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Draft Genome Sequence of the *Saccharomyces cerevisiae* × *Saccharomyces kudriavzevii* HA1836 Interspecies Hybrid Yeast

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ABSTRACT *Saccharomyces cerevisiae* × *Saccharomyces kudriavzevii* interspecies hybrid yeasts have frequently been isolated from alcoholic fermentation environments. Here, we report the draft genome sequence of the *S. cerevisiae* × *S. kudriavzevii* HA1836 strain isolated from grapes from an Austrian vineyard.

Saccharomyces cerevisiae × *Saccharomyces kudriavzevii* hybrids have been identified in environments associated with brewing, wine making, and cider production (1, 2). These hybrids acquired beneficial fermenting properties from the *S. cerevisiae* species and cryotolerance from the *S. kudriavzevii* species (3). The *S. cerevisiae* × *S. kudriavzevii* hybrids have been isolated primarily from cold fermentations, which are characteristic of European regions with cooler continental and oceanic climates (i.e., Austria, Germany, Switzerland, France, and northern Spain). The hybrid strains studied so far differ in the complexity of their genome structures, the proportion of hybridizing yeasts, and their fermentation performances (3–6). Natural, commercial, and artificially constructed hybrid yeasts have shown that the genomic moiety of *S. kudriavzevii* is more unstable than that of *S. cerevisiae* and prone to substantial reduction after a hybridization event (3, 6, 7). *S. cerevisiae* × *S. kudriavzevii* hybrids may have strong advantages over their parental strains due to better adaptation to cold fermentation conditions, better production of esters, higher alcohols and glycerol, and an increased fructose/glucose fermentation rate (4, 5, 8, 9).

During a study of the yeast biodiversity of Austrian vineyards, several strains were isolated from grapes that were shown to have a *S. cerevisiae* × *S. kudriavzevii* hybrid genome by different genetic and molecular markers (7, 10). In order to explore differences in the genome constitutions and gene regulations among the *S. cerevisiae* × *S. kudriavzevii* yeasts, we generated the whole-genome sequence of the HA1836 strain. Genome sequencing was carried out using Ion Torrent technology (Ion PGM Hi-Q View kit; Life Technologies, Inc., Carlsbad, CA, USA) according to the manufacturer's protocols. A total of 1.62 Gb of read data, with a median read length of 315 bp, was produced and assembled with Newbler version 2.9 into a 22.28-Mb genome (~70× coverage) containing 979 contigs (N_{50}, 60,823 bp). Comparative analysis of the genome sequences of the HA1836 and VIN7 (11) strains showed a coverage of 19.51 Mb (87.5%).

Accession number(s). The whole-genome shotgun project reported here has been deposited at DDBJ/EMBL/GenBank under the accession number PQXS00000000. The version described in this paper is the first version, PQXS01000000.

ACKNOWLEDGMENTS

We thank H. Gangl for providing the HA1836 strain. The equipment of the VIBT-Extremophile Center used in this study was financed by BOKU-Equipment GesmbH. The computational results presented have been achieved in part using the Vienna Scientific Cluster (VSC).

Received 20 March 2018 **Accepted** 24 March 2018 **Published** 17 May 2018

Citation Lopandic K, Tafer H, Sterflinger K. 2018. Draft genome sequence of the *Saccharomyces cerevisiae* × *Saccharomyces kudriavzevii* HA1836 interspecies hybrid yeast. Genome Announc 6:e00343-18. https://doi.org/10.1128/genomeA.00343-18.

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