

GEPHE SUMMARY

END3 (<a +end3+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=">https://www.gephebase.org/search-criteria?/and+GeneGephebase="+END3+"#gephebase-summary-title)		Gephebase Gene	GP00000267	GepheID
Published		Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TraitCategory=">https://www.gephebase.org/search-criteria?/and+TraitCategory="+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
Saccharomyces cerevisiae - clinical strain	Trait State in Taxon B
Saccharomyces cerevisiae - laboratory strain	

Trait #2	Trait Category
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TraitCategory=">https://www.gephebase.org/search-criteria?/and+TraitCategory="+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
-	

Data not curated		Ancestral State		
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=">https://www.gephebase.org/search-criteria?/and+TaxonomicStatus="+Intraspecific+"#gephebase-summary-title)		Taxonomic Status		
Taxon A		Taxon B		
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)		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 - clinical strain		Saccharomyces cerevisiae - laboratory strain		Taxon A Description
				Taxon B Description

GENOTYPIC CHANGE

END3

YNL084C; N2307

4932.YNL084C
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YNL084C)

Belongs to the END3 family.

GO - Molecular Function

GO:0005509 : calcium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005509>)
GO:0003779 : actin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003779>)
GO:0030674 : protein binding, bridging (<https://www.ebi.ac.uk/QuickGO/term/GO:0030674>)

GO - Biological Process

GO:0007015 : actin filament organization (<https://www.ebi.ac.uk/QuickGO/term/GO:0007015>)
GO:0006897 : endocytosis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006897>)
GO:0000147 : actin cortical patch assembly (<https://www.ebi.ac.uk/QuickGO/term/GO:0000147>)
GO:0030476 : ascospore wall assembly (<https://www.ebi.ac.uk/QuickGO/term/GO:0030476>)
GO:0007121 : bipolar cellular bud site selection (<https://www.ebi.ac.uk/QuickGO/term/GO:0007121>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0010008 : endosome membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0010008>)
GO:0030479 : actin cortical patch (<https://www.ebi.ac.uk/QuickGO/term/GO:0030479>)

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

S258N

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

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>)

RELATED GEPHE

Related Genes

2 (MKT1, RHO2) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4932~/and+Trait=Temperature+tolerance/or+Taxon+ID=~4932~/and+Trait=Virulence/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~END3~/and+Taxon+ID=~4932~/or+Gene+Gephebase=~END3~/and+Taxon+ID=~4932~#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS