GEPHE SUMMARY

Gephebase Gene
SWS2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SWS2^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001089
Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Sporulation efficiency (https://www.gephebase.org/search-criteria?/and+Trait=^Sporulation efficiency^#gephebase-summary-title)
Trait State in Taxon A
Saccharomyces cerevisiae - SK1 strain
Trait State in Taxon B
Saccharomyces cerevisiae - S288c strain
Ancestral State
Data not curated
Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)
Common Name
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; Saccharomyes cerevisiae; Sccharomyces cerevisiae
Rank
species
Lineage
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
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
is Taxon A an Infraspecies?
Yes
Taxon A Description
Saccharomyces cerevisiae - SK1 strain

Taxon B

Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)
Common Name
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; Saccharomyes cerevisiae; Sccharomyces cerevisiae
Rank
species
Lineage
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
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
is Taxon B an Infraspecies?
Yes
Taxon B Description
Saccharomyces cerevisiae - S288c strain

GENOTYPIC CHANGE

Generic Gene Name
SWS2
Synonyms
YNL081C; N2322
String
4932.YNL081C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YNL081C)
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

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P53937 (http://www.uniprot.org/uniprot/P53937)
GenebankID or UniProtKB
Z71357 (https://www.ncbi.nlm.nih.gov/nuccore/Z71357)

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 hemizygosity 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