



Draft Genome Sequence of the Oleaginous Yeast *Saitozyma podzolica* (syn. *Cryptococcus podzolicus*) DSM 27192

Habibu Aliyu,^a Olga Gorte,^a Anke Neumann,^a Katrin Ochsenreither^a

^aInstitute of Process Engineering in Life Science 2: Technical Biology, Karlsruhe Institute of Technology, Karlsruhe, Germany

ABSTRACT We report here the draft genome of *Saitozyma podzolica* DSM 27192 sequenced based on PacBio chemistry. This yeast isolate produces large amounts of single-cell oil (SCO) and gluconic acid (GA). Information from the genome sequence will provide additional insight into the genetic mechanism of SCO and GA metabolism in this organism.

A yeast isolate from peat bog soil in the Black Forest of Germany was identified using internal transcribed spacer (ITS) region sequencing as *Cryptococcus podzolicus* and deposited as DSM 27192 at the DSMZ (1). This oleaginous yeast was characterized as a simultaneous single-cell oil (SCO) and gluconic acid (GA) producer via a fermentation process with glucose as a carbon source, yielding 18 g/liter SCO and 30 g/liter GA. On xylose, 11.1 g/liter SCO was produced (1). The ability to convert xylose to SCO makes this strain an interesting candidate for the maintenance of the carbon value chain by converting renewable waste material, e.g., hydrolyzed wood and straw, for worthwhile biodiesel production (2).

Saitozyma podzolica DSM 27192 was cultivated in a mineral salt medium described in reference 1. Genomic DNA was extracted from cells grown to early logarithmic phase at 20°C and 130 rpm. Genomic DNA was isolated using a phenol-chloroform protocol (3). Library preparation and PacBio RS long-read sequencing were performed at GATC Biotech AG (Constance, Germany), yielding 203,613 reads of 2,572,991,431 bp, with an N_{50} value and mean read length of 19,167 and 12,636 bp, respectively. The reads were preassembled using HGAP 3.0 and polished using Quiver as part of SMRT Analysis version 2.3 at GATC Biotech AG. To validate this assembly, the reads were assembled and polished using Canu version 1.7.1 (4) and arrow version 2.3.2 (5), respectively. The final assembly comprises 46 contigs of 29,888,215 bp (86.1× coverage) with a mean G+C content of 58.79%. The sizes of the largest and N_{50} contigs were 2,705,151 and 1,066,819 bp, respectively. In comparison, the DSM 27192 draft genome is larger than the genomes of other members of the genera *Dioszegia*, *Saitozyma*, and *Tremella*, whose genome sizes range from 19,344,119 to 28,639,919 bp.

Annotation of DSM 27192 contigs using Funannotate pipeline version 1.5.0-8f86f8c (6) resulted in 10,312 gene predictions comprising 10,224 protein-coding and 88 tRNA genes. Compared to its closest genomic relative (Fig. 1), *Cryptococcus* sp. strain JCM 24511 (GenBank accession number [BCLC00000000](https://www.ncbi.nlm.nih.gov/nuccore/BCLC00000000)), the genome of DSM 27192 encodes 1,689 unique proteins. The completeness of the DSM 27192 draft genome, based on BUSCO (7) *fungi_odb9* and *basidiomycota_odb9*, stands at 92.4% and 90.0%, respectively. In contrast, the completeness of the *Cryptococcus* sp. JCM 24511 genome, based on *fungi_odb9*, was estimated at 94.8%. However, *fungi_odb9* estimate of genome completeness among other members of the genera *Dioszegia*, *Saitozyma*, and *Tremella* ranged from 87.6 to 94.8%. Functional annotation of the predicted proteins revealed that relative to other members of the order Tremellales,

Citation Aliyu H, Gorte O, Neumann A, Ochsenreither K. 2019. Draft genome sequence of the oleaginous yeast *Saitozyma podzolica* (syn. *Cryptococcus podzolicus*) DSM 27192. *Microbiol Resour Announc* 8:e01676-18. <https://doi.org/10.1128/MRA.01676-18>.

Editor Jason E. Stajich, University of California, Riverside

Copyright © 2019 Aliyu 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 Olga Gorte, olga.gorte@kit.edu.

H.A. and O.G. are co-first authors.

Received 13 December 2018

Accepted 28 January 2019

Published 21 February 2019

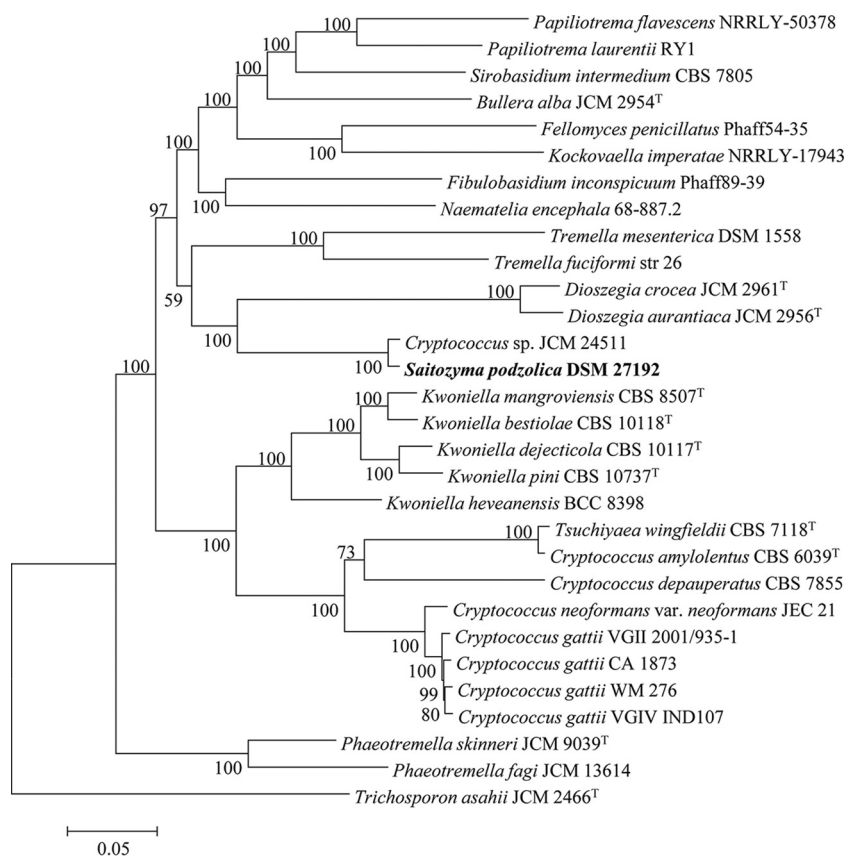


FIG 1 Core genome phylogeny of 31 representative members of the order Tremellales and *Trichosporon asahii* JCM2466^T. Maximum likelihood (ML) tree inferred from concatenated protein alignment (45,703 amino acids in length) of 164 single-copy proteins. The phylogeny was generated using IQ-TREE version 1.6.7 based on the LG+G4+R5 model (8). The ML was generated with confidence values based on 1,000 bootstrap replicates.

DSM 27192 genome encodes a larger number of proteins linked to carbohydrate-active enzymes (CAZymes) and MEROPS, as well as secreted proteins.

The whole-genome sequence of *S. podzolica* DSM 27192 will provide additional insight into the genetic mechanisms and control of fatty acids and gluconic acid synthesis. At the same time, the genomic data will provide an additional point of comparison to other oleaginous yeasts and GA-producing organisms.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [RSCD000000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=RS000000000). The raw reads were deposited in the Sequence Read Archive under the accession number [PRJNA506379](https://www.ncbi.nlm.nih.gov/sra/PRJNA506379).

ACKNOWLEDGMENTS

Bioeconomy International BMBF (grant 031B0452) supported O.G. H.A. acknowledges funding from the Alexander von Humboldt Foundation. We acknowledge support by Deutsche Forschungsgemeinschaft and the Open Access Publishing Fund of Karlsruhe Institute of Technology.

We acknowledge the use of computational resources provided by Siemens.

REFERENCES

- Schulze I, Hansen S, Großhans S, Rudsuck T, Ochsenreither K, Sylđatk C, Neumann A. 2014. Characterization of newly isolated oleaginous yeasts—*Cryptococcus podzolicus*, *Trichosporon porosum* and *Pichia segobiensis*. *AMB Express* 4:24. <https://doi.org/10.1186/s13568-014-0024-0>.
- Li Q, Du W, Liu D. 2008. Perspectives of microbial oils for biodiesel production. *Appl Microbiol Biotechnol* 80:749–756. <https://doi.org/10.1007/s00253-008-1625-9>.
- Sambrook J, Russell DW. 2006. Purification of nucleic acids by extraction with phenol: chloroform. *CSH Protoc* 2006:pdb.prot4455.

4. 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>.
5. Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563. <https://doi.org/10.1038/nmeth.2474>.
6. Palmer J. 2016. Funannotate: pipeline for genome annotation. <https://zenodo.org/record/1471785#.XFO5kvlKi1t>.
7. Waterhouse RM, Seppey M, Simão FA, Manni M, Ioannidis P, Klioutchnikov G, Kriventseva EV, Zdobnov EM. 2018. BUSCO applications from quality assessments to gene prediction and phylogenomics. *Mol Biol Evol* 35: 543–548. <https://doi.org/10.1093/molbev/msx319>.
8. Chernomor O, von Haeseler A, Minh BQ. 2016. Terrace aware data structure for phylogenomic inference from supermatrices. *Syst Biol* 65: 997–1008. <https://doi.org/10.1093/sysbio/syw037>.