

GEPHE SUMMARY

MKT1 (<a +mkt1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+MKT1+"#gephebase-summary-title)	Gephebase Gene	GP00000666	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Trait #1	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
Temperature tolerance (<a +temperature+tolerance+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Temperature+tolerance+"#gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

Trait #2	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
Virulence (<a +virulence+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Virulence+"#gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

Trait #3	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
-	Trait State in Taxon B
-	

Trait #4	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
-	Trait State in Taxon B
-	

Trait #5	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
Xenobiotic resistance (alcohol; ethanol) (<a +xenobiotic+resistance+(alcohol;+ethanol)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic+resistance+(alcohol;+ethanol)+"#gephebase-summary-title)	

title)	Trait State in Taxon A
-	
	Trait State in Taxon B
-	

Trait #6	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)	
	Trait
Xenobiotic resistance (genotoxic DNA-damage agent) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (genotoxic DNA-damage agent)~#gephebase-summary-title)	
	Trait State in Taxon A
-	
	Trait State in Taxon B
-	

	Ancestral State
Data not curated	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)	

	Taxon A		Taxon B
	Latin Name		Latin Name
	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces cerevisiae~#gephebase-summary-title)		Saccharomyces cerevisiae (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 - clinical and industrial strains, RM and SK1 strains		Saccharomyces cerevisiae - laboratory BY strains (eg. s288c)

GENOTYPIC CHANGE

	Generic Gene Name
MKT1	
	Synonyms
YNL085W; N2302	
	String
4932.YNL085W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YNL085W)	
	Sequence Similarities
-	
	GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	
GO:0017108 : 5'-flap endonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0017108)	
GO:0051908 : double-stranded DNA 5'-3' exodeoxyribonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051908)	
GO:0004520 : endodeoxyribonuclease activity	

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P40850 (http://www.uniprot.org/uniprot/P40850)	
GenebankID or UniProtKB AF458981 (https://www.ncbi.nlm.nih.gov/nuccore/AF458981)	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0004520>)
GO:0048256 : flap endonuclease activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048256>)
GO:0045145 : single-stranded DNA 5'-3' exodeoxyribonuclease activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045145>)

GO - Biological Process

GO:0006974 : cellular response to DNA damage stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006974>)
GO:0006281 : DNA repair (<https://www.ebi.ac.uk/QuickGO/term/GO:0006281>)
GO:0044419 : interspecies interaction between organisms
(<https://www.ebi.ac.uk/QuickGO/term/GO:0044419>)

GO - Cellular Component

GO:0034399 : nuclear periphery (<https://www.ebi.ac.uk/QuickGO/term/GO:0034399>)
GO:0010494 : cytoplasmic stress granule
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010494>)
GO:0000932 : P-body (<https://www.ebi.ac.uk/QuickGO/term/GO:0000932>)
GO:0005844 : polysome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005844>)

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

G30D (functionally verified); or haplotype including G30D (functionally verified)

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	Gly	Asp	30

Main Reference

Dissecting the architecture of a quantitative trait locus in yeast. (2002) (<https://pubmed.ncbi.nlm.nih.gov/11907579>)

Authors

Steinmetz LM; Sinha H; Richards DR; Spiegelman JL; Oefner PJ; McCusker JH; Davis RW

Abstract

Most phenotypic diversity in natural populations is characterized by differences in degree rather than in kind. Identification of the actual genes underlying these quantitative traits has proved difficult. As a result, little is known about their genetic architecture. The failures are thought to be due to the different contributions of many underlying genes to the phenotype and the ability of different combinations of genes and environmental factors to produce similar phenotypes. This study combined genome-wide mapping and a new genetic technique named reciprocal-hemizygosity analysis to achieve the complete dissection of a quantitative trait locus (QTL) in *Saccharomyces cerevisiae*. A QTL architecture was uncovered that was more complex than expected. Functional linkages both in cis and in trans were found between three tightly linked quantitative trait genes that are neither necessary nor sufficient in isolation. This arrangement of alleles explains heterosis (hybrid vigour), the increased fitness of the heterozygote compared with homozygotes. It also demonstrates a deficiency in current approaches to QTL dissection with implications extending to traits in other organisms, including human genetic diseases.

Additional References

Complex genetic interactions in a quantitative trait locus. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16462944>)
Identification and dissection of a complex DNA repair sensitivity phenotype in Baker's yeast. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18617998>)
Identification of novel causative genes determining the complex trait of high ethanol tolerance in yeast using pooled-segregant whole-genome sequence analysis. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22399573>)
Dissection of genetically complex traits with extremely large pools of yeast segregants. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20393561>)
Quantitative trait loci mapped to single-nucleotide resolution in yeast. (2005) (<https://pubmed.ncbi.nlm.nih.gov/16273108>)

RELATED GEPHE

Related Genes

23 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, END3, IME1, RAS2, RME1, RME1 [possible pseudo-replicate of laboratory strain entry], RSF1, TAO3, RHO2) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Temperature tolerance/or+Taxon ID=~4932~/and+Trait=Virulence/or+Taxon ID=~4932~/and+Trait=Sporulation efficiency/or+Taxon ID=~4932~/and+Trait=Sporulation efficiency/or+Taxon ID=~4932~/and+Trait=Xenobiotic resistance/or+Taxon ID=~4932~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~MKT1~/and+Taxon ID=~4932~/or+Gene Gephebase=~MKT1~/and+Taxon ID=~4932~#gephebase-summary-title>)

EXTERNAL LINKS

