





Complete Genome Sequence of the Lignocellulose-Degrading Actinomycete *Streptomyces albus* CAS922

Anna Tippelt,^a  Markus Nett,^a  M. Soledad Vela Gurovic^{b,c}

^aDepartment of Biochemical and Chemical Engineering, TU Dortmund University, Dortmund, Germany

^bCenter for Renewable Natural Resources of the Semi-Arid Zone, National Scientific and Technical Research Council, Bahía Blanca, Argentina

^cDepartment of Biology, Biochemistry, and Pharmacy, Universidad Nacional del Sur, Bahía Blanca, Argentina

ABSTRACT *Streptomyces albus* CAS922 was isolated from sunflower seed hulls. Its fully sequenced genome harbors a multitude of genes for carbohydrate-active enzymes, which likely facilitate growth on lignocellulosic biomass. Furthermore, the presence of 27 predicted biosynthetic gene clusters indicates a significant potential for the production of bioactive secondary metabolites.

Actinomycete bacteria are important contributors to the natural degradation of lignocellulosic biomass (1, 2). An illustrative example is *Streptomyces albus* CAS922, which was isolated from sunflower seed hulls discarded by the sunflower oil industry (Cargill S.A.C.I., Bahía Blanca, Argentina) by using ISP-2 agar plates (3) and has been found to grow on diverse lignocellulosic substrates. The strain produces an earthy odor and shows typical streptomycete morphology, including aerial mycelia and substrate hyphae penetrating the agar. Since many actinomycetes are versatile producers of clinically used antibiotics (4, 5), *S. albus* CAS922 might possess the potential to convert lignocellulosic biomass into value-added products. To obtain data to test this hypothesis, its genome was sequenced.

For DNA isolation, a glycerol stock of *S. albus* CAS922 was incubated in ISP-2 broth at 30°C and 250 rpm for 4 days. Genomic DNA was then isolated according to a protocol adapted from a report by Neumann et al. with minor modifications (6). Briefly, cells were harvested from liquid ISP-2 cultures and ground in liquid nitrogen in a mortar. The sample was incubated with lysozyme for 2 h at 300 rpm and proteinase K for 3 h at 300 rpm and was extracted with a mixture of phenol, chloroform, and isoamyl alcohol (25:24:1) followed by RNase treatment. Genome sequencing was executed by CD Genomics (New York, NY, USA) using the Oxford Nanopore sequencing platform. The SQK-LSK109 kit was used for library preparation following the 1D genomic DNA by ligation protocol (7). Adapters were filtered with the software Porechop v0.2.3. Low-quality and short-fragment (<2,000-bp) reads were removed with the MinKNOW software package to obtain a total of 1,543,556,228 bp of clean data from 260,187 clean reads with an N_{50} value of 7,942 bp. The clean reads were assembled using Canu v1.5 software (8), followed by a subsequent data-polishing step with Pilon software (9) to increase accuracy. This resulted in a linear chromosome of 8.06 Mb with 191-fold genome coverage and a G+C content of 72.59%. The Prokaryotic Genome Annotation Pipeline (PGAP) (10) predicted 6,776 protein-coding genes, 80 RNAs, 59 tRNAs, 3 noncoding RNAs, and 312 pseudogenes. A repetitive sequence content of 2.45% was predicted by RepeatMasker (11). Assignment of the strain to the species *S. albus* was verified based on alignments with the nonredundant database (12). Default parameters were used for all software.

A total of 232 carbohydrate-active enzymes were predicted using the CAZy database (13) and dbCAN2 (14). Three of these proteins belong to the AA10 family, recently

Citation Tippelt A, Nett M, Vela Gurovic MS. 2020. Complete genome sequence of the lignocellulose-degrading actinomycete *Streptomyces albus* CAS922. Microbiol Resour Announc 9:e00227-20. <https://doi.org/10.1128/MRA.00227-20>.

Editor David A. Baltus, University of Arizona

Copyright © 2020 Tippelt 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 M. Soledad Vela Gurovic, svela@uns.edu.ar.

Received 2 March 2020

Accepted 27 April 2020

Published 21 May 2020

recognized as copper-dependent lytic polysaccharide monoxygenases involved in the lysis of chitin, cellulose, and xylan (15).

An antiSMASH analysis (16) revealed 27 putative biosynthetic gene clusters. According to this prediction, *S. albus* CAS922 produces the siderophore desferrioxamine E (17), the compatible solute ectoine (18), and the terpenes cyclabdan (19) and geosmin (20). Moreover, the actinomycete harbors the genes for biosynthesis of the antibiotics xantholipin (21) and pseudouridimycin (22). Overall, *S. albus* CAS922 possesses a high potential for the utilization of lignocellulose and the biosynthesis of secondary metabolites.

Data availability. This whole-genome project has been deposited in GenBank with the accession number [CP048875](https://doi.org/10.1093/nar/gkn663). The raw data are available under accession number [SRR11069776](https://doi.org/10.1093/nar/gky418).

ACKNOWLEDGMENTS

M.S.V.G. acknowledges Cristian Gallo for technical assistance.

This study was supported by grants PUE2017 CERZOS-CONICET and PGI 24/B294 SeGCyT-UNS (to M.S.V.G.). The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

REFERENCES

- Antunes PL, Martins FL, Pereira RV, Thomas AM, Barbosa D, Lemos LN, Machado Silva GM, Silva Moura LM, Condomitti Epamino GW, Digiampietri LA, Lombardi KC, Locosque Ramos P, Bento Quaggio R, Franco de Oliveira JC, Castiglioni Pascon R, da Cruz JB, da Silva AM, Setubal JC. 2016. Microbial community structure and dynamics in thermophilic composting viewed through metagenomics and metatranscriptomics. *Sci Rep* 6:38915. <https://doi.org/10.1038/srep38915>.
- Větrovský T, Steffen KT, Baldrian P. 2014. Potential of cometabolic transformation of polysaccharides and lignin in lignocellulose by soil actinobacteria. *PLoS One* 9:e89108. <https://doi.org/10.1371/journal.pone.0089108>.
- Shirling EB, Gottlieb D. 1966. Methods for characterization of *Streptomyces* species. *Int J Syst Bact* 16:313–340. <https://doi.org/10.1099/00207713-16-3-313>.
- van der Meij A, Worsley SF, Hutchings MI, van Wezel GP. 2017. Chemical ecology of antibiotic production by actinomycetes. *FEMS Microbiol Rev* 41:392–416. <https://doi.org/10.1093/femsre/fux005>.
- Nett M, Ikeda H, Moore BS. 2009. Genomic basis for natural product biosynthetic diversity in the actinomycetes. *Nat Prod Rep* 26:1362–1384. <https://doi.org/10.1039/b817069j>.
- Neumann B, Pospiech A, Schairer HU. 1992. Rapid isolation of genomic DNA from Gram-negative bacteria. *Trends Genet* 8:332–333. [https://doi.org/10.1016/0168-9525\(92\)90269-A](https://doi.org/10.1016/0168-9525(92)90269-A).
- Oxford Nanopore Technologies. 2020. Genomic DNA by ligation (SQK-LSK109). Oxford Nanopore Technologies, Oxford, United Kingdom. https://store.nanoporetech.com/us/media/wysiwyg/pdfs/SQK-LSK109/Genomic_DNA_by_Ligation_SQK-LSK109_minion.pdf.
- Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive *k*-mer weighting and repeat separation. *Genome Res* 27:722–736. <https://doi.org/10.1101/gr.215087.116>.
- Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One* 9:e112963. <https://doi.org/10.1371/journal.pone.0112963>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Tarailo-Graovac M, Chen N. 2009. Using RepeatMasker to identify repetitive elements in genomic sequences. *Curr Protoc Bioinformatics* 4.10.1–4.10.14. <https://doi.org/10.1002/0471250953.bi0410s25>.
- Deng YY, Li JQ, Wu SF, Zhu YP, Chen YW, He FC. 2006. Integrated nr database in protein annotation system and its localization. *Comput Eng* 32:71–74.
- Cantarel BL, Coutinho PM, Rancurel C, Bernard T, Lombard V, Henrissat B. 2009. The Carbohydrate-Active EnZymes database (CAZy): an expert resource for glycogenomics. *Nucleic Acids Res* 37:D233–D238. <https://doi.org/10.1093/nar/gkn663>.
- Zhang H, Yohe T, Huang L, Entwistle S, Wu P, Yang Z, Busk PK, Xu Y, Yin Y. 2018. dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. *Nucleic Acids Res* 46:W95–W101. <https://doi.org/10.1093/nar/gky418>.
- Corrêa TLR, Júnior AT, Wolf LD, Buckeridge MS, Dos Santos LV, Murakami MT. 2019. An actinobacteria lytic polysaccharide monoxygenase acts on both cellulose and xylan to boost biomass saccharification. *Biotechnol Biofuels* 12:117. <https://doi.org/10.1186/s13068-019-1449-0>.
- Blin K, Shaw S, Steinke K, Villebro R, Ziemert N, Lee SY, Medema MH, Weber T. 2019. antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. *Nucleic Acids Res* 47:W81–W87. <https://doi.org/10.1093/nar/gkz310>.
- Barona-Gómez F, Wong U, Giannakopoulos AE, Derrick PJ, Challis GL. 2004. Identification of a cluster of genes that directs desferrioxamine biosynthesis in *Streptomyces coelicolor* M145. *J Am Chem Soc* 126:16282–16283. <https://doi.org/10.1021/ja045774k>.
- Louis P, Galinski EA. 1997. Characterization of genes for the biosynthesis of the compatible solute ectoine from *Marinococcus halophilus* and osmoregulated expression in *Escherichia coli*. *Microbiology* 143:1141–1149. <https://doi.org/10.1099/00221287-143-4-1141>.
- Ikeda H, Shin-Ya K, Nagamitsu T, Tomoda H. 2016. Biosynthesis of mercapturic acid derivative of the labdane-type diterpene, cyclabdan that potentiates imipenem activity against methicillin-resistant *Staphylococcus aureus*: cyclabdan is generated by mycothiol-mediated xenobiotic detoxification. *J Ind Microbiol Biotechnol* 43:325–342. <https://doi.org/10.1007/s10295-015-1694-6>.
- Jiang J, He X, Cane DE. 2007. Biosynthesis of the earthy odorant geosmin by a bifunctional *Streptomyces coelicolor* enzyme. *Nat Chem Biol* 3:711–715. <https://doi.org/10.1038/nchembio.2007.29>.
- Zhang W, Wang L, Kong L, Wang T, Chu Y, Deng Z, You D. 2012. Unveiling the post-PKS redox tailoring steps in biosynthesis of the type II polyketide antitumor antibiotic xantholipin. *Chem Biol* 19:422–432. <https://doi.org/10.1016/j.chembiol.2012.01.016>.
- Sosio M, Gaspari E, Iorio M, Pessina S, Medema MH, Bernasconi A, Simone M, Maffoli SI, Ebricht RH, Donadio S. 2018. Analysis of the pseudouridimycin biosynthetic pathway provides insight into the formation of C-nucleoside antibiotics. *Cell Chem Biol* 25:540–549. <https://doi.org/10.1016/j.chembiol.2018.02.008>.