

PMA1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~PMA1~#gephebase-summary-title)	Gephebase Gene	GP00000910	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)		Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Salt tolerance (experimental evolution)^#gephebase-summary-title)		Saccharomyces cerevisiae		Saccharomyces cerevisiae - after 500 generations of selective pressure					
Taxon A		Taxon B		Taxon A		Taxon B		Taxon A		Taxon B	
Saccharomyces cerevisiae		Saccharomyces cerevisiae		Saccharomyces cerevisiae		Saccharomyces cerevisiae		Saccharomyces cerevisiae		Saccharomyces cerevisiae	
(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)		(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)		(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)	
Common Name		Common Name		Common Name		Common Name		Common Name		Common Name	
baker's yeast		baker's yeast		baker's yeast		baker's yeast		baker's yeast		baker's yeast	
Synonyms		Synonyms		Synonyms		Synonyms		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		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		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	
Rank		Rank		Rank		Rank		Rank		Rank	
species		species		species		species		species		species	
Lineage		Lineage		Lineage		Lineage		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		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		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		Parent		Parent		Parent		Parent	
Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	
NCBI Taxonomy ID		NCBI Taxonomy ID		NCBI Taxonomy ID		NCBI Taxonomy ID		NCBI Taxonomy ID		NCBI Taxonomy ID	
4932		4932		4932		4932		4932		4932	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?		is Taxon A an Intraspecies?		is Taxon B an Intraspecies?		is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No		No		No		No		No	

Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)	GenebankID or UniProtKB
PMA1	P05030 (http://www.uniprot.org/uniprot/P05030)	
KT110; YGL008C	X03534 (https://www.ncbi.nlm.nih.gov/nucore/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>)

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

Trp750Cys

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	TGG	TGC	2250
Amino-acid	Trp	Cys	750

Main Reference

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

Authors

Kohn LM; Anderson JB

Abstract

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.

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Additional References

RELATED GEPHE

Related Genes

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 Haplotypes

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>)

EXTERNAL LINKS

COMMENTS

PMID 25016004 includes nucleotidic changes

