



HAL
open science

Draft genome sequence of *Xanthomonas arboricola* pv. *pruni* PVCT 262.1 isolated from *Prunus dulcis* in Italy

Giulio Dimaria, Alexandros Mosca, Marcella Russo, Jaime Cubero, Joël F Pothier, Ralf Koebnik, Vittoria Catara

► To cite this version:

Giulio Dimaria, Alexandros Mosca, Marcella Russo, Jaime Cubero, Joël F Pothier, et al.. Draft genome sequence of *Xanthomonas arboricola* pv. *pruni* PVCT 262.1 isolated from *Prunus dulcis* in Italy. *Microbiology Resource Announcements*, In press, 10.1128/mra.00273-24 . hal-04629914

HAL Id: hal-04629914

<https://hal.inrae.fr/hal-04629914v1>

Submitted on 1 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Draft genome sequence of *Xanthomonas arboricola* pv. *pruni* PVCT 262.1 isolated from *Prunus dulcis* in Italy

Giulio Dimaria,¹ Alexandros Mosca,¹ Marcella Russo,² Jaime Cubero,³ Joël F. Pothier,⁴ Ralf Koebnik,⁵ Vittoria Catara¹

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT Here, we report the draft genome sequence of *Xanthomonas arboricola* pv. *pruni* strain PVCT 262.1, isolated from almond (*Prunus dulcis*) leaves affected by bacterial spots in Italy in 2020. Genome size is 5,076,418 bp and G+C content is 65.44%. A total of 4,096 protein-coding genes and 92 RNAs are predicted.

KEYWORDS *Xanthomonas*, plant pathology, genomics, *Prunus*

Xanthomonas arboricola pv. *pruni* (*Xap*) is the causal agent of bacterial spots of stone fruits and almonds (1). The disease is currently distributed across almost all stone fruit-producing countries and mainly affects peach, nectarine, apricot, and Japanese plum production (2). In Italy, it has been reported on cherry laurel (3), peach, plum (4), and more recently on almond (5).

We report the draft genome sequence of *Xap* strain PVCT 262.1, isolated from almond leaves exhibiting bacterial spot symptoms collected in a commercial orchard in the Agrigento province, Sicily, Italy [Global Positioning System (GPS) coordinates, 37.290807°N, 13.584432°E] in 2020.

For *Xap* isolation, leaf tissue (2 mm) from lesion margins was crushed with sterile water. The suspensions were spread onto Yeast-Peptone-Glucose Agar (YPGA). Plates were incubated at 28°C for 2–3 days.

Xap was identified using conventional duplex PCR with specific primers (*XarbQ-F/XarbQ-R* and *XapY17-F/XapY17-R*) (6), *rpoD* gene partial sequencing (99.63% identity with *Xap* 15-088, GenBank accession number [CP044334.1](#)), and pathogenicity tests on 1-year-old grafted almond plants and detached leaves (7). For total DNA extraction and whole-genome sequencing, a single bacterial colony was transferred from YPGA to lysogenic broth (LB) and incubated overnight (180 rpm, 28°C). DNA was extracted from 1 mL culture (1×10^9 cfu mL⁻¹) with Genra Puregene bacterial DNA extraction kit (Qiagen, Hilden, Germany), following the manufacturer's instructions.

Sequencing libraries were constructed at Beijing Novogene Bioinformatics Technology Co., Ltd using Illumina NEBNext Ultra DNA Library Prep Kit (NEB, USA; 350 bp insert size), according to the manufacturer's recommendations. Sequencing was performed on Illumina NovaSeq 6000 platform (sequencing depth, 312x; paired-end read length, 150 bp). Raw reads (14,580,000 bp) were demultiplexed, recorded in FASTQ file using bcl2fastq v2.19 and quality filtered with Fastp v0.23.1 (8), obtaining 11,366,667 bp clean reads ($Q_{30} = 94.62\%$).

Reads were assembled using SOAPdenovo v2.04 (9), SPAdes v3.11.1 (10), Abyss v1.5.2 (11), and CISA v1.3 (12) for integration. Gaps were solved with SOAP GapCloser v1.12 (9). The annotation was performed on the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.6 (13). Default parameters were used except where otherwise noted.

