

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

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait Category	
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	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	
baker's yeast		baker's yeast	
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; Saccharomyes cerevisiae; Sccharomyces cerevisiae		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; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (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 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Saccharomyces cerevisiae - industrial strain		Saccharomyces cerevisiae - laboratory strains	

SWS2	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / <i>S288c</i>) P53937 (http://www.uniprot.org/uniprot/P53937)
YNL081C; N2322	Synonyms	GenebankID or UniProtKB Z71357 (https://www.ncbi.nlm.nih.gov/nucore/Z71357)
4932.YNL081C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YNL081C)	String	
Sequence Similarities		
Belongs to the universal ribosomal protein uS13 family.		
GO - Molecular Function		
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 - 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>)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	Experimental Evidence
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)	Main Reference
Swinnen S; Schaerlaekens K; Pais T; Claesen J; Hubmann G; Yang Y; Demekle M; Foulqui��-Moreno MR; Goovaerts A; Souvereys K; Clement L; Dumortier F; Thevelein JM	Authors

High ethanol tolerance is an exquisite characteristic of the yeast <i>Saccharomyces cerevisiae</i> , 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.	Abstract
	Additional References

RELATED GEPHE

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

EXTERNAL LINKS

COMMENTS