

Genome Sequence of *Pseudomonas chlororaphis* Strain PA23

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***Pseudomonas chlororaphis* strain PA23 is a plant-beneficial bacterium that is able to suppress disease caused by the fungal pathogen *Sclerotinia sclerotiorum* through a process known as biological control. Here we present a 7.1-Mb assembly of the PA23 genome.**

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Pseudomonas chlororaphis strain PA23 is a soybean root isolate that is able to protect canola from stem rot disease caused by the fungal pathogen *Sclerotinia sclerotiorum* (Lib.) de Bary (1, 2). This bacterium secretes a wide range of compounds, including the antibiotics pyrrolnitrin, phenazine 1-carboxylic acid (PCA), and 2-hydroxyphenazine (2-OH-PHZ), together with chitinase, protease, lipase, and siderophores (3, 4). We have established that pyrrolnitrin is essential for PA23-mediated biocontrol (5). As is the case for many biocontrol pseudomonads, expression of PA23 antifungal factors is governed by a complex regulatory hierarchy. One of the key elements is the GacS/GacA two-component signal transduction system, which works in concert with the Rsm system (4, 6). Additional regulators that oversee production of antifungal compounds include the PhzI/PhzR quorum-sensing system (7), the stationary-phase sigma factor RpoS (8), a transcriptional regulator of RpoS known as PsrA (6), and a global stress response called the stringent response (8).

The genome of *P. chlororaphis* PA23 was sequenced utilizing a Pacific Biosciences data set generated by GenomeQuebec, which was assembled using the PacBio SMRT Analysis pipeline version 2.2.0 (<http://www.pacificbiosciences.com>) with 72-fold coverage to give a single contiguous genome sequence. The sequence was annotated by the NCBI prokaryotic genomes annotation pipeline.

The *P. chlororaphis* PA23 genome consists of 7,122,173 bases with a G+C content of 62.6%. There are 6,179 putative coding sequences, 68 tRNA genes, and 5 rRNA clusters. In addition, bio-synthetic loci for pyrrolnitrin, phenazine, hydrogen cyanide, and alkaline protease have been identified, which is consistent with exoproducts secreted by this bacterium. Comparison of the genome with those of the two other completed *P. chlororaphis* genomes, O6 (CM001490) and subsp. *aureofaciens* 30-84 (CM001559) (9), using Mauve version 2.3.1 (10) revealed a ~600 kbp inversion compared to both O6 and 30-84, together with a short 60-kbp rearrangement relative to O6 alone.

Nucleotide sequence accession number. The genome sequence of *P. chlororaphis* PA23 has been deposited at the NCBI GenBank under the accession number [CP008696](https://doi.org/10.1093/bioinformatics/btu086).

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REFERENCES

- Savchuk S, Fernando WGD. 2004. Effect of timing of application and population dynamics on the degree of biological control of *Sclerotinia sclerotiorum* by bacterial antagonists. *FEMS Microbiol. Ecol.* 49:379–388. <http://dx.doi.org/10.1016/j.femsec.2004.04.014>.
- Zhang Y. 2004. Biocontrol of *Sclerotinia* stem rot of canola by bacterial antagonists and study of biocontrol mechanisms involved. M.Sc. thesis, University of Manitoba, Winnipeg, MB.
- Zhang Y, Fernando WGD, de Kievit TR, Berry C, Daayf F, Paulitz TC. 2006. Detection of antibiotic-related genes from bacterial biocontrol agents with polymerase chain reaction. *Can. J. Microbiol.* 52:476–481. <http://dx.doi.org/10.1139/w05-152>.
- Poritsanos N, Selin C, Fernando WGD, Nakkeeran S, de Kievit TR. 2006. A GacS deficiency does not affect *Pseudomonas chlororaphis* PA23 fitness when growing on canola, in aged batch culture or as a biofilm. *Can. J. Microbiol.* 52:1177–1188. <http://dx.doi.org/10.1139/w06-079>.
- Selin C, Habibian R, Poritsanos N, Athukorala SN, Fernando WGD, de Kievit TR. 2010. Phenazines are not essential for *Pseudomonas chlororaphis* PA23 biocontrol of *Sclerotinia sclerotiorum*, but do play a role in biofilm formation. *FEMS Microbiol. Ecol.* 7:73–83. <http://dx.doi.org/10.1111/j.1574-6941.2009.00792.x>.
- Selin C, Manuel J, Fernando WGD, de Kievit T. 2014. Expression of the *Pseudomonas chlororaphis* strain PA23 Rsm system is under control of GacA, RpoS, PsrA, quorum sensing and the stringent response. *Biol. Contr.* 69:24–33. <http://dx.doi.org/10.1016/j.biocontrol.2013.10.015>.
- Selin C, Fernando WGD, de Kievit T. 2012. The PhzI/PhzR quorum-sensing system is required for pyrrolnitrin and phenazine production, and exhibits cross-regulation with RpoS in *Pseudomonas chlororaphis* PA23. *Microbiol.* 158:896–907. <http://dx.doi.org/10.1099/mic.0.054254-0>.
- Manuel J, Selin C, Fernando WGD, de Kievit T. 2012. Stringent response mutants of *Pseudomonas chlororaphis* PA23 exhibits enhanced antifungal activity against *Sclerotinia sclerotiorum* in vitro. *Microbiol.* 158:207–216. <http://dx.doi.org/10.1099/mic.0.053082-0>.
- Loper J, Hassan KA, Mavrodi DV, Davis II, EW, Lim CK, Shaffer BT, Elbourne LDH, 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 III LS, Pierson EA, Lindow SE, Kobayashi DY, Raaijmakers JM, Weller DM, Thomashow LS, Allen AE, Paulsen IR. 2012. Comparative genomics of plant-associated *Pseudomonas* spp.: insights into diversity and inheritance traits involved in multitrophic interactions. *PLoS Genet.* 8:e1002784. <http://dx.doi.org/10.1371/journal.pgen.1002784>.
- Darling AE, Mau B, Perna NT. 2010. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. *PLoS One* 5:e11147. <http://dx.doi.org/10.1371/journal.pone.0011147>.