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Draft Genome Sequence of *Diplodia seriata* F98.1, a Fungal Species Involved in Grapevine Trunk Diseases

Guillaume Robert-Siegwald,[a] Julie Vallet,[b] Eliane Abou-Mansour,[c] Jiabao Xu,[d] Patrice Rey,[e] Christophe Bertsch,[f] Cecilia Rego,[g] Philippe Larignon,[h] Florence Fontaine,[b] Marc-Henri Lebrun[a]

UMR 1290 BIOGER, INRA, AgroParisTech, Campus AgroParistech, Thiverval-Grignon, France[a]; Université de Reims Champagne-Ardenne, URVVC EA 4707, Laboratoire Stress, Défenses et Reproduction des Plantes, Reims, France[b]; Plant Biology Department, University of Fribourg, Fribourg, Switzerland[c]; BGI-Shenzhen, Shenzhen, China[d]; UMR1065 SAVE, Santé et Agroécologie du Vignoble, INRA, Bordeaux Sciences Agro, Villenave d'Ornon, France[e]; Université Haute Alsace, Laboratoire Vigne Biotechnologie et Environnement EA 3991, Colmar, France[f]; Institut Supérieur d'Agronomie, Tapada da Ajuda, Lisbon, Portugal[g]; Institut Français de la Vigne et du Vin Pôle Rhône-Méditerranée, Rodilhan, France[h]

ABSTRACT The ascomycete *Diplodia seriata* is a causal agent of grapevine trunk diseases. Here, we present the draft genome sequence of *D. seriata* isolate F98.1 (37.27 Mb, 512 contigs, 112 scaffolds, and 8,087 predicted protein-coding genes).

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Address correspondence to Marc-Henri Lebrun, marc-henri.lebrun@inra.fr.

F.F. and M.-H.L. contributed equally to this work.

Diplodia seriata (1, 2) is one of the most common species in the family *Botryosphaeriaceae* that is associated with grapevine trunk diseases (3, 4). In grapevine, *D. seriata* is frequently isolated from necrotic tissues (black spots or sectors) localized in the wood of infected trunks or arms (3–5). This species is also frequently isolated from woody tissues of trees such as *Acer* sp., *Prunus* sp., and *Quercus* sp. (2). Pycnidia are produced on infected grapevine wood or pruning shoots, and liberate pycnidiospores dispersed by rainfall or sprinkler irrigation (6, 7). On grapevine surfaces, pycnidiospores germinate and infectious hyphae penetrate into the plant tissues through pruning wounds (4, 5). Inoculation of *D. seriata* on wounded stems from grafted grapevines of the highly susceptible cultivar tempranillo induces a local brown necrosis in all plants and foliar symptoms in 50% of plants (8). *D. seriata* is known to secrete several plant polymers degrading enzymes such as cellulases, xylanases, lipases, and laccases (9, 10). This fungal species also produces phytotoxic secondary metabolites such as (−)-mellein and its derivates (11, 12).

D. seriata F98.1 was isolated in 1998 at Perpignan, France, from the trunk of a grapevine exhibiting foliar symptoms typical of Syrah decline (13). *D. seriata* F98.1 is pathogenic on grapevine (8, 13). Sequencing was performed by BGI-Tech (China) using Illumina HiSeq 2500 at a coverage of 270× (170-, 500-, and 6,000-bp libraries). After quality filtering, a total of 88,596,792 paired-end reads of 125 bp were obtained. Assembly with SOAPdenovo version 1.05 (14) led to 512 contigs and 112 scaffolds (37.27 Mb; G+C%: 56.8). This high-quality genome (scaffold N_{50}: 2.9 Mb; minimum scaffold length: 1,007 bp; gaps: 250 kb) has 13 scaffolds with a size greater than 1 Mb (90% of the total sequence), likely corresponding to chromosomes. Using GLEAN (15), 8,087 coding sequences (CDSs) were identified, 93% being supported by RNAseq (mycelium on potato dextrose broth or minimal medium for 4 days). Recently, the genome sequence of *D. seriata* DS831, isolated from an infected grapevine (United States, 2011), was released (16). The genome size of DS831 (37.13 Mb) is similar to the genome size of F98.1, but its assembly is five times more fragmented (1,391 contigs; 695 scaffolds), and it carries 9,398 CDSs. Bidirectional best BLAST hit (BDBH) analysis revealed that 82% of F98.1's and DS831's CDSs are similar. OrthoFinder (17) identified

5,935 orthologous single-copy gene families shared between the two genomes. According to BDBH analysis, 1,507 genes are specific to strain F98.1, and 2,763 are specific to strain DS831. Using BLASTN, we found that 2,686 (97.2%) of the genes thought to be specific to strain DS831 were present in the F98.1 genome sequence, and 1,440 (95.6%) of the genes thought to be specific to strain F98.1 are present in the DS831 genome sequence. The difference in CDS numbers between DS831 and F98.1 is likely a consequence of using different annotation software (GLEAN versus Augustus). Fusing the two annotations produces a set of 10,773 CDSs (8,087 from F98.1 and 2,686 from DS831).

Accession number(s). This whole-genome project has been deposited at NCBI GenBank under the accession number MSZU00000000. The version described in this paper is the first version, MSZU01000000.

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