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Draft Genome Sequence of the *Starmerella bacillaris* (syn., *Candida zemplinina*) Type Strain CBS 9494

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ABSTRACT *Starmerella bacillaris* is an ascomycetous yeast ubiquitously present in grapes and fermenting grape musts. In this report, we present the draft genome sequence of the *S. bacillaris* type strain CBS 9494, isolated from sweet botrytized wines, which will contribute to the study of this genetically heterogeneous wine yeast species.

Starmerella bacillaris (syn., *Candida zemplinina*) (1) is a non-*Saccharomyces* yeast ubiquitously present in oenological environments (2–7) and occasionally recognized in soil, fruit insects, and some rotten fruits (5, 8, 9). The species, first recognized in Napa Valley (USA) in *Botrytis*-affected wine fermentations (10), was then identified through a detailed morphological, physiological, and molecular characterization of the *S. bacillaris* type strain 10-372 (=CBS 9494^T=NCAIM Y016667^T), isolated from white wine in Zemplin, Hungary (11). The potential use of *S. bacillaris* in winemaking has been studied in mixed fermentations with *Saccharomyces cerevisiae*, where its fructophilic character and ability to produce wines with reduced ethanol levels represent potential advantages (12–19). Sensory evaluation revealed that pure starters of *S. cerevisiae* were preferred to mixed *S. cerevisiae*/*S. bacillaris* fermentations (20). Phylogenetic analyses of *S. bacillaris* strains isolated from winemaking environments showed that neither clonal-like behavior nor specific genetic signatures were associated with strain populations at the different analyzed vineyards and wineries (21). These studies suggest that *S. bacillaris* is not under selective pressure in winemaking environments since its genetic diversity is shaped by geographical localization (21). The availability of the genome sequence of the *S. bacillaris* type strain CBS 9494 reported here, as well as additional specific molecular tools for population analyses (5, 15, 21–23), will contribute to the knowledge of the genetic and geographic diversity of this species as well as its life cycle (21).

In this study, total DNA from *S. bacillaris* type strain CBS 9494 was prepared using a genomic DNA buffer set and Genomic-tip 100/G kits (Qiagen). Genomic DNA (1 μg) was enzymatically fragmented (10 min) and size selected (315 bp) using the Pippin Prep instrument (Sage Science); a genomic library was generated with the Ion Xpress Plus fragment library kit (ThermoFisher Scientific). The genome sequence (122-fold genome coverage), obtained on the Ion Torrent PGM platform (Life Technologies), was trimmed based on a Phred-type quality threshold score of Q20 (QPhred = 20) and a length threshold of 50 bp using CLC Genomics Workbench version 7.0.3 (CLC bio). A total of

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5,698,579 reads (mean size of 200 bp) were used for *de novo* assembly with Newbler version 2.7 (454 Life Sciences), which resulted in 200 contigs longer than 200 bp (mean, 108,648 bp; maximum, 649,352 bp; N_{50} , 175,910 bp). The genome of *S. bacillaris* type strain 9494 was 9.3 Mb with a G+C content of 39.4%, similar to the recently available genome data for *S. bacillaris* strains FRI751 (24) and PAS13 (25). The *S. bacillaris* type strain CBS 9494 genome sequence reported here will constitute a reference sequence for studying evolutionary and phylogenetic aspects, as well as the geographic biodiversity, of this genetically heterogeneous species (21).

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [QLKO00000000](https://doi.org/10.1007/s10482-012-9762-7). The version described in this paper is the first version, QLKO01000000.

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REFERENCES

- Duarte FL, Pimentel NH, Teixeira A, Fonseca Á. 2012. *Saccharomyces bacillaris* is not a synonym of *Candida stellata*: reinstatement as *Starmerella bacillaris* comb. nov. *Antonie Van Leeuwenhoek* 102:653–658. <https://doi.org/10.1007/s10482-012-9762-7>.
- Nisiotou AA, Nychas G-JE. 2007. Yeast populations residing on healthy or *Botrytis*-infected grapes from a vineyard in Attica, Greece. *Appl Environ Microbiol* 73:2765–2768. <https://doi.org/10.1128/AEM.01864-06>.
- Zott K, Claisse O, Lucas P, Coulon J, Lonvaud-Funel A, Masneuf-Pomarede I. 2010. Characterization of the yeast ecosystem in grape must and wine using real-time PCR. *Food Microbiol* 27:559–567. <https://doi.org/10.1016/j.fm.2010.01.006>.
- Tristezza M, Vetrano C, Bleve G, Spano G, Capozzi V, Logrieco A, Mita G, Grieco F. 2013. Biodiversity and safety aspects of yeast strains characterized from vineyards and spontaneous fermentations in the Apulia Region, Italy. *Food Microbiol* 36:335–342. <https://doi.org/10.1016/j.fm.2013.07.001>.
- Pfiegler WP, Horváth E, Kállai Z, Sipiczki M. 2014. Diversity of *Candida zemplinina* isolates inferred from RAPD, micro/minisatellite and physiological analysis. *Microbiol Res* 169:402–410. <https://doi.org/10.1016/j.micres.2013.09.006>.
- Sun Y, Guo J, Liu F, Liu Y. 2014. Identification of indigenous yeast flora isolated from the five winegrape varieties harvested in Xiangning, China. *Antonie Van Leeuwenhoek* 105:533–540. <https://doi.org/10.1007/s10482-013-0105-0>.
- Raymond Eder ML, Reynoso C, Lauret SC, Rosa AL. 2017. Isolation and identification of the indigenous yeast population during spontaneous fermentation of Isabella (*Vitis labrusca* L.) grape must. *Front Microbiol* 8:532. <https://doi.org/10.3389/fmicb.2017.00532>.
- Csoma H, Sipiczki M. 2008. Taxonomic reclassification of *Candida stellata* strains reveals frequent occurrence of *Candida zemplinina* in wine fermentation. *FEMS Yeast Res* 8:328–336. <https://doi.org/10.1111/j.1567-1364.2007.00339.x>.
- Stamps JA, Yang LH, Morales VM, Boundy-Mills KL. 2012. *Drosophila* regulate yeast density and increase yeast community similarity in a natural substrate. *PLoS One* 7:e42238. <https://doi.org/10.1371/journal.pone.0042238>.
- Mills DA, Johannsen EA, Cocolin L. 2002. Yeast diversity and persistence in *Botrytis*-affected wine fermentations. *Appl Environ Microbiol* 68:4884–4893. <https://doi.org/10.1128/AEM.68.10.4884-4893.2002>.
- Sipiczki M. 2003. *Candida zemplinina* sp. nov., an osmotolerant and psychrotolerant yeast that ferments sweet botrytized wines. *Int J Syst Evol Microbiol* 53:2079–2083. <https://doi.org/10.1099/ijs.0.02649-0>.
- Andorrà I, Landi S, Mas A, Esteve-Zarzo B, Guillamón JM. 2010. Effect of fermentation temperature on microbial population evolution using culture-independent and dependent techniques. *Food Res Int* 43:773–779. <https://doi.org/10.1016/j.foodres.2009.11.014>.
- Comitini F, Gobbi M, Domizio P, Romani C, Lencioni L, Mannazzu I, Ciani M. 2011. Selected non-*Saccharomyces* wine yeasts in controlled multi-starter fermentations with *Saccharomyces cerevisiae*. *Food Microbiol* 28:873–882. <https://doi.org/10.1016/j.fm.2010.12.001>.
- Magyar I, Tóth T. 2011. Comparative evaluation of some oenological properties in wine strains of *Candida stellata*, *Candida zemplinina*, *Saccharomyces uvarum* and *Saccharomyces cerevisiae*. *Food Microbiol* 28:94–100. <https://doi.org/10.1016/j.fm.2010.08.011>.
- Di Maio S, Genna G, Gandolfo V, Amore G, Ciaccio M, Oliva D. 2012. Presence of *Candida zemplinina* in Sicilian musts and selection of a strain for wine mixed fermentations. *S Afr J Enol Vitic* 33:80–87. <https://doi.org/10.21548/33-1-1309>.
- Sadoudi M, Tourdot-Maréchal R, Rousseaux S, Steyer D, Gallardo-Chacón J-J, Ballester J, Vichi S, Guérin-Schneider R, Caixach J, Alexandre H. 2012. Yeast–yeast interactions revealed by aromatic profile analysis of Sauvignon blanc wine fermented by single or co-culture of non-*Saccharomyces* and *Saccharomyces* yeasts. *Food Microbiol* 32:243–253. <https://doi.org/10.1016/j.fm.2012.06.006>.
- Giaramida P, Ponticello G, Di Maio S, Squadrito M, Genna G, Barone E, Scacco A, Corona O, Amore G, di Stefano R, Oliva D. 2013. *Candida zemplinina* for production of wines with less alcohol and more glycerol. *S Afr J Enol Vitic* 34:204–211. <https://doi.org/10.21548/34-2-1095>.
- Rantsiou K, Englezos V, Torchio F, Risse P-A, Cravero F, Gerbi V, Rolle L, Cocolin L. 2017. Modeling the fermentation behavior of *Starmerella bacillaris*. *Am J Enol Vitic* 68:378–385. <https://doi.org/10.5344/ajev.2017.16108>.
- Englezos V, Cocolin L, Rantsiou K, Ortiz-Julien A, Bloem A, Dequin S, Camarasa C. 1 June 2018. Specific phenotypic traits of *Starmerella bacillaris* regarding nitrogen source consumption and central carbon metabolites production during wine fermentation. *Appl Environ Microbiol*. <https://doi.org/10.1128/AEM.00797-18>.
- Bely M, Renault P, da Silva T, Masneuf-Pomarede I, Albertin W, Moine V, Coulon J, Sicard D, de Vienne D, Marullo P. 2013. Non-conventional yeasts and alcohol level reduction, p 33–37. *In Proceedings of the International Symposium on Alcohol Level Reduction in Wine*. Vigne et Vin Publications Internationales, Bordeaux, France.
- Masneuf-Pomarede I, Juquin E, Miot-Sertier C, Renault P, Laizet Y, Salin F, Alexandre H, Capozzi V, Cocolin L, Colonna-Ceccaldi B, Englezos V, Girard P, Gonzalez B, Lucas P, Mas A, Nisiotou A, Sipiczki M, Spano G, Tassou C, Bely M, Albertin W. 2015. The yeast *Starmerella bacillaris* (synonym *Candida zemplinina*) shows high genetic diversity in winemaking environments. *FEMS Yeast Res* 15:fov045. <https://doi.org/10.1093/femsyr/fov045>.
- Tofalo R, Schirone M, Torriani S, Rantsiou K, Cocolin L, Perpetuini G, Suzzi G. 2012. Diversity of *Candida zemplinina* strains from grapes

- and Italian wines. *Food Microbiol* 29:18–26. <https://doi.org/10.1016/j.fm.2011.08.014>.
23. Englezos V, Rantsiou K, Torchio F, Rolle L, Gerbi V, Cocolin L. 2015. Exploitation of the non-*Saccharomyces* yeast *Starmerella bacillaris* (synonym *Candida zemplinina*) in wine fermentation: physiological and molecular characterizations. *Int J Food Microbiol* 199:33–40. <https://doi.org/10.1016/j.ijfoodmicro.2015.01.009>.
24. Lemos Junior WJF, Treu L, da Silva Duarte V, Campanaro S, Nadai C, Giacomini A, Corich V. 2017. Draft genome sequence of the yeast *Starmerella bacillaris* (syn., *Candida zemplinina*) FRI751 isolated from fermenting must of dried Raboso grapes. *Genome Announc* 5(17):e00224-17. <https://doi.org/10.1128/genomeA.00224-17>.
25. Lemos Junior WJF, Treu L, da Silva Duarte V, Carlot M, Nadai C, Campanaro S, Giacomini A, Corich V. 2017. Whole-genome sequence of *Starmerella bacillaris* PAS13, a nonconventional enological yeast with antifungal activity. *Genome Announc* 5(32):e00788-17. <https://doi.org/10.1128/genomeA.00788-17>.



Correction for Rosa et al., “Draft Genome Sequence of the *Candida zemplinina* (syn., *Starmerella bacillaris*) Type Strain CBS 9494”

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Volume 7, no. 3, e00872-18, 2018, <https://doi.org/10.1128/MRA.00872-18>. Page 1: The article title should read as given above.

Page 1, line 1: “*Starmerella bacillaris* (syn., *Candida zemplinina*)” should read “*Candida zemplinina* (syn., *Starmerella bacillaris*).”

Pages 1 and 2: “*S. bacillaris*” should read “*C. zemplinina*” throughout.

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