Title
Draft Genome Sequence of the Grapevine Dieback Fungus Eutypa lata UCR-EL1.

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Eutypa dieback of grapevines is a wood disease caused by the ascomycete Eutypa lata (Pers.: Fr.) Tul. & C. Tul. (also known as E. armeniacae Hansf. and M. V. Carter) (1, 2). E. lata infections result in significant economical losses due to reduced yields, increased crop management costs, and shortened life span of the vines (3, 4).

E. lata enters the host through pruning wounds, colonizes the vascular tissues (1, 5), and gradually kills the plant by secreting phytotoxins (6, 7) and cell wall-degrading enzymes (8). Grape cultivars show differences in their susceptibilities to E. lata (9), but no resistant cultivars or completely effective management practices are available.

E. lata isolate UCR-EL1 was recovered from the margin of a grapevine (Vitis vinifera cv. “Cremson”) wood canker collected in Fresno County (California) in 2011. Fungal colony purification and species identification were performed as described by Rolshausen et al. (10). DNA was extracted using a modified cetyltrimethylammonium bromide (CTAB) method (11), and 7.3 Gb of filtered reads were assembled using CLC Genomic Workbench (v6.0; 2,334 scaffolds (3,322 contigs; median coverage, 97%)).

Scaffolds were masked for repeats using RepeatMasker (13), and gene prediction was performed with the eukaryotic gene finder Augustus (14), trained using the gene models identified by CEGMA (12). A total of 11,818 complete protein-coding sequences were obtained, which is similar to the gene content of other ascomycetes (15, 16). Ninety-two percent of the predicted proteome was annotated based on its sequence homology to proteins in the NCBI nonredundant (nr) database (BLASTp, e-value \( \leq 10^{-3} \)). While these ab initio-discovered gene models need to be further curated and validated using empirical transcript data, they provide us with a first glimpse of the functions encoded in the E. lata genome. In agreement with the known capability of E. lata to degrade woody tissues (8), we found among the 1,224 potentially secreted proteins (SignalP v4.0 (17)) a rich repertoire of cell wall-degrading enzymes comprising 217 putative glycoside hydrolases annotated based on homology with proteins in the CAZy database (18). The most abundant CAZy families identified among the putative secreted proteome were GH61 (26 genes), GH43 (22 genes), and GH16 (17 genes). While GH61 enzymes enhance the breakdown of lignocellulosic material in combination with cellulolytic enzymes (19), GH43 and GH16 enzymes have hemicellulolytic activities. A large number of putative cytochrome P450 monoxygenases (205 genes), known to be involved in lignin oxidation, were also found, as is reported in other genomes of wood-rotting fungi (20–22).

**Nucleotide sequence accession numbers.** This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AORF0000000. The version described in this paper is the first version, accession no. AORF0100000.

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**REFERENCES**

1. Carter MV, Bolay A, English H, Rumbos I. 1985. Variation in the pathogenicity of Eutypa lata (E. armeniacae). Aust. J. Bot. 33:361–366.
2. Carter MV. 1991. The status of Eutypa lata as a pathogen. Phytopathological paper no. 32. CAB International, Wallingford, United Kingdom.
3. Siebert JB. 2001. *Eutypa*: the economic toll on vineyards. Wines Vines April:50–56.

4. Munkvold GP, Duthie JA, Marois JJ. 1994. Reductions in yield and vegetative growth of grapevines due to *Eutypa* dieback. Phytopathology 84:186–192.

5. Péros JP, Berger G. 1994. A rapid method to assess the aggressiveness of *Eutypa lata* isolates and the susceptibility of grapevine cultivars to *Eutypa* dieback. Agronomie 14:515–523.

6. Amborabé B-E, Fleurat-Lessard P, Bonmort J, Roustan J-P, Roblin G. 2001. Effects of eutypine, a toxin from *Eutypa lata*, on plant cell plasma membrane: possible subsequent implication in disease development. Plant Physiol. Biochem. 39:51–58.

7. Smith LR, Mahoney NE, Molyneux RJ, Gubler WD. 1996. Synthesis and structure—phytotoxicity relationships of acetylenic phenols and chromene metabolites, and their analogues, from the grapevine pathogen *Eutypa lata*. J. Nat. Prod. 66:169–176.

8. Rolshauser PE, Greve LC, Labavitch JM, Mahoney NE, Molyneux RJ, Gubler WD. 2008. Pathogenesis of *Eutypa lata* in grapevine: identification of virulence factors and biochemical characterization of cordon dieback. Phytopathology 98:222–229.

9. Sosnowski MR, Lardner R, Wicks TJ, Scott ES. 2007. The influence of grapevine cultivar and isolate of *Eutypa lata* on wood and foliar symptoms. Plant Dis. 91:924–931.

10. Rolshauser PE, Mahoney NE, Molyneux RJ, Gubler WD. 2006. A reassessment of the species concept in *Eutypa lata*, the causal agent of *Eutypa* dieback of grapevine. Phytopathology 96:369–377.

11. Möller EM, Bahnewg G, Sandermann H, Geiger HH. 1992. A simple and efficient protocol for isolation of high molecular weight DNA from filamentous fungi, fruit bodies, and infected plant tissues. Nucleic Acids Res. 20:6115–6116.

12. Parra G, Bradnam K, Ning Z, Keane T, Korf I. 2009. Assessing the gene space in draft genomes. Nucleic Acids Res. 37:289–297.

13. Smit AFA, Hubley R, Green P. 2003. posting date. RepeatMasker. http://repeatmasker.org.

14. Stanke M, Diekhans M, Baertsch R, Haussler D. 2008. Using native and syntenically mapped cDNA alignments to improve de novo gene finding. Bioinformatics 24:637–644.

15. Amselem J, Cuomo CA, van Kan JA, Viaud M, Benito EP, Couloux A, Coutinho PM, de Vries RP, Dyer PS, Fillingier S, Fournier E, Gout L, Hahn M, Kohn L, Lapalu N, Plummer KM, Pradier JM, Quivillon E, Sharon A, Simon A, ten Have A, Tudzynski B, Tudzynski P, Wincker P, Andrew M, Anthouard V, Beever RE, Beffa R, Benoit I, Bouzid O, Braunl B, Chen Z, Choquer M, Collémare J, Cotton P, Danchin EG, Da Silva G, Gauthier A, Giraud C, Giraud T, Gonzalez C, Grosssete S, Gültenner U, Henrisatt B, Howlett BJ, Kodicr A, Kretschmer M, Larpentain A, Leroch M, Levis C, et al. 2011. Genomic analysis of the necrotrrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*. PLoS Genet. 7:e1002230.

16. Gao Q, Jin K, Ying S-H, Zhang Y, Xiao G, Shang Y, Duan Z, Hu X, Xie X-Q, Zhou G, Peng G, Luo Z, Huang W, Wang B, Fang W, Wang S, Zhong Y, Ma L-J, St. Leger RJ, Zhao G-P, Pei Y, Feng M-G, Xia Y, Wang C. 2011. Genome sequencing and comparative transcriptomics of the model entomopathogenic fungi *Metarhizium anisopliae* and *M. acridum*. PLoS Genet. 7:e1001264.

17. Petersen BN, Brunak S, von Heijne G, Nielsen H. 2011. SignalP 4.0: discriminating signal peptides from transmembrane regions. Nat. Methods 8:785–786.

18. Cantarel BL, Coutinho PM, Rancurel C, Bernard T, Lombard V, Henrisatt B. 2009. The carbohydrate-active enzymes database (CAZY): an expert resource for glycomics. Nucleic Acids Res. 37:D233–D238.

19. Harris PV, Welter D, McFarland KC, Re E, Navarro Poulsen JC, Brown K, Salbo R, Ding H, Vlasenko E, Merino S, Xu F, Cherry J, Larsen S, Lo Leggio L. 2010. Stimulation of lignocellulosic biomass hydrolysis by proteins of glycoside hydrolase family 61: structure and function of a large, enigmatic family. Biochemistry 49:3305–3316.

20. Ichinohe H, Wariishi H, Tanaka H. 2002. Identification and characterization of novel cytochrome P450 genes from the white-rot basidiomycete, *Coriolus versicolor*. Appl. Microbiol. Biotechnol. 58:97–105.

21. Martinez D, Challacombe J, Morgenstern I, Hibbert D, Schnoll M, Kubicek CP, Ferreira P, Ruiz-Duenas FJ, Martinez AT, Kersten P, Hammel KE, Vanden Wymelenberg A, Gaskell J, Lindquist E, Sabat G, Bondurant SS, Larrondo LF, Canessa P, Viscuara R, Yadav J, Doddapaneni H, Subramanian V, Pisabarro AG, Lavín JL, Oguiza JA, Master E, Henrisatt B, Coutinho PM, Harris P, Magnusson JK, Baker SE, Bruno K, Kenealy W, Hoeger PJ, Kíes U, Ramaiya P, Lucas S, Salamov A, Shapiro H, Tu H, Che H, Misra M, Xie G, Teter S, Yaver D, James T, Mokrejs M, Pospísek M, Gröger I, Brettin T, Rohdsar D, Berka R, Cullen D. 2009. Genome, transcriptome, and secretome analysis of wood decay fungus *Postia placenta* supports unique mechanisms of lignocellulose conversion. Proc. Natl. Acad. Sci. U. S. A. 106:1954–1959.

22. Martinez D, Larrondo LF, Putnam N, Gelpke MD, Huang K, Chapman J, Helfenbein KG, Ramaiya P, Detter JC, Larimer F, Coutinho PM, Henrisatt B, Berka R, Cullen D, Rohdsar D. 2004. Genome sequence of the lignocellulose degrading fungus *Phanerochaete chrysosporium* strain RP78. Nat. Biotechnol. 22:695–700.