

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait Category
Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Low-glucose adaptation (experimental evolution)^#gephebase-summary-title)	Trait
Saccharomyces cerevisiae	Trait State in Taxon A
Saccharomyces cerevisiae	Trait State in Taxon B
Taxon A	Ancestral State
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#gephebase-summary-title)	Taxonomic Status

Taxon A	Latin Name	Taxon B	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)	
baker's yeast	Common Name	baker's yeast	Common Name
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 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	
Rank		Rank	
species	Lineage	species	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 Infraspecies?		is Taxon B an Infraspecies?	
No		No	

GENOTYPIC CHANGE

CUP1-1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) PoCX80 (http://www.uniprot.org/uniprot/PoCX80)
CUP1; MTH1; YHR053C	Synonyms	GenebankID or UniProtKB K02204 (https://www.ncbi.nlm.nih.gov/nuccore/K02204)
4932.YHR055C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YHR055C)	String	
Belongs to the metallothionein superfamily. Type 12 family.	Sequence Similarities	
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 - Molecular Function	

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=%27Yes%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%27Yes%27#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Coding%27#gephebase-summary-title))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27SNP%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27SNP%27#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=%27Association Mapping%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Association%20Mapping%27#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 *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, MUK1, RAS1, RAS2, RIM15, SLY41, TAF5) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%274932%27/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%274932%27/and+Trait=Low-glucose%20adaptation/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%27MTH1%27/and+Taxon ID=%274932%27/or+Gene Gephebase=%27MTH1%27/and+Taxon ID=%274932%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene%20Gephebase=%27MTH1%27/and+Taxon%20ID=%274932%27/or+Gene%20Gephebase=%27MTH1%27/and+Taxon%20ID=%274932%27#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS