



Improved Draft Genome Sequence of *Pseudomonas poae* A2-S9, a Strain with Plant Growth-Promoting Activity

Ye Xia,^a Seth DeBolt,^b Qin Ma,^c Adam McDermaid,^d Cankun Wang,^d Nicole Shapiro,^e Tanja Woyke,^e Nikos C. Kyrpides^e

^aDepartment of Plant Pathology, The Ohio State University, Columbus, Ohio, USA

^bDepartment of Horticulture, University of Kentucky, Lexington, Kentucky, USA

^cDepartment of Biomedical Informatics, The Ohio State University, Columbus, Ohio, USA

^dDepartment of Agronomy, Horticulture, and Plant Science, South Dakota State University, Brookings, South Dakota, USA

^eDepartment of Energy Joint Genome Institute, Walnut Creek, California, USA

ABSTRACT We report here the improved draft genome sequence of *Pseudomonas poae* strain A2-S9, a bacterium that was originally isolated from switchgrass plants and exhibited the capacity for plant growth promotion. Its genome has a size of 6.68 Mbp and a GC content of 61.3%. The genome encodes 6,022 predicted protein-coding genes.

The plant-associated microbiome performs important functions for plant growth, development, and health (1, 2). These microbes could be beneficial for plant biomass production and sustainable agriculture (3). *Pseudomonas* is a genus of Gram-negative, rod-shaped bacteria. They are among the most representative beneficial microbes associated with diverse plant species and have been documented to enhance plant growth and resistance to biotic and abiotic stresses (4, 5). *Pseudomonas poae* strain A2-S9 was originally isolated from switchgrass plants (*Panicum virgatum*), one of the most important biofuel crops, grown on a reclaimed coal-mining site in western Kentucky (6, 7). Through prior greenhouse experiments, it was found that *Pseudomonas poae* strain A2-S9 (originally named *Pseudomonas* sp. strain 47A) could promote switchgrass plant (*Panicum virgatum* cv. Alamo) growth (6). Therefore, it may have potential to improve the fitness of biofuel crops under stressful environmental conditions. The aim of this study was to obtain the genome of *Pseudomonas poae* strain A2-S9 to provide some insight into the metabolic and molecular mechanisms of the beneficial interactions between this strain and its switchgrass plant host.

The switchgrass plants were collected from a coal-mining site in Kentucky (6). The samples from switchgrass shoots and roots were cut into 1- to 1.5-cm segments, surface sterilized with 20 to 30% bleach, and further washed (3 to 5 times) with sterilized water. Then, the samples were put on plates with tryptic soy agar (TSA) medium (Sigma, USA) and incubated in a 26°C incubator for 3 to 5 days. Different bacterial isolates emerging from the plant segments were further isolated and purified (3 times) on TSA plates. Among these isolates, a single colony of *Pseudomonas poae* strain A2-S9 was cultured in tryptic soy broth (TSB) medium (Sigma, USA) at room temperature for 1 to 2 days (6). The bacterial cells were then centrifuged and pelleted for DNA extraction. The genomic DNA was extracted using the cetyltrimethylammonium bromide (CTAB) approach developed by the U.S. Department of Energy Joint Genome Institute (DOE-JGI; <https://jgi.doe.gov/user-program-info/pmo-overview/protocols-sample-preparation-information/jgi-bacterial-dna-isolation-ctab-protocol-2012>). The genomic DNA was sequenced by Pacific Biosciences (PacBio) technology with 86× depth at DOE-JGI (8), which generated 282,673 filtered subreads totaling 771.7 Mbp. The raw reads were assembled using Hierarchical Genome Assembly Process (HGAP) v. 2.3.0 (9). The average length of reads of >5 kb was 8,467 bp for raw reads and 7,681 bp for filtered

Citation Xia Y, DeBolt S, Ma Q, McDermaid A, Wang C, Shapiro N, Woyke T, Kyrpides NC. 2019. Improved draft genome sequence of *Pseudomonas poae* A2-S9, a strain with plant growth-promoting activity. Microbiol Resour Announc 8:e00275-19. <https://doi.org/10.1128/MRA.00275-19>.

Editor Irene L. G. Newton, Indiana University, Bloomington

Copyright © 2019 Xia et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Ye Xia, xia.374@osu.edu.

Received 8 March 2019

Accepted 18 March 2019

Published 11 April 2019

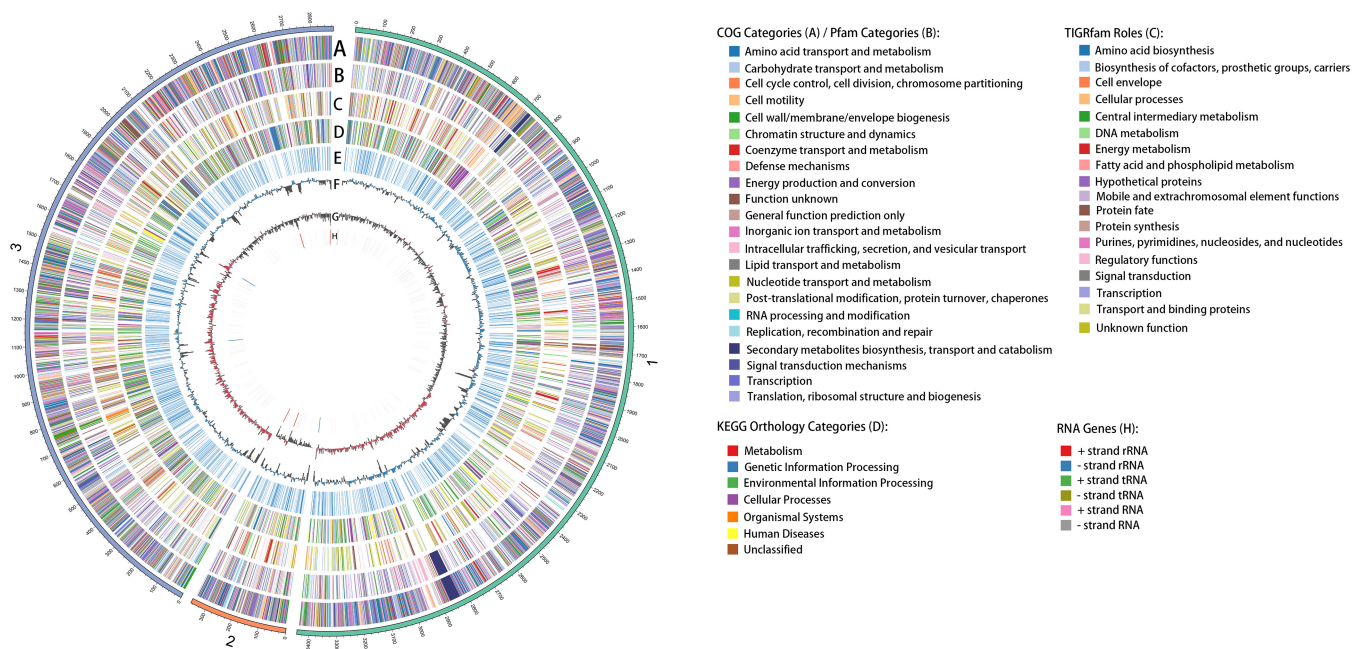


FIG 1 Circular view of the three contigs of the *Pseudomonas poae* A2-S9 genome. The circles from outside to inside denote (i) protein-coding genes with clusters of orthologous groups (COGs), (ii) protein-coding genes with Pfam, (iii) protein-coding genes with TIGRFAMs, (iv) Kyoto Encyclopedia of Genes and Genomes (KEGG) orthology regions, (v) transmembrane helix regions, (vi) GC content (blue indicates above and black indicates below the genome average of 61.3%, 5-kb window), (vii) GC skew (red indicates above and black indicates below zero, 5-kb window), and (viii) RNA genes. The figure was generated using the software Circos (12).

subreads, respectively. Genome annotation was carried out by using the JGI Integrated Microbial Genome (IMG) system (10). The genes were identified using Prodigal v. 2.5 (11). The default parameters were used for all software except where otherwise specified.

The total genome size of *Pseudomonas poae* strain A2-S9 is 6.68 Mbp with 3 contigs (Fig. 1). The GC content of this strain is 61.3%. There are 6,022 protein-coding genes, 5,114 of which have function predictions. The genome of strain A2-S9 encodes 415 genes involved in biosynthetic clusters and 731 genes involved in coding signal peptides. A total of 190 RNA genes were identified, including 22 rRNA genes, 70 tRNA genes, and 98 other RNA genes. Of the 22 rRNA genes, 7 are 5S rRNA, 7 are 16S rRNA, and 8 are 23S rRNA (Fig. 1).

The genome information of *Pseudomonas poae* strain A2-S9 will be a critical resource for studying further the functional potential of this organism and for the application of this beneficial bacterium in enhancing switchgrass yield for biofuel production.

Data availability. The whole-genome sequence described here has been deposited at DDBJ/EMBL/GenBank under BioProject accession no. [PRJNA243959](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA243959), NCBI BioSample accession no. [SAMN02745526](https://www.ncbi.nlm.nih.gov/biosample/SAMN02745526), NCBI SRA accession no. [SRS1644721](https://www.ncbi.nlm.nih.gov/sra/SRS1644721), and GOLD Project identifier Gp0060935. The sequence described in this paper is the first version. The associated sequence data can also be found at the Joint Genome Institute (JGI) portal under the IMG taxon oid no. 2603880217 (https://genome.jgi.doe.gov/portal/PsefluA2S9_FD/PsefluA2S9_FD.info.html).

ACKNOWLEDGMENTS

The genome sequencing and data annotation were carried out in the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility supported under contract no. DE-AC02-05CH11231. This work was also partially supported by the Hatch Project from USDA-NIFA-OHO01392 and OHOA1615 funds from the Ohio Agricultural Research and Development Center (OARDC) and The Ohio State University.

REFERENCES

1. Adesemoye AO, Torbert HA, Kloepper JW. 2009. Plant growth-promoting rhizobacteria allow reduced application rates of chemical fertilizers. *Microb Ecol* 58:921–929. <https://doi.org/10.1007/s00248-009-9531-y>.
2. Duijff BJ, Pouhair D, Olivain C, Alabouvette C, Lemanceau P. 1998. Implication of systemic induced resistance in the suppression of *Fusarium* wilt of tomato by *Pseudomonas fluorescens* WCS417r and by non-pathogenic *Fusarium oxysporum* Fo47. *Eur J Plant Pathol* 104:903–910. <https://doi.org/10.1023/A:1008626212305>.
3. Gouda S, Kerry RG, Das G, Paramithiotis S, Shin H-S, Patra JK. 2018. Revitalization of plant growth promoting rhizobacteria for sustainable development in agriculture. *Microbiol Res* 206:131–140. <https://doi.org/10.1016/j.micres.2017.08.016>.
4. Chu TN, Tran BTH, Van Bui L, Hoang M. 2019. Plant growth-promoting rhizobacterium *Pseudomonas* PS01 induces salt tolerance in *Arabidopsis thaliana*. *BMC Res Notes* 12:11. <https://doi.org/10.1186/s13104-019-4046-1>.
5. Egamberdieva D, Jabborova D, Hashem A. 2015. *Pseudomonas* induces salinity tolerance in cotton (*Gossypium hirsutum*) and resistance to *Fusarium* root rot through the modulation of indole-3-acetic acid. *Saudi J Biol Sci* 22:773–779. <https://doi.org/10.1016/j.sjbs.2015.04.019>.
6. Xia Y, Greissworth E, Mucci C, Williams MA, De Bolt S. 2013. Characterization of culturable bacterial endophytes of switchgrass (*Panicum virgatum* L.) and their capacity to influence plant growth. *Glob Change Biol Bioenergy* 5:674–682. <https://doi.org/10.1111/j.1757-1707.2012.01208.x>.
7. Xia Y, Amna A, Opiyo SO. 2018. The culturable endophytic fungal communities of switchgrass grown on a coal-mining site and their effects on plant growth. *PLoS One* 13:e0198994. <https://doi.org/10.1371/journal.pone.0198994>.
8. Rhoads A, Au KF. 2015. PacBio sequencing and its applications. *Genomics Proteomics Bioinformatics* 13:278–289. <https://doi.org/10.1016/j.gpb.2015.08.002>.
9. Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563. <https://doi.org/10.1038/nmeth.2474>.
10. Chen IMA, Markowitz VM, Chu K, Palaniappan K, Szeto E, Pillay M, Ratner A, Huang J, Andersen E, Huntemann M, Varghese N, Hadjithomas M, Tennessen K, Nielsen T, Ivanova NN, Kyrpides NC. 2017. IMG/M: integrated genome and metagenome comparative data analysis system. *Nucleic Acids Res* 45:D507–D516. <https://doi.org/10.1093/nar/gkw929>.
11. Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <https://doi.org/10.1186/1471-2105-11-119>.
12. Krzywinski M, Schein J, Birol J, Connors J, Gascoyne R, Horsman D, Jones SJ, Marra MA. 2009. Circos: an information aesthetic for comparative genomics. *Genome Res* 19:1639–1645. <https://doi.org/10.1101/gr.092759.109>.