


Draft Genome Sequence of Violacein-Producing Marine Bacterium *Pseudoalteromonas* sp. 520P1

Hoang Tran Dang, Kentarou Yotsumoto,  Keiichi Enomoto

School of Environmental Science and Engineering, Kochi University of Technology, Kochi, Japan

Here, we report a draft 5.25-Mb genome sequence of *Pseudoalteromonas* sp. 520P1, a marine violacein-producing bacterium isolated from the Pacific coast of Japan. Genome annotation by BLAST searches revealed the presence of one acylhomoserine lactone (AHL) synthase (*luxI*) and five AHL receptor protein (*luxR*) gene homologs.

Received 13 November 2014 Accepted 14 November 2014 Published 24 December 2014

Citation Dang HT, Yotsumoto K, Enomoto K. 2014. Draft genome sequence of violacein-producing marine bacterium *Pseudoalteromonas* sp. 520P1. *Genome Announc.* 2(6): e01346-14. doi:10.1128/genomeA.01346-14.

Copyright © 2014 Dang et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Keiichi Enomoto, enomoto.keiichi@kochi-tech.ac.jp.

Pseudoalteromonas sp. 520P1, a Gram-negative marine bacterium isolated from the Pacific coast of Japan, produces violacein only under static culture conditions (1, 2). Violacein, which is produced by several species of terrestrial and marine bacteria, is a secondary metabolite that possesses properties, such as antibacterial, antiviral, antitrypanosomal, and antitumor activities (3). These bioactive properties of violacein suggest that it could be used as a medicine or as a bio-dye because of its purple color. In a previous study, Wang et al. reported that the production of violacein by strain 520P1 was regulated by quorum-sensing mechanisms using an *N*-acylhomoserine lactone (AHL) (4). In *Vibrio fischeri*, two essential components in quorum-sensing-regulated bioluminescence, namely, AHL synthase (*LuxI*) and AHL receptor protein (*LuxR*), and their genes (*luxI/luxR*) have been revealed (5). However, homologous genes for *luxI* and *luxR* in strain 520P1 have not been reported so far. Identification of these genes is pivotal to understand regulatory mechanisms of quorum sensing and the nature of AHL(s) involved in violacein production. Therefore, we sequenced the whole genome of *Pseudoalteromonas* strain 520P1 no. 412 (NBRC 107704) to identify the *luxI* and *luxR* genes.

Genomic DNA of strain 520P1 No. 412 was purified using a QIAGEN Genomic DNA kit with a Genome-tip 100/G column (Qiagen KK, Tokyo, Japan). The genome was sequenced on an Illumina HiSeq 2000 system by MacroGen Japan (Tokyo, Japan). A total of 5,740,346 reads were assembled using SOAPdenovo Assembly into 67 scaffolds with an N_{50} length of 136,339 bp (6). The assembled draft genome sequence was approximately 5.25 Mb long with a total coverage of 110-fold and a G+C content of 34.96%. A total of 4,899 protein-coding regions and 99 RNA-coding sequences were detected using the GLIMMER system and RAST server, respectively (7, 8).

The draft genome was analyzed to locate quorum-sensing-related genes. Annotation and mapping using BLAST and the RAST server revealed that at least one *luxI* homolog and five *luxR* homologs were present in the genome of this strain. A pair of *luxI/luxR* genes was located on the same scaffold (scaffold 19) and

the orientations of the *luxI* and *luxR* genes were in opposite directions.

Genomic analyses of two violacein-producing *Pseudoalteromonas* strains have been reported so far (9, 10). A comparative study of the genomes of these strains and strain 520P1 may help clarify the protein components involved in the quorum-sensing-regulation of violacein synthesis.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. [BBIN000000000](https://www.ncbi.nlm.nih.gov/nuclink/BBIN000000000). The version described in this paper is the first version, [BBIN010000000](https://www.ncbi.nlm.nih.gov/nuclink/BBIN010000000).

ACKNOWLEDGMENT

This work was supported by the research project (2070120) of Kochi University of Technology.

REFERENCES

1. Yada S, Wang Y, Zou Y, Nagasaki K, Hosokawa K, Osaka I, Arakawa R, Enomoto K. 2008. Isolation and characterization of two groups of novel marine bacteria producing violacein. *Mar. Biotechnol.* 10:128–132. [http://dx.doi.org/10.1007/s10126-007-9046-9](https://doi.org/10.1007/s10126-007-9046-9).
2. Zhang X, Enomoto K. 2011. Characterization of a gene cluster and its putative promoter region for violacein biosynthesis in *Pseudoalteromonas* sp. 520P1. *Appl. Microbiol. Biotechnol.* 90:1963–1971. [http://dx.doi.org/10.1007/s00253-011-3203-9](https://doi.org/10.1007/s00253-011-3203-9).
3. Hoshino T. 2011. Violacein and related tryptophan metabolites produced by *Chromobacterium violaceum*: biosynthetic mechanism and pathway for construction of violacein core. *Appl. Microbiol. Biotechnol.* 91: 1463–1475. [http://dx.doi.org/10.1007/s00253-011-3468-z](https://doi.org/10.1007/s00253-011-3468-z).
4. Wang Y, Ikawa A, Okaue S, Taniguchi S, Osaka I, Yoshimoto A, Kishida Y, Arakawa R, Enomoto K. 2008. Quorum sensing signaling molecules involved in the production of violacein by *Pseudoalteromonas*. *Biosci. Biotechnol. Biochem.* 72:1958–1961. [http://dx.doi.org/10.1271/bbb.80090](https://doi.org/10.1271/bbb.80090).
5. Lazdunski AM, Ventre I, Sturgis JN. 2004. Regulatory circuits and communication in gram-negative bacteria. *Nat. Rev. Microbiol.* 2:581–592. [http://dx.doi.org/10.1038/nrmicro924](https://doi.org/10.1038/nrmicro924).
6. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience.* 1:18. [http://dx.doi.org/10.1186/2047-217X-1-18](https://doi.org/10.1186/2047-217X-1-18).

7. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics* 23:673–679. <http://dx.doi.org/10.1093/bioinformatics/btm009>.
8. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res.* 42: D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.
9. Thomas T, Evans FF, Schleheck D, Mai-Prochnow A, Burke C, Pene-syan A, Dalisay DS, Stelzer-Braid S, Saunders N, Johnson J, Ferreira S, Kjelleberg S, Egan S. 2008. Analysis of the *Pseudoalteromonas tunicata* genome reveals properties of a surface-associated life style in the marine environment. *PLoS One* 3:e3252. <http://dx.doi.org/10.1371/journal.pone.0003252>.
10. Cress BF, Erkert KA, Barquera B, Koffas MAG. 2013. Draft genome sequence of *Pseudoalteromonas luteoviolacea* strain B (ATCC 29581). *Genome Announc.* 1(2):e00048-13. <http://dx.doi.org/10.1128/genomeA.00048-13>.