

GEPHE SUMMARY

	Gephebase Gene	GephelD
SWS2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="SWS2">#gephebase-summary-title)	GP00001088	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology">#gephebase-summary-title)	
Xenobiotic resistance (alcohol, ethanol) (https://www.gephebase.org/search-criteria?/and+Trait -^Xenobiotic resistance (alcohol, ethanol)^#gephebase-summary-title)	Trait
Saccharomyces cerevisiae - industrial strain	Trait State in Taxon A
Saccharomyces cerevisiae - laboratory strains	Trait State in Taxon B
Data not curated	Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Domesticated">#gephebase-summary-title)	Taxonomic Status

Taxon A		Taxon B	
	Latin Name		Latin Name
Saccharomyces cerevisiae (#gephebase-summary-title)		Saccharomyces cerevisiae (#gephebase-summary-title)	
baker's yeast	Common Name	baker's yeast	Common Name
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Synonyms	Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Saccharomyces cerevisiae - industrial strain	Taxon A Description	Saccharomyces cerevisiae - laboratory strains	Taxon B Description

GENOTYPIC CHANGE

SWS2	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P53937 (http://www.uniprot.org/uniprot/P53937)
YNL081C; N2322	Synonyms	GenebankID or UniProtKB Z71357 (https://www.ncbi.nlm.nih.gov/nuccore/Z71357)
4932.YNL081C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YNL081C)	String	
Belongs to the universal ribosomal protein uS13 family.	Sequence Similarities	
GO:0003723 : RNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003723) GO:0003735 : structural constituent of ribosome (https://www.ebi.ac.uk/QuickGO/term/GO:0003735)	GO - Molecular Function	
		GO - Biological Process

GO:0032543 : mitochondrial translation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032543>)

GO - Cellular Component

GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)

GO:0005763 : mitochondrial small ribosomal subunit

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005763>)

GO:0015935 : small ribosomal subunit

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015935>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown^#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Cis-regulatory^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

unknown

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title>)

Main Reference

Identification of novel causative genes determining the complex trait of high ethanol tolerance in yeast using pooled-segregant whole-genome sequence analysis. (2012)
(<https://pubmed.ncbi.nlm.nih.gov/22399573>)

Authors

Swinnen S; Schaelaekens K; Pais T; Claesen J; Hubmann G; Yang Y; Demeke M; FoulquiÃ©-Moreno MR; Goovaerts A; Souvereyns K; Clement L; Dumortier F; Thevelein JM

Abstract

High ethanol tolerance is an exquisite characteristic of the yeast *Saccharomyces cerevisiae*, which enables this microorganism to dominate in natural and industrial fermentations. Up to now, ethanol tolerance has only been analyzed in laboratory yeast strains with moderate ethanol tolerance. The genetic basis of the much higher ethanol tolerance in natural and industrial yeast strains is unknown. We have applied pooled-segregant whole-genome sequence analysis to map all quantitative trait loci (QTL) determining high ethanol tolerance. We crossed a highly ethanol-tolerant segregant of a Brazilian bioethanol production strain with a laboratory strain with moderate ethanol tolerance. Out of 5974 segregants, we pooled 136 segregants tolerant to at least 16% ethanol and 31 segregants tolerant to at least 17%. Scoring of SNPs using whole-genome sequence analysis of DNA from the two pools and parents revealed three major loci and additional minor loci. The latter were more pronounced or only present in the 17% pool compared to the 16% pool. In the locus with the strongest linkage, we identified three closely located genes affecting ethanol tolerance: *MKT1*, *SWS2*, and *APJ1*, with *SWS2* being a negative allele located in between two positive alleles. *SWS2* and *APJ1* probably contained significant polymorphisms only outside the ORF, and lower expression of *APJ1* may be linked to higher ethanol tolerance. This work has identified the first causative genes involved in high ethanol tolerance of yeast. It also reveals the strong potential of pooled-segregant sequence analysis using relatively small numbers of selected segregants for identifying QTL on a genome-wide scale.

Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) (<https://www.gephebase.org/search-criteria?/or+TaxonID=^4932^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^SWS2^/and+Taxon+ID=^4932^/or+Gene+Gephebase=^SWS2^/and+Taxon+ID=^4932^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS