *Microbiol Resour Announc* 8:e00247-19. <https://doi.org/10.1128/MRA.00247-19>.

Editor Frank J. Stewart, Georgia Institute of Technology

Copyright © 2019 Khilyas 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 Lydia M. Bogomolnaya, LMBogomolnaya@kpfu.ru.

* Present address: Prerak T. Desai, Janssen Pharmaceuticals, Spring House, Pennsylvania, USA.

Received 18 March 2019

Accepted 1 April 2019

Published 2 May 2019

secondary metabolite biosynthesis, using antiSMASH version 5.0 with default parameter settings (10), indicated the presence of four nonribosomal peptide synthetase (NRPS) clusters and one ribosomally synthesized and posttranslationally modified peptide cluster in the genome of *S. marcescens* SM6. A nucleotide sequence of gene *EG355_08745*, encoded in the NRPS for siderophore biosynthetic cluster 1, shares 70% identity with gene *cbsF* of *Dickeya dadantii* 3937 (11, 12). In *Dickeya chrysanthemi*, *cbsF* is involved in the production of the siderophore chrysochitin (12). Siderophore cluster 2 of *S. marcescens* SM6 contains genes similar to *Serratia plymuthica* V4 genes involved in the biosynthesis of the siderophore serratiochelin (4). These genes (*EG355_01020*, *EG355_01055*, *EG355_01060*, and *EG355_01045*) share 78%, 73%, 78%, and 72% nucleotide identity with *S. plymuthica* V4 genes *schF0*, *schF1*, *schF2*, and *schF3*, respectively (4). The two remaining NRPS clusters contain genes involved in the biosynthesis of a biosurfactant serratamolide (13) and a glucosamine derivative (3).

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [SDUW00000000](https://doi.org/10.1093/bioinformatics/btq000). The version described in this paper is SDUW01000000. Raw sequencing data have been deposited in the SRA under the accession number [PRJNA505622](https://doi.org/10.1093/bioinformatics/btq000).

ACKNOWLEDGMENTS

This work was supported in part by the Program of Competitive Growth of Kazan Federal University, the Russian Science Foundation (project number 16-14-10200 to L.M.B.), and the Russian Foundation for Basic Research (project number 16-34-60200 to I.V.K. and project number 18-34-00458 to T.V.S.). We are grateful to the Interdisciplinary Center for Collective Use (ID number RFMEFI59414X0003), sponsored by the Ministry of Education and Science of the Russian Federation. I.V.K. was also supported by the scholarship of the President of the Russian Federation for Young Scientists and Graduate Students. M.M. and P.T.D. were supported, in part, by USDA grants 2017-67017-26180 and 2017-67015-26085, NIAID contract number HHSN272200900040C, and NIH grant R01AI136520.

REFERENCES

- Mahlen SD. 2011. *Serratia* infections: from military experiments to current practice. *Clin Microbiol Rev* 24:755–791. <https://doi.org/10.1128/CMR.00017-11>.
- Hines DA, Saurugger PN, Ihler GM, Benedik MJ. 1988. Genetic analysis of extracellular proteins of *Serratia marcescens*. *J Bacteriol* 170:4141–4146. <https://doi.org/10.1128/jb.170.9.4141-4146.1988>.
- Dwivedi D, Jansen R, Molinari G, Nimtz M, Johri BN, Wray V. 2008. Antimycobacterial serratamolides and diacyl peptidoglycosamine derivatives from *Serratia* sp. *J Nat Prod* 71:637–641. <https://doi.org/10.1021/np7007126>.
- Seyedsayamdost MR, Cleto S, Carr G, Vlamakis H, João Vieira MJ, Kolter R, Clardy J. 2012. Mixing and matching siderophore clusters: structure and biosynthesis of serratiochelins from *Serratia* sp. V4. *J Am Chem Soc* 134:13550–13553. <https://doi.org/10.1021/ja304941d>.
- Johnstone TC, Nolan EM. 2015. Beyond iron: non-classical biological functions of bacterial siderophores. *Dalton Trans* 44:6320–6339. <https://doi.org/10.1039/C4DT03559C>.
- Falkow S, Marmur J, Carey WF, Spilman WM, Baron LS. 1961. Episomic transfer between *Salmonella typhosa* and *Serratia marcescens*. *Genetics* 46:703–706.
- Ahrenholtz I, Lorenz MG, Wackernagel W. 1994. The extracellular nuclease of *Serratia marcescens*: studies on the activity in vitro and effect on transforming DNA in a groundwater aquifer microcosm. *Arch Microbiol* 161:176–183. <https://doi.org/10.1007/BF00276480>.
- Meier R, Drepper T, Svensson V, Jaeger K-E, Baumann U. 2007. A calcium-gated lid and a large beta-roll sandwich are revealed by the crystal structure of extracellular lipase from *Serratia marcescens*. *J Biol Chem* 282:31477–31483. <https://doi.org/10.1074/jbc.M704942200>.
- Khilyas IV, Shirshikova TV, Matrosova LE, Sorokina AV, Sharipova MR, Bogomolnaya LM. 2016. Production of siderophores by *Serratia marcescens* and the role of MacAB efflux pump in siderophores secretion. *BioNanoScience* 6:480–482. <https://doi.org/10.1007/s12668-016-0264-3>.
- Medema MH, Blin K, Cimermancic P, de Jager V, Zakrzewski P, Fischbach MA, Weber T, Takano E, Breitling R. 2011. antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Res* 39:W339–W346. <https://doi.org/10.1093/nar/gkr466>.
- Glasner JD, Yang C-H, Reverchon S, Hugouvieux-Cotte-Pattat N, Condemine G, Bohin J-P, Van Gijsegem F, Yang S, Franza T, Expert D, Plunkett G, III, San Francisco MJ, Charkowski AO, Py B, Bell K, Rauscher L, Rodriguez-Palenzuela P, Toussaint A, Holeva MC, He SY, Douet V, Boccaro M, Blanco C, Toth I, Anderson BD, Biehl BS, Mau B, Flynn SM, Barras F, Lindeberg M, Birch PRJ, Tsuyumu S, Shi X, Hibbing M, Mee-Ngan Y, Carpentier M, Dassa E, Umehara M, Kim JF, Rusch M, Soni P, Mayhew GF, Fouts DE, Gill SR, Blattner FR, Keen NT, Perna NT. 2011. Genome sequence of the plant-pathogenic bacterium *Dickeya dadantii* 3937. *J Bacteriol* 193:2076–2077. <https://doi.org/10.1128/JB.01513-10>.
- Sandy M, Butler A. 2009. Microbial iron acquisition: marine and terrestrial siderophores. *Chem Rev* 109:4580–4595. <https://doi.org/10.1021/cr9002787>.
- Shanks RMQ, Stella NA, Lahr RM, Wang S, Veverka TI, Kowalski RP, Liu X. 2012. Serratamolide is a hemolytic factor produced by *Serratia marcescens*. *PLoS One* 7:e36398. <https://doi.org/10.1371/journal.pone.0036398>.