# GEPHE SUMMARY

Gephebase Gene

TAF5 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^TAF5^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001710

Main curator

Noor

# PHENOTYPIC CHANGE

Trait Category

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

Trait

Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Low-glucose adaptation (experimental evolution)^#gephebase-summary-title)

Trait State in Taxon A

Saccharomyces cerevisiae

Trait State in Taxon B

Saccharomyces cerevisiae

Ancestral State

Taxon A

Taxonomic Status

Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#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?

No

## 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?

No

# GENOTYPIC CHANGE

Generic Gene Name

TAF5

Synonyms

TAF90; YBR198C; YBR1410

String

4932.YBR198C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBR198C )

Sequence Similarities

Belongs to the WD repeat TAF5 family.

GO - Molecular Function

GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0003682 : chromatin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003682)
GO:0032947 : protein-containing complex scaffold activity (https://www.ebi.ac.uk/QuickGO/term/GO:0032947)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P38129 (http://www.uniprot.org/uniprot/P38129)

GenebankID or UniProtKB

()

GO:0043130 : ubiquitin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043130)

GO - Biological Process

GO:0006325 : chromatin organization (https://www.ebi.ac.uk/QuickGO/term/GO:0006325)
GO:0006366 : transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0006366)
GO:0016573 : histone acetylation (https://www.ebi.ac.uk/QuickGO/term/GO:0016573)
GO:0051123 : RNA polymerase II preinitiation complex assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0051123)

GO - Cellular Component

GO:0000124 : SAGA complex (https://www.ebi.ac.uk/QuickGO/term/GO:0000124)
GO:0046695 : SLIK (SAGA-like) complex (https://www.ebi.ac.uk/QuickGO/term/GO:0046695)
GO:0005669 : transcription factor TFIID complex (https://www.ebi.ac.uk/QuickGO/term/GO:0005669)

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

Gly693Val (G>T at position 616441 according to Table 1) - GGN to GTN position 616441

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

| | Taxon A | Taxon B | Position |
|---|---|---|---|
| Codon | - | - | - |
| Amino-acid | Gly | Val | 693 |

Main Reference

Molecular characterization of clonal interference during adaptive evolution in asexual populations of Saccharomyces cerevisiae. (2008) (https://pubmed.ncbi.nlm.nih.gov/19029899)

Authors

Kao KC; Sherlock G

Abstract

The classical model of adaptive evolution in an asexual population postulates that each adaptive clone is derived from the one preceding it. However, experimental evidence has suggested more complex dynamics, with theory predicting the fixation probability of a beneficial mutation as dependent on the mutation rate, population size and the mutation's selection coefficient. Clonal interference has been demonstrated in viruses and bacteria but not in a eukaryote, and a detailed molecular characterization is lacking. Here we use three different fluorescent markers to visualize the dynamics of asexually evolving yeast populations. For each adaptive clone within one of our evolving populations, we identified the underlying mutations, monitored their population frequencies and used microarrays to characterize changes in the transcriptome. These results represent the most detailed molecular characterization of experimental evolution to date and provide direct experimental evidence supporting both the clonal interference and the multiple mutation models.

Additional References

Reciprocal sign epistasis between frequently experimentally evolved adaptive mutations causes a rugged fitness landscape. (2011) (https://pubmed.ncbi.nlm.nih.gov/21552329)

## RELATED GEPHE

Related Genes

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RAS2, RIM15, SLY41) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS