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EUKARYOTES

Draft Genome Sequence of the Fungus *Lecanicillium psalliotae* Strain HWLR35, Isolated from a Wheat Leaf Infected with Leaf Rust (Caused by *Puccinia triticina*)

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ABSTRACT *Lecanicillium psalliotae* is an entomopathogenic, mycoparasitical, and nematophagous fungus known to produce antibiotic and antifungal compounds. Here, we report the first 36-Mb draft genome sequence of *L. psalliotae* strain HWLR35. The draft genome contains 197 scaffolds and is predicted to have 11,009 protein-coding genes.

Lecanicillium psalliotae, previously described as *Verticillium psalliotae* (1), is a fungal parasite of many different hosts. Previous work has discovered that *L. psalliotae* is a mycoparasite of soybean rust (caused by *Phakopsora pachyrhizi*) urediniospores (2), is a nematophagous parasite (3), and is entomopathogenic against *Rhipicephalus annulatus* (4). *L. psalliotae* exhibits antagonistic inhibition of its hosts by a variety of means, including the excretion of natural products. *L. psalliotae* is a known producer of oosporein, a red-pigmented dibenzoquinone with antibiotic (5) and antifungal (6) activities. The *L. psalliotae* strain HWLR35 was isolated from a wheat leaf infected with leaf rust (caused by *Puccinia triticina*) from the Plant Breeding Institute, Cobbitty, NSW, Australia. Rust diseases of cereal crops are a threat to global food security (7) and present an interesting opportunity for the implementation of biocontrol agents, such as a fungal mycoparasite. Preliminary identification of *L. psalliotae* HWLR35 was proposed based on internal transcribed spacer (ITS) analysis but has not been confirmed morphologically.

L. psalliotae strain HWLR35 was grown on potato dextrose agar from a single-spore culture, and DNA was extracted with the PowerSoil DNA isolation kit (Mo Bio Laboratories, Inc., USA). Genomic DNA was sequenced with 125-bp paired-end reads on the Illumina HiSeq 2500 platform at the Western Sydney University Sequencing Facility. FastQC (8) was used for quality control after the raw reads had adapters removed, and low-quality reads were trimmed through Trimmomatic (9). Blue (10) was used for error correction. To identify the optimum assembly, the error-corrected read data were separately assembled with ABySS (11), SPAdes (12), and SOAP*denovo*2 (13). Error-corrected read data assembled with SOAP*denovo*2 ($k = 103$) performed best according to the following assembly metrics: scaffolds smaller than 1 kb were discarded, and the total assembly length was 36,139,470 bp in 197 remaining sequences, with the largest scaffold being 4,365,396 bp. The N_{50} was 2,330,369 bp, the L_{50} was 6, the G+C content was 52.74%, and the genome coverage was 80-fold. Two hundred ninety benchmarking universal single-copy ortholog (BUSCO) genes were used to test the genome assembly completeness by gene content (14) and showed that the assembly had 99.3% completeness with 288 single-copy BUSCOs, 2 being duplicated, 1 being fragmented, and

Received 29 November 2017 **Accepted** 1 December 2017 **Published** 11 January 2018

Citation Harm GFS, Papanicolaou A, Cuddy WS, Park RF, Moffitt MC. 2018. Draft genome sequence of the fungus *Lecanicillium psalliotae* strain HWLR35, isolated from a wheat leaf infected with leaf rust (caused by *Puccinia triticina*). Genome Announc 6:e01442-17. https://doi.org/10.1128/genomeA.01442-17.

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1 missing. TransposonPSI (15) and RepeatModeler (16) were used to mine the genome for transposons and repeats. The genome was masked with RepeatMasker (17) from the mined elements and the complete fungal RepBase data set (18), with 3.33% of the genome masked. Then, GeneMark-ES (19) and Augustus (20) were used for gene prediction in the masked genome, with 11,009 and 11,575 protein-coding genes predicted, respectively. To investigate biosynthetic gene clusters, antiSMASH 3.0 (21) was used, and the program identified 10 type I polyketide synthase (T1PKS) clusters, 9 nonribosomal peptide synthases (NRPS), 4 T1PKS-NRPS hybrid clusters, 5 terpenes, and 6 "other" clusters, for a total of 34 gene clusters. BLASTn (22) of ITS, 5.8S, and partial 18S and partial 28S rRNA sequences from the draft genome revealed a 100% match to *L. psalliotae* strain KYK00175 (GenBank accession no. AB360364) (23). The novel genome sequence of *L. psalliotae* HWLR35 will contribute to biosynthetic gene cluster discovery and help foster research into the genes relating to mycoparasitical interactions.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession no. PHFE00000000. The version described in this paper is the first version, PHFE01000000.

ACKNOWLEDGMENTS

This project was funded by an internal grant from Western Sydney University.

We acknowledge the Western Sydney University Next Generation Sequencing Facility and the Plant Breeding Institute for providing sequencing and the infected wheat leaf from which *L. psalliotae* was isolated, respectively.

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