

	Gephebase Gene	GepheID
PMA1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~PMA1~#gephebase-summary-title)	GP00000905	Main curator
	Entry Status	
Published		

Trait Category		Trait	
Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology ^#gephebase-summary-title)			
Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=~Salt tolerance (experimental evolution)^#gephebase-summary-title)			
Saccharomyces cerevisiae	Trait State in Taxon A		
	Trait State in Taxon B		
Saccharomyces cerevisiae - after 500 generations of selective pressure	Ancestral State		
Taxon A	Taxonomic Status		
Experimental Evolution (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Experimental Evolution ^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin 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	Common Name	baker's yeast	Common Name
	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	Rank	species	Rank
	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
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
is Taxon A an Infrappecies?		is Taxon B an Infrappecies?	
No		No	

Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
PMA1	P05030 (http://www.uniprot.org/uniprot/P05030)
KT110; YGL008C	GenebankID or UniProtKB X03534 (https://www.ncbi.nlm.nih.gov/nuccore/X03534)
4932.YGL008C	
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=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 (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)	
GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism (https://www.ebi.ac.uk/QuickGO/term/GO:0008553)	
GO - Biological Process	
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>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Gly337Ser	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title)	Experimental Evidence

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

The underlying structure of adaptation under strong selection in 12 experimental yeast populations. (2014) (https://pubmed.ncbi.nlm.nih.gov/25016004)	Main Reference
Kohn LM; Anderson JB	Authors
The aims of this study were to determine (i) whether adaptation under strong selection occurred through mutations in a narrow target of one or a few nucleotide sites or a broad target of numerous sites and (ii) whether the programs of adaptation previously observed from three experimental populations were unique or shared among populations that underwent parallel evolution. We used archived population samples from a previous study, representing 500 generations of experimental evolution in 12 populations under strong selection, 6 populations in a high-salt environment and 6 populations in a low-glucose environment. Each set of six populations included four with sexual reproduction and two with exclusively asexual reproduction. Populations were sampled as resequenced genomes of 115 individuals and as bulk samples from which frequencies of mutant alleles were estimated. In a high-salt environment, a broad target of 11 mutations within the proton exporter, PMA1, was observed among the six populations, in addition to expansions of the ENA gene cluster. This pattern was shared among populations that underwent parallel evolution. In a low-glucose environment, two programs of adaptation were observed. The originally observed pattern of mutation in MDS3/MKT1 in population M8 was a narrow target of a single nucleotide, unique to this population. Among the other five populations, the three mutations were shared in a broad target, sensing/signaling genes RAS1 and RAS2. RAS1/RAS2 mutations were not observed in the high-salt populations; PMA1 mutations were observed only in a high-salt environment.	Abstract
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RELATED GEPHE

4 (CYC8, ENA1-2-5 cluster, TRK1, MEP2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
10 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~PMA1~/and+Taxon ID=~4932~/or+Gene Gephebase=~PMA1~/and+Taxon ID=~4932~#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

PMID 25016004 includes nucleotidic changes

