

# Draft Genome Sequence of the Phosphate-Solubilizing Bacterium *Pseudomonas argentinensis* Strain SA190 Isolated from the Desert Plant *Indigofera argentea*

Feras F. Lafi,<sup>a,b</sup> Intikhab Alam,<sup>b</sup> Rene Geurts,<sup>c</sup> Ton Bisseling,<sup>c</sup> Vladimir B. Bajic,<sup>b</sup> Heribert Hirt,<sup>a</sup>  Maged M. Saad<sup>a</sup>

King Abdullah University of Science and Technology (KAUST), Biological and Environmental Sciences and Engineering Division (BESE), Thuwal, Kingdom of Saudi Arabia<sup>a</sup>; Computational Bioscience Research Center (CBRC), King Abdullah University of Science and Technology (KAUST), Thuwal, Kingdom of Saudi Arabia<sup>b</sup>; Department of Plant Sciences, Laboratory of Molecular Biology, Wageningen University, Wageningen, Netherlands<sup>c</sup>

***Pseudomonas argentinensis* strain SA190 is a plant endophytic-inhabiting bacterium that was isolated from root nodules of the desert plant *Indigofera argentea* collected from the Jizan region of Saudi Arabia. Here, we report the genome sequence of SA190, highlighting several functional genes related to plant growth-promoting activity, environment adaption, and antifungal activity.**

Received 26 October 2016 Accepted 28 October 2016 Published 22 December 2016

**Citation** Lafi FF, Alam I, Geurts R, Bisseling T, Bajic VB, Hirt H, Saad MM. 2016. Draft genome sequence of the phosphate-solubilizing bacterium *Pseudomonas argentinensis* strain SA190 isolated from the desert plant *Indigofera argentea*. *Genome Announc* 4(6):e01431-16 doi:10.1128/genomeA.01431-16.

**Copyright** © 2016 Lafi 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 Heribert Hirt, [heribert.hirt@kaust.edu.sa](mailto:heribert.hirt@kaust.edu.sa).

In an effort to explore the microbial diversity of the desert pioneer plants, the Darwin21 project (<http://www.darwin21.net>) has been established. Under the project, extensive microbial isolations from the roots of different desert plants have been conducted. Preliminary results have revealed a large diversity of bacterial species with a potential to promote the growth of *Arabidopsis thaliana* plants under abiotic stresses. A select number of these strains were sequenced and characterized as described previously (1). Phosphate-solubilizing bacteria, particularly *Pseudomonas* spp., dominated our collection and are encountered in other plants (2–5). *P. argentinensis* strain SA190 is an endophytic bacterium that was isolated from surface-sterilized root nodules of the pioneer plant *Indigofera argentea* Burm.f. (*Fabaceae*). Plants were collected in the Jizan area (16°56.475'N, 42°36.694'E) of Saudi Arabia. Based on the 16S rRNA gene sequences, the strain SA190 is closely related (99% gene similarity) to *P. argentinensis* strain CH01 (NR\_043115.1) and *P. argentinensis* strain PA01 (AY691189.2) (6).

The genomic DNA of strain SA190 was extracted using the Qiagen DNeasy blood and tissue kit, following the manufacturer's protocol. The DNA was then sequenced using paired-end Illumina MiSeq reads, with the library prepared as described previously (1). Contig assembly was done with SPAdes assembler version 3.6 (7) with a 1-kb contig cutoff size. *De novo* assembly of MiSeq reads for *P. argentinensis* strain SA190 resulted in 27 contigs with a total length of 5,055,230 bp and a mean contig size of 187,230 bp. The  $N_{50}$  was 496,934 bp, and the  $L_{50}$  was reached in four contigs. The GC content of this genome was 64%. MegaBLAST (8) searches of strain SA190 concatenated genomes against the NCBI reference genome database (<http://www.ncbi.nlm.nih.gov/genome>) revealed that the closest relative genomes with a 78% query coverage and 96% sequence identity belonged to *P. fulva* 12-X (NC\_015556.1) isolated from a rice paddy. The annotation of *P. argentinensis* SA190 was carried out using the default INDIGO pipeline (9) with the exception of open reading

frame (ORF) prediction by FragGeneScan (10). The annotation of SA190 resulted in 3,661 ORFs, six rRNAs, 57 tRNAs, and 125 ncRNAs. The annotation predicted a number of genes related to growth-promotion activity, including gene-coding clusters for phosphate solubilization: six genes for pyrroloquinoline quinone synthesis (PQQ) (EC: 1.1.5.2) organized in one operon *pqqEDCBAF*; a gene (*acdS*) that encodes for 1-aminocyclopropane-1-carboxylic acid deaminase (ACC deaminase) (EC: 3.5.99.7, K01505); and a key enzyme involved in plant growth-promotion activities (11, 12). Furthermore, genes involved in antifungal activity were found, e.g., glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) and chitinase (EC: 3.2.1.14), which has been reported to be involved in fending off plant pathogenic fungi (13). Further analysis of the genome sequence of strain SA190 will help to elucidate the metabolic pathways involved in plant growth-promoting interaction and further an understanding of molecular mechanisms for controlling some pathogens of soil-borne plant diseases.

**Accession number(s).** The genome of *P. argentinensis* SA190 was deposited at DDBJ/EMBL/GenBank under the accession number [LWDZ000000000](https://www.ncbi.nlm.nih.gov/nuccore/LWDZ000000000). The version described in this paper is the first version, LWDZ01000000.

## ACKNOWLEDGMENTS

Genome sequencing was performed at the Bioscience Core Laboratory of the King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia. Authors are grateful for the use of Dragon and snapdragon compute clusters at the Computational Bioscience Research Center (CBRC) of KAUST.

This work was supported by a base fund research grant to H.H. from the King Abdullah University of Science and Technology (KAUST). Computational aspects of this work have been supported by the KAUST Office of Sponsored Research (OSR) under awards URF/1/1976-02 and FCS/1/2448-01 to V.B.B.

## FUNDING INFORMATION

This work, including the efforts of Heribert Hirt, was funded by KAUST (BAS/1/1062-01-01). This work, including the efforts of Vladimir B. Bajic, was funded by Office of Sponsored Research, KAUST (URF/1/1976-02 and FCS/1/2448-01).

## REFERENCES

- Lafi FF, Bokhari A, Alam I, Bajic VB, Hirt H, Saad MM. 2016. Draft genome sequence of the plant growth-promoting *Cupriavidus gilardii* strain JZ4 isolated from the desert plant *Tribulus terrestris*. *Genome Announc* 4(4):e00678-16. <http://dx.doi.org/10.1128/genomeA.00678-16>.
- Oteino N, Lally RD, Kiwanuka S, Lloyd A, Ryan D, Germaine KJ, Dowling DN. 2015. Plant growth promotion induced by phosphate solubilizing endophytic *Pseudomonas* isolates. *Front Microbiol* 6:745. <http://dx.doi.org/10.3389/fmicb.2015.00745>.
- Rosas SB, Andrés JA, Rovera M, Correa NS. 2006. Phosphate-solubilizing *Pseudomonas putida* can influence the rhizobia-legume symbiosis. *Soil Biol Biochem* 38:3502–3505. <http://dx.doi.org/10.1016/j.soilbio.2006.05.008>.
- Peix A, Rivas R, Mateos PF, Martínez-Molina E, Rodríguez-Barrueco C, Velázquez E. 2003. *Pseudomonas rhizosphaerae* sp. nov., a novel species that actively solubilizes phosphate in vitro. *Int J Syst Evol Microbiol* 53: 2067–2072. <http://dx.doi.org/10.1099/ijs.0.02703-0>.
- Peix A, Rivas R, Santa-Regina I, Mateos PF, Martínez-Molina E, Rodríguez-Barrueco C, Velázquez E. 2004. *Pseudomonas lutea* sp. nov., a novel phosphate-solubilizing bacterium isolated from the rhizosphere of grasses. *Int J Syst Evol Microbiol* 54:847–850. <http://dx.doi.org/10.1099/ijs.0.02966-0>.
- Peix A, Berge O, Rivas R, Abril A, Velázquez E. 2005. *Pseudomonas argentinensis* sp. nov., a novel yellow pigment-producing bacterial species, isolated from rhizospheric soil in Córdoba, Argentina. *Int J Syst Evol Microbiol* 55:1107–1112. <http://dx.doi.org/10.1099/ijs.0.63445-0>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski 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. <http://dx.doi.org/10.1089/cmb.2012.0021>.
- Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL. 2009. BLAST+: architecture and applications. *BMC Bioinformatics* 10:421. <http://dx.doi.org/10.1186/1471-2105-10-421>.
- Alam I, Antunes A, Kamau AA, Ba Alawi WB, Kalkatawi M, Stingl U, Bajic VB. 2013. INDIGO—integrated data warehouse of microbial genomes with examples from the Red Sea extremophiles. *PLoS One* 8:e82210. <http://dx.doi.org/10.1371/journal.pone.0082210>.
- Rho MN, Tang HX, Ye YZ. 2010. FragGeneScan: predicting genes in short and error-prone reads. *Nucleic Acids Res* 38:e191. <http://dx.doi.org/10.1093/nar/gkq747>.
- Choi O, Kim J, Kim JG, Jeong Y, Moon JS, Park CS, Hwang I. 2008. Pyrroloquinoline quinone is a plant growth promotion factor produced by *Pseudomonas fluorescens* B16. *Plant Physiol* 146:657–668. <http://dx.doi.org/10.1104/pp.107.112748>.
- Loper JE, Hassan KA, Mavrodi DV, Davis EW, 2nd, Lim CK, Shaffer BT, Elbourne LD, Stockwell VO, Hartney SL, Breakwell K, Henkels MD, Tetu SG, Rangel LI, Kidarsa TA, Wilson NL, van de Mortel JE, Song C, Blumhagen R, Radune D, Hostetler JB, Brinkac LM, Durkin AS, Kluepfel DA, Wechter WP, Anderson AJ, Kim YC, Pierson LS III, Pierson EA, Lindow SE, Kobayashi DY, Raaijmakers JM, Weller DM, Thomashow LS, Allen AE, Paulsen IT. 2012. Comparative genomics of plant-associated *Pseudomonas* spp.: insights into diversity and inheritance of traits involved in multitrophic interactions. *PLoS Genet* 8:e1002784. <http://dx.doi.org/10.1371/journal.pgen.1002784>.
- Aktuganov G, Melentjev A, Galimzianova N, Khalikova E, Korpela T, Susi P. 2008. Wide-range antifungal antagonism of *Paenibacillus ehimensis* IB-X-b and its dependence on chitinase and  $\beta$ -1,3-glucanase production. *Can J Microbiol* 54:577–587. <http://dx.doi.org/10.1139/w08-043>.