The draft genome assembly generated 60 scaffolds (>500 bp) with 5,076,418 bp total length (genome coverage, 99.99x; N_{50} length, 165,685 bp) and 65.44% GC content. Genome completeness was estimated at 99.8% using BUSCO v5.6.1 (14) and

Editor David A. Baltrus, The University of Arizona, Tucson, Arizona, USA

Address correspondence to Vittoria Catara, vcatara@unict.it.

The authors declare no conflict of interest.

Received 18 March 2024

Accepted 16 May 2024

Published 11 June 2024

Copyright © 2024 Dimaria et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

xanthomonadales_odb10 (2024-01-08) lineage. PGAP predicted 4,096 protein-coding genes, 188 pseudogenes, and 92 RNAs.

PVCT 262.1 genome harbors copper resistance genes (e.g., *copB*, *copD*- and *copL*-family, *cutA*, *cutC*), suggesting copper resistance acquisition. The latter was observed *in vitro* for Italian *Xap* isolates, although *copLAB* gene cluster was not detected, suggesting different copper resistance mechanisms (4). The type III effector gene *xopE3*, specific to pathovar *pruni* within *X. arboricola* (15), was identified.

The genome sequence provided here will help further studies on bacterial spot ecology and epidemiology, contributing to elucidate almond-*Xap* interactions.

ACKNOWLEDGMENTS

This article is based upon work from COST Action CA16107 “EuroXanth,” supported by COST (European Cooperation in Science and Technology). The work was financially supported by Incentive Plan for Research (PIA.CE.RI.) 2020–2022 line 2 (MEDIT-ECO 5A722192155 Research Project) of the University of Catania (Italy).

AUTHOR AFFILIATIONS

¹Department of Agriculture, Food, and Environment, University of Catania, Catania, Italy

²Agrobiotech Soc. Coop., Catania, Italy

³Departamento de Protección Vegetal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria/Consejo Superior de Investigaciones Científicas (INIA/CSIC), Madrid, Spain

⁴Environmental Genomics and Systems Biology Research Group, Institute for Natural Resource Sciences, Zurich University of Applied Sciences (ZHAW), Wädenswil, Switzerland

⁵Plant Health Institute of Montpellier, University of Montpellier, CIRAD, INRAE, Institut Agro, IRD, Montpellier, France

AUTHOR ORCIDs

Giulio Dimaria  <http://orcid.org/0009-0004-5210-1070>

Joël F. Pothier  <http://orcid.org/0000-0002-9604-7780>

Vittoria Catara  <http://orcid.org/0000-0001-8076-258X>

AUTHOR CONTRIBUTIONS

Giulio Dimaria, Conceptualization, Formal analysis, Investigation, Methodology, Resources, Software, Writing – original draft, Writing – review and editing | Alexandros Mosca, Formal analysis, Investigation, Methodology, Resources, Software, Validation, Writing – original draft, Writing – review and editing | Marcella Russo, Investigation, Methodology | Jaime Cubero, Methodology, Supervision, Validation, Writing – review and editing | Joël F. Pothier, Methodology, Software, Supervision, Validation, Writing – review and editing | Ralf Koebnik, Methodology, Supervision, Validation, Writing – review and editing | Vittoria Catara, Conceptualization, Data curation, Formal analysis, Funding acquisition, Methodology, Resources, Supervision, Validation, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

This Whole-Genome Shotgun project was deposited in GenBank under the accession number [JAZHEZ000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAZHEZ000000000), BioProject accession number [PRJNA1061488](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1061488), BioSample accession number [SAMN39271251](https://www.ncbi.nlm.nih.gov/biosample/SAMN39271251). The version described is [JAZHEZ010000000](https://www.ncbi.nlm.nih.gov/nuccore/JAZHEZ010000000). SRA accession number is [SRR27587392](https://www.ncbi.nlm.nih.gov/sra/SRR27587392).

