

GEPHE SUMMARY

	Gephebase Gene		GepheID
HXT6/7 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~HXT6/7~#gephebase-summary-title)		GP00000494	
	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		
Data not curated			
	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)
HXT6		P39003 (http://www.uniprot.org/uniprot/P39003)	
	Synonyms		GenebankID or UniProtKB
YDR343C; D9651.12		U51032 (https://www.ncbi.nlm.nih.gov/nuccore/U51032)	
	String		
4932.YDR343C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YDR343C)			
	Sequence Similarities		
Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family.			
	GO - Molecular Function		
GO:0005351 : carbohydrate:proton symporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005351)			
GO:0005353 : fructose transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005353)			
GO:0005355 : glucose transmembrane transporter activity			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005355>)
GO:0015149 : hexose transmembrane transporter activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015149>)
GO:0015578 : mannose transmembrane transporter activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015578>)

GO - Biological Process

GO:0055085 : transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)
GO:0098704 : carbohydrate import across plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0098704>)
GO:0008645 : hexose transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008645>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

	Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	
	Molecular Type
Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Amplification~#gephebase-summary-title)	
	Aberration Type
Complex Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Complex Change~#gephebase-summary-title)	
	Molecular Details of the Mutation
expansion by unequal recombination between HXT6 and HXT7 (99% nucleotide similarity) : replicated in two independent studies and in multiple lines	
	Experimental Evidence
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title)	
	Main Reference
Multiple duplications of yeast hexose transport genes in response to selection in a glucose-limited environment. (1998) (https://pubmed.ncbi.nlm.nih.gov/9718721)	
	Authors
Brown CJ; Todd KM; Rosenzweig RF	

Abstract

When microbes evolve in a continuous, nutrient-limited environment, natural selection can be predicted to favor genetic changes that give cells greater access to limiting substrate. We analyzed a population of baker’s yeast that underwent 450 generations of glucose-limited growth. Relative to the strain used as the inoculum, the predominant cell type at the end of this experiment sustains growth at significantly lower steady-state glucose concentrations and demonstrates markedly enhanced cell yield per mole glucose, significantly enhanced high-affinity glucose transport, and greater relative fitness in pairwise competition. These changes are correlated with increased levels of mRNA hybridizing to probe generated from the hexose transport locus HXT6. Further analysis of the evolved strain reveals the existence of multiple tandem duplications involving two highly similar, high-affinity hexose transport loci, HXT6 and HXT7. Selection appears to have favored changes that result in the formation of more than three chimeric genes derived from the upstream promoter of the HXT7 gene and the coding sequence of HXT6. We propose a genetic mechanism to account for these changes and speculate as to their adaptive significance in the context of gene duplication as a common response of microorganisms to nutrient limitation.

Additional References

Characteristic genome rearrangements in experimental evolution of *Saccharomyces cerevisiae*. (2002) (<https://pubmed.ncbi.nlm.nih.gov/12446845>)
Molecular characterization of clonal interference during adaptive evolution in asexual populations of *Saccharomyces cerevisiae*. (2008) (<https://pubmed.ncbi.nlm.nih.gov/19029899>)
Reciprocal sign epistasis between frequently experimentally evolved adaptive mutations causes a rugged fitness landscape. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21552329>)
The repertoire and dynamics of evolutionary adaptations to controlled nutrient-limited environments in yeast. (2008) (<https://pubmed.ncbi.nlm.nih.gov/19079573>)

RELATED GEPHE

	Related Genes
12 (COX18, IRA1, MDS3, MKT1, MNN4, MTH1, 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
No matches found.	

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes