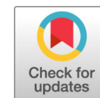
AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™



Genome Sequence of the Thermophilic Biomass-Degrading Fungus *Malbranchea cinnamomea* FCH 10.5

Zoraide Granchi,[a] Sake van Pelt,[a] Vu Nguyen Thanh,[b] Lisbeth Olsson,[c,d] Silvia Hüttner[c,d]

GenomeScan B.V., Leiden, The Netherlands[a]; Center for Industrial Microbiology, Food Industries Research Institute, Thanh Xuan, Hanoi, Vietnam[b]; Division of Industrial Biotechnology, Department of Biology and Biological Engineering, Chalmers University of Technology, Gothenburg, Sweden[c]; Wallenberg Wood Science Center, Chalmers University of Technology, Gothenburg, Sweden[d]

ABSTRACT We report here the annotated draft genome sequence of the thermophilic biomass-degrading fungus *Malbranchea cinnamomea* strain FCH 10.5, isolated from compost at a waste treatment plant in Vietnam. The genome sequence contains 24.96 Mb with an overall GC content of 49.79% and comprises 9,437 protein-coding genes.

Received 22 June 2017 **Accepted** 28 June 2017 **Published** 17 August 2017

Citation Granchi Z, van Pelt S, Thanh VN, Olsson L, Hüttner S. 2017. Genome sequence of the thermophilic biomass-degrading fungus *Malbranchea cinnamomea* FCH 10.5. Genome Announc 5:e00779-17. https://doi.org/10.1128/genomeA.00779-17.

Copyright © 2017 Granchi et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Silvia Hüttner, huttner@chalmers.se.

Malbranchea cinnamomea is a thermophilic fungus belonging to the order *Onygenales* (1) that is naturally found in composting soil and has the capability of degrading plant biomass. It is a promising source of thermostable enzymes, such as α-glucosidases, xylanases, α-amylases, and glucanases, that have industrial relevance as biocatalysts, particularly in biorefinery contexts (2–5). To be able to fully exploit the enzymatic system of *M. cinnamomea* and investigate its strategy of growth on various lignocellulosic materials, we sequenced the strain FCH 10.5, which was isolated from compost at the Cau Dien waste treatment factory in Hanoi, Vietnam. The fungus was cultivated at 50°C for 48 h in liquid medium with the following composition: 4 g liter^{-1} KH_2PO_4, 13.6 g liter^{-1} $(NH_4)_2SO_4$, 0.8 g liter^{-1} $CaCl_2$-$2H_2O$, 0.6 g liter^{-1} $MgSO_4$-$7H_2O$, 6 g liter^{-1} Bacto peptone, 10 mg liter^{-1} $FeSO_4$-$7H_2O$, 3.2 mg liter^{-1} $MnSO_4$-H_2O, 2.8 mg liter^{-1} $ZnSO_4$-$7H_2O$, 4 mg liter^{-1} $CoCl_2-6H_2O$, 200 mL liter^{-1} Tween 80, and 20 g liter^{-1} glucose. DNA for sequencing was extracted with cetyltrimethylammonium bromide (CTAB) buffer (2% CTAB, 100 mM Tris HCl, pH 8.0, 20 mM EDTA, 1.4 M NaCl) and purified from the supernatant by a combination of phenol-chloroform extraction and isopropanol precipitation (6) and a DNeasy Plant minikit (Qiagen).

Genome sequencing was performed in GenomeScan facilities. The NEBNext Ultra DNA library prep kit for Illumina (catalog no. NEB E7370S/L) was used according to the manufacturer's protocol for library preparation. Quality and yield after sample preparation were measured using Bioanalyzer (Agilent Technologies).

Clustering and DNA sequencing using the Illumina cBot and HiSeq 2500 systems were performed according to the manufacturer's protocols using a concentration of 8.0 pM of DNA, standard Illumina primers, and HiSeq control software HCS version 2.2.58. Image analysis, base calling, and quality checking were performed with the Illumina data analysis pipeline RTA version 1.18.64 and Bcl2fastq version 1.8.4.

The 250-nt paired-end reads were trimmed for adapter sequences and filtered for sequence quality using our in-house tool FASTQFilter version 2.05. The short-read genome assembler based on De Bruijn graphs, Abyss version 1.3.7 (7), was used for assembly with an optimized *k*-mer length of 64. Scaffolds shorter than 500 bp were removed.

For gene finding, two approaches were used and combined to obtain the presented data. The HMM-based algorithm Glimmer version 3.02 (8) was trained using the

Downloaded from http://genomea.asm.org/ on August 21, 2017 by Chalmers University

genome of *Uncinocarpus reesii* (downloaded from JGI, http://genome.jgi.doe.gov). Furthermore, mapped mRNA-Seq reads were used by the CodingQuarry (9) software tool for an evidence-based method of gene finding. Combining the two methods, gene models for 9,437 genes were obtained. For annotation, coding sequences were translated into amino acid sequences, and a BLASTp search (version 2.2.28+) was performed on the SwissProt database with default parameters.

Accession number(s). The *M. cinnamomea* FCH 10.5 whole-genome sequence has been deposited in DDBJ/EMBL/GenBank under the assembly accession no. FQSS00000000. The version described in this paper is the second version, FQSS02000000.

ACKNOWLEDGMENTS

This work was funded by the European Union OPTIBIOCAT project (FP7 KBBE. 2013/3/3-04; grant agreement no. 613868) and by Swedish Research Council (Vetenskapsrådet) grant no. 2014-03523.

REFERENCES

1. Morgenstern I, Powlowski J, Ishmael N, Darmond C, Marqueteau S, Moisan MC, Quenneville G, Tsang A. 2012. A molecular phylogeny of thermophilic fungi. Fungal Biol 116:489–502. https://doi.org/10.1016/j.funbio.2012.01.010.
2. Han P, Zhou P, Hu S, Yang S, Yan Q, Jiang Z. 2013. A novel multifunctional α-amylase from the thermophilic fungus *Malbranchea cinnamomea*: biochemical characterization and three-dimensional structure. Appl Biochem Biotechnol 170:420–435. https://doi.org/10.1007/s12010-013-0198-y.
3. Fan G, Yang S, Yan Q, Guo Y, Li Y, Jiang Z. 2014. Characterization of a highly thermostable glycoside hydrolase family 10 xylanase from *Malbranchea cinnamomea*. Int J Biol Macromol 70:482–489. https://doi.org/10.1016/j.ijbiomac.2014.07.025.
4. Matsuo M, Yasui T. 1985. Properties of xylanase of malbranchea. Agric Biol Chem 49:839–841.
5. Yang S, Xiong H, Yan Q, Yang H, Jiang Z. 2014. Purification and characterization of a novel alkaline β-1,3–1,4-glucanase (lichenase) from thermophilic fungus *Malbranchea cinnamomea*. J Ind Microbiol Biotechnol 41:1487–1495. https://doi.org/10.1007/s10295-014-1494-4.
6. Sambrook J, Russell DW. 2006. Purification of nucleic acids by extraction with phenol:chloroform. CSH Protoc 2006:prot4455. https://doi.org/10.1101/pdb.prot4455.
7. Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. 2009. ABySS: a parallel assembler for short read sequence data. Genome Res 19:1117–1123. https://doi.org/10.1101/gr.089532.108.
8. Majoros WH, Pertea M, Salzberg SL. 2004. TigrScan and GlimmerHMM: two open source ab initio eukaryotic gene-finders. Bioinformatics 20:2878–2879. https://doi.org/10.1093/bioinformatics/bth315.
9. Testa AC, Hane JK, Ellwood SR, Oliver RP. 2015. CodingQuarry: highly accurate hidden Markov model gene prediction in fungal genomes using RNA-seq transcripts. BMC Genomics 16:170. https://doi.org/10.1186/s12864-015-1344-4.

Downloaded from http://genomea.asm.org/ on August 21, 2017 by Chalmers University