REFERENCES

1. Garita-Cambroner J, Palacio-Bielsa A, Cubero J. 2018. *Xanthomonas arboricola* pv. pruni, causal agent of bacterial spot of stone fruits and almond: its genomic and phenotypic characteristics in the *X. arboricola* species context. *Mol Plant Pathol* 19:2053–2065. <https://doi.org/10.1111/mpp.12679>
2. Stefani E. 2010. Economic significance and control of bacterial spot/canker of stone fruits caused by *Xanthomonas arboricola* pv. pruni. *J Plant Pathol*:S99–S103. <https://doi.org/10.4454/jpp.v92i1sup.2511>
3. Marchi G, Cinelli T, Surico G. 2011. Bacterial leaf spot caused by the quarantine pathogen *Xanthomonas arboricola* pv. pruni on cherry laurel in central Italy. *Plant Dis* 95:74. <https://doi.org/10.1094/PDIS-07-10-0529>
4. Giovanardi D, Dallai D, Stefani E. 2017. Population features of *Xanthomonas arboricola* pv. pruni from *Prunus* spp. orchards in northern Italy. *Eur J Plant Pathol* 147:761–771. <https://doi.org/10.1007/s10658-016-1040-5>
5. Gerin D, Cariddi C, De Miccolis Angelini RM, Dongiovanni C, Faretra F, Pollastro S. 2019. First report of bacterial spot caused by *Xanthomonas arboricola* pv. pruni on almond in Italy. *Plant Dis* 103:1018. <https://doi.org/10.1094/PDIS-11-18-2006-PDN>
6. Pothier JF, Pagani MC, Pelludat C, Ritchie DF, Duffy B. 2011. A duplex-PCR method for species- and pathovar-level identification and detection of the quarantine plant pathogen *Xanthomonas arboricola* pv. pruni. *J Microbiol Methods* 86:16–24. <https://doi.org/10.1016/j.mimet.2011.03.019>
7. Randhawa PS, Civerolo EL. 1985. A detached-leaf bioassay for *Xanthomonas campestris* pv. pruni. *Phytopathology* 75:1060–1063. <https://doi.org/10.1094/Phyto-75-1060>
8. Chen S, Zhou Y, Chen Y, Gu J. 2018. Fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* 34:i884–i890. <https://doi.org/10.1093/bioinformatics/bty560>
9. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, et al. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* 1:1–6. <https://doi.org/10.1186/2047-217X-1-18>
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>
11. Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJM, Birol I. 2009. ABySS: a parallel assembler for short read sequence data. *Genome Res* 19:1117–1123. <https://doi.org/10.1101/gr.089532.108>
12. Lin SH, Liao YC. 2013. CISA: contig integrator for sequence assembly of bacterial genomes. *PLoS ONE* 8:e60843. <https://doi.org/10.1371/journal.pone.0060843>
13. Li W, O'Neill KR, Haft DH, DiCuccio M, Chetvernin V, Badretdin A, Coulouris G, Chitsaz F, Derbyshire MK, Durkin AS, Gonzales NR, Gwadz M, Lanczycki CJ, Song JS, Thanki N, Wang J, Yamashita RA, Yang M, Zheng C, Marchler-Bauer A, Thibaud-Nissen F. 2021. RefSeq: expanding the prokaryotic genome annotation pipeline reach with protein family model curation. *Nucleic Acids Res* 49:D1020–D1028. <https://doi.org/10.1093/nar/gkaa1105>
14. Manni M, Berkeley MR, Seppey M, Simão FA, Zdobnov EM. 2021. BUSCO update: novel and streamlined workflows along with broader and deeper phylogenetic coverage for scoring of eukaryotic, prokaryotic, and viral genomes. *Mol Biol Evol* 38:4647–4654. <https://doi.org/10.1093/molbev/msab199>
15. Hajri A, Pothier JF, Fischer-Le Saux M, Bonneau S, Poussier S, Boureau T, Duffy B, Manceau C. 2012. Type three effector gene distribution and sequence analysis provide new insights into the pathogenicity of plant-pathogenic *Xanthomonas arboricola*. *Appl Environ Microbiol* 78:371–384. <https://doi.org/10.1128/AEM.06119-11>