



Whole-Genome Sequence of a *Pantoea* sp. Strain Isolated from an Olive (*Olea europaea* L.) Knot

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ABSTRACT Here, we present the total genome sequence of *Pantoea* sp. strain paga, a plant-associated bacterium isolated from knots present on olive trees grown on the Adriatic Coast. The genome size of *Pantoea* sp. paga is 5.08 Mb, with a G+C content of 54%. The genome contains 4,776 predicted coding DNA sequences (CDSs), including 70 tRNA genes and 1 ribosomal operon. Obtained genome sequence data will provide insight on the physiology, ecology, and evolution of *Pantoea* spp.

Pantoea is a genus of Gram-negative bacteria belonging to phylum *Proteobacteria*, class *Gammaproteobacteria*, order *Enterobacteriales*, family *Erwiniaceae*. In the olive knot disease, the nonpathogenic bacterial species *Pantoea agglomerans* and *Erwinia toletana*, olive plant epiphytes and endophytes, coexist with the pathogenic bacterium *Pseudomonas savastanoi* pv. *savastanoi*, the causal agent of disease (1–3).

P. agglomerans strains inhabiting olive trees as nonpathogenic endophytes have been shown to cooperate with strains of *P. savastanoi*, forming a stable bacterial consortium that increases the severity of disease (1). It has been suggested that the indole-3-acetic acid (IAA) and cytokinins produced by *P. agglomerans* may increase the size of the knots on olive caused by *P. savastanoi* and also that the growth of *P. agglomerans* is apparently supported by the copresence of an actively growing population of *P. savastanoi* (2).

Bacterial cells were isolated from olive knots isolated in the central region of Dalmatia, Croatia (global positioning system [GPS] coordinates 43°30'19.6"N, 16°29'55.0"E). Fresh olive knots were surface sterilized by 75% ethanol, sliced with a sterile scalpel, and plated onto King's medium agar plates (4). Plates were kept in the dark at 25°C for 48 h. An isolated single colony was transferred into 10 ml of liquid lysogeny broth (LB) medium and grown at 28°C for 24 h with shaking. DNA was isolated from bacterial cells using a microbial DNA kit (Macherey-Nagel, Hoerd, France).

Two micrograms of genomic DNA was used for fragmentation and 300-bp library preparation using a Nextera XT DNA library prep kit and protocol (Illumina, Evry, France), and 2 × 150-bp paired-end sequencing was done using Illumina technology at GATC Biotech (Mulhouse, France). Quality controls were made with FastQC (5) and Trimmomatic (6). We obtained a total of 7,822,775 reads, with 462× coverage and a G+C content of 54%. Genome assembly was realized using Unicycler v0.4.3 software, and annotation was done with the MicroScope platform v3.10.0 using default parameters, with a minimum contig length of 200 bp (7–9). The *Pantoea* sp. genome is assembled in 52 contigs, with the largest contigs of 1,219,567 bp. The genome size has 5,077,592 bp, an N_{50} value of 580,527 bp, a G+C content of 54.58%, and 4,786 annotated genes.

Data availability. The complete genome sequence described here has been deposited at NCBI/GenBank under BioProject number [PRJNA555164](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA555164), BioSample number

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SAMN12302724, and GenBank accession number VLTf00000000. Raw reads were deposited at NCBI under SRA accession number SRX6799334. The version described in this paper is the first version. The *Pantoea* sp. paga strain is available on request from the Institute for Adriatic Crops (IAC).

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We declare no conflict of interest.

REFERENCES

- 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. <https://doi.org/10.1038/ismej.2011.65>.
- Marchi G, Sisto A, Cimmino A, Andolfi A, Cipriani MG, Evidente A, Surico G. 2006. Interaction between *Pseudomonas savastanoi* and *Pantoea agglomerans* in the olive knots. *Plant Pathol* 55:614–624. <https://doi.org/10.1111/j.1365-3059.2006.01449.x>.
- Buonauro R, Moretti C, Passos da Silva D, Cortese C, Ramos C, Venturi V. 2015. The olive knot disease as a model to study the role of interspecies bacterial communities in plant disease. *Front Plant Sci* 6:434. <https://doi.org/10.3389/fpls.2015.00434>.
- King EO, Ward MK, Raney DE. 1954. Two simple media for the demonstration of pyocyanin and fluorescin. *J Lab Clin Med* 44:301–307.
- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
- Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Comput Biol* 13:e1005595. <https://doi.org/10.1371/journal.pcbi.1005595>.
- Vallenet D, Calteau A, Cruveiller S, Gachet M, Lajus A, Josso A, Mercier J, Renaux A, Rollin J, Rouy Z, Roche D, Scarpelli C, Médigue C. 2017. MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. *Nucleic Acids Res* 45:D517–D528. <https://doi.org/10.1093/nar/gkw1101>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.