

MDS3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MDS3^#gephebase-summary-title)	Gephebase Gene	GP00000641	GepheID
Published	Entry Status	Martin	Main curator

Trait Category		Trait		Trait State in Taxon A		Trait State in Taxon B		Ancestral State		Taxonomic Status	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)		Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=~Low-glucose+adaptation+(experimental+evolution)^#gephebase-summary-title)		Saccharomyces cerevisiae		Saccharomyces cerevisiae		Taxon A		Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Experimental+Evolution^#gephebase-summary-title)	
Taxon A		Taxon B		Latin Name		Latin Name		Common Name		Common 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)		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		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		NCBI Taxonomy ID		NCBI Taxonomy ID	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		is Taxon A an Infrasppecies?		is Taxon B an Infrasppecies?		No		No	

Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)	GenebankID or UniProtKB
MDS3	P53094 (http://www.uniprot.org/uniprot/P53094)	
YGL197W; G1307	Z72719 (https://www.ncbi.nlm.nih.gov/nuccore/Z72719)	
4932.YGL197W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YGL197W)		
Sequence Similarities		
-		
GO - Molecular Function		
-		
GO - Biological Process		
GO:0051321 : meiotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051321)		
GO:0007124 : pseudohyphal growth (https://www.ebi.ac.uk/QuickGO/term/GO:0007124)		
GO:0030435 : sporulation resulting in formation of a cellular spore		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030435>)
GO:0075297 : negative regulation of ascospore formation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0075297>)
GO:0031929 : TOR signaling (<https://www.ebi.ac.uk/QuickGO/term/GO:0031929>)
GO - Cellular Component
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

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

Phe - Val substitution

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	-	-	-

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

12 (COX18, HXT6/7, IRA1, 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