Genome sequence of the food spoilage Yeast
Zygosaccharomyces bailii CLIB 213T.
Virginie Galeote, Frédéric Bigey, Hugo Devillers, Cécile Neuvéglise, Sylvie Dequin

To cite this version:
Virginie Galeote, Frédéric Bigey, Hugo Devillers, Cécile Neuvéglise, Sylvie Dequin. Genome sequence of the food spoilage Yeast Zygosaccharomyces bailii CLIB 213T.. Genome Announcements, American Society for Microbiology, 2013, 1 (4), 10.1128/genomeA.00606-13. hal-01837764

HAL Id: hal-01837764
https://hal.archives-ouvertes.fr/hal-01837764
Submitted on 29 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.
The ascomycetous yeast *Zygosaccharomyces bailii* is one of the most problematic spoilage yeasts in food and beverage industries, due to its exceptional resistance to various stresses. A better understanding of the molecular mechanisms underlying these stress resistance phenotypes might help develop strategies to improve food quality. Thus, we determined and annotated the genome sequence of the strain *Z. bailii* CLIB 213T (= CBS 680).

The genus *Zygosaccharomyces* belongs to the hemiascomycetous yeast phylum and includes six previously described species (*Zygosaccharomyces bailii*, *Zygosaccharomyces bisporus*, *Zygosaccharomyces kombuchaensis*, *Zygosaccharomyces lentus*, *Zygosaccharomyces mellsii*, and *Zygosaccharomyces rouxii*) (1) and six recently proposed novel species (2–6). *Z. bailii* is widespread in food spoilage because of its unusual physiological characteristics, such as resistance to weak-acid preservatives and the ability to adapt to high sugar concentrations and high temperatures, vigorously ferment sugar, and grow at low pH (7–9). Great phenotypic diversity has been observed among *Z. bailii* strains (10). In wine fermentation, although this species is generally considered to have detrimental effects, potentially beneficial aspects have also been proposed (10, 11). More recently, the potential of *Z. bailii* for the production of bioethanol has also been reported (12).

While *Z. bailii* is frequently encountered in wines, it has been shown to be the donor of a 17-kb DNA region to *Saccharomyces cerevisiae*. This transferred region was first discovered in the genome of the commercial wine yeast strain *S. cerevisiae* EC1118 and thereafter was widely found in other *S. cerevisiae* wine yeast genomes, in multiple copies and showing different structures and organization (13, 14). Such eukaryote-to-eukaryote gene transfer is remarkable, given the phylogenetic distance between these two species and the large amount of DNA transferred. The *Zygosaccharomyces* genus has been poorly investigated, and so only the *Z. rouxii* genome sequence is available. Sequencing the genome of *Z. bailii* strain CLIB 213T may therefore give clues to better control and exploit this species in the context of food quality improvement and biotechnological applications.

The draft genome was sequenced by using the Illumina HiSeq2000 platform (2 × 100-bp, sequencing depth, 250×), with a total of 50,868,918 reads hard-clipped to 75 bp and processed using SOAPdenovo v1.05 (15) using a k-mer size of 51. A high-contiguity assembly was obtained of 212 contigs with an N₅₀ contig length of 226,975 bp, further assembled into 56 scaffolds for a total size of 10,361,356 bp (N₅₀ scaffold length of 932,251 bp). Twenty-seven scaffolds of >10 kb (cumulative size of 10,268,813 bp with a 42.5% G+C content) were suitable for automatic annotation. A total of 5,084 putative protein-coding genes, including 217 pseudogenes, were predicted using Amadea BioPack (ISoft, France) and were further curated manually. BLASTp comparison revealed that 98.2% of these genes have a homolog in *Z. rouxii*, only 8 are species-specific genes, and 5 were acquired by interkingdom lateral transfer. A total of 162 tRNAs were identified using tRNAscan-SE v1.3.1 (16).

The 17-kb gene cluster transferred to *S. cerevisiae* was found in a single copy in *Z. bailii*, suggesting that the amplification is specific to *S. cerevisiae*. Genes encoding key enzymes for glucose and fructose assimilation were identified. The FFS1 gene, encoding a low-affinity facilitator protein specific for fructose, previously identified in *Z. bailii* strain ISA1307 (17), was found on scaffold 5. We also identified a gene encoding a protein that is highly similar (77% identity) to EC1118 Fsy1p, a high-affinity fructose/H⁺ symporter (18). Three other genes showed a high similarity with *S. cerevisiae* Hxtp glucose transporters. The large number of genes that potentially encode sugar transporters with different characteristics might explain the high fermentative performance of *Z. bailii*.

**Nucleotide sequence accession numbers.** The sequence of the *Z. bailii* genome has been deposited at EMBL under the accession no. HG316454 to HG316480 (as 27 scaffolds).

**ACKNOWLEDGMENTS**

The development of the annotation transfer tool based on Amadea BioPack was financially supported by the ANR project GB-3G (2010 BLAN 1606).

We thank Jean-Luc Legras for his helpful advice and discussions.
REFERENCES

1. James S, Stratford M. 2011. Zygosaccharomyces Barker 1901, p 937–947. In Kurtzman CP, Fell JW, Boekhout T (ed), The yeasts: a taxonomic study, vol 1. Elsevier, London, United Kingdom.

2. Rosa CA, Lachance M-A. 2005. Zygosaccharomyces machadoi sp. n., a yeast species isolated from a nest of the stingless bee Tetragonisca angustula. Lundiana 6:27–29.

3. Saksinchai S, Suzuki M, Chantawannakul P, Ohkuma M, Lumyong S. 2012. A novel ascosporogenous yeast species, Zygosaccharomyces siamensis, and the sugar tolerant yeasts associated with raw honey collected in Thailand. Fungal Divers. 52:123–139.

4. Torriani S, Lorenzini M, Salvetti E, Felis GE. 2011. Zygosaccharomyces gambellarensis sp. nov., an ascosporogenous yeast isolated from an Italian “passito” style wine. Int. J. Syst. Evol. Microbiol. 61:3084–3088.

5. Solieri L, Cassanelli S, Croce MA, Giudici P. 2008. Genome size and ploidy level: new insights for elucidating relationships in Zygosaccharomyces species. Fungal Genet. Biol. 45:1582–1590.

6. Suh SO, Gujjari P, Beres C, Beck B, Zhou J. 2013. Proposal of Zygosaccharomyces parabailii sp. nov. and Zygosaccharomyces pseudobailii sp. nov., two new species closely related to Zygosaccharomyces bailii. Int. J. Syst. Evol. Microbiol. 63:1922–1929.

7. Guerreiro JF, Mira NP, Sá-Correia I. 2012. Adaptive response to acetic acid in the highly resistant yeast species Zygosaccharomyces bailii revealed by quantitative proteomics. Proteomics 12:2303–2318.

8. Kurtzman CP. 1998. Zygosaccharomyces Barker, p 424–432. In Kurtzman CP, Fell JW (ed), The yeasts, a taxonomic study. Elsevier, Amsterdam, The Netherlands.

9. Martorell P, Stratford M, Steels H, Fernández-Espinar MT, Querol A. 2007. Physiological characterization of spoilage strains of Zygosaccharomyces bailii and Zygosaccharomyces rouxii isolated from high sugar environments. Int. J. Food Microbiol. 114:234–242.

10. Domizio P, Romani C, Lencioni L, Comitini F, Gobbi M, Mannazzu I, Ciani M. 2011. Outlining a future for non-Saccharomyces yeasts: selection of putative spoilage wine strains to be used in association with Saccharomyces cerevisiae for grape juice fermentation. Int. J. Food Microbiol. 147:170–180.

11. Romano P, Fiore C, Paraggio M, Caruso M, Capece A. 2003. Function of yeast species and strains in wine flavour. Int. J. Food Microbiol. 86:169–180.

12. Paixão SM, Teixeira PD, Silva TP, Teixeira AV, Alves L. Screening of novel yeast inulinases and further application to bioprocesses. New Biotechnol., in press.

13. Galeote V, Bigey F, Beyne E, Novo M, Legras JL, Casaregola S, Dequin S. 2011. Amplification of a Zygosaccharomyces bailii DNA segment in wine yeast genomes by extrachromosomal circular DNA formation. PLOS One 6:e17872. doi:10.1371/journal.pone.0017872.

14. Novo M, Bigey F, Beyne E, Galeote V, Gavory F, Mallet S, Cambon B, Legras JL, Wincker P, Casaregola S, Dequin S. 2009. Eukaryote-to-eukaryote gene transfer events revealed by the genome sequence of the wine yeast Saccharomyces cerevisiae EC1118. Proc. Natl. Acad. Sci. U. S. A. 106:16333–16338.

15. Li R, Zhu H, Ruan J, Qian W, Fang X, Shi Z, Li Y, Li S, Shan G, Kristiansen K, Li S, Yang H, Wang J, Wang J. 2010. De novo assembly of human genomes with massively parallel short read sequencing. Genome Res. 20:265–272.

16. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25:955–964.

17. Pina C, Goncalves P, Prista C, Loureiro-Dias MC. 2004. Ffz1, a new transporter specific for fructose from Zygosaccharomyces bailii. Microbiology 150:2429–2433.

18. Galeote V, Novo M, Salena-Oom M, Brion C, Valério E, Gonçalves P, Dequin S. 2010. FSY1, a horizontally transferred gene in the Saccharomyces cerevisiae EC1118 wine yeast strain, encodes a high-affinity fructose/H+ symporter. Microbiology 156:3754–3761.