



# High-Quality Draft Genome Sequence of *Xanthomonas arboricola* pv. *juglandis* CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment

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**ABSTRACT** Here, we report the draft genome sequence of *Xanthomonas arboricola* pv. *juglandis* CPBF 1521, isolated from symptomatic leaves of an ornamental walnut in a public site in Portugal without any record of phytosanitary treatment. This isolate may constitute a genomic reference of a wild-type strain in comparative genomics studies.

*Xanthomonas arboricola* pv. *juglandis* (*Gammaproteobacteria* class, *Xanthomonadales* order, *Xanthomonadaceae* family) is a threatening and important pathogen of the principal commercial nut trees Persian walnut and English walnut (*Juglans regia* L.) (1, 2). Diseases caused by *X. arboricola* pv. *juglandis* have been demonstrated by the development of several symptoms, namely the presence of necrotic lesions on leaves and fruits, the presence of external apical necrosis near the blossom end evolving into fruit necrosis, and the presence of vertical cankers, brown to black exudates, and distortions on trunks (3–5). Not surprisingly, *X. arboricola* pv. *juglandis* is responsible for increasing losses in walnut production resulting in a negative economic impact for walnut crop regions in many countries worldwide (1, 2, 6).

The present announcement reports the whole-genome sequence of a *X. arboricola* pv. *juglandis* strain, CPBF 1521, isolated in October 2014 from the leaves of an ornamental *J. regia* specimen in a public site in Loures, Portugal, showing typical symptoms of walnut bacterial blight, and for which no phytosanitary treatments were applied. This set of features suggests that this strain has not been exposed to selective pressures caused by phytosanitary treatments, such as copper-based compound sprays, making this genomic data set particularly interesting for comparative genomics studies.

*X. arboricola* pv. *juglandis* CPBF 1521 was obtained from infected leaf samples as previously described (7) and was grown on M2 medium (yeast extract, 2 g liter<sup>-1</sup>; Bacto peptone, 5 g liter<sup>-1</sup>; NaCl, 5 g liter<sup>-1</sup>; KH<sub>2</sub>PO<sub>4</sub>, 0.45 g liter<sup>-1</sup>; and Na<sub>2</sub>HPO<sub>4</sub> 12H<sub>2</sub>O, 2.39 g liter<sup>-1</sup>) at 28°C for 48 h with shaking (100 rpm). The EZNA bacterial DNA purification kit (Omega Bio-Tek, Norcross, GA) was used for DNA extraction. Standard genomic library preparation and sequencing was carried out with at the GATC Biotech AG (Konstanz, Germany) using an Illumina HiSeq platform with 2 × 150-bp paired-end reads. Raw sequence data with approximately 10,113,730 reads were assembled

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*de novo* using MIRA version 4.0 (8) in accurate mode with standard settings. The set of contigs obtained was reassembled using SeqMan Pro from the Lasergene genomics package version 12.1.0 (DNASTar, Madison, WI) with Pro Assembler parameters and reads were mapped using SeqMan NGen with standard settings to check for inconsistencies. Contigs were ordered according to the related reference genome of *X. arboricola* pv. *juglandis* (strain CFBP 2528; GenBank accession number [NZ\\_JZEF00000000](https://doi.org/10.1093/nucleic-acids/nz-jzef0000000)) (9) using the Move Contigs function in Mauve version 20150226 build 10 (10, 11). Genome annotation was performed with Prokka version 1.12 (12) based on *de novo* discovery of genes using a *Xanthomonas* genus database.

The *X. arboricola* pv. *juglandis* CPBF 1521 genome contains 56 contigs with an  $N_{50}$  value of 173,159 bp, has a total size of 5,194,740 bp, and a G+C content of 65.41%. A total of 4,494 coding sequences (CDS) with 4 rRNAs and 53 tRNAs were found using Prokka. Initial comparative analysis using EDGAR version 2.0 (13) identified 3,984 CDS shared between CPBF 1521 and *X. arboricola* pv. *juglandis* CFBP 2528 that was used as a reference genome. Moreover, a high average nucleotide identity value (98%) was obtained between these two strains.

This newly sequenced genome expands the existing genomic data for *X. arboricola* pv. *juglandis* (8, 14–16). Further genomic comparison studies are being conducted to identify unique genomic features of *X. arboricola* pv. *juglandis* CPBF 1521.

**Data availability.** This whole-genome shotgun project has been deposited in the European Nucleotide Archive (ENA) under the BioProject accession number [PRJEB27248](https://www.ebi.ac.uk/bioproject/12248) and in GenBank under the accession number [UIHD00000000](https://www.ncbi.nlm.nih.gov/genbank/100000000). The version described in this paper is the first version, UIHD01000000.

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