AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of *Raffaelea quercivora* JCM 11526, a Japanese Oak Wilt Pathogen Associated with the Platypodid Beetle, *Platypus quercivorus*

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The Japanese oak wilt pathogen *Raffaelea quercivora* and the platypodid beetle, *Platypus quercivorus*, cause serious mass mortality of *Quercus* spp. in Japan. Here, we present the first draft genome sequence of *R. quercivora* JCM 11526 to increase our understanding of the mechanism of pathogenicity and symbiosis with the ambrosia beetle.

Received 6 June 2016 **Accepted** 10 June 2016 **Published** 28 July 2016

Citation Masuya H, Manabe R-I, Ohkuma M, Endoh R. 2016. Draft genome sequence of *Raffaelea quercivora* JCM 11526, a Japanese oak wilt pathogen associated with the platypodid beetle, *Platypus quercivorus*. Genome Announc 4(4):e00755-16. doi:10.1128/genomeA.00755-16.

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The genus *Raffaelea*, belonging to the order *Ophiostomatales*, class *Sordariomycetes*, and phylum *Ascomycota*, is closely associated with various wood-boring beetles in the *Scolytinae* and *Platypodinae* families (1, 2). The fungi strongly depend on the beetles for their dispersal, and the beetle larvae consume the fungi for their own growth (3). A wide variety of platypodid/scolytid beetles possess mycangia, specialized structures for storing fungal spores, on their body or in the mouth (4).

Several *Raffaelea* spp. show virulence toward trees (5, 6). Among them, *R. quercivora* is the causal agent of Japanese oak wilt, together with *Platypus quercivorus* (*Platypodidae*, *Coleoptera*) (7). Since the 1990s, Japanese oak forests have been heavily damaged by the *R. quercivora*/*P. quercivorus* complex. Although virulence tests have been performed in many previous studies (5), they have not been addressed in the context of molecular biology due to a lack of genomic information.

Here, we present the draft genome sequence of *R. quercivora* JCM 11526, an ex-type strain, isolated from an adult *P. quercivorus* and maintained at JCM (7). Genomic DNA of the fungus was extracted with a phenol-chloroform/isoamyl alcohol series, followed by purification using the QIAGEN Genomic-tip 100/G kit (Qiagen) and a PowerClean Pro DNA cleanup kit (Mo Bio Laboratories, Inc.). A paired-end (PE) shotgun library and a mate-pair (MP) library were constructed using the TruSeq DNA sample prep kit (Illumina) and the Nextera mate-pair library prep kit (Illumina); the genomic sequence reads from the PE and MP libraries were generated on the Illumina HiSeq 2500 and MiSeq platforms, respectively. The obtained reads were assembled using ALLPATHS-LG version 52488, where the ploidy was set to 2. The genome was assembled into 33,925,930 bp, with a G+C content of 57.1% in 82 contigs and 26 scaffolds, an N_{50} metric of 3,655 kb, and a largest scaffold of 5,014 kb. RepeatMasker (http://www.repeatmasker.org) was used to identify and mask repetitive and low-complex regions within the assembly, and 25% of the genome was estimated to be repetitive. CEGMA (8) was used to assess gene space, resulting in 234 of 248 (94.3%) core eukaryotic genes being identified in the assembly. Gene prediction was performed using the MAKER annotation pipeline (9), including AUGUSTUS version 3.0.3 (10), SNAP (2013-02-16) (11), and GeneMark-ES (12). A total of 8,906 protein-coding genes were predicted using AUGUSTUS trained on *Neurospora crassa*. A total of 214 noncoding RNA genes were predicted using RepeatMasker and RepeatRunner (http://www.yandell-lab.org/software/repeatrunner.html). A total of 126 tRNA genes were predicted using tRNAscan-SE (13). The draft functional annotation was performed using Sma3S (14), where the UniProt-TrEMBL (release 2015_11) and UniProt-SwissProt (release 2015_11) databases were used, resulting in 7,890 and 2,551 genes being functionally annotated by UniProt-TrEMBL and UniProt-SwissProt, respectively.

R. quercivora is the first sequenced species in this genus. Information about its genome sequence will provide novel insights into the pathogenicity of *R. quercivora* and the coevolutionary symbiosis between ambrosia beetles, fungi, and host trees.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the BioProject PRJDB3607 with accession numbers BCFZ01000001 to BCFZ01000026. The version described in this paper is the first one.

ACKNOWLEDGMENTS

This study was part of the Genome Information Upgrading Program FY2014, National Bioresource Project (NBRP), MEXT, Japan. This study was also supported by JSPS KAKENHI, grant number 15K18720.

We thank Shihomi Uzuhashi for her support in extracting genomic DNA.

FUNDING INFORMATION

This work, including the efforts of Ri-ichiroh Manabe, Moriya Ohkuma, and Rikiya Endoh, was funded by Ministry of Education,

Culture, Sports, Science, and Technology (MEXT) (FY2014). This work, including the efforts of Rikiya Endoh, was funded by Japan Society for the Promotion of Science (JSPS) (15K18720).

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