

Draft Genome Sequence of *Pseudomonas savastanoi* pv. *savastanoi* Strain DAPP-PG 722, Isolated in Italy from an Olive Plant Affected by Knot Disease

Chiaraluca Moretti,^a Chiara Cortese,^a Daniel Passos da Silva,^b Vittorio Venturi,^b Cayo Ramos,^c Giuseppe Firrao,^d Roberto Buonauro^a

Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Università degli Studi di Perugia, Perugia, Italy^a; International Centre for Genetic Engineering and Biotechnology, Trieste, Italy^b; Instituto de Hortofruticultura Subtropical y Mediterránea La Mayora, Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC), Área de Genética, Málaga, Spain^c; Dipartimento di Scienze Agrarie e Ambientali, Università degli Studi di Udine, Udine, Italy^d

Olive knot disease, caused by the bacterium *Pseudomonas savastanoi* pv. *savastanoi*, seriously affects olive trees in the Mediterranean basin. Here, we report the draft genome sequence of *P. savastanoi* pv. *savastanoi* DAPP-PG 722, a strain isolated in Italy from an olive plant affected by knot disease.

Received 26 August 2014 Accepted 28 August 2014 Published 2 October 2014

Citation Moretti C, Cortese C, Passos da Silva D, Venturi V, Ramos C, Firrao G, Buonauro R. 2014. Draft genome sequence of *Pseudomonas savastanoi* pv. *savastanoi* strain DAPP-PG 722, isolated in Italy from an olive plant affected by knot disease. *Genome Announc.* 2(5):e00864-14. doi:10.1128/genomeA.00864-14.

Copyright © 2014 Moretti et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Chiaraluca Moretti, chiaraluca.moretti@unipg.it.

There is an increasing interest in olive (*Olea europaea* L.) growing in many countries, probably due to the benefit of olive oil in human health. Olive knot caused by *Pseudomonas savastanoi* pv. *savastanoi* represents a serious disease in many olive-producing areas, which can cause a progressive plant decline that leads to reductions in the number of fruit-bearing shoots and in tree yield potential (1). Disease symptoms are characterized by knots on different parts of the plant, mainly on twigs and young branches (2). Many other bacterial species have been reported to be associated with olive knots (3), in particular *Pantoea agglomerans*, *Erwinia oleae* (4), and *Erwinia toletana*. These olive knot associated bacteria have been reported to form a stable inter-species community with *P. savastanoi* pv. *savastanoi*; to communicate through a quorum-sensing system mediated by *N*-acyl-homoserine lactone signals, and to increase the disease severity when coinoculated with the pathogen in olive plants (5, 6).

Genomics analyses reported to date for *P. savastanoi* pv. *savastanoi* include only the draft genome sequence of strain NCPPB3335 (7), isolated from an olive knot in France, and the complete plasmid sequence of the three-plasmid complement of this strain (8). We report here the draft genome sequence of *P. savastanoi* pv. *savastanoi* strain DAPP-PG722, isolated from an olive knot in Perugia (central Italy). Genomic DNA was prepared using the Nextera DNA sample preparation kit (Illumina), according to the manufacturer's instructions. Sequencing was performed on an IlluminaMiSeq platform using indexed paired-end 250-nucleotide v2 chemistry. The sequencing produced an output of 1,854,337 reads representing approximately 70-fold coverage of the genome. Assembly, made by Edena assembler (9), yielded 412 contigs with a maximum length of 150 kb and an N_{50} of 46 kb, assuming a genome size of 6.42 Mb. The G+C content is 57.9%, which is similar to the 57.12% G+C content reported for *P. savastanoi* pv. *savastanoi* strain NCPPB3335 (7).

Automatic annotation of the genome, performed using RAST (10), predicted a total of 5,972 candidate protein-coding genes in

the draft genome sequence of *P. savastanoi* pv. *savastanoi* DAPP-PG722, with 1,573 of them (35.7%) annotated as hypothetical proteins. This draft genome also contains 57 tRNA and 16 rRNA sequences. A comparative analysis was performed with the genome sequence of *P. savastanoi* pv. *savastanoi* NCPPB3335 (accession no. CM001834.1) using MUMmer (11). The results showed that 89% of the *P. savastanoi* pv. *savastanoi* DAPP-PG722 genome aligned with that of NCPPB3335 with an average of 85% of identity.

Several genes encoding ABC transporters for sugars and urea were found exclusively in the DAPP-PG722 genome. Furthermore, it contains genes involved in the biosynthesis of secretion systems I, II, III, IV, and VI. In agreement with data reported for NCPPB3335, the genome of DAPP-PG722 encoded a complete type III secretion system (T3SS). Additionally, a comparison of the effector repertoire of the two strains revealed that they share all 33 T3SS effectors reported for NCPPB3335 (12). However, the DAPP-PG722 genome also encodes the effector gene *hopA1'*, which is absent in NCPPB3335.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JOJV00000000. The version described in this paper is version JOJV00000000.

ACKNOWLEDGMENTS

This study was supported by a grant from Fondazione Cassa di Risparmio di Perugia "Indagini sul ruolo dei fenoli dell'olivo nello sviluppo della rogna, per individuare nuove strategie di lotta alla malattia" and by the Spanish plan Nacional I+D+i grant AGL2011-30343-CO2-01, co-financed by FEDER funds.

We thank Luca Bonciarelli for technical assistance.

REFERENCES

1. Quesada JM, Penyalver R, Pérez-Panadés J, Salcedo CI, Carbonell EA, López MM. 2010. Comparison of chemical treatments for reducing epiphytic *Pseudomonas savastanoi* pv. *savastanoi* populations and for im-

- proving subsequent control of olive knot disease. *Crop Protect.* 29: 1413–1420. <http://dx.doi.org/10.1016/j.cropro.2010.07.024>.
2. Ramos C, Matas IM, Bardaji L, Aragon IM, Murillo J. 2012. *Pseudomonas savastanoi* pv. *savastanoi*: some like it knot. *Mol. Plant Pathol.* 13: 998–1009. <http://dx.doi.org/10.1111/j.1364-3703.2012.00816.x>.
 3. Passos da Silva D, Castañeda-Ojeda MP, Moretti C, Buonauro R, Ramos C, Venturi V. 2014. Bacterial multispecies studies and microbiome analysis of a plant disease. *Microbiology* 160:556–566. <http://dx.doi.org/10.1099/mic.0.074468-0>.
 4. Moretti C, Hosni T, Vandemeulebroecke K, Brady C, De Vos P, Buonauro R, Cleenwerck I. 2011. *Erwinia oleae* sp. nov., isolated from olive knots caused by *Pseudomonas savastanoi* pv. *savastanoi*. *Int. J. Syst. Evol. Microbiol.* 61:2745–2752. <http://dx.doi.org/10.1099/ijs.0.026336-0>.
 5. Hosni T, Moretti C, Devescovi G, Suarez-Moreno ZR, Fatmi MB, Guarnaccia C, Pongor S, Onofri A, Buonauro R, Venturi V. 2011. Sharing of quorum-sensing signals and role of interspecies communities in a bacterial plant disease. *ISME J.* 5:1857–1870. <http://dx.doi.org/10.1038/ismej.2011.65>.
 6. Hosni T. 2010. Interaction between *Pseudomonas savastanoi* pv. *savastanoi*, the causal agent of olive knot, and the endophytic bacterial species associated with the knot. Ph.D. thesis. University of Perugia, Italy.
 7. Rodríguez-Palenzuela P, Matas IM, Murillo J, López-Solanilla E, Bardaji L, Pérez-Martínez I, Rodríguez-Mosquera E, Penyalver R, López MM, Quesada JM, Biehl BS, Perna NT, Glasner JD, Cabot EL, Neeno-Eckwall E, Ramos C. 2010. Annotation and overview of the *Pseudomonas savastanoi* pv. *savastanoi* NCPPB 3335 draft genome reveals the virulence gene complement of a tumour-inducing pathogen of woody hosts. *Environ. Microbiol.* 12:1604–1620. <http://dx.doi.org/10.1111/j.1462-2920.2010.02207.x>.
 8. Bardaji L, Perez-Martinez I, Rodriguez-Moreno L, Rodriguez-Palenzuela P, Sundin GW, Ramos C, Murillo J. 2011. Sequence and role in virulence of the three plasmid complement of the model tumour-inducing bacterium *Pseudomonas savastanoi* pv. *savastanoi* NCPPB 3335. *PLoS One* 6:e25705. <http://dx.doi.org/10.1371/journal.pone.0025705>.
 9. Hernandez D, François P, Farinelli L, Osterås M, Schrenzel J. 2008. *De novo* bacterial genome sequencing: millions of very short reads assembled on a desktop computer. *Genome Res.* 18:802–809. <http://dx.doi.org/10.1101/gr.072033.107>.
 10. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
 11. Kurtz S, Phillippy A, Delcher AL, Smoot M, Shumway M, Antonescu C, Salzberg SL. 2004. Versatile and open software for comparing large genomes. *Genome Biol.* 5:R12. <http://dx.doi.org/10.1186/gb-2004-5-2-r12>.
 12. Matas IM, Castañeda-Ojeda MP, Aragón IM, Antúnez-Lamas M, Murillo J, Rodríguez-Palenzuela P, López-Solanilla E, Ramos C. 2014. Translocation and functional analysis of *Pseudomonas savastanoi* pv. *savastanoi* NCPPB 3335 type III secretion system effectors reveals two novel effector families of the *Pseudomonas syringae* complex. *Mol. Plant Microbe Interact.* 27:424–436. <http://dx.doi.org/10.1094/MPMI-07-13-0206-R>.