AMERICAN SOCIETY FOR MICROBIOLOGY
Microbiology® Resource Announcements

Draft Genome Sequence of *Daldinia childiae* JS-1345, an Endophytic Fungus Isolated from Stem Tissue of Korean Fir

Jung A Kim,[a] Jongbum Jeon,[b] Sook-Young Park,[c] Mi Jin Jeon,[a] Joo-Hong Yeo,[a] Yong-Hwan Lee,[b] Soonok Kim[a]

[a]Genetic Resources Assessment Division, National Institute of Biological Resources, Incheon, South Korea

[b]Department of Agricultural Biotechnology, Interdisciplinary Program in Agricultural Genomics, Center for Fungal Genetic Resources, Center for Fungal Pathogenesis, Seoul National University, Seoul, South Korea

[c]Department of Plant Medicine, Sunchon National University, Suncheon, South Korea

Jung A Kim, Jongbum Jeon, and Sook-Young Park contributed equally to this work. Author order was determined in order of increasing seniority.

ABSTRACT The fungus *Daldinia childiae* strain JS-1345, isolated from stem tissue of *Abies koreana* (Korean fir), has shown strong anti-inflammatory activity. Here, we report the genome sequence of *D. childiae* JS-1345. The final assembly consisted of 133 scaffolds totaling 38,652,569 bp (G+C content, 44.07%).

Abies koreana Wilson (Korean fir) is a shrub and an evergreen plant that is endemic in the mountain region of South Korea at an altitude of 1,000 to 1,900 m (1). It has been used as traditional medicine to treat colds, stomachache, indigestion, and rheumatic disease (2). Essential oil from *A. koreana* has exhibited antioxidant, anti-inflammatory, and antimicrobial activities (1, 3, 4).

Recently, we isolated one of its endophytic fungi, *Daldinia childiae* JS-1345, from stem tissue of an *A. koreana* specimen collected in 2013 from Mount Moodeung (35°06′29.6″N, 127°01′09.1″E) in Hwasoon, South Korea, according to previously reported protocols (5, 6). This strain was deposited in the Wildlife Genetic Resources Bank at the National Institute of Biological Resources (Incheon, South Korea) under accession no. NIBRGR0000180467. *D. childiae* is a widely distributed wood-inhabiting ascomycete fungus belonging to the family *Hypoxylaceae* and the order *Xylariales* (7). Although many studies of this fungus have focused on taxonomy and ecology, little is known about the bioactivity of its metabolites and its genomics. We report here the draft genome sequence of *D. childiae* strain JS-1345, an endophytic fungus isolated from *A. koreana*.

Genomic DNA was extracted from young mycelia grown in potato dextrose broth at 25°C with shaking at 120 rpm for 2 days using a DNeasy minikit (Qiagen, CA). A short-insert paired-end library was generated using a TruSeq Nano DNA sample prep kit (Illumina, CA) with a fragment size of 350 bp, and a long-insert mate pair library was generated using a Nextera mate pair library prep kit (Illumina, CA) with a fragment size of 10 kb. The PacBio sequencing library was prepared using the SMRTbell template prep kit (Pacific Biosciences, CA). Genome sequencing was performed at Theragen Etex Bio Institute in Suwon, South Korea, following the strategies described previously (8). A total of 615,019 reads with an average length of 7,965 bp were generated from 4 cells of the PacBio Sequel platform using the overlap-layout-consensus (OLC) algorithm (9). About 5.6 Gb of short sequences from a paired-end library with an average insert length of 350 bp and about 11.6 Gb of sequences with 9,026,794 high-quality reads from a mate-paired library with an average insert length of 10 kb after filtering with NextClip v1.3 (10) were generated. Short-read sequences were assembled using SOAPdenovo v2.04 (9) with a kmer value of 41. These two assemblies were merged with HaploMerger2 (11). Merged sequences were cleaned twice using the faDnaPolishing.pl

Citation Kim JA, Jeon J, Park S-Y, Jeon MJ, Yeo J-H, Lee Y-H, Kim S. 2020. Draft genome sequence of *Daldinia childiae* JS-1345, an endophytic fungus isolated from stem tissue of Korean fir. Microbiol Resour Announc 9:e01284-19. https://doi.org/10.1128/MRA.01284-19.

Editor Jason E. Stajich, University of California, Riverside

Address correspondence to Soonok Kim, sokim90@korea.kr.

Received 12 October 2019
Accepted 14 November 2019
Published 2 April 2020

script provided by HaploMerger2 (removeShortSeq=500) (11). Scaffolding and gap filling were performed using SSPACE-Standard v3.0 (12), SSPACE-LongRead v1.1 (13), and GapFiller v1.10 (14) using default parameters. To summarize, the genome reads containing the nuclear genome were assembled into 133 scaffolds (263 contigs) with a total length of 38,652,569 bp and an N_{50} value of 3.27 Mb from the 22.16 Gb (556× genome size) of genome sequences. Genome assembly was validated using BUSCO v3.0.2b, which showed 98.2% of the benchmarked universal single copy orthologs (BUSCOs) as complete, including 3 complete and duplicated BUSCOs, against a set of 290 fungal genes (15). The G+C content of the assembled genome was 44.07%.

Gene prediction was performed by AUGUSTUS v3.2.1 (16) and produced 10,072 protein-coding gene models, of which 9,824 had homologs in the UniProt or NCBI nr and InterPro databases. Biosynthetic gene clusters with 25 polyketide synthases and 14 nonribosomal protein synthetases were found by antiSMASH v5.0 (17, 18). We further identified 418 genes encoding transcription factor genes using the Fungal Transcription Factor Database (FTFD) v1.0 (19), 124 cytochrome P450 genes using the Fungal Cytochrome P450 Database v1.0 (20), 61 genes encoding plant cell wall-degrading enzymes using the Fungal Plant Cell Wall-Degrading Enzyme Database v1.0 (21), and 6 genes encoding laccases and 26 genes encoding peroxidases using fPoxDB v1.0 (22). This draft genome sequence will contribute to phylogenomic analyses of fungi in *Xylariales* and to the identification and functional analyses of genes involved in active compound biosynthesis.

Data availability. The whole-genome sequence of *D. childiae* JS-1345 obtained in this study has been deposited in GenBank under accession no. VYXO00000000. The version described in this article is the first version, VYXO01000000. PacBio and Illumina sequence data were also deposited in the SRA under accession no. SRR10154460 to SRR10154462 (BioProject no. PRJNA566056).

ACKNOWLEDGMENT

This work was supported by the National Institute of Biological Resources, funded by the Ministry of Environment of the Republic of Korea (projects NIBR201830101 and NIBR201921101).

