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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.

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