Draft Genome Sequence of the Basidiomycetous Fungus *Flammulina velutipes* TR19

Atsushi Kurata, Yasuhisa Fukuta, Miho Mori, Noriaki Kishimoto, Norifumi Shirasaka

Faculty of Agriculture, Kindai University, Nakamachi, Nara City, Nara, Japan

All authors contributed equally to this work.

Here, we report the draft genome sequence of *Flammulina velutipes* TR19, which was newly isolated from commercial strains in Japan. The genes related to fruiting body formation in the basidiomycete were identified by whole-genome analysis.

**Received** 23 April 2016  **Accepted** 28 April 2016  **Published** 9 June 2016

**Citation** Kurata A, Fukuta Y, Mori M, Kishimoto N, Shirasaka N. 2016. Draft genome sequence of the basidiomycetous fungus *Flammulina velutipes* TR19. Genome Announc 4(3): e00505-16. doi:10.1128/genomeA.00505-16.

**Copyright** © 2016 Kurata et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

**Address correspondence to** Norifumi Shirasaka, sirasaka@nara.kindai.ac.jp.

Fruiting bodies of basidiomycetous fungi are referred to as mushrooms. The production of mushrooms is important in the food, pharmaceutical, and biotechnological industries (1). Although the demand for mushrooms has expanded all over the world, it is difficult to constitutively develop fruiting bodies in many basidiomycetes (2). Fruiting body formation is proposed to start with the formation of an aggregate from mycelium, the formation of a primordium, and the outgrowth of the mature fruiting body (3). Although insights into fruiting body development have been provided in several basidiomycetes (4–6), the complex molecular mechanism in each developmental stage remains to be revealed.

We newly isolated *Flammulina velutipes* TR19 by mating. *F. velutipes*, which belongs to the order *Agaricales*, is known as winter mushroom. Strain TR19 stably forms a fruiting body using potato dextrose agar (PDA) liquid medium. In order to elucidate the molecular mechanisms in formation of fruiting body, we sequenced the whole genome of strain TR19 using the Illumina HiSeq (Hokkaido System Science Co., Ltd., Japan). The genomic DNA of dikaryotic TR19 cells was prepared using Isoplant II (Nippon Gene Co., Ltd., Japan). Paired-end libraries of 100-bp fragments were prepared, and the genome sequencing generated 45,722,056 raw reads covering a total of 4,618 Mbp (Phred > Q30, 92.52%). Quality-trimmed DNA reads conferring 132-fold coverage were assembled *de novo* by Velvet 1.2.08. As a result, the genome sequence comprised 5,130 contigs totaling 34,792,959 bp, with an average length of 6,782 bp (largest, 792,880 bp; smallest, 169 bp). An N$_{50}$ contig length of 150,115 bp and a N$_{90}$ contig length of 8,389 bp were obtained. The G+C content was 49.6%. All assembly data were deposited in the DDBJ/EMBL/GenBank nucleotide sequence database.

The gene prediction and annotation were carried out using an Augustus tool (7) and the Microbial Genome Annotation Pipeline (MiGAP, [http://www.migap.org](http://www.migap.org)) (8, 9). A total of 13,843 protein-coding genes were predicted. As a result, we identified six genes encoding proteins involved in the fruiting body development by MiGAP and local blast program with Geneious R9 (Biomatters Ltd., Auckland, New Zealand), namely, two hydrophobin genes (*hyd1* and *hyd2*), one mitochondrial ATP-synthase gene (*atp*), one fruiting body-specific gene (*fds*), and two transcription factor genes (*fst* and *gat*). The nucleotide sequences of *hyd1*, *hyd2*, and *atp* from strain TR19 were similar to those of the hydrophobin gene *vh1* (GenBank accession no. AB026721.1) from *F. velutipes*, the hydrophobin gene *Fv-hyd1* (GenBank accession no. AB126868.1) from *F. velutipes*, and the mitochondrial ATP-synthase gene *atp9* (GenBank accession no. NC_013731 [83400.83621]) from *F. velutipes*, respectively, with 100% identities. The nucleotide sequences of *fds*, *fst*, and *gat* from strain TR19 exhibited the closest similarities to those of the fruiting body-specific gene *fds* (GenBank accession no. D83658.1) from *F. velutipes* with 81% identity, the transcription factor gene *fst3* (GenBank accession no. XM_003031274) from *Schizophyllum commune* with 80% identity (10), and the transcription factor gene *gat1* (GenBank accession no. XM_003036543) from *S. commune* with 71% identity (10), respectively. We plan to analyze the functions of the genes and detect other genes involved in fruiting body development in the genome of *F. velutipes* TR19.

**Nucleotide sequence accession number.** The genome sequence of *F. velutipes* TR19 is available in DDBJ/EMBL/GenBank under the accession no. BDAN00000000.

**FUNDING INFORMATION**

This work, including the efforts of Norifumi Shirasaka, was funded by Ministry of Education, Culture, Sports, Science, and Technology (MEXT) (S1512004). This study was supported in part by a grant of the Strategic Research Foundation Grant-aided Project for Private Universities from the Ministry of Education, Culture, Sport, Science, and Technology, Japan (MEXT), 2015-2017 (S1512004).

**REFERENCES**

1. Aida FMNA, Shuhami M, Yazid M, Maaruf AG. 2009. Mushroom as a potential source of prebiotics: a review. Trends Food Sci Technol 20: 567–575. [http://dx.doi.org/10.1016/j.tifs.2009.07.007](http://dx.doi.org/10.1016/j.tifs.2009.07.007).
2. Couto SR, Sanromán MA. 2006. Application of solid-state fermentation to food industry—a review. J Food Eng 76:291–302. [http://dx.doi.org/10.1016/j.jfoodeng.2005.05.022](http://dx.doi.org/10.1016/j.jfoodeng.2005.05.022).
3. Kües U, Liu Y. 2000. Fruiting body production in basidiomycetes. Appl...
4. Ohm RA, de Jong JF, de Bekker C, Wösten HA, Lugones LG. 2011. Transcription factor genes of Schizophyllum commune involved in regulation of mushroom formation. Mol Microbiol 81:1433–1445. http://dx.doi.org/10.1111/j.1365-2958.2011.07776.x.

5. Park YJ, Baek JH, Lee S, Kim C, Rhee H, Kim H, Seo J-S, Park HR, Yoon DE, Nam JY, Kim HI, Kim JG, Yoon H, Kang HW, Cho JY, Song ES, Sung GH, Yoo YB, Lee CS, Lee BM. 2014. Whole genome and global gene expression analyses of the model mushroom Flammulina velutipes reveal a high capacity for lignocellulose degradation. PLoS One 9:e93560. http://dx.doi.org/10.1371/journal.pone.0093560.

6. Stajich JE, Wilke SK, Ahrén D, Au CH, Birren BW, Borodovsky M, Burns C, Canbäck B, Casselton LA, Cheng J, Dietrich FS, Fargo DC, Farman ML, Gathman AC, Goldberg J, Guigó R, Hoeggjer PJ, Hooker JB, Huggins A. 2010. Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom Coprinopsis cinerea (Coprinus cinereus). Proc Natl Acad Sci USA 107:11889–11894. http://dx.doi.org/10.1073/pnas.1003391107.

7. Stanke M, Tzvetkova A, Morgenstern B. 2006. AUGUSTUS at EGASP: using EST, protein and genomic alignments for improved gene prediction in the human genome. Genome Biol 7(Suppl 1):S11. http://dx.doi.org/10.1186/gb-2006-7-s1-s11.

8. Sugawara H, Ohyama A, Mori H, Kurokawa K. 2009. Microbial genome annotation pipeline (MiGAP) for diverse users, Poster S001-1-2. 20th Int Conf Genome Inform (GIW2009), 14 to 16 December 2009, Kanagawa.

9. Lagesen K, Hallin P, Rødland EA, Staerfeldt H-H, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35:3100–3108. http://dx.doi.org/10.1093/nar/gkm160.

10. Ohm RA, De Jong JF, Lugones LG, Aerts A, Kothe E, Stajich JE, De Vries RP, Record E, Levasseur A, Baker SE, Bartholomew KA, Coutinho PM, Erdmann S, Fowler TJ, Gathman AC, Lombard V, Henrissat B, Knabe N, Kües U, Lilly WW. 2010. Genome sequence of the model mushroom Schizophyllum commune. Nat Biotechnol 28:957–963. http://dx.doi.org/10.1038/nbt.1643.