

GEPHE SUMMARY

Gephebase Gene
TAF5

Entry Status
Published

GepheID
GP00001710

Main curator
Noor

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Low-glucose adaptation (experimental evolution)

Trait State in Taxon A
Saccharomyces cerevisiae

Trait State in Taxon B
Saccharomyces cerevisiae

Ancestral State
Taxon A

Taxonomic Status
Experimental Evolution

Taxon A

Latin Name

Saccharomyces cerevisiae

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; Saccharomyces 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)

NCBI Taxonomy ID

4932

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Saccharomyces cerevisiae

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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

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Parent

Saccharomyces () - (Rank: genus)

NCBI Taxonomy ID

4932

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name
TAF5

Synonyms

TAF90; YBR198C; YBR1410

String

4932.YBR198C

Sequence Similarities

Belongs to the WD repeat TAF5 family.

GO - Molecular Function

GO:0042802 : identical protein binding

GO:0003682 : chromatin binding

GO:0032947 : protein-containing complex scaffold activity

GO:0043130 : ubiquitin binding

GO - Biological Process

GO:0006325 : chromatin organization

GO:0006366 : transcription by RNA polymerase II

GO:0016573 : histone acetylation

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P38129

GenebankID or UniProtKB

GO:0051123 : RNA polymerase II preinitiation complex assembly

GO - Cellular Component

GO:0000124 : SAGA complex

GO:0046695 : SLIK (SAGA-like) complex

GO:0005669 : transcription factor TFIID complex

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

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

	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)

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)

RELATED GEPHE

Related Genes

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RAS2, RIM15, SLY41)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS