

CYC8 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^CYC8^#gephebase-summary-title)	Gephebase Gene	GP00000195	GepheID
Published	Entry Status	Martin	Main curator

	Trait Category				
Physiology (#https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology)					
	Trait				
Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=~Salt tolerance (experimental evolution))					
	Trait State in Taxon A				
<i>Saccharomyces cerevisiae</i>					
	Trait State in Taxon B				
<i>Saccharomyces cerevisiae</i>					
	Ancestral State				
Taxon A					
	Taxonomic Status				
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Experimental Evolution)					
	Taxon A				Taxon B
	Latin Name				Latin Name
<i>Saccharomyces cerevisiae</i>					<i>Saccharomyces cerevisiae</i>
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces cerevisiae)					(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces cerevisiae)
	Common Name				Common Name
baker's yeast					baker's yeast
	Synonyms				Synonyms
<i>Saccharomyces capensis</i> ; <i>Saccharomyces italicus</i> ; <i>Saccharomyces oviformis</i> ; <i>Saccharomyces uvarum</i> var. <i>melibiosus</i> ; baker's yeast; <i>S. cerevisiae</i> ; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; <i>Saccaromyces cerevisiae</i> ; <i>Saccharomyce cerevisiae</i> ; <i>Saccharomyes cerevisiae</i> ; <i>Sccharomyces cerevisiae</i>					<i>Saccharomyces capensis</i> ; <i>Saccharomyces italicus</i> ; <i>Saccharomyces oviformis</i> ; <i>Saccharomyces uvarum</i> var. <i>melibiosus</i> ; baker's yeast; <i>S. cerevisiae</i> ; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; <i>Saccaromyces cerevisiae</i> ; <i>Saccharomyce cerevisiae</i> ; <i>Saccharomyes cerevisiae</i> ; <i>Sccharomyces cerevisiae</i>
	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
<i>Saccharomyces ()</i> - (Rank: genus)					<i>Saccharomyces ()</i> - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)					(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)
	NCBI Taxonomy ID				NCBI Taxonomy ID
4932					4932
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=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

CYC8	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) P14922 (http://www.uniprot.org/uniprot/P14922)
CRT8; SSN6; YBR112C; YBR0908	Synonyms	GenebankID or UniProtKB X78993 (https://www.ncbi.nlm.nih.gov/nuccore/X78993)
4932.YBR112C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YBR112C)	String	
Belongs to the CYC8/SSN6 family.	Sequence Similarities	
GO:0042826 : histone deacetylase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042826) GO:0003714 : transcription corepressor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003714) GO:0003713 : transcription coactivator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003713)	GO - Molecular Function	

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0006338 : chromatin remodeling (<https://www.ebi.ac.uk/QuickGO/term/GO:0006338>)
GO:0035955 : negative regulation of dipeptide transport by negative regulation of transcription from RNA polymerase II promoter
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035955>)
GO:0016584 : nucleosome positioning
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016584>)
GO:2000531 : regulation of fatty acid biosynthetic process by regulation of transcription from RNA polymerase II promoter (<https://www.ebi.ac.uk/QuickGO/term/GO:2000531>)
GO:2001020 : regulation of response to DNA damage stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:2001020>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0090568 : nuclear transcriptional repressor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090568>)
GO:0017053 : transcriptional repressor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0017053>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title](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](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](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](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping~#gephebase-summary-title))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Determinants of divergent adaptation and Dobzhansky-Muller interaction in experimental yeast populations. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20637622>)

Authors

Anderson JB; Funt J; Thompson DA; Prabhu S; Socha A; Sirjusingh C; Dettman JR; Parreiras L; Guttman DS; Regev A; Kohn LM

Abstract

Divergent adaptation can be associated with reproductive isolation in speciation [1]. We recently demonstrated the link between divergent adaptation and the onset of reproductive isolation in experimental populations of the yeast *Saccharomyces cerevisiae* evolved from a single progenitor in either a high-salt or a low-glucose environment [2]. Here, whole-genome resequencing and comparative genome hybridization of representatives of three populations revealed 17 mutations, six of which explained the adaptive increases in mitotic fitness. In two populations evolved in high salt, two different mutations occurred in the proton efflux pump gene *PMA1* and the global transcriptional repressor gene *CYC8*; the *ENA* genes encoding sodium efflux pumps were overexpressed once through expansion of this gene cluster and once because of mutation in the regulator *CYC8*. In the population from low glucose, one mutation occurred in *MDS3*, which modulates growth at high pH, and one in *MKT1*, a global regulator of mRNAs encoding mitochondrial proteins, the latter recapitulating a naturally occurring variant. A Dobzhansky-Muller (DM) incompatibility between the evolved alleles of *PMA1* and *MKT1* strongly depressed fitness in the low-glucose environment. This DM interaction is the first reported between experimentally evolved alleles of known genes and shows how reproductive isolation can arise rapidly when divergent selection is strong.

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Additional References

Cellular effects and epistasis among three determinants of adaptation in experimental populations of *Saccharomyces cerevisiae*. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21856932>)

RELATED GEPHE

Related Genes

4 (ENA1-2-5 cluster, PMA1, TRK1, MEP2) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4932~/and+Trait=Salt+tolerance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

