



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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