

GEPHE SUMMARY

	Gephebase Gene	GepheID
RME1 [possible pseudo-replicate of laboratory strain entry] (<a +rme1+[possible+pseudo-replicate+of+laboratory+strain+entry]"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+RME1+[possible+pseudo-replicate+of+laboratory+strain+entry]"#gephebase-summary-title)		Main curator
	Entry Status	
Published		

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology"#gephebase-summary-title)		Trait	
Sporulation efficiency (<a +sporulation+efficiency"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Sporulation+efficiency"#gephebase-summary-title)			
	Trait State in Taxon A		
Saccharomyces cerevisiae - oak strain		Trait State in Taxon B	
Saccharomyces cerevisiae - vineyard strain			
	Ancestral State		
Taxon A		Taxonomic Status	
Intraspecific (<a +intraspecific"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Saccharomyces cerevisiae (<a +saccharomyces+cerevisiae"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Saccharomyces+cerevisiae"#gephebase-summary-title)		Saccharomyces cerevisiae (<a +saccharomyces+cerevisiae"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Saccharomyces+cerevisiae"#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; 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	
	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 Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Saccharomyces cerevisiae - oak strain		Saccharomyces cerevisiae - vineyard strain	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
RME1		P32338 (http://www.uniprot.org/uniprot/P32338)
	Synonyms	GenebankID or UniProtKB
CSP1; YGR044C		M76447 (https://www.ncbi.nlm.nih.gov/nuccore/M76447)
	String	
4932.YGR044C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YGR044C)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)		

GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)

GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)

GO:0051301 : cell division (<https://www.ebi.ac.uk/QuickGO/term/GO:0051301>)

GO:0045835 : negative regulation of meiotic nuclear division
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045835>)

GO:0051038 : negative regulation of transcription involved in meiotic cell cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051038>)

GO:0036095 : positive regulation of invasive growth in response to glucose limitation by positive regulation of transcription from RNA polymerase II promoter
(<https://www.ebi.ac.uk/QuickGO/term/GO:0036095>)

GO:0071931 : positive regulation of transcription involved in G1/S transition of mitotic cell cycle (<https://www.ebi.ac.uk/QuickGO/term/GO:0071931>)

GO - Cellular Component

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)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	Molecular Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)	Aberration Type
1-9 bp	Deletion Size
single nucleotide deletion in promoter region	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	Experimental Evidence
Genetic interactions between transcription factors cause natural variation in yeast. (2009) (https://pubmed.ncbi.nlm.nih.gov/19164747)	Main Reference
Gerke J; Lorenz K; Cohen B	Authors
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.	Abstract
	Additional References

RELATED GEPHE

7 (IME1, RAS2, RME1, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS