

GEPHE SUMMARY

APJ1 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^APJ1^#gephebase-summary-title)	Gephebase Gene	GP00000097	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

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	Latin Name	Taxon B	Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Common Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Common Name
baker's yeast	Synonyms	baker's yeast	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	Rank	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	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	NCBI Taxonomy ID	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	is Taxon A an Infraspecies?	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	is Taxon B an Infraspecies?
Yes	Taxon A Description	Yes	Taxon B Description
Saccharomyces cerevisiae - industrial strain		Saccharomyces cerevisiae - laboratory strains	

GENOTYPIC CHANGE

APJ1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P53940 (http://www.uniprot.org/uniprot/P53940)
YNL077W; N2342	Synonyms	GenebankID or UniProtKB Z71353 (https://www.ncbi.nlm.nih.gov/nuccore/Z71353)
4932.YNL077W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YNL077W)	String	
-	Sequence Similarities	
	GO - Molecular Function	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		
GO:0001671 : ATPase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0001671)		
GO:0031072 : heat shock protein binding		

(https://www.ebi.ac.uk/QuickGO/term/GO:0031072)	
GO:0051082 : unfolded protein binding	
(https://www.ebi.ac.uk/QuickGO/term/GO:0051082)	
GO - Biological Process	
GO:0006457 : protein folding (https://www.ebi.ac.uk/QuickGO/term/GO:0006457)	
GO:0016925 : protein sumoylation (https://www.ebi.ac.uk/QuickGO/term/GO:0016925)	
GO - Cellular Component	
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)	
GO:0034399 : nuclear periphery (https://www.ebi.ac.uk/QuickGO/term/GO:0034399)	
	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 <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: <i>MKT1</i> , <i>SWS2</i> , and <i>APJ1</i> , with <i>SWS2</i> being a negative allele located in between two positive alleles. <i>SWS2</i> and <i>APJ1</i> probably contained significant polymorphisms only outside the ORF, and lower expression of <i>APJ1</i> 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

15 (ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS