

IME1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase%3D%27IME1%27#gephebase-summary-title)	Gephebase Gene	GP00000498	GepheID
Published	Entry Status	Martin	Main curator

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)			
Sporulation efficiency (https://www.gephebase.org/search-criteria?/and+Trait=^Sporulationefficiency^#gephebase-summary-title)	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 (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)	Taxonomic Status		
Taxon A		Taxon B	
Latin Name		Latin Name	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Saccharomycescerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Saccharomycescerevisiae^#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; 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	
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 Infrasppecies?		is Taxon B an Infrasppecies?	
No		Yes	
		Taxon B Description	
		Saccharomyces cerevisiae - vineyard strain	

IME1	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)
	Synonyms	P21190 (http://www.uniprot.org/uniprot/P21190)
YJR094C; J1916	String	X52152 (https://www.ncbi.nlm.nih.gov/nucore/X52152)
4932.YJR094C (http://string-db.org/newstring_cgj/show_network_section.pl?identifier=4932.YJR094C)	Sequence Similarities	
-	GO - Molecular Function	
GO:0008134 : transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008134)	GO - Biological Process	
GO:0045944 : positive regulation of transcription by RNA polymerase II		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006357 : regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006357>)
GO:0051321 : meiotic cell cycle (<https://www.ebi.ac.uk/QuickGO/term/GO:0051321>)
GO:0007124 : pseudohyphal growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0007124>)
GO:0040020 : regulation of meiotic nuclear division
(<https://www.ebi.ac.uk/QuickGO/term/GO:0040020>)
GO:0030435 : sporulation resulting in formation of a cellular spore
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030435>)

GO - Cellular Component

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

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L325M and/or 1bp synonymous substitution

Experimental Evidence

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

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

Main Reference

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

Authors

Gerke J; Lorenz K; Cohen B

Abstract

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.

Additional References

RELATED GEPHE

Related Genes

7 (RAS2, 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

No matches found.

EXTERNAL LINKS

COMMENTS