

GEPHE SUMMARY

TAF5 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^TAF5^#gephebase-summary-title)	Gephebase Gene	GP00001710	Gepheid
	Entry Status	Noor	Main curator
Published			

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		Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Latin Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Latin Name
baker's yeast	Common Name	baker's yeast	Common Name
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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

TAF5	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P38129 (http://www.uniprot.org/uniprot/P38129)
TAF90; YBR198C; YBR1410	Synonyms	GenebankID or UniProtKB
4932.YBR198C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBR198C)	String	0
	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)		

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

