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EUKARYOTES

Draft Genome Sequence of the Fungus Associated with Oak Wilt Mortality in South Korea, *Raffaelea quercus-mongolicae* KACC44405

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ABSTRACT The fungus *Raffaelea quercus-mongolicae* is the causal agent of Korean oak wilt, a disease associated with mass mortality of oak trees (e.g., *Quercus* spp.). The fungus is vectored and dispersed by the ambrosia beetle, *Platypus koryoensis*. Here, we present the 27.0-Mb draft genome sequence of *R. quercus-mongolicae* strain KACC44405.

Received 29 June 2017 **Accepted** 12 July 2017 **Published** 24 August 2017

Citation Jeon J, Kim K-T, Song H, Lee G-W, Cheong K, Kim H, Choi G, Lee Y-H, Stewart JE, Klopfenstein NB, Kim M-S. 2017. Draft genome sequence of the fungus associated with oak wilt mortality in South Korea, *Raffaelea quercus-mongolicae* KACC44405. Genome Announc 5:e00797-17. https://doi.org/10.1128/genomeA.00797-17.

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Oak wilt disease has emerged rapidly across South Korea since 2004, and the putative causal agent of the disease has been identified as a filamentous ascomycetous fungus, *Raffaelea quercus-mongolicae* (1). This fungus has a symbiotic relationship with an insect vector, *Platypus koryoensis* (ambrosia beetle), which attacks oak trees (e.g., *Quercus mongolica*, *Q. aliena*, and *Q. serrata*) (2). After the fungus has been vectored into a beetle gallery of an oak tree, it can cause sapwood discoloration and disrupt sap flow in the host. Thus, *R. quercus-mongolicae* is considered to be the putative cause of wilt and blight symptoms that subsequently cause tree mortality. Previously, to evaluate the cause of mass mortality of oak trees in South Korea, the virulence of *R. quercus-mongolicae* on oak trees was assessed; however, these previous pathogenicity tests were inconclusive (3). Molecular biological investigations on the pathogenicity of *R. quercus-mongolicae* have not been addressed, largely due to the need for genomic information. Here, we present the draft genome sequence to assist further genome-based analyses of *R. quercus-mongolicae* and its host interactions.

The isolate of *R. quercus-mongolicae* (KACC44405) originated from discolored sapwood of *Platypus koryoensis*-infested *Q. mongolica* that was displaying pronounced symptoms of oak wilt (collected by K. H. Kim at Gwangreung Experimental Forest, Pocheon, South Korea, 12 May 2005). The fungal isolate was cultured on potato dextrose agar, and genomic DNA was extracted using a standard phenol-chloroform method.

The draft genome was sequenced with the Illumina NextSeq and MiSeq systems for paired-end reads and the HiSeq 2000 system for mate pair reads. The short reads were assembled with the A5-miseq pipeline (4), and gaps were filled with the GapCloser module in SOAPdenovo2 (5). The estimated genome size of *R. quercus-mongolicae* was 27,005,990 bp with a 54.25% GC content, which was assembled to 43 scaffolds with an N_{50} of 2.2 Mb obtained from 200 contigs. The protein-coding genes were predicted using the MAKER genome annotation pipeline (6). A total of 8,155 coding genes were predicted, and 147 genes were identified as tRNA genes by tRNAscan-SE software (7).

Using the previously developed gene family prediction pipelines, six gene families that possibly contribute major roles in the physiology and pathogenicity of *R. quercus-mongolicae* were annotated (8–12). The numbers of transcription factor and cytochrome P450 coding genes were 425 and 52, respectively. The genome had 625 secreted protein-coding genes, and, of those, 118 were small secreted polypeptides of less than 300 amino acids. Plant cell wall-degrading enzymes were encoded by 28 genes, in addition to 11 genes encoding laccases and 14 genes encoding peroxidases that may be involved in lignin degradation. Also, 13 polyketide synthase and 18 nonribosomal peptide synthetase genes were identified with antiSMASH software (13). The genome sequence of *R. quercus-mongolicae* strain KACC44405, along with other *Raffaelea* spp., will provide valuable resources for comparative genomic analyses and identifying genes that contribute to a potential pathogenic relationship between the fungus and host, as well as a potential symbiotic relationship between the fungus and insect vector.

Accession number(s). This genome sequence has been deposited in GenBank under the accession no. NIPS00000000.

REFERENCES

1. Kim KH, Choi YJ, Seo ST, Shin HD. 2009. *Raffaelea quercus-mongolicae* sp. nov. associated with *Platypus koryoensis* on oak in Korea. Mycotaxon 110:189–197. https://doi.org/10.5248/110.189.
2. Suh DY, Hyun MW, Kim SH, Seo ST, Kim KH. 2011. Filamentous fungi isolated from *Platypus koryoensis*, the insect vector of oak wilt disease in Korea. Mycobiology 39:313–316. https://doi.org/10.5941/MYCO.2011.39.4.313.
3. Torii M, Matsuda Y, Seo ST, Kim KH, Ito S, Moon MJ, Kim SH, Yamada T. 2014. The effect of *Raffaelea quercus-mongolicae* inoculations on the formation of non-conductive sapwood of *Quercus mongolica*. Mycobiology 42:210–214. https://doi.org/10.5941/MYCO.2014.42.2.210.
4. Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics 31:587–589. https://doi.org/10.1093/bioinformatics/btu661.
5. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. Gigascience 1:18. https://doi.org/10.1186/2047-217X-1-18.
6. Cantarel BL, Korf I, Robb SM, Parra G, Ross E, Moore B, Holt C, Sánchez Alvarado A, Yandell M. 2008. MAKER: an easy-to-use annotation pipeline designed for emerging model organism genomes. Genome Res 18:188–196. https://doi.org/10.1101/gr.6743907.
7. Lowe TM, Eddy SR. 1997. TRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–964.
8. Park J, Park J, Jang S, Kim S, Kong S, Choi J, Ahn K, Kim J, Lee S, Kim S, Park B, Jung K, Kim S, Kang S, Lee YH. 2008. FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. Bioinformatics 24:1024–1025. https://doi.org/10.1093/bioinformatics/btn058.
9. Park J, Lee S, Choi J, Ahn K, Park B, Park J, Kang S, Lee YH. 2008. Fungal cytochrome P450 database. BMC Genomics 9:402. https://doi.org/10.1186/1471-2164-9-402.
10. Kim KT, Jeon J, Choi J, Cheong K, Song H, Choi G, Kang S, Lee YH. 2016. Kingdom-wide analysis of fungal small secreted proteins (SSPs) reveals their potential role in host association. Front Plant Sci 7:186. https://doi.org/10.3389/fpls.2016.00186.
11. Choi J, Kim KT, Jeon J, Lee YH. 2013. Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and oomycetes. BMC Genomics 14(suppl 5):S7. https://doi.org/10.1186/1471-2164-14-S5-S7.
12. Choi J, Détry N, Kim KT, Asiegbu FO, Valkonen JP, Lee YH. 2014. fPoxDB: fungal peroxidase database for comparative genomics. BMC Microbiol 14:117. https://doi.org/10.1186/1471-2180-14-117.
13. Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Res 43:W237–W243. https://doi.org/10.1093/nar/gkv437.