

GEPHE SUMMARY

	Gephebase Gene		GepheID
MTH1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MTH1~#gephebase-summary-title)		GP00000679	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

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

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
CUP1-1		PoCX80 (http://www.uniprot.org/uniprot/PoCX80)	
	Synonyms		GenebankID or UniProtKB
CUP1; MTH1; YHR053C		K02204 (https://www.ncbi.nlm.nih.gov/nuccore/K02204)	
	String		
4932.YHR055C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YHR055C)			
	Sequence Similarities		
Belongs to the metallothionein superfamily. Type 12 family.			
	GO - Molecular Function		
GO:0016209 : antioxidant activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016209)			
GO:0005507 : copper ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005507)			
GO:0046870 : cadmium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046870)			
GO:0004784 : superoxide dismutase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004784)			

GO - Biological Process

GO:0071585 : detoxification of cadmium ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071585>)
GO:0010273 : detoxification of copper ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010273>)
GO:0046688 : response to copper ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046688>)
GO:0019430 : removal of superoxide radicals
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019430>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

	Presumptive Null
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#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
Nonsense	
	Molecular Details of the Mutation
1bp substitution resulting in premature stop codon	
	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	-	-	-

	Main Reference
Molecular characterization of clonal interference during adaptive evolution in asexual populations of <i>Saccharomyces cerevisiae</i> . (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, MUK1, RAS1, RAS2, RIM15, SLY41, TAF5) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title)	Related Haplotypes
1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~MTH1~/and+Taxon ID=~4932~/or+Gene Gephebase=~MTH1~/and+Taxon ID=~4932~#gephebase-summary-title)	

EXTERNAL LINKS

COMMENTS