

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	GP00000268	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
-	

	Ancestral State		
Data not curated	Taxonomic Status		
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)			
	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)	Common 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)	Common Name
baker's yeast	Synonyms	baker's yeast	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	Rank	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
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon A an Intraspecies?	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon B an Intraspecies?
Yes	Taxon A Description	Yes	Taxon B Description
Saccharomyces cerevisiae - clinical strain		Saccharomyces cerevisiae - laboratory strain	

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>)

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

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

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

Nonsynonymous

D268N

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

Generic Gene Name

Synonyms

String

Sequence Similarities

GO - Molecular Function

GO - Biological Process

GO - Cellular Component

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

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

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

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

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.

Complex genetic interactions in a quantitative trait locus. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16462944>)

Main Reference

Authors

Abstract

Additional References

RELATED GEPHE

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>)

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>)

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS