

University of Groningen

Draft genome sequence of *Coniochaeta ligniaria* NRRL 30616, a lignocellulolytic fungus for bioabatement of inhibitors in plant biomass hydrolysates

Jiménez, Diego Javier; Hector, Ronald E.; Riley, Robert; Lipzen, Anna; Kuo, Rita C.; Amirebrahimi, Mojgan; Barry, Kerry M.; Grigoriev, Igor V.; van Elsas, Jan; Nichols, Nancy N.

Published in:
Genome Announcements

DOI:
[10.1128/genomeA.01476-16](https://doi.org/10.1128/genomeA.01476-16)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Final author's version (accepted by publisher, after peer review)

Publication date:
2017

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Jiménez, D. J., Hector, R. E., Riley, R., Lipzen, A., Kuo, R. C., Amirebrahimi, M., ... Nichols, N. N. (2017). Draft genome sequence of *Coniochaeta ligniaria* NRRL 30616, a lignocellulolytic fungus for bioabatement of inhibitors in plant biomass hydrolysates. *Genome Announcements*, 5(4). DOI: 10.1128/genomeA.01476-16

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).


Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.



Draft Genome Sequence of *Coniochaeta ligniaria* NRRL 30616, a Lignocellulolytic Fungus for Bioabatement of Inhibitors in Plant Biomass Hydrolysates

Diego Javier Jiménez,^a Ronald E. Hector,^b Robert Riley,^c Anna Lipzen,^c Rita C. Kuo,^c Mojgan Amirebrahimi,^c Kerrie W. Barry,^c Igor V. Grigoriev,^c Jan Dirk van Elsas,^a  Nancy N. Nichols^b

Cluster of Microbial Ecology, Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands^a; Bioenergy Research Unit, National Center for Agricultural Utilization Research, USDA-ARS, Peoria, Illinois, USA^b; U.S. Department of Energy Joint Genome Institute, Walnut Creek, California, USA^c

ABSTRACT Here, we report the first draft genome sequence (42.38 Mb containing 13,657 genes) of *Coniochaeta ligniaria* NRRL 30616, an ascomycete with biotechnological relevance in the bioenergy field given its high potential for bioabatement of toxic furanic compounds in plant biomass hydrolysates and its capacity to degrade lignocellulosic material.

Coniochaeta ligniaria is an ascomycete (order Coniochaetales), inhabiting decaying wood, leaf litter, and soil (1). *C. ligniaria* NRRL 30616 was isolated from furfural-contaminated soil based on its ability to metabolize furan-aldehyde mixtures (2). This strain has the potential to remove a variety of inhibitory compounds (e.g., 5-hydroxymethylfurfural) from plant biomass (e.g., wheat straw, switchgrass, corn stover, alfalfa stems, and rice hulls) dilute-acid hydrolysates, facilitating subsequent microbial fermentation of sugars (3–6). Moreover, *C. ligniaria*-like isolates have also been recovered from torrefied grass (7) as well as from various soil-derived lignocellulolytic microbial consortia (8, 9). Previous studies revealed that *C. ligniaria* contains key enzymatic machinery that efficiently works in lignocellulose deconstruction (10, 11). However, direct confirmation of the genomic potential has until now been missing.

To support information about the metabolism of furanic compounds and degradation of lignocellulosic biomass, we report here the draft genome sequence of *C. ligniaria* NRRL 30616. The strain was cultivated in yeast extract-peptone-dextrose (YPD) broth containing 50 μ g/ml kanamycin. Total genomic DNA extraction was performed using the OmniPrep kit for fungi (G-Biosciences, St. Louis, MO). The genome was sequenced using the Illumina HiSeq 2000 platform at the Joint Genome Institute (JGI). The obtained quality reads were assembled with AllPathsLG version R47710 (12). The size of the assembled genome is 42.38 Mb (94.4 \times coverage), comprising 135 scaffolds (118 with more than 2 kb) and 230 contigs. The three largest scaffolds had 4.64, 4.17, and 3.94 Mb. Fungal genome annotation was performed using the JGI pipeline and is available via the JGI-MycoCosm platform (13). A total of 13,657 genes were predicted. Analysis of the genes with the CAZy database (14) identified 304 glycoside hydrolases, 100 glycosyl transferases, seven polysaccharide lyases, 45 carbohydrate esterases, 92 carbohydrate-binding modules, and 23 lytic polysaccharide monooxygenases (LPMOs) (AA9 and AA11 families), a new type of copper-dependent metalloenzymes that catalyze the oxidative cleavage of (1-4)-linked glycosidic bonds of plant polysaccharides and chitin (15). Regarding genes that could be involved in furanic compound metabolism (16), the *C. ligniaria* NRRL 30616 genome was found to contain 1,070 oxidoreduc-

Received 7 November 2016 Accepted 22 November 2016 Published 26 January 2017

Citation Jiménez DJ, Hector RE, Riley R, Lipzen A, Kuo RC, Amirebrahimi M, Barry KW, Grigoriev IV, van Elsas JD, Nichols NN. 2017. Draft genome sequence of *Coniochaeta ligniaria* NRRL 30616, a lignocellulolytic fungus for bioabatement of inhibitors in plant biomass hydrolysates. Genome Announc 5:e01476-16. <https://doi.org/10.1128/genomeA.01476-16>.

Copyright © 2017 Jiménez 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 Nancy N. Nichols, nancy.nichols@ars.usda.gov.

tases, 926 dehydrogenases, and 227 decarboxylases. Based on gene ontology analysis, 23 genes are involved in the response to oxidative stress (GO:0006979).

The genomic information in this report will provide a better understanding of the genetic mechanism involved in the bioabatement of inhibitory by-products on plant biomass hydrolysates. In addition, the plethora of enzymes involved in lignocellulose degradation could be a relevant source for the production of new proteins useful in efficient saccharification of plant biomass. The availability of a genetic system for modification of *C. ligniaria* NRRL 30616 could enable engineering of the strain for conversion of biomass sugars to any number of value-added products.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [MNPNO000000](https://doi.org/10.1101/1000000). The version described in this paper is version MNPNO1000000.

ACKNOWLEDGMENTS

The work conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, is supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231. This work was also supported by the BE-Basic Foundation (<http://www.be-basic.org/>).

We thank Sarah E. Frazer and Katherine Card for excellent technical assistance.

The mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

REFERENCES

- Weber E. 2002. The *Lecythophora–Coniochaeta* complex I. Morphological studies on *Lecythophora* species isolated from *Picea abies*. *Nova Hedwigia* 74:159–185. <https://doi.org/10.1127/0029-5035/2002/0074-0159>.
- López MJ, Nichols NN, Dien BS, Moreno J, Bothast RJ. 2004. Isolation of microorganisms for biological detoxification of lignocellulosic hydrolysates. *Appl Microbiol Biotechnol* 64:125–131. <https://doi.org/10.1007/s00253-003-1401-9>.
- Nichols NN, Sharma LN, Mowery RA, Chambliss CK, Van Walsum GP, Dien BS, Iten LB. 2008. Fungal metabolism of fermentation inhibitors present in corn stover dilute acid hydrolysate. *Enzyme Microb Technol* 42: 624–630. <https://doi.org/10.1016/j.enzmictec.2008.02.008>.
- Nichols NN, Dien BS, Cotta MA. 2010. Fermentation of bioenergy crops into ethanol using biological abatement for removal of inhibitors. *Bioresour Technol* 101:7545–7550 <https://doi.org/10.1016/j.biortech.2010.04.097>.
- Saha BC, Nichols NN, Cotta MA. 2011. Ethanol production from wheat straw by recombinant *Escherichia coli* strain FBR5 at high solid loading. *Bioresour Technol* 102:10892–10897. <https://doi.org/10.1016/j.biortech.2011.09.041>.
- Nichols NN, Hector RE, Saha BC, Frazer SE, Kennedy GJ. 2014. Biological abatement of inhibitors in rice hull hydrolysate and fermentation to ethanol using conventional and engineered microbes. *Biomass Bioenerg* 67:79–88. <https://doi.org/10.1016/j.biombioe.2014.04.026>.
- Trifonova R, Babini V, Postma J, Ketelaars JJM, van Elsas JD. 2009. Colonization of torrefied grass fibers by plant-beneficial microorganisms. *Appl Soil Ecol* 41:98–106. <https://doi.org/10.1016/j.apsoil.2008.09.005>.
- Jiménez DJ, Korenblum E, van Elsas JD. 2014. Novel multispecies microbial consortia involved in lignocellulose and 5-hydroxymethylfurfural bioconversion. *Appl Microbiol Biotechnol* 98:2789–2803. <https://doi.org/10.1007/s00253-013-5253-7>.
- de Lima Brossi MJ, Jiménez DJ, Cortes-Talpa L, van Elsas JD. 2015. Soil-derived microbial consortia enriched with different plant biomass reveal distinct players acting in lignocellulose degradation. *Microb Ecol* 71:616–627. <https://doi.org/10.1007/s00248-015-0683-7>.
- López MJ, Vargas-García MdC, Suárez-Estrella F, Nichols NN, Dien BS, Moreno J. 2007. Lignocellulose-degrading enzymes produced by the ascomycete *Coniochaeta ligniaria* and related species: application for a lignocellulosic substrate treatment. *Enzyme Microb Technol* 40: 794–800. <https://doi.org/10.1016/j.enzmictec.2006.06.012>.
- Ravindran A, Adav SS, Sze SK. 2012. Characterization of extracellular lignocellulolytic enzymes of *Coniochaeta* sp. during corn stover bioconversion. *Proc Biochem* 47:2440–2448. <https://doi.org/10.1016/j.procbio.2012.10.003>.
- 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>.
- Grigoriev IV, Nikitin R, Haridas S, Kuo A, Ohm R, Otilar 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>.
- Lombard V, Golaconda-Ramulu H, Drula E, Coutinho PM, Henrissat B. 2014. The carbohydrate-active enzymes database (CAZY) in 2013. *Nucleic Acids Res* 42:D490–D495. <https://doi.org/10.1093/nar/gkt1178>.
- Forsberg Z, Røhr AK, Mekasha S, Andersson KK, Eijsink VG, Vaaje-Kolstad G, Sørlie M. 2014. Comparative study of two chitin-active and two cellulose-active AA10-type lytic polysaccharide monoxygenases. *Biochemistry* 53:1647–1656. <https://doi.org/10.1021/bi5000433>.
- Wang X, Gao Q, Bao J. 2015. Transcriptional analysis of *Amorphotheca resinae* ZN1 on biological degradation of furfural and 5-hydroxymethylfurfural derived from lignocellulose pretreatment. *Bio-technol Biofuels* 8:136. <https://doi.org/10.1186/s13068-015-0323-y>.