

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (alcohol, ethanol) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (alcohol, ethanol)^#gephebase-summary-title)			
	Trait State in Taxon A		
Saccharomyces cerevisiae - industrial strain			
	Trait State in Taxon B		
Saccharomyces cerevisiae - laboratory strains			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
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)	
	Common Name		Common Name
baker’s yeast		baker’s yeast	
	Synonyms		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; 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	
	Rank		Rank
species		species	
	Lineage		Lineage
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	
	Parent		Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		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	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
APJ1		P53940 (http://www.uniprot.org/uniprot/P53940)	
	Synonyms		GenebankID or UniProtKB
YNL077W; N2342		Z71353 (https://www.ncbi.nlm.nih.gov/nuccore/Z71353)	
	String		
4932.YNL077W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YNL077W)			
	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; Schaerlaekens K; Pais T; Claesen J; Hubmann G; Yang Y; Demeke M; Foulqui  -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 (ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, 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 Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS