

GEPHE SUMMARY

TAO3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~TAO3~#gephebase-summary-title)		Gephebase Gene	GP00001103	GepheID
Published		Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait Category	
Sporulation efficiency (https://www.gephebase.org/search-criteria?/and+Trait=~Sporulationefficiency~#gephebase-summary-title)		Trait	
Saccharomyces cerevisiae - SK1 strain		Trait State in Taxon A	
Saccharomyces cerevisiae - S288c strain		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
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)	
baker’s yeast		baker’s yeast	
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	
species		species	
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	
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)	
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)	
Yes		Yes	
Saccharomyces cerevisiae - SK1 strain		Saccharomyces cerevisiae - S288c strain	

GENOTYPIC CHANGE

TAO3		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P40468 (http://www.uniprot.org/uniprot/P40468)	
PAG1; YIL129C		GenebankID or UniProtKB DQ116824 (https://www.ncbi.nlm.nih.gov/nuccore/DQ116824)	
4932.YIL129C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YIL129C)			
To S.pombe mor2.			
-			
GO:0000902 : cell morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0000902)			
GO:0007118 : budding cell apical bud growth			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007118>)
GO:0007114 : cell budding (<https://www.ebi.ac.uk/QuickGO/term/GO:0007114>)
GO - Cellular Component
GO:0005933 : cellular bud (<https://www.ebi.ac.uk/QuickGO/term/GO:0005933>)
GO:0005938 : cell cortex (<https://www.ebi.ac.uk/QuickGO/term/GO:0005938>)
GO:0000131 : incipient cellular bud site
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000131>)
GO:0043332 : mating projection tip (<https://www.ebi.ac.uk/QuickGO/term/GO:0043332>)

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
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)	Aberration Type
E1493Q	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	Experimental Evidence
Quantitative trait loci mapped to single-nucleotide resolution in yeast. (2005) (https://pubmed.ncbi.nlm.nih.gov/16273108)	Main Reference
Deutschbauer AM; Davis RW	Authors

Identifying the genetic variation underlying quantitative trait loci remains problematic. Consequently, our molecular understanding of genetically complex, quantitative traits is limited. To address this issue directly, we mapped three quantitative trait loci that control yeast sporulation efficiency to single-nucleotide resolution in a noncoding regulatory region (RME1) and to two missense mutations (TAO3 and MKT1). For each quantitative trait locus, the responsible polymorphism is rare among a diverse set of 13 yeast strains, suggestive of genetic heterogeneity in the control of yeast sporulation. Additionally, under optimal conditions, we reconstituted approximately 92% of the sporulation efficiency difference between the two genetically distinct parents by engineering three nucleotide changes in the appropriate yeast genome. Our results provide the highest resolution to date of the molecular basis of a quantitative trait, showing that the interaction of a few genetic variants can have a profound phenotypic effect.	Abstract
	Additional References

RELATED GEPHE

7 (IME1, RAS2, RME1, RME1 [possible pseudo-replicate of laboratory strain entry], RSF1, SWS2, 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