Data Article

Data on the genome analysis of the wood-rotting fungus *Steccherinum ochraceum* LE-BIN 3174

Konstantin Moiseenko a,*, Olga Glazunova a, Natalia Shakhova b, Olga Savinova a, Daria Vasina a, Tatiana Tyazhelova c, Nadezhda Psurtseva b, Tatiana Fedorova a

a A.N. Bach Institute of Biochemistry, Research Center of Biotechnology, Russian Academy of Sciences, Leninsky Ave. 33/2, Moscow, 119071, Russian Federation
b Komarov Botanical Institute of the Russian Academy of Sciences, Professor Popov St. 2, St. Petersburg, 197376, Russian Federation
c N.I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Gubkin St. 3, Moscow, 117809, Russian Federation

A R T I C L E   I N F O

Article history:
Received 30 November 2019
Received in revised form 30 December 2019
Accepted 15 January 2020
Available online 22 January 2020

Keywords:
Steccherinum ochraceum
Draft genome sequence
White-rot
Wood decay

A B S T R A C T

In the present article, we report data on the whole-genome sequencing of wood-rotting (white-rot) fungus *Steccherinum ochraceum* LE-BIN 3174. The *S. ochraceum* LE-BIN 3174 genome consists of 770 scaffolds (N50 = 62,812 bp) with the total length of assembly ~35 Mb. The structural annotation of the genome resulted in the prediction of 12,441 gene models, among which 181 were models of tRNA-coding genes, and 12,260 – protein-coding genes. The protein-coding genes were annotated with different databases (Pfam, InterPro, eggNOG, dbCAN, and MEROPS). The whole genome sequence and functional annotation provide an important information for the deep investigation of biochemical processes that take place during the late stages of wood decomposition by Basidiomycetes. The Whole Genome project of *S. ochraceum* LE-BIN 3174 had been deposited at DDBJ/ENA/GenBank under the accession RWJN00000000. The version described in this work is version RWJN00000000.1. For further interpretation of the data provided in this article, please refer to the research article “Fungal Adaptation to the Advanced Stages of...
Wood Decomposition: Insights from the Steccherinum ochraceum® [1].

© 2020 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

1. Data description

Steccherinum ochraceum is a white-rot basidiomycete with wide ecological amplitude. It occurs in different regions of Russia and throughout the world occupying different climatic zones. The obtained draft genome of S. ochraceum LE-BIN 3174 (DDBJ/ENA/GenBank accession/version – RWJN00000000.1) is represented by the 770 scaffolds with the total length of 35.27 Mb and of comparable quality with other previously sequenced genomes of polypore fungi [2]. The gene prediction resulted in 12,441 gene models. The general information regarding genome’s assembly, structural and functional annotation is presented in Table 1. The summary of the Gene Ontology (GO) classification of the protein coding genes is illustrated in Fig. 1. The whole genome sequence of S. ochraceum LE-BIN 3174 showed that it harbors 361 carbohydrate-active enzymes (CAZymes). The auxiliary activity enzymes (AA), carbohydrate

Specifications Table

| Subject | Biology |
|---------|---------|
| Specific subject area | Microbiology, Mycology, Genomics. |
| Type of data | Genome sequence data. |
| How data were acquired | Shotgun method using Illumina HiSeq 2500 with paired end runs. |
| Parameters for data collection | The mycelium derived from field-collected basidiospores was statically cultivated on glucose-peptone (GP) medium at 26–28 °C in 750-mL Erlenmeyer flasks. The mycelium was ground in liquid nitrogen, and total DNA was extracted using DNeasy Plant Mini Kit (Qiagen, US). |
| Data format | Raw and analyzed data. |
| Description of data collection | The genome was assembled with CLC Genomics Workbench 11.0 (Qiagen, US) and annotated with Funannotate pipeline v1.5.0 (https://github.com/nextgenusfs/funannotate) |
| Data source location | The fungal strain of Steccherinum ochraceum (Pers. ex J.F. Gmel.) Gray was isolated (August 01, 2013) from basidiospores collected from a fallen dry aspen branch in the polydominant temperate deciduous broadleaf forest (Kaluzhskiye Zaseki Nature Reserve, Russia; N 53°33′28.4″; E 35°38′24.4″). The strain was deposited in the Komarov Botanical Institute Basidiomycetes Culture Collection (LE-BIN; St. Petersburg, Russia) as S. ochraceum LE-BIN 3174 |
| Data accessibility | The whole genome sequence of Steccherinum ochraceum LE-BIN 3174 had been deposited at DDBJ/ENA/GenBank under the accession RWJN00000000. The version described in this paper is version RWJN00000000.1. The BioSample and BioProject accession numbers are SAMN10505049 and PRJNA507755, respectively. All other data are within this article. |
| Related research article | K.V. Moiseenko, O.A. Glazunova, N.V. Shakhova, O.S. Savinova, D.V. Vasina, T.V. Tyazhelova, N.V. Psurtseva, T.V. Fedorova, Fungal Adaptation to the Advanced Stages of Wood Decomposition: Insights from the Steccherinum ochraceum, Microorganisms. 7 (2019) 527. https://doi.org/10.3390/microorganisms7110527 [1]. |

Value of the Data

- The genome of Steccherinum ochraceum LE-BIN 3174 is the first genome under the family Steccherinaceae to be reported.
- This draft genome will accelerate functional genomics research, increase the knowledge of the biochemical process of wood degradation and create an opportunity for comparative studies with other fungi.
- The CAZyme content of this genome will provide a valuable insight into the fungal adaptation to an ecological niche of pre-degraded wood.

1. Data description
esterase (CE), glycoside hydrolases (GH), glycosyl transferase (GT), and polysaccharide lyase (PL) superfamilies were represented by 109, 37, 151, 55, and 9 CAZymes from 9, 8, 48, 25, and 3 families, respectively. The comparison of the *S. ochraceum* CAZymes genome content with those from other lignocellulose decaying fungi belonging to different trophic groups is presented in Fig. 2 and Fig. 3.

### Table 1
| General data on the genome sequencing of *S. ochraceum* LE-BIN 3174. |
|---------------------------------|---------------------------------|
| **Sequencing**                  |                                 |
| Sequencing technology           | Illumina HiSeq 2500             |
| Length of paired-reads (2\(\times\), bp) | 2 × 100                        |
| Total number of paired-reads (2\(\times\)) | 2 × 47 868 586                  |
| Insert size, bp                 | 300–500                         |
| **Assembly**                    | Structural annotation           |
| Assembly size                   | 35.27 (Mb)                      |
| Overall coverage                | 100×                            |
| Number of scaffolds             | 770                             |
| Longest scaffold                | 464 123 (bp)                    |
| N50 length of scaffolds         | 62 812 (bp)                     |
| Mean size of scaffolds          | 45 812 (bp)                     |
| Median size of scaffolds        | 33 955 (bp)                     |
| Repeat content                  | 1.4 (%)                         |
| Overall GC                      | 52.7 (%)                        |
| Number of predicted genes       | 12 441                          |
| Proportion covered by genes     | 64.1 (%)                        |
| Number of trRNA-coding genes    | 181                             |
| Number of protein-coding genes  | 12 260                          |
| Mean protein size               | 483 (aa)                        |
| **Main functional annotation**  |                                 |
| General-content databases       |                                 |
| Pfam                            | 6965                            |
| InterPro                        | 8186                            |
| eggNOG                          | 9237                            |
| Domain-specific databases       |                                 |
| dbCAN                           | 369                             |
| MEROPS                          | 382                             |
| **Additional functional features** |                                 |
| Proteins with signal peptides   | 1093                            |
| Proteins with transmembrane helices | 2585                        |

![Fig. 1. The Gene Ontology (GO) functional annotation of *S. ochraceum* LE-BIN 3174.](image)
2. Experimental design, materials, and methods

2.1. Fungal strain isolation and genetic verification

The fungal strain of *Steccherinum ochraceum* (Pers. ex J.F. Gmel.) Gray was isolated (August 01, 2013) from basidiospores collected from a fallen dry aspen branch in the polydominant temperate deciduous broadleaf forest (Kaluzhskiy Zaseki Nature Reserve, Russia; N 53°33'28.40"; E 35°38'24.40"). After morphological and genetic verifications, the strain was deposited in the Komarov Botanical Institute Basidiomycetes Culture Collection (LE-BIN; St. Petersburg, Russia) as *S. ochraceum* LE-BIN 3174.
### Families of carbohydrate-degrading enzymes (CAZymes) related to plant polysaccharide degradation in *S. ochraceum* LE-BIN 3174 and other fungal genomes.

| Subcategory | Enzyme activity | EC no. | Abbreviation | CAZyme family | Frequency | Total | High |
|-------------|-----------------|--------|--------------|---------------|-----------|-------|------|
| **Lignin**  | Class II peroxidase | 1.11.1.13/14 | POX | AA1 | 27 | 42 | 38 | 32 | 14 | 1 | 11 |
|             | Glucose oxidase  | 1.1.3.12 | GOX | AAL1 | 7 | 14 | 11 | 9 | 5 | 1 | 1 |
| **Cellulose** | 1.4.1.14 | FG | GH45 | 13 | 21 | 19 | 17 | 10 | 8 | 6 |
|             | 1.1.1.78 | XV | GH7 | 34 | 51 | 45 | 39 | 23 | 19 | 15 |
|             | 1.1.1.75 | CM | GH5 | 4 | 6 | 5 | 4 | 3 | 2 | 2 |
|             | 1.1.1.21 | RG | GH4 | 3 | 5 | 4 | 3 | 3 | 2 | 2 |
|             | 1.1.1.98 | CH | AA1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| **Xylan**   | 1.4.1.8 | KLN | GH3 | 6 | 9 | 8 | 7 | 6 | 3 | 3 |
| **Galactomannans** | 1.1.1.78 | MAN | GH5 | 21 | 34 | 31 | 29 | 19 | 16 | 13 |
|             | 1.1.1.25 | XYL | GH5 | 10 | 17 | 15 | 13 | 9 | 6 | 6 |
|             | 1.1.1.23 | LOC | GH5 | 9 | 15 | 13 | 12 | 10 | 8 | 8 |
| **Hemicelluloses** | 1.4.1.22 | XYL | GH5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
|             | 1.3.1.19 | MIPS | GH5 | 2 | 4 | 3 | 3 | 2 | 2 | 2 |
|             | 1.1.2.27 | KDX | GH4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Kraft lignin** | 1.4.2.5 | KFL | GH5 | 15 | 23 | 20 | 18 | 12 | 10 | 10 |
| **Pectin**  | 1.3.1.56 | AAT | GH5 | 15 | 23 | 20 | 18 | 12 | 10 | 10 |
|             | 1.3.1.109 | LTB | GH5 | 2 | 4 | 3 | 3 | 2 | 2 | 2 |
|             | 1.4.4.10 | RMM | GH5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Eukaryotic** | 1.4.4.10 | LTB | GH5 | 15 | 23 | 20 | 18 | 12 | 10 | 10 |
|             | 1.3.1.109 | LTB | GH5 | 2 | 4 | 3 | 3 | 2 | 2 | 2 |
|             | 1.4.4.10 | RMM | GH5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Pectin**  | 1.4.1.20 | RMM | GH5 | 15 | 23 | 20 | 18 | 12 | 10 | 10 |
|             | 1.3.1.109 | LTB | GH5 | 2 | 4 | 3 | 3 | 2 | 2 | 2 |
|             | 1.4.4.10 | RMM | GH5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Pectin**  | 1.4.1.20 | RMM | GH5 | 15 | 23 | 20 | 18 | 12 | 10 | 10 |
|             | 1.3.1.109 | LTB | GH5 | 2 | 4 | 3 | 3 | 2 | 2 | 2 |
|             | 1.4.4.10 | RMM | GH5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| **Classification** | **Enzyme activity** | **EC no.** | **Abbreviation** | **CAZyme family** | **Frequency** | **Total** | **High** |
|--------------------|---------------------|------------|-----------------|-------------------|---------------|-----------|--------|
| **Endoglucanase**  | 1.4.1.11 | XRE | GH7 | 9 | 16 | 13 | 11 | 7 | 6 |
| **Cellulase**      | 1.4.1.4 | XRE | GH7 | 9 | 16 | 13 | 11 | 7 | 6 |
| **Pectinase**      | 2.2.2.10 | FEL | R1 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Polysaccharidase** | 2.2.2.2 | FEL | R1 | 1 | 2 | 1 | 1 | 1 | 1 |
| **Cellulase**      | 1.4.1.4 | XRE | GH7 | 9 | 16 | 13 | 11 | 7 | 6 |
| **Pectinase**      | 2.2.2.10 | FEL | R1 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Polysaccharidase** | 2.2.2.2 | FEL | R1 | 1 | 2 | 1 | 1 | 1 | 1 |

### Notes
1. **Row-wise color guide:** Low, Medium, High. 
2. **Classification** is based on the EC (EC). Please note the redundancy in the classification scheme: the same CAZyme can simultaneously act on several components of lignocellulose.
3. **Frequency** denotes the number of times an enzyme is found in the dataset. 
4. **Total** represents the sum of frequencies for each enzyme. 
5. **High** indicates the number of unique entries for each enzyme.

---

**Fig. 3.** Families of carbohydrate-degrading enzymes (CAZymes) related to plant polysaccharide degradation in *S. ochraceum* LE-BIN 3174 and other fungal genomes.
For the genetic verification, the genomic DNA (gDNA) was extracted as described later in the “Genomic DNA Isolation, Library Preparation and Sequencing” section of this manuscript, and the sequence of ITS1-5.8S rRNA-ITS2 region was obtained using the standard primers: ITS1F 5′—CTT GGT CAT TTA GAG GAA GTA A—3′ and ITS4B 5′—CAG GAG ACT TGT ACA CGG TCC AG—3′. The PCR amplification was performed using the Encyclo PCR kit (Evrogen, Russia) under the following conditions: 1 cycle of 5 min at 95 °C; 25 cycles of 1 min at 90 °C, 1 min at 56 °C, and 1 min at 72 °C; 1 cycle of 10 min at 72 °C. Obtained PCR reaction mixture was resolved using 1.2% agarose gel. The performed PCR amplification produced the single PCR-product with approximate length of 830 bp. The obtained product was ceased from the gel and purified with QIAquick Gel Extraction Kit (Qiagen, USA), according to the manufacturer’s instructions. The Sanger sequencing of the obtained fragment was performed at the Evrogen JSC (Russia, Moscow).

2.2. Genomic DNA isolation, Library Preparation and Sequencing

For gDNA extraction, *S. ochraceum* LE-BIN 3174 was statically cultivated at 26–28 °C in 750-mL Erlenmeyer flasks contained 200 mL of glucose-peptone (GP) medium (per 1 L of dH2O): 3.0 g peptone, 10.0 g glucose, 0.6 g KH2PO4, 0.4 g K2HPO4, 0.5 g MgSO4, 50 mg MnSO4, 1 mg ZnSO4 and 0.5 mg FeSO4. The mycelium was ground in liquid nitrogen, and gDNA was extracted using DNeasy Plant Mini Kit (Qiagen, US). The quality and quantity of the isolated DNA were checked using Agilent Bioanalyzer 2100 (Agilent Technologies, US) and Qubit fluorimeter (Thermo Fisher Scientific, US).

After ultrasonic fragmentation the gDNA was prepared for sequencing using TruSeq DNA Sample Prep Kit (Illumina, US). The quality and quantity of the obtained DNA-library were checked using Agilent Bioanalyzer 2100 and StepOnePlus Real-Time PCR System (Thermo Fisher Scientific, US). The whole genome sequencing was carried out with Illumina HiSeq 2500 system (Illumina, US) using HiSeq Rapid SBS Kit v2 at the Evrogen JSC (Russia, Moscow).

2.3. Genome sequencing, assembly and annotation

The shotgun sequencing produced 2 × 47,868,586 paired-end reads (2 × 100 bp) with an insert size of 300–500 bp. The reads were further processed with CLC Genomics Workbench 11.0 (Qiagen, US) as follows: (1) adapters were removed from all reads; (2) all reads were trimmed based on their quality; (3) reads were sampled to reduce coverage to a maximum average coverage of 100 × ; (4) reads were *de novo* assembled, and resulted contigs were scaffolded.

Genome structural and functional annotations were performed using Funannotate pipeline v1.5.0 (https://github.com/nextgenusfs/funannotate).

The structural annotation step included: (1) repeat masking with the RepeatMasker package (http://www.repeatmasker.org/) using the RepBase repeats libraries [3]; (2) *ab initio* protein-coding gene prediction with self-trained GeneMark-ES [4] and AUGUSTUS [5] trained using BUSCO 2.0 [6] gene models (*Phanerochaete chrysosporium* was selected as a closely-related species); (3) *ab initio* tRNA-coding gene prediction with tRNAscan-SE [7]; (4) integration and filtering of the obtained gene models.

The functional annotation of the predicted protein-coding genes was performed with three general-content databases: the protein families database – Pfam [8], the integrative protein signature database – InterPro [9], and the orthologous groups database – eggNOG [10]. Additionally, two domain-specific databases were employed: carbohydrate-active enzyme (CAZyme) database – dbCAN [11], and peptidase database – MEROPS [12]. The prediction of transmembrane topologies and signal peptides was performed with Phobius [13] and SignalP [14], respectively.

The data on genome sequencing, assembly and annotation are presented in Table 1.

As a result of general functional prediction, 6019 genes were annotated with the GO terms. In total, 10,648 GO terms were assigned, from which 1707 were GO terms related to “Cellular component” class, 5207 – to “Molecular function” class, and 3734 – to “Biological process” class (Fig. 1).
2.4. The peculiarities of the *S. ochraceum* LE-BIN 3174 CAZymes genome content

Based on the sequenced genome, the CAZymes repertoire of *S. ochraceum* LE-BIN 3174 was inferred and compared with those of the 8 fungi belonging to the different ecological niches and trophic groups. From the Polyporales order: *Trametes versicolor*, *Trametes pubescens*, and *Trametes hirsuta* (all are primary colonizers on lignum). From the Agaricales order: *Gymnopilus junonius* (secondary colonizer on lignum), *Hymenopellis radicata* (deep root mushroom, lignum), *Mycena galopus* (saprotroph on *folia dejecta*), *Crucibulum laeve* (saprotroph on *stramentum*), and *Agrocybe praecox* (saprotroph on humus).

Comparison of the total CAZymes content is present in Fig. 2. Comparison of the content of CAZymes acting on different polymeric components of lignocellulose [15] is presented in Fig. 3. Please note, that the numbers do not add up properly due to the redundancy in the classification scheme that was advanced to reflect different enzymatic activities possessed by fungi rather than different CAZymes, since the same CAZyme can simultaneously act on several components of lignocellulose.

Acknowledgments

We would like to thank everyone who contributed directly or indirectly to this study, especially Vasil R. Sultanov for his excellent bioinformatical assistance.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2020.105169.

References

[1] K.V. Moiseenko, O.A. Glazunova, N.V. Shakhova, O.S. Savinova, D.V. Vasina, T.V. Tyazhelova, N.V. Psurtseva, T.V. Fedorova, Fungal adaptation to the advanced stages of wood decomposition: Insights from the *Steccherinum ochraceum*, Microorganisms 7 (2019) 527, https://doi.org/10.3390/microorganisms7110527.

[2] H. Nordberg, M. Cantor, S. Dusheyko, S. Hua, A. Poliakov, I. Shabalov, T. Smirnova, I.V. Grigoriev, I. Dubchak, The genome portal of the department of energy joint genome Institute: 2014 updates, Nucleic Acids Res. 42 (2014) D26–D31, https://doi.org/10.1093/nar/gkt1069.

[3] W. Bao, K.K. Kojima, O. Kohany, Repbase Update, a database of repetitive elements in eukaryotic genomes, Mobile DNA 6 (2015) 11, https://doi.org/10.1186/s13100-015-0041-9.

