

RSF1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~RSF1^#gephebase-summary-title)	Gephebase Gene	GP00001016	GepheID
Published	Entry Status	Martin	Main curator

Physiology (#www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology)		Trait Category
Sporulation efficiency (#www.gephebase.org/search-criteria?/and+Trait=~Sporulation+efficiency)		Trait
Saccharomyces cerevisiae - oak strain		Trait State in Taxon A
Saccharomyces cerevisiae - vineyard strain		Trait State in Taxon B
Data not curated		Ancestral State
Intraspecific (#www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific)		Taxonomic Status
Taxon A	Taxon B	
Saccharomyces cerevisiae (#www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae)	Saccharomyces cerevisiae (#www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae)	Latin Name
baker's yeast	baker's yeast	Common Name
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	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	Synonyms
species	species	Rank
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	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	Parent
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)	NCBI Taxonomy ID
Yes	Yes	is Taxon A an Intraspecies?
Saccharomyces cerevisiae - oak strain	Saccharomyces cerevisiae - vineyard strain	Taxon A Description
		Taxon B Description

UniProtKB	Generic Gene Name	UniProtKB Arabidopsis thaliana
HFR1		Q9FE22 (http://www.uniprot.org/uniprot/Q9FE22)
	Synonyms	GenebankID or UniProtKB
FBI1; LONG HYPOCOTYL IN FAR-RED; REDUCED PHYTOCHROME SIGNALING 1; REDUCED SENSITIVITY TO FAR-RED LIGHT 1; REP1; RSF1; T6A9.4; T6A9_4; BHLH26; EN68; At1g02340; T6A9_13		KZV08876 (https://www.ncbi.nlm.nih.gov/nuccore/KZV08876)
	String	
3702.AT1G02340.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT1G02340.1)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0046983 : protein dimerization activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0046983>)
GO:0003700 : DNA-binding transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)
GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)
GO:0003712 : transcription coregulator activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003712>)

GO - Biological Process

GO:0009785 : blue light signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009785>)
GO:0009738 : abscisic acid-activated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009738>)
GO:0009585 : red, far-red light phototransduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009585>)
GO:0010218 : response to far red light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010218>)
GO:0009642 : response to light intensity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009642>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

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

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

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

Nonsynonymous

D181G

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Genetic interactions between transcription factors cause natural variation in yeast. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19164747>)

Gerke J; Lorenz K; Cohen B

Our understanding of the genetic basis of phenotypic diversity is limited by the paucity of examples in which multiple, interacting loci have been identified. We show that natural variation in the efficiency of sporulation, the program in yeast that initiates the sexual phase of the life cycle, between oak tree and vineyard strains is due to allelic variation between four nucleotide changes in three transcription factors: IME1, RME1, and RSF1. Furthermore, we identified that selection has shaped quantitative variation in yeast sporulation between strains. These results illustrate how genetic interactions between transcription factors are a major source of phenotypic diversity within species.

RELATED GEPHE

7 (IME1, RAS2, RME1, RME1 [possible pseudo-replicate of laboratory strain entry], SWS2, TAO3, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932^/and+Trait=Sporulation efficiency/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS

