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Xanthomonas euroxanthea sp. nov., a new xanthomonad species including pathogenic and non-pathogenic strains of walnut

Leonor Martins1,2,* Camila Fernandes1,2,3 Jochen Blom4 Nay C. Dia5,6 Joël F. Pothier5 and Fernando Tavares1,2,*

Abstract
We describe a novel species isolated from walnut (Juglans regia) which comprises non-pathogenic and pathogenic strains on walnut. The isolates, obtained from a single ornamental walnut tree showing disease symptoms, grew on yeast extract–dextrose–carbonate agar as mucoid yellow colonies characteristic of Xanthomonas species. Pathogenicity assays showed that while strain CPBF 424T causes disease in walnut, strain CPBF 367 was non-pathogenic on walnut leaves. Biolog GEN III metabolic profiles disclosed some differences between strains CPBF 367 and CPBF 424T and other xanthomonads. Multilocus sequence analysis with seven housekeeping genes (gyrB, rpoD, atpD, dnaK, efp, gltA) grouped these strains in a distinct cluster from Xanthomonas arboricola pv. juglandis and closer to Xanthomonas prunicola and Xanthomonas arboricola pv. populi. Average nucleotide identity (ANI) analysis results displayed similarity values below 93% to X. arboricola strains. Meanwhile ANI and digital DNA–DNA hybridization similarity values were below 89 and 50% to non-arboricola Xanthomonas strains, respectively, revealing that they do not belong to any previously described Xanthomonas species. Furthermore, the two strains show over 98% similarity to each other. Genomic analysis shows that strain CPBF 424T harbours a complete type III secretion system and several type III effector proteins, in contrast with strain CPBF 367, shown to be non-pathogenic in plant bioassays. Taking these data altogether, we propose that strains CPBF 367 and CPBF 424T belong to a new species herein named Xanthomonas euroxanthea sp. nov., with CPBF 424T (=LMG 31037T=CCOS 1891T=NCPPB 4675T) as the type strain.

INTRODUCTION
The taxonomy of the genus Xanthomonas has been extensively studied and categorized over last century, raising some disputes regarding classification and nomenclature of its members, largely due to the wide plant host diversity associated with the genus. Recorded Xanthomonas hosts include numerous economically relevant crop species, severely impacting agricultural productivity worldwide [1].

Introduction of molecular methods such as DNA–DNA hybridization allowed the first big reclassification within the genus Xanthomonas [2]. Recently, studies relying on multilocus sequence analysis (MLSA), whole-genome average nucleotide identity (ANI) and biochemical analysis have proved fruitful in the reclassification of Xanthomonas species and description amendments of several strains [3, 4]. These techniques have allowed us to reach a deeper discriminatory insight into the genetic diversity of Xanthomonas at the intrasubspecific level, consequently leading to the proposal of novel species [5–7].

Increasing reports of non-pathogenic Xanthomonas strains, such as Xanthomonas arboricola isolates recovered from asymptomatic and symptomatic host tissues, points to the uncertainty of several Xanthomonas strains regarding their host-associated lifestyle and likely host diversity [8–10].

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Abbreviations: ANI, average nucleotide identity; BLASTn, nucleotide Basic Local Alignment Search Tool; dDDH, digital DNA–DNA hybridization; MLSA, multilocus sequence analysis; T3E, type III effectors; T3SS, type III secretion system; WBB, walnut bacterial blight; YDC, yeast extract-dextrose-carbonate.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CPBF 424T is MT036365. The GenBank accession numbers for genome sequences of CPBF 367 and CPBF 424T are UNRN00000000.1 and UHHB00000000.1, respectively.

One supplementary figure and two supplementary tables are available with the online version of this article.

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Interestingly, *X. arboricola* is the species with most non-pathogenic strains within the genus *Xanthomonas* [11]. Characterization of several of these non-pathogenic *X. arboricola* strains has revealed that they are phylogenetically distant from the disease-causing strains that were isolated from their specific hosts [8]. Furthermore, plants are host to a consortium of both distant and genetically similar bacteria, displaying different host-associated phenotypes. It has been suggested that the sympatry of pathogenic and non-pathogenic strains may favour horizontal gene transfer events, likely leading to the emergence of new pathogenic lineages [8, 11].