[4] J. Besemer, A. Lomsadze, M. Borodovsky, GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions, Nucleic Acids Res. 29 (2001) 2607–2618. http://www.ncbi.nlm.nih.gov/pubmed/11410670.

[5] M. Stanke, R. Steinkamp, S. Waack, B. Morgenstern, AUGUSTUS: a web server for gene finding in eukaryotic genomes. Implications for finding sequence motifs in regulatory regions, Nucleic Acids Res. 32 (2004) W309–W312, https://doi.org/10.1093/nar/gkh379.

[6] F.A. Simão, R.M. Waterhouse, P. Ioannidis, E.V. Kriventseva, E.M. Zdobnov, BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs, Bioinformatics 31 (2015) 3210–3212, https://doi.org/10.1093/bioinformatics/btv351.

[7] T.M. Lowe, S.R. Eddy, tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence, Nucleic Acids Res. 25 (1997) 955–964. http://www.ncbi.nlm.nih.gov/pubmed/9023104.

[8] R.D. Finn, P. Coggill, R.V. Eberhardt, S.R. Eddy, J. Mistry, A.L. Mitchell, S.C. Potter, M. Punta, M. Qureshi, A. Sangrador-Vegas, G.A. Salazar, J. Tate, A. Bateman, The Pfam protein families database: towards a more sustainable future, Nucleic Acids Res. 44 (2016) D279–D285, https://doi.org/10.1093/nar/gkv1344.

[9] S. Hunter, R. Apweiler, T.K. Attwood, A. Bairoch, A. Bateman, D. Birns, P. Bork, U. Das, L. Daugherty, L. Duquenne, R.D. Finn, J. Gough, D. Haft, N. Hulo, D. Kahn, E. Kelly, A. Laugraud, I. Letunic, D. Lonsdale, R. Lopez, M. Madera, J. Maslen, C. McAnulla, J. McDowall, J. Mistry, A. Mitchell, N. Mulder, D. Natale, C. Orens, A.F. Quinn, J.D. Selengut, C.J.A. Sigrist, M. Sin, P.D. Thomas, F. Valencia, D. Wilson, C.H. Wu, C. Yeats, InterPro: the integrative protein signature database, Nucleic Acids Res. 37 (2009) D211–D215, https://doi.org/10.1093/nar/gkn785.

[10] J. Huerta-Cepas, D. Szklarczyk, K. Forslund, H. Cook, D. Heller, M.C. Walter, T. Rattee, D.R. Mende, S. Sunagawa, M. Kuhn, L.J. Jensen, C. von Mering, P. Bork, eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences, Nucleic Acids Res. 44 (2016) D286–D293, https://doi.org/10.1093/nar/gkv1248.
[11] Y. Yin, X. Mao, J. Yang, X. Chen, F. Mao, Y. Xu, dbCAN: a web resource for automated carbohydrate-active enzyme annotation, Nucleic Acids Res. 40 (2012) W445–W451, https://doi.org/10.1093/nar/gks479.

[12] N.D. Rawlings, A.J. Barrett, A. Bateman, MEROPS: the database of proteolytic enzymes, their substrates and inhibitors, Nucleic Acids Res. 40 (2012) D343–D350, https://doi.org/10.1093/nar/gkr987.

[13] L. Käll, A. Krogh, E.L.L. Sonnhammer, Advantages of combined transmembrane topology and signal peptide prediction - the Phobius web server, Nucleic Acids Res. 35 (2007) W429–W432, https://doi.org/10.1093/nar/gkm256.

[14] H. Nielsen, Predicting secretory proteins with SignalP, in: D. Kihara (Ed.), Protein Funct. Predict. Methods Mol. Biol. v.1611, Humana Press Inc., New York, 2017, pp. 59–73, https://doi.org/10.1007/978-1-4939-7015-5_6.

[15] J. Rytioja, K. Hildén, J. Yuzon, A. Hatakka, R.P. de Vries, M.R. Makela, Plant-polysaccharide-degrading enzymes from basidiomycetes, Microbiol. Mol. Biol. Rev. 78 (2014) 614–649, https://doi.org/10.1128/MMBR.00035-14.