

GEPHE SUMMARY

MKT1 (#gephebase-summary-title)	Gephebase Gene	GP00000662	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category	
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 - 30G laboratory strain	Trait State in Taxon B
Saccharomyces cerevisiae - experimentally evolved lines	Ancestral State
Taxon A	Taxonomic Status
Experimental Evolution (#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Saccharomyces cerevisiae (#gephebase-summary-title)		Saccharomyces cerevisiae (#gephebase-summary-title)	
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; 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	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=4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	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
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Saccharomyces cerevisiae - 30G laboratory strain	Taxon A Description	Saccharomyces cerevisiae - 30G laboratory strain + experimental evolution regimen	Taxon B Description

GENOTYPIC CHANGE

MKT1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P40850 (http://www.uniprot.org/uniprot/P40850)	GenebankID or UniProtKB
YNL085W; N2302	Synonyms	X03534 (https://www.ncbi.nlm.nih.gov/nuccore/X03534)	
4932.YNL085W (https://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YNL085W)	String		
-	Sequence Similarities		
	GO - Molecular Function		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			
GO:0017108 : 5'-flap endonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0017108)			

GO:0051908 : double-stranded DNA 5'-3' exodeoxyribonuclease activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0051908>)

GO:0004520 : endodeoxyribonuclease activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0004520>)

GO:0048256 : flap endonuclease activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048256>)

GO:0045145 : single-stranded DNA 5'-3' exodeoxyribonuclease activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045145>)

GO - Biological Process

GO:0006974 : cellular response to DNA damage stimulus

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006974>)

GO:0006281 : DNA repair (<https://www.ebi.ac.uk/QuickGO/term/GO:0006281>)

GO:0044419 : interspecies interaction between organisms

(<https://www.ebi.ac.uk/QuickGO/term/GO:0044419>)

GO - Cellular Component

GO:0034399 : nuclear periphery (<https://www.ebi.ac.uk/QuickGO/term/GO:0034399>)

GO:0010494 : cytoplasmic stress granule

(<https://www.ebi.ac.uk/QuickGO/term/GO:0010494>)

GO:0000932 : P-body (<https://www.ebi.ac.uk/QuickGO/term/GO:0000932>)

GO:0005844 : polysome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005844>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title>)

Molecular Type

Coding (<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>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D30G (reversion; functionally verified); evolved independently in 3 lines

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

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

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

Main Reference

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

Authors

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

12 (COX18, HXT6/7, IRA1, MDS3, 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

1 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^MKT1^/and+Taxon+ID=^4932^/or+Gene+Gephebase=^MKT1^/and+Taxon+ID=^4932^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

@Parallelism. Mutation replicated 3 times by experimental evolution; the reverse mutation (see other MKT1 entry) has evolved in BY laboratory strains by domestication