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# Draft Genome Sequence of *Plasmopara viticola*, the Grapevine Downy Mildew Pathogen

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***Plasmopara viticola* is a biotrophic pathogenic oomycete responsible for grapevine downy mildew. We present here the first draft of the *P. viticola* genome. Analysis of this sequence will help in understanding plant-pathogen interactions in oomycetes, especially pathogen host specialization and adaptation to host resistance.**

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*Plasmopara viticola* is a heterothallic diploid oomycete (*Stramenopiles*) responsible for grapevine downy mildew, one of the most serious grapevine diseases worldwide (1, 2). The pathogen is native to North America and was accidentally introduced in Europe at the end of the 19th century (3). *P. viticola* is a good candidate for the study of host adaptation in biotrophic plant pathogens, especially host-plant specialization (4), and adaptation to plant resistance (5, 6). Analyses of transcriptomic data for the species have recently been published (7, 8), but until now, no reference genome sequence was available.

The sequenced isolate INRA-PV221 was collected in 2009 from a grapevine leaf lesion in a vineyard in the Bordeaux region (Blanquefort, France). The isolate was propagated on detached grapevine leaves, and genomic DNA of sporangia was extracted using either the DNeasy blood and tissue kit or the DNeasy plant minikit (both from Qiagen). A paired-end and two mate-pair libraries (3- and 8-kb inserts) were prepared and sequenced on Illumina HiSeq2000 sequencers at the GeT-PlaGe GenoToul facility (Toulouse, France) and by Eurofins MWG Operon (Ebersberg, Germany), respectively, producing around 615 million reads. Paired-end reads were cleaned and transformed into virtual long reads using boost-r (J. Gouzy, unpublished data), and then assembled into contigs using Velvet (9). After removal of contigs included in longer contigs, scaffolding of contigs using mate-pair read information was carried out with LYNX (J. Gouzy, unpublished data).

After removing contaminating bacterial sequences, the assembly included 1,883 scaffolds with a size greater than 1 kb (maximum size: 763.2 kb), for a total size of 74.74 Mb (N content: 2.12 Mb). The  $N_{50}$  and  $N_{90}$  of the assembly were 180.6 kb and 33.5 kb, respectively ( $L_{50}$ : 130 scaffolds;  $L_{90}$ : 450 scaffolds). The average GC content was 44.3%. Completeness of the genome as estimated by CEGMA (10, 11), using a set of 248 conserved eukaryote genes, was 91% (95% when counting partial matches).

The gene annotation and analysis of the genome of *P. viticola* will lead to the identification of the effector gene repertoire of this

pathogen, allowing a better understanding of the molecular interactions governing this pathosystem and facilitating the identification of genes involved in gene-for-gene interactions with grapevine. The availability of a reference genome will also be helpful for population genomics studies addressing the worldwide invasion of *P. viticola* and the mechanisms responsible for its rapid adaptation to fungicides and to resistant grapevine cultivars (5, 6).

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number [MBPM00000000](https://www.ncbi.nlm.nih.gov/nuccore/MBPM00000000). The version described in this paper is the first version, MBPM01000000.

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