

GEPHE SUMMARY

<p>SWS2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~SWS2~#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001089</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
--	---	---------------------------------	------------------------------------

PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)</p> <p>Sporulation efficiency (https://www.gephebase.org/search-criteria?/and+Trait=~Sporulation+efficiency~#gephebase-summary-title)</p> <p>Saccharomyces cerevisiae - SK1 strain</p> <p>Saccharomyces cerevisiae - S288c strain</p> <p>Data not curated</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Saccharomyces cerevisiae</p> <p>baker's yeast</p> <p>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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces</p> <p>Saccharomyces () - (Rank: genus)</p> <p>4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)</p> <p>Yes</p> <p>Saccharomyces cerevisiae - SK1 strain</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Infrappecies?</p> <p>Taxon A Description</p>	<p>Saccharomyces cerevisiae</p> <p>baker's yeast</p> <p>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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces</p> <p>Saccharomyces () - (Rank: genus)</p> <p>4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)</p> <p>Yes</p> <p>Saccharomyces cerevisiae - S288c strain</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Infrappecies?</p> <p>Taxon B Description</p>
---	---	---	--	---	--

GENOTYPIC CHANGE

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

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

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 hemizyosity 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, RAS2, RME1, RME1 [possible pseudo-replicate of laboratory strain entry], RSF1, TAO3, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4932^/and+Trait=Sporulation+efficiency/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