

GEPHE SUMMARY

	Gephebase Gene		GepheID
MTH1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MTH1~#gephebase-summary-title)		GP00000680	
	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>)

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title)	Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title)	Aberration Type
1-10 kb	Insertion Size
Ty retrotransposition resulting in a coding frameshift	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title)	Experimental Evidence
The repertoire and dynamics of evolutionary adaptations to controlled nutrient-limited environments in yeast. (2008) (https://pubmed.ncbi.nlm.nih.gov/19079573)	Main Reference
Gresham D; Desai MM; Tucker CM; Jenq HT; Pai DA; Ward A; DeSevo CG; Botstein D; Dunham MJ	Authors

The experimental evolution of laboratory populations of microbes provides an opportunity to observe the evolutionary dynamics of adaptation in real time. Until very recently, however, such studies have been limited by our inability to systematically find mutations in evolved organisms. We overcome this limitation by using a variety of DNA microarray-based techniques to characterize genetic changes -- including point mutations, structural changes, and insertion variation -- that resulted from the experimental adaptation of 24 haploid and diploid cultures of <i>Saccharomyces cerevisiae</i> to growth in either glucose, sulfate, or phosphate-limited chemostats for approximately 200 generations. We identified frequent genomic amplifications and rearrangements as well as novel retrotransposition events associated with adaptation. Global nucleotide variation detection in ten clonal isolates identified 32 point mutations. On the basis of mutation frequencies, we infer that these mutations and the subsequent dynamics of adaptation are determined by the batch phase of growth prior to initiation of the continuous phase in the chemostat. We relate these genotypic changes to phenotypic outcomes, namely global patterns of gene expression, and to increases in fitness by 5-50%. We found that the spectrum of available mutations in glucose- or phosphate-limited environments combined with the batch phase population dynamics early in our experiments allowed several distinct genotypic and phenotypic evolutionary pathways in response to these nutrient limitations. By contrast, sulfate-limited populations were much more constrained in both genotypic and phenotypic outcomes. Thus, the reproducibility of evolution varies with specific selective pressures, reflecting the constraints inherent in the system-level organization of metabolic processes in the cell. We were able to relate some of the observed adaptive mutations (e.g., transporter gene amplifications) to known features of the relevant metabolic pathways, but many of the mutations pointed to genes not previously associated with the relevant physiology. Thus, in addition to answering basic mechanistic questions about evolutionary mechanisms, our work suggests that experimental evolution can also shed light on the function and regulation of individual metabolic pathways.	Abstract
	Additional References

RELATED GEPHE

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 Genes
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)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

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