



Draft Genome Sequence of the Ectomycorrhizal Ascomycete *Sphaerosporella brunnea*

Gian Maria Niccolò Benucci, Sajeet Haridas, Kurt Labutti, Giorgio Marozzi,
Livio Antonielli, Sergio Sánchez, Pedro Marco, Xinxin Wang, Kerrie Barry,
Anna Lipzen, et al.

► To cite this version:

Gian Maria Niccolò Benucci, Sajeet Haridas, Kurt Labutti, Giorgio Marozzi, Livio Antonielli, et al..
Draft Genome Sequence of the Ectomycorrhizal Ascomycete *Sphaerosporella brunnea*. Microbiology
Resource Announcements, 2019, 10.1128/MRA.00857-19 . hal-02913048

HAL Id: hal-02913048

<https://hal.univ-lorraine.fr/hal-02913048>

Submitted on 7 Aug 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Draft Genome Sequence of the Ectomycorrhizal Ascomycete *Sphaerosporella brunnea*

 Gian Maria Niccolò Benucci,^{a,b} Sajeet Haridas,^c Kurt Labutti,^c Giorgio Marozzi,^d Livio Antonielli,^e Sergio Sanchez,^f Pedro Marco,^f Xinxin Wang,^a Kerrie Barry,^c Anna Lipzen,^c Mansi Chovatia,^c Hope Hundley,^c Leonardo Baciarelli Falini,^d Claude Murat,^g Francis Martin,^g Emidio Albertini,^d Domizia Donnini,^d Igor V. Grigoriev,^{c,h}  Gregory Bonito^{a,b}

^aDepartment of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, Michigan, USA

^bGreat Lakes Bioenergy Research Center (GLBRC), East Lansing, Michigan, USA

^cU.S. Department of Energy Joint Genome Institute, Walnut Creek, California, USA

^dDepartment of Agricultural, Food and Environmental Science, University of Perugia, Perugia, Italy

^eAIT Austrian Institute of Technology, Center for Health and Bioresources, Tulln, Austria

^fCentro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Zaragoza, Spain

^gUMR1136 Interactions Arbres-Microorganismes, Laboratoire d'Excellence ARBRE, INRA, Université de Lorraine, Champenoux, France

^hDepartment of Plant and Microbial Biology, University of California Berkeley, Berkeley, California, USA

ABSTRACT *Sphaerosporella brunnea* is a pioneer ectomycorrhizal fungus with facultative saprophytic capacities. Here, we sequenced the genome of *S. brunnea* strain Sb_GMNB300, which is estimated at 51.6 Mb in size with 872 assembled contigs accounting for 12,597 predicted coding genes. This genome will be useful for comparative studies of Pezizales ectomycorrhizal symbioses.

Sphaerosporella brunnea (Alb. & Schwein.) Svrček & Kubička is an ectomycorrhizal ascomycete in the Pyrenomataceae family (Pezizales) that produces cup-shaped apothecia (1), often after rain or disturbance (2). *S. brunnea* grows in North America, Europe, Asia, and Oceania in association with trees and shrubs (3). It is a common cooccurring fungus of truffle-mycorrhized seedlings (2, 4, 5).

Sphaerosporella brunnea strain Sb_GMNB300 (NRRL 66913) was isolated from soil in Perugia, Italy, in April 2014. Mycelium from a single spore was grown in potato dextrose agar (PDA) medium for 10 days at 24°C. DNA was extracted with a modified cetyltrimethylammonium bromide (CTAB) protocol (6) and sequenced with PacBio technology using a low-input protocol for 10-kb libraries. The genome was assembled with Falcon v. 0.3.0 (7), improved with finisherSC v. 2.1 (8), and polished with Arrow SMRTLink v. 6.0.0.47841 (Pacific Biosciences, CA). Genome completeness was assessed using CEGMA v. 2.5 (9) and BBTools v. 38.38 (<http://sourceforge.net/projects/bbmap>). Contigs of less than 1,000 bp were excluded from the assembly. Mitochondrial reads were assembled separately. The genome was annotated using the Joint Genome Institute (JGI) annotation pipeline v. 2.0 (10, 11). The contents of the annotation pipeline are described in detail at <https://mycocosm.jgi.doe.gov/programs/fungi/FungalGenomeAnnotationSOP.pdf>.

For transcriptome analysis, mycelium was grown in PDA and malt extract agar (MEA) media at 24°C and 4°C for 10 and 20 days, respectively. RNA was extracted with the RNeasy plant minikit (Qiagen, Germany), and the library was prepared with an Illumina TruSeq stranded mRNA HT sample prep kit with poly(A) selection of mRNA and sequenced using a NovaSeq 6000 2 × 150-bp sequencer (Illumina, CA). After sequencing, read artifacts (kmer = 25 bp, 1 mismatch) were detected with BBDuk v. 38.34 (<https://sourceforge.net/projects/bbmap/>). Detected artifacts were trimmed from the 3' end of reads. General quality trimming was performed with the Phred trimming method set at Q6. Reads shorter than 25 bp or one-third of the original read length were removed, as

Citation Benucci GMN, Haridas S, Labutti K, Marozzi G, Antonielli L, Sanchez S, Marco P, Wang X, Barry K, Lipzen A, Chovatia M, Hundley H, Baciarelli Falini L, Murat C, Martin F, Albertini E, Donnini D, Grigoriev IV, Bonito G. 2019. Draft genome sequence of the ectomycorrhizal ascomycete *Sphaerosporella brunnea*. Microbiol Resour Announc 8:e00857-19. <https://doi.org/10.1128/MRA.00857-19>.

Editor Antonis Rokas, Vanderbilt University

Copyright © 2019 Benucci 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 Gian Maria Niccolò Benucci, benucci@msu.edu.

Received 20 September 2019

Accepted 1 October 2019

Published 12 December 2019

well as RNA spike-in reads, PhiX reads, and reads containing any ambiguous characters (Ns). Clean transcriptome sequencing (RNA-Seq) reads were assembled in Trinity v. 2.3.2 (12). RNA-Seq capture was performed by aligning a 1% subsample of RNA reads to the final DNA assembly using BBTools v. 38.67. Gene clusters of interest were searched in the clustering table available at the JGI MycoCosm portal (<https://mycocosm.jgi.doe.gov/clm/run/Sphbr2-comparative-qc.3266?organism=Sphbr2>). Clusters were computed following the TRIBE-Markov cluster (MCL) clustering method of Enright et al. (13), from all-versus-all BLAST analysis of the proteins in the set of organisms included in a clustering run.

The *Sphaerospora brunnea* draft genome had an estimated size of 51,598,955 bp, sequence coverage depth of 907.91×, 872 (≥2 kbp) total contigs (and scaffolds), an N_{50} value (i.e., the smallest number of contigs whose length sum makes up half of the genome size) of 130, an L_{50} value (i.e., half of the genome sequence is in contigs larger than or equal to this length) of 119,241 bp, and an estimated average GC content of 52.64% ± 2.33%. The mitochondrion genome is in 5 contigs and is 265,525 bp in size ($N_{50} = 2$, $L_{50} = 78,073$ bp). A Core Eukaryotic Genes Mapping Approach (CEGMA) completeness score of 99.34% and an RNA-Seq capture of 96.85% were obtained for the final assembly.

The *Sphaerospora brunnea* genome size is similar to those of other Pyronemataceae species (e.g., *Pyronema confluens* [50.0 Mbp] [14]) but smaller than those of Tubercularia species (e.g., *Tuber aestivum* [145.0 Mbp] [15], *Tuber melanosporum* [125.0 Mbp] [16], and *Tuber borchii* [97.2 Mbp] [17]). A total of 12,597 protein-coding genes were detected, with average lengths of 1,555 bp and 397 amino acids for genes and proteins, respectively. The number of genes is similar to those of *P. confluens* (13,367) and *T. borchii* (12,346) but greater than those of *T. melanosporum* (10,058) and *T. aestivum* (9,344). Predicted proteins in the genome of *S. brunnea* demonstrate an enriched capacity to produce plant cell wall-degrading enzymes compared to that of its relatives, which includes 2 genes in glycoside hydrolase family 6 (GH6) compared to 1 present in *P. confluens* and 3 genes in GH7 compared to 2 in *P. confluens* that are absent in *Tuber* spp. (16). Only the mating type locus MAT1-2-1 with the high-mobility-group (HMG) box (protein identifier 924729, <https://mycocosm.jgi.doe.gov/cgi-bin/dispatch/GeneModel?db=Sphbr2&id=924729>) was identified in the genome of *S. brunnea* Sb_GMNB300, in contrast to reports by Sánchez and colleagues (3) and expectations of homothallism.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [VXIS00000000](#). The version described in this paper is the first version, VXIS01000000. Genome and transcriptome data are available in DDBJ/ENA/GenBank under BioProject number [PRJNA554466](#), BioSample number [SAMN12268380](#), and Sequence Read Archive accession numbers [SRP214822](#) and [SRP215074](#), or on the U.S. Department of Energy (DOE) JGI MycoCosm portal (9) (comparative).

ACKNOWLEDGMENTS

This research was performed within the Community Sequence Program “1KFG: Deep Sequencing of Ecologically-relevant Dikarya (Proposal ID: 1974),” conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, which was supported by the Office of Science of the U.S. Department of Energy under contract DE-AC02-05CH11231 and supported in part by the Great Lakes Bioenergy Research Center, U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, under award number DE-SC0018409. Participation of S. Sanchez and P. Marco was supported by the Spanish National Institute of Agricultural Research under project RTA2015-00053-00.

REFERENCES

1. Danielson RM. 1984. Ectomycorrhiza formation by the operculate discomycete *Sphaerospora brunnea* (Pezizales). *Mycologia* 76: 454–461. <https://doi.org/10.1080/00275514.1984.12023866>.
2. García-Montero LG, Galán R, Massimo G, Manjón JL, Díez J. 1997. *Sphaerospora brunnea* (Alb. et Schwein) Svrcek et Kubicka, un discomicete con incidencia en la truficultura e interés forestal. *Revista Catalana de Micologia* 20:99–104.
3. Sánchez S, Gómez E, Martín M, De Miguel AM, Urban A, Barriuso J. 2014.

- Experiments on the life cycle and factors affecting reproduction of *Sphaerospora brunnea* provide evidence for rapid asexual propagation by conidiospores and for homothallism in an ectomycorrhizal competitor of cultivated truffle species. *Fungal Ecology* 8:59–65. <https://doi.org/10.1016/j.funeco.2013.12.003>.
4. Palazón C, Barriuso J, Delgado I. 2005. Lucha química contra el contaminante *Sphaerospora brunnea* (Alb. et Schwein.) Svrcek et Kubicka, responsable de la “micorriza marrón” de los invernaderos de producción de planta micorrizada con trufa negra (*Tuber melanosporum* Vitt.). *Actas del IV Congreso Forestal*. Zaragoza, Spain.
 5. Donnini D, Bencivenga M, Calandra R, Tanfulli M. 1997. Influenza della reazione del substrato sulla micorizzazione di *Ostrya carpinifolia* Scop. con *Tuber melanosporum* Vitt. e *Sphaerospora brunnea* (A. e S.) Svrcek e Kubicka. *Micologia Italiana* 26:17–22.
 6. Kohler A, Kuo A, Nagy LG, Morin E, Barry KW, Buscot F, Canbäck B, Choi C, Cichocki N, Clum A, Colpaert J, Copeland A, Costa MD, Doré J, Floudas D, Gay G, Girlanda M, Henrissat B, Herrmann S, Hess J, Högberg N, Johansson T, Khouja H-R, LaButti K, Lahrmann U, Levasseur A, Lindquist EA, Lipzen A, Marmeisse R, Martino E, Murat C, Ngan CY, Nehls U, Plett JM, Pringle A, Ohm RA, Perotto S, Peter M, Riley R, Rineau F, Ruytinx J, Salamov A, Shah F, Sun H, Tarkka M, Tritt A, Veneault-Fourrey C, Zuccaro A, Mycorrhizal Genomics Initiative Consortium, Tunlid A, Grigoriev IV, Hibbett DS, Martin FM. 2015. Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. *Nature Genetics*. *Nat Genet* 47:410–415. <https://doi.org/10.1038/ng.3223>.
 7. Chin C-S, Peluso P, Sedlazeck FJ, Nattestad M, Concepcion GT, Clum A, Dunn C, O'Malley R, Figueroa-Balderas R, Morales-Cruz A, Cramer GR, Delledonne M, Luo C, Ecker JR, Cantu D, Rank DR, Schatz MC. 2016. Phased diploid genome assembly with single-molecule real-time sequencing. *Nat Methods* 13:1050–1054. <https://doi.org/10.1038/nmeth.4035>.
 8. Lam KK, LaButti K, Khalak A, Tse D. 2015. FinisherSC: a repeat-aware tool for upgrading de-novo assembly using long reads. *Bioinformatics* 31: 3207–3209. <https://doi.org/10.1093/bioinformatics/btv280>.
 9. 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>.
 10. Grigoriev IV, Nikitin R, Haridas S, Kuo A, Ohm R, Otillar R, Riley R, Salamov A, Zhao X, Korzeniewski F, Smirnova T, Nordberg H, Dubchak I, Shabalov I. 2014. MycoCosm portal: gearing up for 1000 fungal genomes. *Nucleic Acids Res* 42:D699–D704. <https://doi.org/10.1093/nar/gkt1183>.
 11. Kuo A, Bushnell B, Grigoriev IV. 2014. Fungal genomics: sequencing and annotation, p 1–52. In Martin F (ed), *Fungi. Advances in botanical research*. Elsevier Academic Press, Cambridge, United Kingdom.
 12. Grabherr MG, Haas BJ, Yassour M, Levin JZ, Thompson DA, Amit I, Adiconis X, Fan L, Raychowdhury R, Zeng Q, Chen Z, Mauceli E, Hacohen N, Gnirke A, Rhind N, di Palma F, Birren BW, Nusbaum C, Lindblad-Toh K, Friedman N, Regev A. 2011. Full-length transcriptome assembly from RNA-seq data without a reference genome. *Nat Biotechnol* 29:644–652. <https://doi.org/10.1038/nbt.1883>.
 13. Enright AJ, Van Dongen S, Ouzounis CA. 2002. An efficient algorithm for large-scale detection of protein families. *Nucleic Acids Res* 30:1575–1584. <https://doi.org/10.1093/nar/30.7.1575>.
 14. Traeger S, Altegoer F, Freitag M, Gabaldon T, Kempken F, Kumar A, Marcet-Houben M, Pöggeler S, Stajich EJ, Nowrousian M. 2013. The genome and development-dependent transcriptomes of *Pyronema confluens*: a window into fungal evolution. *PLoS Genet* 9:e1003820. <https://doi.org/10.1371/journal.pgen.1003820>.
 15. Murat C, Payen T, Noel B, Kuo A, Morin E, Chen J, Kohler A, Krizsán K, Balestrini R, Da Silva C, Montanini B, Hainaut M, Levati E, Barry KW, Belfiori B, Cichocki N, Clum A, Dockter RB, Fauchery L, Guy J, Iotti M, Le Tacon F, Lindquist EA, Lipzen A, Malmagac F, Mello A, Molinier V, Miyauchi S, Poulain J, Riccioni C, Rubini A, Sitrit Y, Splivallo R, Traeger S, Wang M, Žifčáková L, Wipf D, Zambonelli A, Paolocci F, Nowrousian M, Ottonello S, Baldrian P, Spatafora JW, Henrissat B, Nagy LG, Aury J-M, Wincker P, Grigoriev IV, Bonfante P, Martin FM. 2018. Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. *Nat Ecol Evol* 2:1956–1965. <https://doi.org/10.1038/s41559-018-0710-4>.
 16. Martin F, Kohler A, Murat C, Balestrini R, Coutinho PM, Jaillon O, Montanini B, Morin E, Noel B, Percudani R, Porcel B, Rubini A, Amicucci A, Amselem J, Anthouard V, Arcioni S, Artiguenave F, Aury J-M, Ballario P, Bolchi A, Brenna A, Brun A, Buée M, Cantarel B, Chevalier G, Couloux A, Da Silva C, Denoeud F, Duplessis S, Ghignone S, Hilselberger B, Iotti M, Marçais B, Mello A, Miranda M, Pacioni G, Quesneville H, Riccioni C, Ruotolo R, Splivallo R, Stocchi V, Tisserant E, Viscomi AR, Zambonelli A, Zampieri E, Henrissat B, Lebrun M-H, Paolocci F, Bonfante P, Ottonello S, Wincker P. 2010. Périgord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. *Nature* 464:1033–1038. <https://doi.org/10.1038/nature08867>.
 17. Murat C, Kuo A, Barry KW, Clum A, Dockter RB, Fauchery L, Iotti M, Kohler A, LaButti K, Lindquist EA, Lipzen A, Morin E, Wang M, Grigoriev IV, Zambonelli A, Martin FM. 2018. Draft genome sequence of *Tuber borchii* Vittad., a whitish edible truffle. *Genome Announc* 6:e00537-18. <https://doi.org/10.1128/genomeA.00537-18>.