3-26-2015

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Kai Nesemann
Georg-August Universität

Susanna A. Braus-Stromeyer
Georg-August Universität

Andrea Thuermer
Georg-August Universität

Rolf Daniel
Georg-August Universität

Dmitri V. Mavrodi
University of Southern Mississippi, dmitri.mavrodi@usm.edu

See next page for additional authors

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Draft Genome Sequence of the Phenazine-Producing *Pseudomonas fluorescens* Strain 2-79

Kai Nesemann,[a] Susanna A. Braus-Stromeyer,[a] Andrea Thuermer,[b] Rolf Daniel,[b] Dmitri V. Mavrodi,[c] Linda S. Thomashow,[d] David M. Weller,[d] Gerhard H. Braus[a]

Department of Molecular Microbiology and Genetics, Institute of Microbiology and Genetics, Georg-August Universität, Göttingen, Germany[a]; Department of Genomic and Applied Microbiology and Göttingen Genomics Laboratory, Institute of Microbiology and Genetics, Georg-August Universität, Göttingen, Germany[b]; Department of Biological Sciences, University of Southern Mississippi, Hattiesburg, Mississippi, USA[c]; USDA-ARS Root Disease and Biological Control Research Unit, Washington State University, Pullman, Washington, USA[d]

***Pseudomonas fluorescens* strain 2-79, a natural isolate of the rhizosphere of wheat (*Triticum aestivum* L.), possesses antagonistic potential toward several fungal pathogens. We report the draft genome sequence of strain 2-79, which comprises 5,674 protein-coding sequences.**

Received 4 February 2015 **Accepted** 18 February 2015 **Published** 26 March 2015

Citation Nesemann K, Braus-Stromeyer SA, Thuermer A, Daniel R, Mavrodi DV, Thomashow LS, Weller DM, Braus GH. 2015. Draft genome sequence of the phenazine-producing *Pseudomonas fluorescens* strain 2-79. Genome Announc 3(2):e00130-15. doi:10.1128/genomeA.00130-15.

Address correspondence to Gerhard H. Braus, gbraus@gwdg.de.

The concentration and composition of antibiotic-producing, root-colonizing organisms are important factors that partially determine the suppressiveness of soils toward certain soil-borne diseases (1).

Fluorescent pseudomonads play a major role in suppressing take-all disease of wheat caused by the fungal pathogen *Gaeumannomyces graminis* var. *tritici* (Sacc.) (2). In 1979, Weller and Cook isolated bacteria from roots of wheat plants grown in take-all suppressive soils in Washington state, USA (3). *Pseudomonas fluorescens* 2-79 (NRRL B-15132) was characterized as a strong biological control agent suppressing *G. graminis* in vitro and *in planta*. Wheat plants infected with *G. graminis* var. *tritici* and additionally treated with *P. fluorescens* 2-79 resulted in taller plants, more heads, and fewer symptoms of root disease compared to the control plants without bacterial treatment. Bacterial treatment could increase the yield up to 147% in soils fumigated with methyl bromide and up to 27% in natural soils (3). *P. fluorescens* 2-79 produces phenazines, which represent a diverse chemical group of nitrogen-containing heterocyclic pigments possessing broadly inhibitory properties toward bacteria and fungi (4). Phenazines undergo redox reactions with NADH/NADPH, leading to an increase of toxic superoxide radicals and hydrogen peroxide in the target cells (5). Mavrodi et al. investigated the biosynthesis pathway of phenazines in *P. fluorescens* 2-79 (6).

Genomic DNA of *P. fluorescens* 2-79 was isolated by using the MasterPure Complete DNA and RNA purification kit (Epicentre, Madison, WI, USA). A shotgun sequencing library was generated employing the Nextera DNA sample preparation kit following the manufacturer's instructions. The whole genome of *P. fluorescens* 2-79 was sequenced with the Genome Analyzer IIx (Illumina, San Diego, CA, USA). In total, 8.5 million paired-end reads of 112 bp were generated. *De novo* assembly of all shotgun reads using SPAdes version 3.0.0 (7) resulted in 143 contigs >3 kb and 123-fold coverage. The draft genome sequence comprises 6.4 Mb and a GC content of 59.83%. Genome annotation was performed by using Prokka (8). The draft genome harbored 1 rRNA cluster, 47 tRNA genes, 4,286 protein-encoding genes with function prediction, and 1,388 genes coding for hypothetical proteins.

Proteins involved in secondary metabolism were analyzed. The gene *hcnA* (GenBank accession no. 15560558) involved in HCN synthesis and the phenazine operon (GenBank accession no. L48616.1) are present in *P. fluorescens* 2-79. The gene *phlD* (GenBank accession no. 15563828) necessary for the synthesis of 2,4-diacetylphloroglucinol (DAPG) is absent in 2-79.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JXCQ00000000. The version described in this paper is the first version, JXCQ01000000.

ACKNOWLEDGMENTS

This work was supported by the Federal Ministry of Education and Research (BMBF) BioFung project and the DFG through grants awarded to G.H.B. We also are grateful for support provided by USDA-NRI grant no. 2011-67019-30212 from the USDA-NIFA Soil Processes program.

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