



Draft Genome Sequence of the D-Xylose-Fermenting Yeast *Spathaspora xylofermentans* UFMG-HMD23.3

Daiane D. Lopes,^a Samuel P. Cibulski,^b Fabiana Q. Mayer,^b Franciele M. Siqueira,^c Carlos A. Rosa,^d Ronald E. Hector,^e Marco Antônio Z. Ayub^a

Biotechnology and Biochemical Engineering Laboratory (BiotechLab), Science and Food Technology Institute, Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil^a; Veterinary Research Institute, Fepagro Animal Health, Eldorado do Sul, Rio Grande do Sul, Brazil^b; Centro de Biotecnologia, Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil^c; Department of Microbiology, Biological Science Institute, Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil^d; Bioenergy Research Unit, National Center for Agricultural Utilization Research, USDA-ARS, Peoria, Illinois, USA^e

ABSTRACT Here, we report the draft genome sequence of the yeast *Spathaspora xylofermentans* UFMG-HMD23.3 (=CBS 12681), a D-xylose-fermenting yeast isolated from the Amazonian forest. The genome consists of 298 contigs, with a total size of 15.1 Mb, including the mitochondrial genome, and 5,948 predicted genes.

Spathaspora xylofermentans UFMG-HMD23.3 (=CBS 12681) is an asexual D-xylose-fermenting yeast isolated from rotting wood of the Amazonian environment in Brazil (1). Species of the *Spathaspora* clade are known for their ability to convert xylose to ethanol and have the potential for lignocellulosic ethanol production (2–6). Limitations in lignocellulosic ethanol production associated with poor xylose assimilation by engineered *Saccharomyces cerevisiae* strains could be solved through knowledge about the mechanisms for xylose fermentation in natural, or wild-type, yeasts (7–10). Considering the importance of the genus *Spathaspora* and the species closely related to this clade, we proceeded to annotate the genomic information of the strain presented here. The genomic information from this yeast will contribute to advancing technologies to efficiently produce lignocellulosic-based ethanol, the so-called second-generation ethanol, either by the direct use of a genetically improved strain or as a source of genes needed for xylose fermentation in genetically modified industrial strains of *S. cerevisiae*.

S. xylofermentans DNA was isolated using the Wizard genomic DNA purification kit (Promega). DNA libraries were prepared with a Nextera DNA library prep kit (Illumina) and sequenced in the MiSeq system (Illumina) (paired-end, 500-cycle version 2 kit). The raw sequence data comprise 3,827,910 high-quality paired-end reads. Reads were imported into CLC Genomics Workbench version 10, trimmed, and *de novo* assembled. Gene prediction was performed with AUGUSTUS (11), and genome statistics were generated by QUASt (12). The genome of *S. xylofermentans* HMD23.3 consists of 293 contigs (largest contig, 639,790 bp; N_{50} , 142,604 bp), with a total size of 15,098,813 bp (mean coverage, $\sim 55\times$) and a G+C content of 35.34%. Among 5,948 potential protein-coding genes, 92.8% encode proteins with assigned functional roles and showed similarity to yeast species of the CTG clade, mainly to *S. passalidarum* strain NRRL Y-27907 (13). The mitochondrial DNA was assembled into a 23,201-bp fragment (contig 138, mean coverage of 483 \times). tRNAscan-SE (14) predicted 249 tRNA genes scattered across the contigs. RNAmmer (15) identified 28S, 18S, and 5.8S rRNA genes at contig 178.

S. xylofermentans HMD23.3 has genes required for xylose assimilation and fermentation, which are important for lignocellulosic-based ethanol production. Genes for conversion of D-xylose to D-xylulose (*XYL1* and *XYL2*) and xylulokinase for incorporation

Received 30 June 2017 Accepted 3 July 2017 Published 17 August 2017

Citation Lopes DD, Cibulski SP, Mayer FQ, Siqueira FM, Rosa CA, Hector RE, Ayub MAZ. 2017. Draft genome sequence of the D-xylose-fermenting yeast *Spathaspora xylofermentans* UFMG-HMD23.3. Genome Announc 5:e00815-17. <https://doi.org/10.1128/genomeA.00815-17>.

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

Address correspondence to Marco Antônio Z. Ayub, mazayub@ufrgs.br.

of D-xylulose-5P into the pentose phosphate pathway were identified at contigs 27, 110, and 124. Only one *XYL1* gene was identified (contig 124), and the Xyl1p is 93% and 76% identical to Xyl1.1p and Xyl1.2p of *S. passalidarum* NRRL Y-27907, respectively. Xyl1.2p showed a preference for NADH over NADPH in activity tests of xylose reductase, which allows for the anaerobic fermentation of xylose (7). At least 21 sugar transporters were identified, and some of them were related as possible xylose transporters.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [NDXA00000000](https://doi.org/10.1093/nar/gkt418). The version described in this paper is the first version, NDXA01000000.

ACKNOWLEDGMENTS

We acknowledge the financial support and scholarships from CNPq, CAPES, and FINEP (grant 01.10.0783.04), all Brazilian research-funding agencies.

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

- Cadete RM, Melo MA, Zilli JE, Vital MJS, Mouro A, Prompt AH, Gomes FCO, Stambuk BU, Lachance MA, Rosa CA. 2013. *Spathaspora brasiliensis* sp. nov., *Spathaspora suhii* sp. nov., *Spathaspora roraimanensis* sp. nov. and *Spathaspora xylofermentans* sp. nov., four novel D-xylose-fermenting yeast species from Brazilian Amazonian forest. *Antonie Van Leeuwenhoek* 103:421–431. <https://doi.org/10.1007/s10482-012-9822-z>.
- da Cunha-Pereira F, Hickert LR, Sehnem NT, de Souza-Cruz PB, Rosa CA, Ayub MAZ. 2011. Conversion of sugars present in rice hull hydrolysates into ethanol by *Spathaspora arborariae*, *Saccharomyces cerevisiae*, and their co-fermentations. *Bioresour Technol* 102:4218–4225. <https://doi.org/10.1016/j.biortech.2010.12.060>.
- Hickert LR, de Souza-Cruz PB, Rosa CA, Ayub MA. 2013. Simultaneous saccharification and co-fermentation of un-detoxified rice hull hydrolysate by *Saccharomyces cerevisiae* ICV D254 and *Spathaspora arborariae* NRRL Y-48658 for the production of ethanol and xylitol. *Bioresour Technol* 143:112–116. <https://doi.org/10.1016/j.biortech.2013.05.123>.
- Hou X. 2012. Anaerobic xylose fermentation by *Spathaspora passalidarum*. *Appl Microbiol Biotechnol* 94:205–214. <https://doi.org/10.1007/s00253-011-3694-4>.
- Long TM, Su YK, Headman J, Higbee A, Willis LB, Jeffries TW. 2012. Cofermentation of glucose, xylose, and cellobiose by the beetle-associated yeast *Spathaspora passalidarum*. *Appl Environ Microbiol* 78: 5492–5500. <https://doi.org/10.1128/AEM.00374-12>.
- Martiniano SE, Philippini RR, Chandel AK, Rosa CA, Pagnocca FC, da Silva SS. 2014. Evaluation of rice bran extract as a nitrogen source for improved hemicellulosic ethanol production from sugarcane bagasse by new xylose-fermenting yeast strains isolated from Brazilian forests. *Sugar Tech* 16:1–8. <https://doi.org/10.1007/s12355-013-0219-8>.
- Cadete RM, de las Heras AM, Sandström AG, Ferreira C, Gírio F, Gorwa-Grauslund MF, Rosa CA, Fonseca C. 2016. Exploring xylose metabolism in *Spathaspora* species: XYL1.2 from *Spathaspora passalidarum* as the key for efficient anaerobic xylose fermentation in metabolic engineered *Saccharomyces cerevisiae*. *Biotechnol Biofuels* 9:167. <https://doi.org/10.1186/s13068-016-0570-6>.
- Hahn-Hägerdal B, Karhumaa K, Fonseca C, Spencer-Martins I, Gorwa-Grauslund MF. 2007. Towards industrial pentose-fermenting yeast strains. *Appl Microbiol Biotechnol* 74:937–953. <https://doi.org/10.1007/s00253-006-0827-2>.
- Lopes MR, Morais CG, Kominek J, Cadete RM, Soares MA, Uetanabaro APT, Fonseca C, Lachance MA, Hittinger CT, Rosa CA. 2016. Genomic analysis and D-xylose fermentation of three novel *Spathaspora* species: *Spathaspora girioi* sp. nov., *Spathaspora hagerdaliae* f. a., sp. nov. and *Spathaspora gorwiae* f. a., sp. nov. *FEMS Yeast Res* 16:1–12. <https://doi.org/10.1093/femsyr/fow044>.
- Wohlbach DJ, Kuo A, Sato TK, Potts KM, Salamov AA, LaButti KM, Sun H, Clum A, Pangilinan JL, Lindquist EA, Lucas S, Lapidus A, Jin M, Gunawan C, Balan V, Dale BE, Jeffries TW, Zinkel R, Barry KW, Grigoriev IV, Gasch AP. 2011. Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. *Proc Natl Acad Sci U S A* 108:13212–13217. <https://doi.org/10.1073/pnas.1103039108>.
- Hoff KJ, Stanke M. 2013. WebAUGUSTUS—a Web service for training AUGUSTUS and predicting genes in eukaryotes. *Nucleic Acids Res* 41: W123–W128. <https://doi.org/10.1093/nar/gkt418>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
- Maguire SL, ÓhÉigeartaigh SS, Byrne KP, Schröder MS, O’Gaora P, Wolfe KH, Butler G. 2013. Comparative genome analysis and gene finding in *Candida* species using CGOB. *Mol Biol Evol* 30:1281–1291. <https://doi.org/10.1093/molbev/mst042>.
- Lowe TM, Eddy SR. 1997. TRNAScan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* 25:955–964.
- Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res* 35:3100–3108. <https://doi.org/10.1093/nar/gkm160>.