High-Quality Draft Genome Sequences of Five *Xanthomonas arboricola* pv. fragariae Isolates

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ABSTRACT *Xanthomonas arboricola* pv. fragariae was described in 2001 as the causal agent of strawberry bacterial leaf blight. We report here the first draft whole-genome sequences of five *X. arboricola* pv. fragariae isolates from Italy and France.

Xanthomonas arboricola pv. fragariae was described in 2001 as the causal agent of strawberry bacterial leaf blight (1). The first symptoms related to this bacterium were observed in 1993 in strawberry cultivations in northern Italy (1). Afterward, the disease has only been reported in plantlets from Turkey in 2004 (2). The bacterium was under quarantine status in Europe starting in 2002 (3), but it was derestricted in 2007 (see https://www.eppo.int/MEETINGS/2007_meetings/phytomeasures.htm). This was partly due to the observation that the pathogen was sometimes coisolated with *Xanthomonas fragariae* (4, 5), which is the causal agent of bacterial angular leaf spot and is under quarantine status in Europe (6, 7). Also, the reported pathogenicity of *X. arboricola* pv. fragariae upon artificial inoculation on strawberry has often been ambiguous (4, 5, 8; M. Gétaz and J. F. Pothier, unpublished data). This could be related to the important heterogeneity among *X. arboricola* pv. fragariae strains, as observed in previous studies (4, 5, 9–11). Very recently, the pathogenicity of the pathotype strain was proved to produce typical symptoms in the strawberry cultivars Candonga, Sabrina, and Murano (12).

Until now, no whole-genome data for this bacterium were available in GenBank. In this study, whole-genome sequences of five *X. arboricola* pv. fragariae strains isolated from strawberry plants in Italy and France between 1986 and 1993 were obtained (Table 1).

Genomic DNA was extracted using the NucleoSpin tissue kit (Macherey-Nagel AG, Düren, Germany) following the manufacturer's protocol. Paired-end libraries constructed by the Nextera XT DNA library prep kit (Illumina, San Diego, CA) were sequenced on a MiSeq system (Illumina) using a 600-cycle MiSeq reagent kit v3 (Illumina). *De novo* assemblies were created using SeqMan NGen from the Lasergene genomics package version 12.1.0 (DNAStar, Madison, WI). This was followed by contig reassembly using SeqMan Pro and read mapping using SeqMan NGen to check for inconsistencies.

The five genomes displayed an overall size between 4,692,498 and 4,906,785 bp, which is in the range previously observed with other *X. arboricola* genomes (13–17). The G+C contents in all the genomes were similar (65.75 to 65.95%). Genomes were annotated automatically using GenDB (18), and a total of 3,852 to 4,044 coding sequences (CDSs) were detected (Table 1). Using EDGAR 2.0 (19), a total of 3,523 CDSs were found to be shared between these five genomes.

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TABLE 1 Draft whole-genome sequences of five *Xanthomonas arboricola* pv. fragariae strains submitted to the ENA database

Strain[a]	Synonym(s)	Yr, country of isolation	ENA accession no.	No. of contigs	Genome size (bp)	G+C content (%)	No. of CDSs
LMG 19145[b]	CFBP 6771, PD 2780	1993, Italy	OEQL00000000	39	4,906,785	65.88	4,019
LMG 19144	CFBP 6770, PD 2696	1993, Italy	OEQF00000000	58	4,842,182	65.94	3,954
CFBP 6762	PD 2694	1993, Italy	OEQE00000000	38	4,889,284	65.75	4,044
LMG 19146	CFBP 3548, PD 3164	1986, France	OEQG00000000	39	4,884,039	65.75	4,020
CFBP 6773	NA[c]	NA	OEQD00000000	39	4,692,498	65.95	3,852

[a]The culture collections providing strains are abbreviated in the strain names as LMG (Collection of the Laboratorium voor Microbiologie en Microbiele Genetica, Ghent, Belgium), CFBP (Collection Française de Bactéries Associées aux Plantes, Beaucouzé, France), or PD (Culture Collection of Plant Pathogenic Bacteria, Wageningen, the Netherlands).
[b]Pathotype strain.
[c]NA, not applicable.

Average nucleotide identities (ANIs) between these five genomes ranged from 96.57% to 97.69%, thus confirming the species designation but also suggesting some genome content heterogeneity.

The *X. arboricola* pv. fragariae draft genome sequences presented here add to the existing genomic information and further clarify the complexity of the species *X. arboricola*.

Accession number(s). The annotated draft whole-genome sequences of the five *X. arboricola* pv. fragariae isolates were deposited at ENA under the sequencing project number PRJEB23514. The accession numbers for the isolates are shown in Table 1.

REFERENCES

1. Janse JD, Rossi MP, Gorkink RFJ, Derks JHJ, Swings J, Janssens D, Scortichini M. 2001. Bacterial leaf blight of strawberry (*Fragaria (x) ananassa*) caused by a pathovar of *Xanthomonas arboricola*, not similar to *Xanthomonas fragariae* Kennedy & King. Description of the causal organism as *Xanthomonas arboricola* pv. fragariae (pv. nov., comb. nov.). Plant Pathol 50:653–665. https://doi.org/10.1046/j.1365-3059.2001.00644.x.

2. Ustun N, Tjou-Tam-Sin NNA, Janse JD. 2007. First report on bacterial leaf blight of strawberry caused by *Xanthomonas arboricola* pv. fragariae Janse et al. in Turkey. J Plant Pathol 89:109–112.

3. Anonymous. 2002. A new pathogen, *Xanthomonas arboricola* pv. fragariae, causing bacterial leaf blight of strawberry: addition to the EPPO Alert List. OEPP/EPPO Reporting Serv 2012(4):10–11.

4. Scortichini M, Rossi MP. 2003. Genetic diversity of *Xanthomonas arboricola* pv. fragariae strains and comparison with some other *X. arboricola* pathovars using repetitive PCR genomic fingerprinting. J Phytopathol 151:113–119. https://doi.org/10.1046/j.1439-0434.2003.00591.x.

5. Vandroemme J, Cottyn B, Pothier JF, Pflüger V, Duffy B, Maes M. 2013. *Xanthomonas arboricola* pv. fragariae: what's in a name? Plant Pathol 62:1123–1131. https://doi.org/10.1111/ppa.12028.

6. Anonymous. 1986. *Xanthomonas fragariae* Kennedy & King. EPPO Bull16:17–20.

7. European Union. 2000. Council Directive 2000/29/EC of 8 May 2000 on protective measures against the introduction into the community of organisms harmful to plants and plant products and their spread within the community. Council of the European Union, Brussels, Belgium.

8. Merda D, Bonneau S, Guimbaud J-F, Durand K, Brin C, Boureau T, Lemaire C, Jacques M-A, Fischer-Le Saux M. 2016. Recombination-prone bacterial strains form a reservoir from which epidemic clones emerge in agroecosystems. Environ Microbiol Rep 8:572–581. https://doi.org/10.1111/1758-2229.12397.

9. 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.

10. Cesbron S, Pothier J, Gironde S, Jacques MA, Manceau C. 2014. Development of multilocus variable-number tandem repeat analysis (MLVA) for *Xanthomonas arboricola* pathovars. J Microbiol Methods 100:84–90. https://doi.org/10.1016/j.mimet.2014.02.017.

11. Fischer-Le Saux M, Bonneau S, Essakhi S, Manceau C, Jacques MA. 2015. Aggressive emerging pathovars of *Xanthomonas arboricola* represent widespread epidemic clones distinct from poorly pathogenic strains, as revealed by multilocus sequence typing. Appl Environ Microbiol 81:4651–4668. https://doi.org/10.1128/AEM.00050-15.

12. Ferrante P, Scortichini M. 2017. *Xanthomonas arboricola* pv. fragariae: a confirmation of the pathogenicity of the pathotype strain. Eur J Plant Pathol https://doi.org/10.1007/s10658-017-1326-2.

13. Ibarra Caballero J, Zerillo MM, Snelling J, Boucher C, Tisserat N. 2013. Genome sequence of *Xanthomonas arboricola* pv. corylina, isolated from Turkish filbert in Colorado. Genome Announc 1:e00246-00213. https://doi.org/10.1128/genomeA.00246-13.

14. Garita-Cambronero J, Sena-Vélez M, Palacio-Bielsa A, Cubero J. 2014. Draft genome sequence of *Xanthomonas arboricola* pv. pruni, strain Xap33, causal agent of bacterial spot disease on almond. Genome Announc 2:e00440-14. https://doi.org/10.1128/genomeA.00440-14.

15. Ignatov AN, Kyrova EI, Vinogradova SV, Kamionskaya AM, Schaad NW, Luster DG. 2015. Draft genome sequence of *Xanthomonas arboricola* strain 3004, a causal agent of bacterial disease on barley. Genome Announc 3:e01572-14. https://doi.org/10.1128/genomeA.01572-14.

16. Pereira UP, Gouran H, Nascimento R, Adaskaveg JE, Goulart LR, Dandekar AM. 2015. Complete genome sequence of *Xanthomonas arboricola* pv. juglandis 417, a copper-resistant strain isolated from

Juglans regia L. Genome Announc 3:e01126-15. https://doi.org/10.1128/genomeA.01126-15.

17. Garita-Cambronero J, Palacio-Bielsa A, López MM, Cubero J. 2016. Draft genome sequence for virulent and avirulent strains of *Xanthomonas arboricola* isolated from *Prunus* spp. in Spain. Stand Genomic Sci 11:12. https://doi.org/10.1186/s40793-016-0132-3.

18. Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. Nucleic Acids Res 31:2187–2195. https://doi.org/10.1093/nar/gkg312.

19. Blom J, Kreis J, Spänig S, Juhre T, Bertelli C, Ernst C, Goesmann A. 2016. EDGAR 2.0: an enhanced software platform for comparative gene content analyses. Nucleic Acids Res 44:W22–W28. https://doi.org/10.1093/nar/gkw255.