GEPHE SUMMARY

Gephebase Gene

END3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^END3^#gephebase-summary-title)

GepheID

GP00000268

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Temperature tolerance (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 (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Virulence (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 (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

Common Name

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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

Rank

species

Lineage

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

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Saccharomyces cerevisiae - clinical strain

Taxon B

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

Common Name

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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

Rank

species

Lineage

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

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Saccharomyces cerevisiae - laboratory strain

GENOTYPIC CHANGE

Generic Gene Name

END3

Synonyms

YNL084C; N2307

String

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

Sequence Similarities

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)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P39013 (http://www.uniprot.org/uniprot/P39013)

GenebankID or UniProtKB

AF458981 (https://www.ncbi.nlm.nih.gov/nuccore/AF458981)

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

D268N

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 JI; 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