GEPHE SUMMARY

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

GepheID
GP00001710

Entry Status
Published

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