

24 whole genome of *X. arboricola* pv *corylina*, isolated from infected hazelnut trees in the
25 southern of Chile.

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27 **Genome announcement**

28 Chile is the largest hazelnut producer in the Southern Hemisphere and this cultivation
29 covers more than 20000 ha (Guerrero et al, 2020 Chavez et al, 2020). One important
30 loss of productivity of hazelnut cultivation is due to the disease caused by *X. arboricola*
31 pv. *corylina* (Ellena et al. 2014). Disease control conventionally involves the application
32 of copper compounds, 3-4 sprays per year (Ellena et al. 2014), whose use in Chile has
33 been shown to be related to copper resistance acquisition in *X. arboricola* pv. *corylina*
34 isolates (Chavez et al. 2020).

35 This genome announcement describes the whole genome of *X.arboricola* pv. *corylina* A7
36 isolated from infected hazelnut trees with a potential of copper resistance. *X. arboricola*
37 pv. *corylina* stain A7 was selected from 12 isolated obtained from hazelnut trees with
38 characteristic symptoms of bacterial blight according to Lamichhane et al. 2014 from
39 Camarico, Región del Maule, Chile (latitude 35° 15' 23" S and longitude 71° 20' 41" W).
40 This site has been consistently managed with copper (II) hydroxide and copper (II)
41 sulfate pentahydrate to treat bacterial blight considering two application/season, in
42 leaf fall and at the beginning of sprouting. The bacterial isolate was selected for its
43 capacity of growing *in vitro* with high copper concentration (130 µg/mL Cu²⁺),
44 according to Moya Elizondo, et al. 2018.

45 *X. arboricola* pv. *corylina* A7 was grown in YPG medium (10 g peptone, 5 g yeast extract,
46 5 g glucose per litre, Difco, Detroit) for 48h. Genomic DNA was isolated using QIAamp

47 DNA Mini Kit (Qiagen), following the manufacture's protocol. DNA Sequencing was
48 performed on an Illumina Hiseq4000 platform using Truseq DNA 350bp library with a
49 2 X 100 bp paired-end protocol (Macrogen, Korea). A total of 11,206,268 reads were
50 obtained. The reads quality were check using FastQC (Andrews 2010) and low-quality
51 sequences were trimmed using Trim Galore (Krueger 2016). For long reads sequencing,
52 a 20Kb SMRTbell library was prepared and sequenced on Pacbio platform (Macrogen,
53 Korea). 55,637 raw Pacbio reads were longer than 18,317 bp.

54 Genome assembly was performed using hybrid assembler Unicycler (Wick et al. 2017)
55 with default parameters for hybrid assembly. One circular chromosome of 5166498bp
56 (65.47 %G/C content) was obtained, with a coverage over 500x. The chromosome was
57 visualized with Geneious Prime 2020 1.2 (<https://www.geneious.com>).

58 The assembled genome was annotated by NCBI Prokaryotic Genome Annotation
59 Pipeline (Tatusova et al. 2016). A total of 4344 coding sequencing, 160 pseudogenes, 2
60 complete rRNA operon (5S, 16S, 23S), 54 tRNA, and 36 non-coding RNAs were
61 predicted by this pipeline.

62 Regarding copper resistance genes, the operon *copAB*, *copL*, *cutC* and *PCuAC* gene were
63 found in the genome annotation. In *Xanthomonas axonopodis* pv. *citri* genome, *copAB*
64 gene products may play an important role in copper resistance mechanism and *copL*
65 could regulate *copAB* operon (Teixeira et al. 2008). It has also been found that Copper
66 homeostasis protein CutC (*cutC*) and copper chaperone *PCu_AC* could be implicated in
67 the survival of *X. arboricola* pv. *corylina* in a high concentration of copper (Latorre et al.
68 2011; Thompson et al. 2013).

69 Identification of the copAB operon and copL, cutC and PCuAC genes in the genome
70 suggests the inefficacy of copper-based compounds for the treatment of *Xanthomona*
71 *arboricola* pv. *corylina* strain A7 in hazelnut. To our knowledge, this is the first report
72 of the whole genome of *X. arboricola* pv. *corylina* isolate in productive crop of hazelnuts
73 in the southern of Chile and complement the information described by Caballero et al.
74 2013, providing a valuable resource for future studies.

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76 **Accession Numbers**

77 The draft assembly of *X. arboricola* pv. *corylina* strain A7 has been deposited in the
78 National Centre for Biotechnology Information (NCBI) GenBank database under the
79 accession number CP062164. Raw Illumina Hiseq reads and PacBio reads have been
80 deposited in NCBI SRA under the accession number of BioProject PRJNA661460,
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