



# Draft Genome Sequences of the Oomycete *Pilasporangium apinafurcum* Strains JCM 30513 and JCM 30514, Formerly Classified as *Pythium apinafurcum*

Shihomi Uzuhashi,<sup>a</sup> Rikiya Endoh,<sup>b</sup> Ri-ichiroh Manabe,<sup>c</sup> Moriya Ohkuma<sup>b</sup>

Genetic Resources Center, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan<sup>a</sup>; Microbe Division/Japan Collection of Microorganisms (JCM), RIKEN BioResource Center, Tsukuba, Ibaraki, Japan<sup>b</sup>; Division of Genomic Technologies, RIKEN Center for Life Science Technologies, Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, Japan<sup>c</sup>

**ABSTRACT** *Pilasporangium apinafurcum*, formerly classified as *Pythium apinafurcum*, is a unique oomycete that infects plants asymptotically. Here, we present the draft genome sequences of two variants of *P. apinafurcum*, JCM 30513 and JCM 30514, isolated from uncultivated field soil in Wakayama Prefecture, Japan.

*Pilasporangium apinafurcum* is an oomycete formerly classified as *Pythium apinafurcum* based on its morphological similarity with many *Pythium* spp. (1, 2). The species was transferred from *Pythium* to a new genus, *Pilasporangium*, because of its unique phylogenetic position, and since then, only the single species has been assigned to the genus (3). *P. apinafurcum* infects some plants asymptotically (1). Two phylogenetic subgroups in *P. apinafurcum* are known. They were distinguished from each other based on the nucleotide sequences of the internal transcribed spacer regions of the rRNA gene and mitochondrial cytochrome *c* oxidase genes 1 and 2, but no apparent difference was observed in terms of morphology or pathogenicity between the two subgroups (1).

Here, we present the draft genome sequences of *P. apinafurcum* strains JCM 30513 and JCM 30514, each belonging to a different subgroup. Methods for cultivation, genomic DNA extraction, and purification were described previously (4). Briefly, *P. apinafurcum* was cultured on potato dextrose agar, and DNA was extracted using phenol-chloroform-isoamyl alcohol followed by purification using the Genomic-tip 100/G (Qiagen) and PowerClean Pro DNA cleanup kit (Mo Bio Laboratories, Inc.). A paired-end (PE) shotgun library and a mate-pair (MP) library were constructed using a TruSeq DNA library prep kit (Illumina) and a Nextera mate-pair library prep kit (Illumina), respectively. Sequencing for the PE and MP libraries was performed using the Illumina HiSeq 2500 platform. The MP reads were processed with NextClip version 0.8 (5) to remove adapter sequences. The PE and MP reads were assembled using ALLPATHS-LG version 52488 (6) into scaffolds with total lengths of 37,582,498 bp (JCM 30513) and 37,444,745 bp (JCM 30514), and the genome sizes and proportions of repetitive regions were 53.05 Mb and 37% and 49.48 Mb and 32%, respectively. The G+C content, number of contigs, number of scaffolds, and  $N_{50}$  (scaffold) were 43.5%, 899, 310, and 400.6 kb (JCM 30513) and 43.9%, 855, 280, and 449.6 kb (JCM 30514), respectively. Total sequencing depths (total read yields divided by estimated genome size) were  $211\times$  ( $158\times$  for PE,  $53\times$  for MP libraries) for JCM 30513 and  $278\times$  ( $217\times$  for PE,  $61\times$  for MP libraries) for JCM 30514. Completeness of the assemblies was estimated by CEGMA (7) to be 95.56% (JCM 30513) and 96.37% (JCM 30514), respectively. Gene

Received 20 July 2017 Accepted 26 July 2017 Published 31 August 2017

**Citation** Uzuhashi S, Endoh R, Manabe R-I, Ohkuma M. 2017. Draft genome sequences of the oomycete *Pilasporangium apinafurcum* strains JCM 30513 and JCM 30514, formerly classified as *Pythium apinafurcum*. *Genome Announc* 5:e00899-17. <https://doi.org/10.1128/genomeA.00899-17>.

**Copyright** © 2017 Uzuhashi et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Shihomi Uzuhashi, [uzuhashi@affrc.go.jp](mailto:uzuhashi@affrc.go.jp).

prediction was performed using the MAKER annotation pipeline version 2.31.8 (8), including AUGUSTUS version 3.0.3 (9), SNAP version 2013-02-16 (10), and GeneMark-ES suite 4.21 (11), where AUGUSTUS and SNAP were trained on *Pythium ultimum* var. *sporangiiferum* BR650 (12); 13,996 (JCM 30153) and 14,069 (JCM 30514) protein-coding genes were predicted. These numbers are similar with those reported for other pythiaceus species (12, 13). Sma3s version 2013-09-01 (14) with the UniProt-TrEMBL release 2015\_11 and UniProt-SwissProt release 2015\_11 databases enabled functional annotation of 2,665 and 1,369 genes for JCM 30513 and 2,697 and 1,373 genes for JCM 30514, respectively.

The draft genome sequences reported here will contribute to a more detailed understanding of pythiaceus species, including the mechanisms of asymptomatic infection of plants by *P. apinafurcum*.

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under BioProject no. PRJDB3796 (JCM 30513) and PRJDB3797 (JCM 30514) with GenBank accession no. [BCKD01000001](https://doi.org/10.1007/S10267-009-0486-0) to [BCKD01000310](https://doi.org/10.1007/S10267-009-0486-0) (JCM 30513) and [BCKE01000001](https://doi.org/10.1007/S10267-010-0046-7) to [BCKE01000280](https://doi.org/10.1007/S10267-010-0046-7) (JCM 30514). The versions described here are the first versions.

## ACKNOWLEDGMENTS

We thank Toshiya Iida and Keiko Kitamura for their support in quality checking the extracted DNA and the Genome Network Analysis Support Facility, RIKEN CLST (Yokohama, Japan), for sequence data production.

This work was funded by the National Bioresource Project/Genome Information Upgrading Program FY2014 from the Ministry of Education, Culture, Sports Science, and Technology, Japan, to R.-I.M. and M.O., and by the Japan Society for the Promotion of Science KAKENHI (15K18720) to R.E.

## REFERENCES

- Uzuhashi S, Kakishima M, Tojo M, Kobayashi S. 2009. *Pythium apinafurcum*: its morphology, molecular phylogeny, and infectivity for plants. *Mycoscience* 50:281–290. <https://doi.org/10.1007/S10267-009-0486-0>.
- van der Plaats-Niterink AJ. 1981. Monograph of the genus *Pythium*. *Stud Mycol* 21:1–242.
- Uzuhashi S, Kakishima M, Tojo M. 2010. Phylogeny of the genus *Pythium* and description of new genera. *Mycoscience* 51:337–365. <https://doi.org/10.1007/S10267-010-0046-7>.
- 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. <https://doi.org/10.1128/genomeA.00755-16>.
- 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>.
- Gnerre S, Maccallum I, Przybylski D, Ribeiro FJ, Burton JN, Walker BJ, Sharpe T, Hall G, Shea TP, Sykes S, Berlin AM, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander ES, Jaffe DB. 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc Natl Acad Sci U S A* 108:1513–1518. <https://doi.org/10.1073/pnas.1017351108>.
- Parra G, Bradnam K, Korf I. 2007. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. *Bioinformatics* 23:1061–1067. <https://doi.org/10.1093/bioinformatics/btm071>.
- 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>.
- Stanke M, Schöffmann O, Morgenstern B, Waack S. 2006. Gene prediction in eukaryotes with a generalized hidden Markov model that uses hints from external sources. *BMC Bioinformatics* 7:62. <https://doi.org/10.1186/1471-2105-7-62>.
- Johnson AD, Handsaker RE, Pulit SL, Nizzari MM, O'Donnell CJ, de Bakker PIW. 2008. SNAP: A Web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics* 24:2938–2939. <https://doi.org/10.1093/bioinformatics/btn564>.
- Ter-Hovhannisyanyan V, Lomsadze A, Chernoff YO, Borodovsky M. 2008. Gene prediction in novel fungal genomes using an *ab initio* algorithm with unsupervised training. *Genome Res* 18:1979–1990. <https://doi.org/10.1101/gr.081612.108>.
- Lévesque CA, Brouwer H, Cano L, Hamilton JP, Holt C, Huitema E, Raffaele S, Robideau GP, Thines M, Win J, Zerillo MM, Beakes GW, Boore JL, Busam D, Dumas B, Ferriera S, Fuerstenberg SI, Gachon CMM, Gaulin E, Govers F, Grenville-Briggs L, Horner N, Hostetler J, Jiang RHY, Johnson J, Krajaejun T, Lin H, Meijer HJG, Moore B, Morris P, Phuntmart V, Puii D, Shetty J, Stajich JE, Tripathy S, Wawra S, van West P, Whitty BR, Coutinho PM, Henrissat B, Martin F, Thomas PD, Tyler BM, De Vries RP, Kamoun S, Yandell M, Tisserat N, Buell CR. 2010. Genome sequence of the necrotrophic plant pathogen *Pythium ultimum* reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol* 11:R73. <https://doi.org/10.1186/gb-2010-11-7-r73>.
- Adhikari BN, Hamilton JP, Zerillo MM, Tisserat N, Lévesque CA, Buell CR. 2013. Comparative genomics reveals insight into virulence strategies of plant pathogenic oomycetes. *PLoS One* 8:e75072. <https://doi.org/10.1371/journal.pone.0075072>.
- Muñoz-Mérida A, Viguera E, Claros MG, Trelles O, Pérez-Pulido AJ. 2014. Sma3s: a three-step modular annotator for large sequence datasets. *DNA Res* 21:341–353. <https://doi.org/10.1093/dnares/dsu001>.