

# Draft Genome Sequence of the *Xylella fastidiosa* CoDiRO Strain

Annalisa Giampetruzzi,<sup>a</sup> Michela Chiumenti,<sup>a</sup> Maria Saponari,<sup>a</sup> Giacinto Donvito,<sup>b</sup> Alessandro Italiano,<sup>b</sup> Giuliana Loconsole,<sup>a</sup> Donato Boscia,<sup>a</sup> Corrado Cariddi,<sup>c</sup> Giovanni Paolo Martelli,<sup>c</sup> Pasquale Saldarelli<sup>a</sup>

Institute for Sustainable Plant Protection, National Research Council (CNR), Bari, Italy<sup>a</sup>; Department of Physics, University of Bari Aldo Moro, Bari, Italy<sup>b</sup>; Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro, Bari, Italy<sup>c</sup>

A.G. and M.C. contributed equally to this work.

**We determined the draft genome sequence of the *Xylella fastidiosa* CoDiRO strain, which has been isolated from olive plants in southern Italy (Apulia). It is associated with olive quick decline syndrome (OQDS) and characterized by extensive scorching and desiccation of leaves and twigs.**

Received 22 December 2014 Accepted 5 January 2015 Published 12 February 2015

**Citation** Giampetruzzi A, Chiumenti M, Saponari M, Donvito G, Italiano A, Loconsole G, Boscia D, Cariddi C, Martelli GP, Saldarelli P. 2015. Draft genome sequence of the *Xylella fastidiosa* CoDiRO strain. *Genome Announc* 3(1):e01538-14. doi: 10.1128/genomeA.01538-14.

**Copyright** © 2015 Giampetruzzi et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Annalisa Giampetruzzi, [a.giampetruzzi@ba.ivv.cnr.it](mailto:a.giampetruzzi@ba.ivv.cnr.it).

*Xylella fastidiosa* is a xylem-restricted Gram-negative bacterium and the agent of diseases of a wide range of hosts (1). Currently, seven *X. fastidiosa* genomes have been completely sequenced, including citrus-variegated chlorosis strain 9a5c, Pierce's disease strains Temecula 1 and GB514, almond leaf scorch strains M12 and M23, oleander strain Ann1, and mulberry strain MUL0034.

In 2013, the first confirmed outbreak of *X. fastidiosa* in the European Union was reported from southern Italy (Apulia), the infection occurring on olive trees affected by olive quick decline syndrome (OQDS) and characterized by extensive scorching and desiccation of leaves and twigs (2). Investigations were therefore initiated to determine the taxonomic allocation, host range, and vector(s) of the bacterial strain associated with OQDS, which was denoted CoDiRO, the abbreviation of the Italian name of the disease.

Genomic DNA was recovered from a pure *X. fastidiosa* CoDiRO culture from infected periwinkle. A paired-end DNA library was constructed and sequenced using Illumina technology, which resulted in 9,008,814 reads and 345× coverage.

Reads were assembled *de novo* using EDENA, Velvet, and SOAPdenovo (3–5) with different *k*-mers. The best contig assemblies from each program were merged using CISA (6) and scaffolded with SSPACE (7) on the Orione instance of Galaxy (8). This reconstruction resulted in a final assembly of 12 scaffolds with sizes ranging from 1,790 to 678,618 bp and an average scaffold size of 211,911 bp. Scaffolds were ordered on the backbone of the reference genome sequence of *X. fastidiosa* subsp. *pauca* 9a5c, which, according to multilocus sequence typing, was the most related strain. Where necessary, PCR and Sanger sequencing were performed by primer walking to fix the position of contigs showing conflicting ordering information.

The draft genome of *X. fastidiosa* CoDiRO consisted of a total of 2,507,614 bp (with a GC content of 51.8%), likely representing >95% of the full genomic sequence since other *X. fastidiosa* strains have genomes ranging from 2.39 to 2.73 Mbp (9).

The draft genome was annotated through submission to the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP),

resulting in the identification of 6 rRNA genes, 49 tRNA loci, 2,053 protein-encoding genes, and 2 noncoding RNAs. A plasmid of 35,318 bp was also found sharing 98% similarity in the *tra* and *trb* loci with the conjugative plasmid pXF-RIV5 (10), but differing from it for the accessory module containing genes of a toxin-antitoxin system.

Comparative analyses showed that (i) variations (insertion/deletion of nucleotide) exist in genes encoding important virulence factors (*rpf* cluster gene, polygalacturonase-*pglA* gene) that are likely to be involved with recognition of specific host factors, which may influence host specificity, infectivity, and/or development of virulence capacity; and (ii) CoDiRO is genetically related with *X. fastidiosa* subsp. *pauca* isolates with the highest similarity with an isolate from Central America but not with the *X. fastidiosa* strain infecting olives in California (11).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JUJW00000000](https://www.ncbi.nlm.nih.gov/nuccore/JUJW00000000). The version described in this paper is version [JUJW01000000](https://www.ncbi.nlm.nih.gov/nuccore/JUJW01000000).

## ACKNOWLEDGMENTS

This work was supported by grants from the Regional Plant Health Service of Apulia and from CNR CISA-“Valorizzazione delle risorse genetiche di colture mediterranee attraverso approcci di metagenomica, tracciatomica e analisi funzionale per la caratterizzazione di germoplasma autoctono, endofiti, agenti di biocontrollo e fitopatogeni (METARGERM)” and was conducted using equipment of “Rete di Laboratori Pubblici SELGE- Regione Puglia (cod. 14).”

## REFERENCES

- Hopkins DL, Purcell AH. 2002. *Xylella fastidiosa*: cause of Pierce's disease of grapevine and other emergent diseases. *Plant Dis* 86:1056–1066. [http://dx.doi.org/10.1094/PDIS.2002.86.10.1056](https://doi.org/10.1094/PDIS.2002.86.10.1056).
- Saponari M, Boscia D, Nigro F, Martelli GP. 2013. Identification of DNA sequences related to *Xylella fastidiosa* in oleander, almond and olive trees exhibiting leaf scorch symptoms in Apulia (Southern Italy). *J Plant Pathol* 95:659–668. [http://dx.doi.org/10.4454/JPP.V95I3.035](https://doi.org/10.4454/JPP.V95I3.035).
- Hernandez D, François P, Farinelli L, Osterås M, Schrenzel J. 2008. *De novo* bacterial genome sequencing: millions of very short reads assembled

- on a desktop computer. *Genome Res* 18:802–809. <http://dx.doi.org/10.1101/gr.072033.107>.
4. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
  5. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam T, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *GigaScience* 1:18. <http://dx.doi.org/10.1186/2047-217X-1-18>.
  6. Lin SH, Liao YC. 2013. CISA: contig integrator for sequence assembly of bacterial genomes. *PLoS One* 8:e60843. <http://dx.doi.org/10.1371/journal.pone.0060843>.
  7. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics* 27: 578–579. <http://dx.doi.org/10.1093/bioinformatics/btq683>.
  8. Cuccuru G, Orsini M, Pinna A, Sbardellati A, Soranzo N, Travaglione A, Uva P, Zanetti G, Fotia G. 2014. Orione, a Web-based framework for NGS analysis in microbiology. *Bioinformatics* 30:1928–1929. <http://dx.doi.org/10.1093/bioinformatics/btu135>.
  9. Varani AM, Monteiro-Vitorello CB, de Almeida LG, Souza RC, Cunha OL, Lima WC, Civerolo E, Van Sluys MA, Vasconcelos AT. 2012. *Xylella fastidiosa* comparative genomic database is an information resource to explore the annotation, genomic features, and biology of different strains. *Genet Mol Biol* 35:149–152. <http://dx.doi.org/10.1590/S1415-47572012005000019>.
  10. Rogers EE, Stenger DC. 2012. A conjugative 38-kB plasmid is present in multiple subspecies of *Xylella fastidiosa*. *PLoS One* 7:e52131. <http://dx.doi.org/10.1371/journal.pone.0052131>.
  11. Krugner R, Sisterson MS, Chen J, Stenger DC, Johnson MW. 2014. Evaluation of olive as a host of *Xylella fastidiosa* and associated sharpshooter vectors. *Plant Dis* 98:1186–1193. <http://dx.doi.org/10.1094/PDIS-01-14-0014-RE>.