

## GEPHE SUMMARY

**Gephebase Gene**  
PMA1

**Entry Status**  
Published

**GepheID**  
GP00000901

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Salt tolerance (experimental evolution)

**Trait State in Taxon A**  
Saccharomyces cerevisiae

**Trait State in Taxon B**  
Saccharomyces cerevisiae - after 500 generations of selective pressure

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Experimental Evolution

### Taxon A

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
baker's yeast

**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

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
baker's yeast

**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

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
PMA1

**Synonyms**  
KTI10; YGL008C

**String**  
4932.YGL008C

**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  
GO:0046872 : metal ion binding  
GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism

**GO - Biological Process**  
GO:0055085 : transmembrane transport  
GO:0006885 : regulation of pH  
GO:1902906 : proteasome storage granule assembly  
GO:0120029 : proton export across plasma membrane

**UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)**  
P05030

**GenebankID or UniProtKB**  
X03534

GO:1902600 : proton transmembrane transport  
GO:0051453 : regulation of intracellular pH

**GO - Cellular Component**

GO:0016021 : integral component of membrane  
GO:0005886 : plasma membrane  
GO:0045121 : membrane raft

**Presumptive Null**

No

**Molecular Type**

Coding

**Aberration Type**

SNP

**SNP Coding Change**

Nonsynonymous

**Molecular Details of the Mutation**

Ser234Cys

**Experimental Evidence**

Association Mapping

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

**Main Reference**

Determinants of divergent adaptation and Dobzhansky-Muller interaction in experimental yeast populations. (2010)

**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.

Copyright (c) 2010 Elsevier Ltd. All rights reserved.

**Additional References**

Cellular effects and epistasis among three determinants of adaptation in experimental populations of *Saccharomyces cerevisiae*. (2011)

The underlying structure of adaptation under strong selection in 12 experimental yeast populations. (2014)

## RELATED GEPHE

**Related Genes**

4 (*CYC8*, *ENA1-2-5* cluster, *TRK1*, *MEP2*)

**Related Haplotypes**

10

## COMMENTS

PMID 25016004 includes nucleotidic changes