

RAS2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~RAS2~#gephebase-summary-title)		Gephebase Gene	GP00000956	GepheID
Published		Entry Status	Martin	Main curator

Physiology (#gephebase-summary-title)		Trait Category	
Sporulation efficiency (#gephebase-summary-title)		Trait	
Saccharomyces cerevisiae - SK1 strain		Trait State in Taxon A	
Saccharomyces cerevisiae - S288c strain		Trait State in Taxon B	
Taxon A		Ancestral State	
Domesticated (#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (#gephebase-summary-title)		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=4930)		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)		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 - SK1 strain		Saccharomyces cerevisiae - S288c strain	

RAS2 CTN5; CYR3; GLC5; TSL7; ASC1; YNL098C; N2198 4932.YNL098C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YNL098C) Belongs to the small GTPase superfamily. Ras family. GO - Molecular Function GO:0005525 : GTP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005525) GO:0003924 : GTPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003924) GO - Biological Process GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)	Generic Gene Name Synonyms String Sequence Similarities GO - Molecular Function GO - Biological Process	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / <i>S288c</i>) P01120 (http://www.uniprot.org/uniprot/P01120) GenebankID or UniProtKB Z71374 (https://www.ncbi.nlm.nih.gov/nucleotide/Z71374)
--	---	---

GO:0032880 : regulation of protein localization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032880>)
GO:0016236 : macroautophagy (<https://www.ebi.ac.uk/QuickGO/term/GO:0016236>)
GO:0007190 : activation of adenylate cyclase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007190>)
GO:0030437 : ascospore formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030437>)
GO:0045762 : positive regulation of adenylate cyclase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045762>)
GO:2000222 : positive regulation of pseudohyphal growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000222>)
GO:0000411 : positive regulation of transcription by galactose
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000411>)
GO:0032258 : protein localization by the Cvt pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032258>)
GO:0097271 : protein localization to bud neck
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097271>)
GO:0010603 : regulation of cytoplasmic mRNA processing body assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010603>)
GO:0001302 : replicative cell aging (<https://www.ebi.ac.uk/QuickGO/term/GO:0001302>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

1bp insertion in promoter

Experimental Evidence

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

Main Reference

Four linked genes participate in controlling sporulation efficiency in budding yeast. (2006) (<https://pubmed.ncbi.nlm.nih.gov/17112318>)

Authors

Ben-Ari G; Zenvirth D; Sherman A; David L; Klutstein M; Lavi U; Hillel J; Simchen G

Abstract

Quantitative traits are conditioned by several genetic determinants. Since such genes influence many important complex traits in various organisms, the identification of quantitative trait loci (QTLs) is of major interest, but still encounters serious difficulties. We detected four linked genes within one QTL, which participate in controlling sporulation efficiency in *Saccharomyces cerevisiae*. Following the identification of single nucleotide polymorphisms by comparing the sequences of 145 genes between the parental strains SK1 and S288c, we analyzed the segregating progeny of the cross between them. Through reciprocal hemizygosy analysis, four genes, *RAS2*, *PMS1*, *SWS2*, and *FKH2*, located in a region of 60 kilobases on Chromosome 14, were found to be associated with sporulation efficiency. Three of the four “high” sporulation alleles are derived from the “low” sporulating strain. Two of these sporulation-related genes were verified through allele replacements. For *RAS2*, the causative variation was suggested to be a single nucleotide difference in the upstream region of the gene. This quantitative trait nucleotide accounts for sporulation variability among a set of ten closely related winery yeast strains. Our results provide a detailed view of genetic complexity in one “QTL region” that controls a quantitative trait and reports a single nucleotide polymorphism-trait association in wild strains. Moreover, these findings have implications on QTL identification in higher eukaryotes.

Additional References

RELATED GEPHE

Related Genes

7 (IME1, RME1, RME1 [possible pseudo-replicate of laboratory strain entry], RSF1, SWS2, TAO3, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Sporulation efficiency/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

2 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~RAS2~/and+Taxon ID=~4932~/or+Gene Gephebase=~RAS2~/and+Taxon ID=~4932~#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