The advent of increasingly powerful genomic tools and improved bacterial genome assemblers and accurate annotation has led to a more confident examination of bacterial evolution and phylogeny, allowing microbiologists and plant pathologists to assign specific differences to the existing taxonomy, even at the pathovar level. A pathovar of a pathogenic species refers to an infrasubspecific group that includes strains with the same host range [9, 14]. Indeed, a previous study has revealed the identification of two *X. arboricola* strains isolated from symptomatic leaves of a pecan tree (*Carya illinoinensis*), which are pathogenic to both pecan and walnut trees [14]. These data raise the need to understand how the genetic makeup of plant bacterial pathogens, such as *Xanthomonas*, links with a diversifying range of plant hosts. Walnut (Juglans *regia*) being the main cultivated species for walnut fruits and timber production with the Persian walnut (*Juglans regia* cv. robusta) showing bacterial blight symptoms in leaves and fruits, located in a municipal garden in the city of Loures, Portugal (Fig. S1, available in the online version of this article). Distinct organs were sampled including symptomatic leaves (CPBF 1521 in 2014) and asymptomatic buds (CPBF 367, CPBF 424 T, CPBF 1480, CPBF 1521 in 2016). The procedure for preparation of plant material for bacteria isolation has been described previously [20]. Briefly, the excised plant material was disinfected by immersion in 70% ethanol followed by washing with sterile distilled water (SDW) and then macerated in extraction bags with 5 ml SDW [21]. Suspension and correspondent dilutions were streaked on yeast extract–dextrose–carbonate (YDC) agar [22] and incubated at 26±2 °C for 4 days. Single colonies were picked and streaked on fresh nutrient agar (NA) medium to ensure purity. Suspension and correspondent dilutions were streaked on yeast extract–dextrose–carbonate (YDC) agar [22] and incubated at 26±2 °C for 4 days. Single colonies were picked and streaked on fresh nutrient agar (NA) medium to ensure purity.

### ISOLATION AND GROWTH OF BACTERIA

Several isolates were obtained over three consecutive years (2014–2016) from an isolated ornamental walnut tree (*Juglans regia*) showing bacterial blight symptoms in leaves and fruits, located in a municipal garden in the city of Loures, Portugal (Fig. S1, available in the online version of this article). Distinct organs were sampled including symptomatic leaves (CPBF 1521 in 2014) and asymptomatic buds (CPBF 367, CPBF 424 T, CPBF 426 and CPBF 427 in 2016). The procedure for preparation of plant material for bacteria isolation has been described previously [20]. Briefly, the excised plant material was disinfected by immersion in 70% ethanol followed by washing with sterile distilled water (SDW) and then macerated in extraction bags with 5 ml SDW [21]. Suspension and correspondent dilutions were streaked on yeast extract–dextrose–carbonate (YDC) agar [22] and incubated at 26±2 °C for 4 days. Single characteristic mucoid yellow colonies of *Xanthomonas* were streaked on fresh nutrient agar (NA) medium to ensure purity. Selected isolates (CPBF 424 T and CPBF 367) were stored at −80 °C in cryovials containing LB medium (Difco) and glyc erol to a final concentration of 30%. The strains were deposited in international bacterial collections with the accession numbers CPBF 367=LMG 31036=CCOS 1890; CPBF 424 T =LMG 31037 T =CCOS 1891 T =NCPPB 4675 T ; CPBF 427=LMG 31039=CCOS 1893; CPBF 1521=LMG 31040=CCOS 1894=NCPPB 4676. (CPBF, Portuguese Collection of Phytopathogenic Bacteria in Oeiras, Portugal; BCCM/LMG, the Belgian Coordinated Collections of Microorganisms/LMG Bacteria Collection in Gent, Belgium; CCOS, Culture Collection of Switzerland in Wädenswil, Switzerland; NCPPB, National Collection of Plant Pathogenic Bacteria in York, UK; CFBP, French Collection of Plant associated Bacteria, France).
numbers CPBF 367 (LMG 31036=CCOS 1890) and CPBF 424T (=LMG 31037=CCOS 1891T=NCPPB 4675T). Isolates CPBF 367 and CPBF 424T were grown in YDC medium for analysis of colony morphology and pigment production for a 10 day period. The bacterial strains used throughout this study are disclosed in Table 1.

PATHOGENICITY ASSAYS

Plantlets used in the pathogenicity tests were grown from seeds collected from Juglans regia cv. Hartley on the same day. After 30 days of cold stratification treatment at 3–5 °C to break dormancy, seeds were sown in sterilized sand substrate and germinated over 60 days at alternated temperatures, 16 h day at 30 °C and 8 h night at 20 °C [23]. Walnut plantlets were then maintained in a climatic chamber under controlled environmental conditions of 16 h photoperiod (16 h of light at 24 °C and 8 h of darkness at 18 °C). Pathogenicity determination of strains CPBF 424T and CPBF 367 was carried out as previously described [20]. Briefly, inoculum suspensions of approximately 10^8 c.f.u. ml^-1 were prepared with SDW. Plantlets with at least four young leaves expanded were inoculated by spraying with a manual atomizer until runoff. SDW was used for negative control, while X. arboricola pv. juglandis strains LMG 747T and CPBF 1480 were used as positive controls of infection. Three replicates were included for each strain tested. Symptoms were registered after 7 days and further followed for over 5 weeks. Necrotic bacterial spots were observed 7 days post inoculation on leaves of plants inoculated with walnut isolate CPBF 424T, and with positive-control strains LMG 747T and CPBF 1480 (Fig. 1). Walnut isolate CPBF 367 and negative controls did not produce any disease symptoms on walnut plantlets. In order to fulfil Koch’s postulates, typical Xanthomonas yellow mucoid bacterial colonies were re-isolated from the symptoms and confirmed by sequencing analysis of gyrB and fyuA.

PHENOTYPIC CHARACTERIZATION

Phenotypic characterization was carried out with Biolog GEN III MicroPlates (Biolog) according to the manufacturer’s instructions, on walnut isolates CPBF 367, CPBF 424T, CPBF 427, CPBF 1521 and reference strains X. arboricola pv. juglandis LMG 747T and X. arboricola pv. populi CFBP 3123PT. For all strains except CFBP 3123PT, three MicroPlates were assayed on different dates. Selected strains were first grown on solid NYGA medium (5 g l^-1 peptone, 3 g l^-1 yeast extract, 20 g l^-1 glycerol and 15 g l^-1 agar) for 48 h at 28 °C. The strains were subsequently grown on solid Biolog Dehydrated Growth agar for 24 h at 28 °C. Fresh colonies were then transferred into Inoculating Fluid A vials using a cotton-tipped swab. The density of the inoculum was checked and adjusted to a transmittance of 95–98% using a turbidimeter. A total of 100 µl prepared inoculum was then dispensed into each well of the Biolog MicroPlate. MicroPlates were then incubated at 28 °C and read using a MicroStation 2 Reader (Biolog) at 24, 48, 72, 120, 192 and 240 h.

Considering compound metabolism, values 160% superior to the negative control (water) value were considered positive, while those below 130% the negative control were taken as negative. Values in between were considered borderline [10]. The data measured at 72 h was shown to provide the most consistent results between replicates and thus was selected for further analysis. Isolates CPBF 367 and CPBF 424T seemed to metabolize mucic acid and d-saccharic acid, in contrast to X. arboricola pv. juglandis CPBF 427, CPBF 1521 and LMG 747T. Additionally, comparisons with results from other Xanthomonas strains [4–6] revealed differences in metabolizing d-salacin, sucrose, acetic acid, melibiose, formic acid, d-arabitol, d-glucose-6-phosphate, maltose and gentiobiose (Table 2). The metabolization of some substrates was inconclusive due to the inconsistencies observed between replicates.
Table 2. Biolog profiles of *Xanthomonas euroxanthea* strains in comparison with members of *Xanthomonas arboricola* pv. *juglandis* and other related *Xanthomonas* species.

<table>
<thead>
<tr>
<th>Test</th>
<th><em>X. euroxanthea</em> CPBF 367</th>
<th><em>X. euroxanthea</em> CPBF 424†</th>
<th><em>X. arboricola</em> pv. <em>juglandis</em> CPBF 427</th>
<th><em>X. arboricola</em> pv. <em>juglandis</em> CPBF 1521</th>
<th><em>X. arboricola</em> pv. <em>populi</em> CFBP 3123‡</th>
<th><em>X. floridensis</em></th>
<th><em>X. nasturtii</em></th>
<th><em>X. campestris</em> pv. <em>campestris</em></th>
<th><em>X. axonopodis</em> pv. <em>phaseoli</em></th>
<th><em>X. prunicola</em></th>
<th><em>X. arboricola</em> pv. <em>pruni</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>d-Salicin</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Mucic acid</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>D-Saccharic acid</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>+/BL</td>
<td>+/BL</td>
<td>−</td>
<td>−</td>
<td>−/BL</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>Sucrose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>Acetic acid</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>n/a</td>
<td>n/a</td>
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<tr>
<td>Melibiose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>Formic acid</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)/+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>d-Arabitol</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>BL</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>D-Glucose-6-phosphate</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Maltose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>n/a</td>
<td>+</td>
</tr>
<tr>
<td>Gentiose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>n/a</td>
<td>+</td>
</tr>
</tbody>
</table>

MULTILOCUS SEQUENCE ANALYSIS

MLSA based on the concatenated partial sequences of seven genes \textit{fyuA} (684 bp), \textit{gyrB} (735 bp), \textit{rpoD} (586 bp), atp\textit{D} (750 bp), \textit{dnaK} (759 bp), efp (339 bp) and gln\textit{A} (675 bp) was performed. Sequences were retrieved from the NCBI database from 118 strains, including eight different \textit{X. arboricola} pathovars previously used to describe the diversity of \textit{X. arboricola} [24] and another 15 \textit{Xanthomonas} species. The analysis was carried out using Geneious version 9.1.7 software (Biomatters) and a maximum-likelihood tree based on the General Time Reversible (GTR+G+I) model in mega 7.0 was reconstructed (Fig. 2). The novel strains CPBF 424$^T$ CPBF 367 and CPBF 426 formed a separate cluster from all other walnut-associated strains. Interestingly, although isolated from walnut trees, these strains are more closely related to \textit{X. prunicola} and \textit{X. arboricola} pv. \textit{pruni} strains, which are known phytopathogens of \textit{Prunus} trees.

GENOMIC CHARACTERIZATION

The draft genome sequence of CPBF 424$^T$ was previously published [25]. Whole genome sequencing of strains CPBF

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\textbf{Fig. 2.} Maximum-likelihood tree based on the nucleotide alignments of 118 concatenated sequences of atp\textit{D}, \textit{dnaK}, \textit{efp}, \textit{fyuA}, \textit{glnA}, \textit{gyrB} and \textit{rpoD} partial sequences (total length of 4528 bp), emphasizing the phylogenetic relatedness of \textit{Xanthomonas euroxanthea} strains CPBF 367, CPBF 424$^T$ and CPBF 426 (highlighted in bold) within the genus \textit{Xanthomonas}. Bootstrap values >50 from 1000 iterations are shown over and below the branches.
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Genomes of strains CPBF 367 and CPBF 424 were deposited in GenBank under accession numbers UNRN00000000.1 and UIHB00000000.1, respectively.

ANI and digital DNA–DNA hybridization (dDDH) values between CPBF 367 and CPBF 424, and genomes of X. arboricola species were calculated using the edgar version 2.0 platform [26, 27] and formula 2 of the Genome-to-Genome Distance Calculator (GGDC 2.1; http://ggdc.dsmz.de/ggdc.php) [28]. ANI analysis included the genomes of 10 X. arboricola strains, belonging to eight distinct pathovars, and 10 other Xanthomonas species (Table S1). ANI values of strains CPBF 367 and CPBF 424 were less than 93 % with X. arboricola species and less than 89 % with non-arboricola Xanthomonas species (Fig. 3). These values reside below the threshold of 95–96 % commonly considered for representatives of the same species [29]. Furthermore, these CPBF 367 and CPBF 424 strains share 98 % ANI with each other (Fig. 3). The dDDH analysis considered 20 strains representing different species of the genus Xanthomonas and revealed similarities values below the 70 % threshold (Table S2) considered for delimitation of new species [28]. Taken together, the results of ANI and dDDH analyses suggest that these strains belong to a new Xanthomonas species.

**Fig. 3.** Average nucleotide identity (ANI) between novel isolates CPBF 367 and CPBF 424T (in bold) and 20 different Xanthomonas genomes using edgar. Pairwise ANI values are shown in percentages and indicated within the cells of the heat-map. Accession numbers of sequences are available in Table S1.

**Fig. 4.** Distribution of protein homologs of the type III secretion system (T3SS) and type III effectors (T3E) among the Xanthomonas euroxanthea strains (CPBF 367, CPBF 424T, CPBF 426) and Xanthomonas arboricola pv. juglandis strains based on blastn analysis. Dark blue corresponds to the presence of T3SS protein homologous, and dark green corresponds to the presence of T3E homologous. The light blue and green indicate absence of T3SS and T3E homologous, respectively. The threshold criteria applied were minimal e-value of 1e−10, query length similarity cut-off ≥40 % and sequence identity with a cut-off ≥70 % (Fig. 4). The walnut pathogenic strain CPBF 424T has a T3SS gene profile similar to the strains X. arboricola pv. juglandis CPBF 427 and CPBF 1521 and possesses gene homologs described for pathogenic strains of X. arboricola [10, 33–35]. In contrast, strains CPBF 367 and CPBF 426 lack the majority of the T3SS- and T3E-encoding genes (Fig. 4), resembling the T3SS and T3E profile of atypical non-pathogenic strains of Xanthomonas species described previously [33, 35]. The absence of some of the components from the Hrp2 family and of genes that are part...
of the macromolecular structure of the T3SS may explain the non-pathogenic phenotype of CPBF 367, even while harbouring regulators genes of T3SS, such as hrpX and hrpG [36, 37]. Additionally, the fact that strain CPBF 426 is deficient for most T3SS genes, suggests that this strain may not be pathogenic as shown for CPBF 367. Intriguingly, CPBF 424 \(^7\) seems to have a functional T3SS and holds a narrow gene repertoire of T3E homologs in comparison with other X. arboricola pv. juglandis strains [9, 30, 33]. This differs markedly from X. arboricola pv. juglandis CPBF 247 and CPBF 1521 and strains CPBF 367 and CPBF 426. Although the pathogenic strain CPBF 424 \(^7\) possesses homologs for eight known effectors, from which only three were identified in non-pathogenic X. euroxanthea (CPBF 367 and CPBF 426), no homologs were found for most of the genes assigned as important for pathogenicity of Xanthomonas species, namely avrBs2, avrB3, avrXccA1, avrXccA2, xopAW, xopC, xopG, xopK, xopL, xopN, xopQ, xopV, xopX, xopZ and xopZI. All the aforementioned genes, with the exception of xopZ2, were present in both X. arboricola pv. juglandis CPBF 427 and CPBF 1521 strains (Fig. 4). The genomic features of this new species and the pathogen phenotype of strain CPBF 424 \(^7\) in walnut make these strains particularly appealing to elucidate the evolutionary hypothesis of pathogenicity in walnut, to uncover the genetic footprints of adaptation and to address speciation in Xanthomonas.

**DESCRIPTION OF XANTHOMonas EUROXANtheA SP. NOV.**

Xanthomonas euroxanthea (eu.ro.xan.thea. N.L. fem. adj. euroxanthea referring to the EuroXanth COST Action CA 16107, the EU-funded network in which the isolates of this species were characterized).

Cells are Gram-stain-negative straight rods and form colonies that are yellow, circular, smooth, mucoid and slightly convex with entire margins when grown on YDC agar for 2 days. Regarding carbon source metabolism, X. euroxanthea is positive for 34 substrates (dextrin, maltose, trehalose, cellobiose, gentiobiose, sucrose, melibiose, N-acetyl-d-glucosamine, α-d-glucose, d-mannose, d-fructose, d-galactose, l-fucose, glycerol, gelatin, glycyl-l-proline, l-alanine, l-glutamic acid, l-serine, mucic acid, d-saccharic acid, methyl pyruvate, l-lactic acid, citric acid, α-keto-glutaric acid, l-malic acid, bromo-succinic acid, Tween 40, α-hydroxy-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid) and negative for 25 compounds (turanose, stachyose, raffinose, methyl β-d-glucoside, d-salicin, N-acetyl-β-d-mannosamine, N-acetyl-d-galactosamine, N-acetyl-neuraminic acid, 3-methyl glucose, l-rhamnose, d-sorbitol, d-arabitol, myo-inositol, d-glucose-6-phosphate, d-aspartic acid, l-serine, l-arginine, l-lygopyrlutamic acid, d-gluconic acid, quinic acid, p-hydroxy-phenylacetic acid, d-lactic acid methyl ester, d-malic acid, γ-amino-butyric acid and β-hydroxy-β-l-butyric acid).

This species includes non-pathogenic (CPBF 367) and pathogenic (CPBF 424 \(^7\)) strains. The type strain is CPBF 424 \(^7\) (LMG 31037\(^T\)=CCOS 1891\(^T\)=NCPPB 4675\(^T\)), isolated from an asymptomatic bud of an isolated ornamental diseased walnut tree (J. regia) tree growing in a municipal garden of Loures, Portugal. The high-quality draft genome of the type strain is characterized by a size of 4.8 Mb and a G+C content of 65.9 mol%. The GenBank accession number of the 16S rRNA gene sequence of strain CPBF 424 \(^7\) is MT036365 and its draft genome sequence accession number is GCA_900476395.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


