



HAL
open science

Draft genome sequence of *Plasmopara viticola*, the grapevine downy mildew pathogen

Yann Dussert, Jerome Gouzy, Sylvie Richart-Cervera, Isabelle D. Mazet, Laurent Deliere, Carole Couture, Ludovic Legrand, Marie-Christine Piron, Pere Mestre, François F. Delmotte

► To cite this version:

Yann Dussert, Jerome Gouzy, Sylvie Richart-Cervera, Isabelle D. Mazet, Laurent Deliere, et al.. Draft genome sequence of *Plasmopara viticola*, the grapevine downy mildew pathogen. *Genome Announcements*, 2016, 4 (5), 2 p. 10.1128/genomeA.00987-16 . hal-02637044

HAL Id: hal-02637044

<https://hal.inrae.fr/hal-02637044v1>

Submitted on 27 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Yann Dussert,^a Jérôme Gouzy,^b Sylvie Richart-Cervera,^a Isabelle D. Mazet,^a Laurent Delière,^a Carole Couture,^a Ludovic Legrand,^b Marie-Christine Piron^c Pere Mestre,^c François Delmotte^a

SAVE, Bordeaux Sciences Agro, INRA, Villenave d'Ornon, France^a; LIPM, Université de Toulouse, INRA, CNRS, Castanet-Tolosan, France^b; SVQV, INRA, Université de Strasbourg, Colmar, France^c

***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.**

Received 26 July 2016 Accepted 3 August 2016 Published 22 September 2016

Citation Dussert Y, Gouzy J, Richart-Cervera S, Mazet ID, Delière L, Couture C, Legrand L, Piron M-C, Mestre P, Delmotte F. 2016. Draft genome sequence of *Plasmopara viticola*, the grapevine downy mildew pathogen. *Genome Announc* 4(5):e00987-16. doi:10.1128/genomeA.00987-16.

Copyright © 2016 Dussert et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Yann Dussert, dussert.yann@gmail.com.

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/nuclink/MBPM00000000). The version described in this paper is the first version, MBPM01000000.

ACKNOWLEDGMENTS

We thank Dario Cantu, Francis Martin, and Christophe Plomion for their useful advice.

FUNDING INFORMATION

This work, including the efforts of François Delmotte, was funded by INRA AIP-Bioressources. This work, including the efforts of François Delmotte, was funded by European Commission (EC) (INNOVINE FP7-KBBE-311775). This work, including the efforts of François Delmotte, was funded by Agence Nationale de la Recherche (ANR) (GANDALF ANR-12-ADAP-0009). This work, including the efforts of Pere Mestre, was funded by Agence Nationale de la Recherche (ANR) (EFFECTOORES ANR-13-ADAP-0003).

REFERENCES

- Kamoun S, Furzer O, Jones JD, Judelson HS, Ali GS, Dalio RJ, Roy SG, Schena L, Zambounis A, Panabières F, Cahill D, Ruocco M, Figueiredo A, Chen X-R, Hulvey J, Stam R, Lamour K, Gijzen M, Tyler BM, Grünwald NJ, Mukhtar MS, Tomé DFA, Tör M, Van Den Ackerveken G, McDowell J, Daayf F, Fry WE, Lindqvist-Kreuzer H, Meijer HJG, Petre B, Ristaino J, Yoshida K, Birch PRJ, Govers F. 2015. The top 10 oomycete pathogens in molecular plant pathology. *Mol Plant Pathol* 16: 413–434. <http://dx.doi.org/10.1111/mpp.12190>.
- Gessler C, Pertot I, Perazzolli M. 2011. *Plasmopara viticola*: a review of knowledge on downy mildew of grapevine and effective disease management. *Phytopathol Mediterr* 50:3–44.
- Fontaine MC, Austerlitz F, Giraud T, Labbé F, Papura D, Richard-

- Cervera S, Delmotte F. 2013. Genetic signature of a range expansion and leap-frog event after the recent invasion of Europe by the grapevine downy mildew pathogen *Plasmopara viticola*. *Mol Ecol* 22:2771–2786. <http://dx.doi.org/10.1111/mec.12293>.
4. Rouxel M, Mestre P, Comont G, Lehman BL, Schilder A, Delmotte F. 2013. Phylogenetic and experimental evidence for host-specialized cryptic species in a biotrophic oomycete. *New Phytol* 197:251–263. <http://dx.doi.org/10.1111/nph.12016>.
 5. Delmotte F, Mestre P, Schneider C, Kassemeyer H-H, Kozma P, Richart-Cervera S, Rouxel M, Delière L. 2014. Rapid and multiregional adaptation to host partial resistance in a plant pathogenic oomycete: evidence from European populations of *Plasmopara viticola*, the causal agent of grapevine downy mildew. *Infect Genet Evol* 27:500–508. <http://dx.doi.org/10.1016/j.meegid.2013.10.017>.
 6. Delmas CE, Fabre F, Jolivet J, Mazet ID, Richart Cervera S, Delière L, Delmotte F. 2016. Adaptation of a plant pathogen to partial host resistance: selection for greater aggressiveness in grapevine downy mildew. *Evol Appl* 9:709–725. <http://dx.doi.org/10.1111/eva.12368>.
 7. Mestre P, Carrere S, Gouzy J, Piron M-C, Tourvieille de Labrouhe D, Vincourt P, Delmotte F, Godiard L. 2016. Comparative analysis of expressed CRN and RXLR effectors from two *Plasmopara* species causing grapevine and sunflower downy mildew. *Plant Pathol* 65:767–781. <http://dx.doi.org/10.1111/ppa.12469>.
 8. Yin L, Li X, Xiang J, Qu J, Zhang Y, Dry IB, Lu J. 2015. Characterization of the secretome of *Plasmopara viticola* by *de novo* transcriptome analysis. *Physiol Mol Plant Pathol* 91:1–10. <http://dx.doi.org/10.1016/j.pmpp.2015.05.002>.
 9. 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>.
 10. Parra G, Bradnam K, Korf I. 2007. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. *Bioinformatics* 23:1061–1067. <http://dx.doi.org/10.1093/bioinformatics/btm071>.
 11. Parra G, Bradnam K, Ning Z, Keane T, Korf I. 2009. Assessing the gene space in draft genomes. *Nucleic Acids Res* 37:289–297. <http://dx.doi.org/10.1093/nar/gkn916>.