Complete Genome of *Xanthomonas arboricola* pv. *corylina* Strain A7 Isolated from Southern Chile

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Abstract

The complete genome sequence of *Xanthomonas arboricola* pv. *corylina* A7 was obtained by a hybrid approach combining PacBio and Illumina HiSeq sequence data. A single circular chromosome of 5.1 mb with 65.47% G + C content was obtained, including 4,344 coding sequences identified as well as some genes involved in copper resistance. The information obtained corresponds to the first report of a high-quality whole genome of *X. arboricola* pv. *corylina*, isolated from infected hazelnut trees in southern Chile.

Genome Announcement

Chile is the largest hazelnut producer in the Southern Hemisphere and this cultivation covers more than 20,000 hectares (Ellena et al. 2014; Guerrero Contreras et al. 2020). One important loss of productivity of hazelnut cultivation is due to the disease caused by *X. arboricola* pv. *corylina* (Ellena et al. 2014). Disease control conventionally involves the application of copper compounds, three to four sprays per year (Ellena et al. 2014), whose use in Chile has been shown to be related to copper resistance acquisition in *X. arboricola* pv. *corylina* isolates (Chavez and Durán 2020).

This announcement describes the whole genome of *X. arboricola* pv. *corylina* strain A7 isolated from infected hazelnut trees with a potential of copper resistance. *X. arboricola* pv. *corylina* A7 was selected from 12 strains isolated from hazelnut trees with characteristic symptoms of bacterial blight from Camarico, Región del Maule, Chile (Lamichhane and Varvaro 2014). This site has been consistently managed with copper (II) hydroxide and copper (II) sulfate pentahydrate to treat bacterial blight considering two applications per season, in leaf fall and at the beginning of sprouting. The bacterial isolate was selected for its capacity for growing in vitro with high copper concentration (130 µg of Cu²⁺ per milliliter) (Moya-Elizondo et al. 2018).

X. arboricola pv. *corylina* A7 was grown in YPG medium (10 g of peptone, 5 g of yeast extract, and 5 g of glucose per liter [Difco]) for 48 h. Genomic DNA was isolated using a QIAamp DNA mini kit (Qiagen), following manufacturer protocols. DNA sequencing was performed on an Illumina HiSeq 4000 platform, using a TruSeq DNA 350-bp library with a 2 × 100 bp paired-end protocol (Macrogen). A total of 11,206,268 reads were obtained. Read quality was checked using FastQC (Andrews 2010), and low-quality sequences were trimmed, using Trim Galore (Krueger 2016). For long-read sequencing, a 20-kb SMRTbell library was prepared and was sequenced on the PacBio platform (Macrogen). In all, 55,637 raw PacBio reads were longer than 18,317 bp.

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Keywords

bacterial blight, hazelnut, whole genome

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Genome assembly was performed using hybrid assembler Unicycler (Wick et al. 2017) with default parameters for hybrid assembly. One circular chromosome of 5,166,498 bp (65.47% G/C content) was obtained, with a coverage over 500x. The chromosome was visualized with Geneious Prime 2020 1.2.

The assembled genome was annotated using the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (Tatusova et al. 2016). A total of 4,344 coding sequences, 160 pseudogenes, two complete ribosomal RNA operons (each operon containing 5S, 16S, 23S), 54 transfer RNAs, and 36 noncoding RNAs were predicted by this pipeline.

Regarding copper resistance genes, the operon *copAB*, *copL*, *cutC*, and a PCuAC protein-encoding gene were found in the genome annotation. In the *Xanthomonas axonopodis* pv. *citri* genome, *copAB* gene products may play an important role in the copper-resistance mechanism and *copL* could regulate the *copAB* operon (Teixeira et al. 2008). It has also been found that copper homeostasis protein CutC (*cutC*) and copper chaperone PCuAC could be implicated in the survival of *X. arboricola* pv. *corylina* in a high concentration of copper (Latorre et al. 2011; Thompson et al. 2013).

Identification of the *copAB* operon and *copL*, *cutC*, and PCuAC genes in the genome suggests the inefficacy of copper-based compounds for the treatment of *Xanthomona arboricola* pv. *corylina* A7 in hazelnut. To our knowledge, this is the first report of the whole genome of *X. arboricola* pv. *corylina* isolate in productive hazelnut crops in southern Chile and it complements the information described by Ibarra Caballero et al. (2013), providing a valuable resource for future studies.

Data Availability

The draft assembly of the *X. arboricola* pv. *corylina* strain A7 has been deposited in the NCBI GenBank database under accession number CP062164. Raw Illumina HiSeq reads and PacBio reads have been deposited in NCBI Short Read Archive under BioProject accession number PRJNA661460, SRR12693513/SRR12693512.

Author-Recommended Internet Resource

Geneious Prime 2020 1.2: <https://www.geneious.com>

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