



Genome Sequence of *Pseudomonas chlororaphis* Lzh-T5, a Plant Growth-Promoting Rhizobacterium with Antimicrobial Activity

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ABSTRACT *Pseudomonas chlororaphis* Lzh-T5 is a plant growth-promoting rhizobacterium (PGPR) with antimicrobial activity isolated from tomato rhizosphere in the city of Dezhou, Shandong Province, China. Here, the draft genome sequence of *P. chlororaphis* Lzh-T5 is reported, and several functional genes related to antifungal antibiotics and siderophore biosynthesis have been found in the genome.

Rhizobacteria referred to as plant growth-promoting rhizobacteria (PGPRs) (1, 2), which have antimicrobial activity and could influence plant growth, have the potential for use as bioagents in controlling plant diseases and improving crop production. *Pseudomonas chlororaphis* is a widespread bacterium in the rhizosphere soil which can produce phenazine antibiotics that exhibit antifungal activity (3–6).

Strain *P. chlororaphis* Lzh-T5 was isolated from tomato rhizosphere in an area affected by root rot, a fungal disease caused by *Fusarium moniliforme*. Here, we report the draft genome sequence of *P. chlororaphis* Lzh-T5. Genomic DNA of *P. chlororaphis* Lzh-T5 was extracted and then sequenced using the PacBio and Illumina MiSeq systems, respectively.

The raw data were filtered and assembled by SPAdes software version 3.9.0 (7) and A5-MiSeq version 20150522 (8) to generate 1,224 Mb of total clean data, and the genome coverage was 164.0×. The assembled genome of *P. chlororaphis* Lzh-T5 comprises a single circular chromosome of 6,826,693 bp in length, with a GC content of 63.06%. Its genome comprises 6,282 genes, 6,116 open reading frames (ORFs), 67 tRNA genes, and 16 rRNA genes, which is similar to *P. chlororaphis* PA23 (99%) (GenBank accession number CP008696), *P. chlororaphis* ATCC 13985 (99%) (GenBank accession number LT629738), and *P. chlororaphis* LMG 21630 (98%) (GenBank accession number LT629747).

Like most *Pseudomonas* spp., *P. chlororaphis* Lzh-T5 possessed several gene clusters to generate siderophores, such as pyoverdine (PVD) and achromobactin. There were two nonadjacent clusters involved in PVD synthesis, including 4 nonribosomal peptide synthetase (NRPS) genes (GenBank accession numbers CXP47_RS20395, CXP47_RS20400, CXP47_RS20405, and CXP47_RS20875) (9). Clusters to synthesize achromobactin consisted of the synthesis genes *acsA-F* (CXP47_RS15760, CXP47_RS15765, CXP47_RS15770, CXP47_RS15780, CXP47_RS15785 and CXP47_RS15790) and achromobactin transporter genes *cbrA* through *cbrD* (CXP47_RS15755, CXP47_RS15750, CXP47_RS15745, and CXP47_RS15740) (10).

P. chlororaphis Lzh-T5 can also synthesize antifungal antibiotics, and gene clusters for antibiotics synthesis were found. For example, *prnA* through *prnD* (CXP47_RS17640,

Received 20 March 2018 Accepted 29 March 2018 Published 3 May 2018

Citation Li Z, Li X, Zeng Q, Chen M, Liu D, Wang J, Shen L, Song F. 2018. Genome sequence of *Pseudomonas chlororaphis* Lzh-T5, a plant growth-promoting rhizobacterium with antimicrobial activity. *Genome Announc* 6: e00328-18. <https://doi.org/10.1128/genomeA.00328-18>.

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CXP47_RS17635, CXP47_RS17630, and CXP47_RS17625) coding for pyrrolnitrin (11), *hcnA* through *hcnC* (CXP47_RS12080, CXP47_RS12085, and CXP47_RS12090) coding for volatile compound hydrogen cyanide (12), and *phzI*, *phzR*, *phzA* through *phzG*, and *phzO* (CXP47_RS25500, CXP47_RS25505, CXP47_RS25510, CXP47_RS25515, CXP47_RS25520, CXP47_RS25525, CXP47_RS25530, CXP47_RS25535, CXP47_RS25540, and CXP47_RS25545) coding for phenazine, were found (3). Meanwhile, as nitrogen-containing pigments, phenazine and its derivatives also have many biotechnological applications, such as colorimetric redox indicators (13).

In conclusion, the genome sequence and annotation of *P. chlororaphis* Lzh-T5 contributed to revealing the molecular mechanism of its antimicrobial activity, which suggests that *P. chlororaphis* Lzh-T5 could be used as a biocontrol agent of various soilborne diseases.