REFERENCES

1. Yoon WJ, Kim SS, Oh TH, Lee NH, Hyun CG. 2009. *Abies koreana* essential oil inhibits drug-resistant skin pathogen growth and LPS-induced inflammatory effects of murine macrophage. Lipids 44:471–476. https://doi.org/10.1007/s11745-009-3297-3.
2. Yeşilada E, Honda G, Sezik E, Tabata M, Fujita T, Tanaka T, Takeda Y, Takaishi Y. 1995. Traditional medicine in Turkey. V. Folk medicine in the inner Taurus Mountains. J Ethnopharmacol 46:133–152. https://doi.org/10.1016/0378-8741(95)01241-5.
3. Jeong SI, Lim JP, Jeon H. 2007. Chemical composition and antibacterial activities of the essential oil from *Abies koreana*. Phytother Res 21:1246–1250. https://doi.org/10.1002/ptr.2229.
4. Lee JH, Hong SK. 2009. Comparative analysis of chemical compositions and antimicrobial activities of essential oils from *Abies holophylla* and *Abies koreana* activities of essential oils from *Abies holophylla* and *Abies koreana*. J Microbiol Biotechnol 19:372–377. https://doi.org/10.4014/jmb.0811.630.
5. Lee C, Kim S, Li W, Bang S, Lee H, Lee HJ, Noh EY, Park JE, Bang WY, Shim SH. 2017. Bioactive secondary metabolites produced by an endophytic fungus *Gaeumannomyces* sp. JS0464 from a maritime halophyte *Phragmites communis*. J Antibiot (Tokyo) 70:737–742. https://doi.org/10.1038/ja.2017.39.
6. Nguyen HT, Kim S, Yu NH, Park AR, Yoon H, Bae CH, Yeo JH, Kim IS, Kim JC. 2019. Antimicrobial activities of an oxygenated cyclohexanone derivative isolated from *Amphirosellinia nigrospora* JS-1675 against various plant pathogenic bacteria and fungi. J Appl Microbiol 126:894–904. https://doi.org/10.1111/jam.14138.
7. Stadler M, Hawksworth DL, Fournier J. 2014. The application of the name *Xylaria hypoxylon*, based on *Clavaria hypoxylon* of Linnaeus. IMA Fungus 5:57–66. https://doi.org/10.5598/imafungus.2014.05.01.07.
8. Jeon J, Park SY, Kim JA, Yu NH, Park AR, Kim JC, Lee YH, Kim S. 2019. Draft genome sequence of *Amphirosellinia nigrospora* JS-1675, an endophytic fungus from *Pteris cretica*. Microbiol Resour Announc 8:e00069-19. https://doi.org/10.1128/MRA.00069-19.
9. Wang A, Wang Z, Li Z, Li LM. 2018. BAUM: improving genome assembly by adaptive unique mapping and local overlap-layout-consensus approach. Bioinformatics 34:2019–2028. https://doi.org/10.1093/bioinformatics/bty020.
10. Leggett RM, Clavijo BJ, Clissold L, Clark MD, Caccamo M. 2014. NextClip: an analysis and read preparation tool for Nextera long mate pair libraries. Bioinformatics 30:566–568. https://doi.org/10.1093/bioinformatics/btt702.
11. Huang S, Chen Z, Huang G, Yu T, Yang P, Li J, Fu Y, Yuan S, Chen S, Xu A. 2012. HaploMerger: reconstructing allelic relationships for polymorphic diploid genome assemblies. Genome Res 22:1581–1588. https://doi.org/10.1101/gr.133652.111.
12. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics 27:578–579. https://doi.org/10.1093/bioinformatics/btq683.
13. Boetzer M, Pirovano W. 2014. SSPACE-LongRead: scaffolding bacterial draft genomes using long read sequence information. BMC Bioinformatics 15:211. https://doi.org/10.1186/1471-2105-15-211.
14. Nadalin F, Vezzi F, Policriti A. 2012. GapFiller: a *de novo* assembly approach to fill the gap within paired reads. BMC Bioinformatics 13(Suppl 14):S8. https://doi.org/10.1186/1471-2105-13-S14-S8.
15. Waterhouse RM, Seppey M, Simao FA, Manni M, Ioannidis P, Klioutchnikov G, Kriventseva EV, Zdobnov EM. 2018. BUSCO applications from quality assessments to gene prediction and phylogenomics. Mol Biol Evol 35:543–548. https://doi.org/10.1093/molbev/msx319.

16. Stanke M, Steinkamp R, Waack S, Morgenstern B. 2004. AUGUSTUS: a Web server for gene finding in eukaryotes. Nucleic Acids Res 32: W309–W312. https://doi.org/10.1093/nar/gkh379.
17. Hunter S, Jones P, Mitchell A, Apweiler R, Attwood TK, Bateman A, Bernard T, Binns D, Bork P, Burge S, de Castro E, Coggill P, Corbett M, Das U, Daugherty L, Duquenne L, Finn RD, Fraser M, Gough J, Haft D, Hulo N, Kahn D, Kelly E, Letunic I, Lonsdale D, Lopez R, Madera M, Maslen J, McAnulla C, McDowall J, McMenamin C, Mi H, Mutowo-Muellenet P, Mulder N, Natale D, Orengo C, Pesseat S, Punta M, Quinn AF, Rivoire C, Sangrador-Vegas A, Selengut JD, Sigrist CJ, Scheremetjew M, Tate J, Thimmajanarthanan M, Thomas PD, Wu CH, Yeats C, Yong SY. 2012. InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Res 40:D306–D312. https://doi.org/10.1093/nar/gkr948.
18. Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Muller 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.
19. 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.
20. 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.
21. 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.
22. Choi J, Detry 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.