

# GEPHE SUMMARY

PMA1 ( <a href="https://www.gephebase.org/search-criteria/?and+Gene">https://www.gephebase.org/search-criteria/?and+Gene</a> Gephebase="PMA1">#gephebase-summary-title)	Gephebase Gene	GP00000900	GepheID
	Entry Status	Martin	Main curator
Published			

## PHENOTYPIC CHANGE

Trait Category		Trait	Taxon A	Taxonomic Status	Taxon B	Latin Name
Physiology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait">https://www.gephebase.org/search-criteria/?and+Trait</a> Category="Physiology">#gephebase-summary-title)		Salt tolerance (experimental evolution) ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=Salt+tolerance+(experimental+evolution)#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=Salt+tolerance+(experimental+evolution)#gephebase-summary-title</a> )	Trait State in Taxon A		Trait State in Taxon B	
Saccharomyces cerevisiae		Saccharomyces cerevisiae - after 500 generations of selective pressure	Ancestral State		Experimental Evolution ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic">https://www.gephebase.org/search-criteria/?and+Taxonomic</a> Status="Experimental Evolution">#gephebase-summary-title)	
Taxon A		Taxonomic Status		Taxon B		Latin Name
Saccharomyces cerevisiae		Saccharomyces cerevisiae		Saccharomyces cerevisiae		( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=Saccharomyces+cerevisiae#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=Saccharomyces+cerevisiae#gephebase-summary-title</a> )
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
Rank		Lineage		Rank		Lineage
species		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		species		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
Saccharomyces () - (Rank: genus)		Parent		Saccharomyces () - (Rank: genus)		Parent
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )		NCBI Taxonomy ID		( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )		NCBI Taxonomy ID
4932		4932		4932		4932
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932</a> )		is Taxon A an Infraspecies?		is Taxon B an Infraspecies?		No

## GENOTYPIC CHANGE

PMA1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P05030 ( <a href="http://www.uniprot.org/uniprot/P05030">http://www.uniprot.org/uniprot/P05030</a> )	GenebankID or UniProtKB
KTh10; YGL008C	Synonyms	X03534 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/X03534">https://www.ncbi.nlm.nih.gov/nuccore/X03534</a> )	
4932.YGL008C	String		
( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YGL008C">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YGL008C</a> )	Sequence Similarities		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIIA subfamily.	GO - Molecular Function		
GO:0005524 : ATP binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005524">https://www.ebi.ac.uk/QuickGO/term/GO:0005524</a> )	GO - Biological Process		
GO:0046872 : metal ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046872">https://www.ebi.ac.uk/QuickGO/term/GO:0046872</a> )			
GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0008553">https://www.ebi.ac.uk/QuickGO/term/GO:0008553</a> )			
GO:0055085 : transmembrane transport			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)  
 GO:0006885 : regulation of pH (<https://www.ebi.ac.uk/QuickGO/term/GO:0006885>)  
 GO:1902906 : proteasome storage granule assembly  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:1902906>)  
 GO:0120029 : proton export across plasma membrane  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0120029>)  
 GO:1902600 : proton transmembrane transport  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:1902600>)  
 GO:0051453 : regulation of intracellular pH  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0051453>)

#### GO - Cellular Component

GO:0016021 : integral component of membrane  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)  
 GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)  
 GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Coding%22#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22SNP%22#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Leu363Trp

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Association+Mapping%22#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>)

The underlying structure of adaptation under strong selection in 12 experimental yeast populations. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25016004>)

## RELATED GEPHE

Related Genes  
 4 (CYC8, ENA1-2-5 cluster, TRK1, MEP2) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%224932%22/and+Trait=Salt+tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

Related Haplotypes  
 10 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%22PMA1%22/and+Taxon+ID=%224932%22/or+Gene+Gephebase=%22PMA1%22/and+Taxon+ID=%224932%22#gephebase-summary-title>)

## EXTERNAL LINKS

## COMMENTS

PMID 25016004 includes nucleotidic changes