Accession number(s). The whole-genome shotgun project of *Pseudomonas chlororaphis* Lzh-T5 has been deposited at GenBank under the accession number [CP025309](#).

ACKNOWLEDGMENTS

This work was supported by Natural Science Foundation of Shandong Province (grant ZR2015CQ002), the Taishan Young Scholars Program of Shandong Province of China (grant tsqn20161049), the Talent Introduction Project of Dezhou University of China (grant 2016kjrc10), Projects of Science and Technology for Colleges and Universities in Shandong Province (grants J17KA099 and J15LE09), the National Natural Science Foundation of China (grants 31500606 and 61671107), and the Shandong Provincial Key Laboratory of Agricultural Microbiology Open Fund (grant SDKL2017015).

REFERENCES

- Handelsman J, Stabb EV. 1996. Biocontrol of soilborne plant pathogens. *Plant Cell* 8:1855–1869. <https://doi.org/10.1105/tpc.8.10.1855>.
- Bhattacharyya PN, Jha DK. 2012. Plant growth-promoting rhizobacteria (PGPR): emergence in agriculture. *World J Microbiol Biotechnol* 28:1327–1350. <https://doi.org/10.1007/s11274-011-0979-9>.
- Calderón CE, Ramos C, de Vicente A, Cazorla FM. 2015. Comparative genomic analysis of *Pseudomonas chlororaphis* PCL1606 reveals new insight into antifungal compounds involved in biocontrol. *Mol Plant Microbe Interact* 28:249–260. <https://doi.org/10.1094/MPMI-10-14-0326-FI>.
- Ranjbariyan A, Shams-Ghahfarokhi M, Razzaghi-Abyaneh M. 2014. Antifungal activity of a soil isolate of *Pseudomonas chlororaphis* against medically important dermatophytes and identification of a phenazine-like compound as its bioactive metabolite. *J Mycol Med* 24:e57–e64. <https://doi.org/10.1016/j.mycmed.2014.01.117>.
- Morohoshi T, Wang WZ, Suto T, Saito Y, Ito S, Someya N, Ikeda T. 2013. Phenazine antibiotic production and antifungal activity are regulated by multiple quorum-sensing systems in *Pseudomonas chlororaphis* subsp. *aurantiaca* StFRB508. *J Biosci Bioeng* 116:580–584. <https://doi.org/10.1016/j.jbiosc.2013.04.022>.
- Kiprianova EA, Shepelevich VV, Klochko VV, Ostapchuk AN, Varbanets LD, Skokliuk LB, Berezkina AE, Avdeeva LV. 2013. Antifungal and antiviral substances of *Pseudomonas chlororaphis* subsp. *aureofaciens* strains—components of gaupsin. *Mikrobiol Z* 75:28–35. (In Russian.)
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski 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. <https://doi.org/10.1089/cmb.2012.0021>.
- Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. *Bioinformatics* 31:587–589. <https://doi.org/10.1093/bioinformatics/btu661>.
- Ringel MT, Dräger G, Brüser T. 2016. PvdN enzyme catalyzes a periplasmic pyoverdine modification. *J Biol Chem* 291:23929–23938. <https://doi.org/10.1074/jbc.M116.755611>.
- Berti AD, Thomas MG. 2009. Analysis of achromobactin biosynthesis by *Pseudomonas syringae* pv. *syringae* B728a. *J Bacteriol* 191:4594–4604. <https://doi.org/10.1128/JB.00457-09>.
- Costa R, van Aarle IM, Mendes R, van Elsas JD. 2009. Genomics of pyrrolnitrin biosynthetic loci: evidence for conservation and whole-operon mobility within Gram-negative bacteria. *Environ Microbiol* 11:159–175. <https://doi.org/10.1111/j.1462-2920.2008.01750.x>.
- Michelsen CF, Stougaard P. 2012. Hydrogen cyanide synthesis and antifungal activity of the biocontrol strain *Pseudomonas fluorescens* In5 from Greenland is highly dependent on growth medium. *Can J Microbiol* 58:381–390. <https://doi.org/10.1139/w2012-004>.
- Bilal M, Guo S, Iqbal HMN, Hu H, Wang W, Zhang X. 2017. Engineering *Pseudomonas* for phenazine biosynthesis, regulation, and biotechnological applications: a review. *World J Microbiol Biotechnol* 33:191. <https://doi.org/10.1007/s11274-017-2356-9>.