

GEPHE SUMMARY

HXT6/7 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^HXT6/7^#gephebase-summary-title)	Gephebase Gene	GP00000494	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		
Data not curated	Ancestral State		
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Experimental Evolution^#gephebase-summary-title)	Taxonomic Status		
	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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes 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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes 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=4932)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	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
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

HXT6	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P39003 (http://www.uniprot.org/uniprot/P39003)	GenebankID or UniProtKB
YDR343C; D9651.12	Synonyms	U51032 (https://www.ncbi.nlm.nih.gov/nuccore/U51032)	
4932.YDR343C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YDR343C)	String		
Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family.	Sequence Similarities		
GO:0005351 : carbohydrate:proton symporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005351)	GO - Molecular Function		
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>)

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

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

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 Genes

No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes