

	Gephebase Gene	GepheID
PMA1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~PMA1~#gephebase-summary-title)	GP00000907	Main curator
	Entry Status	
Published	Martin	

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		
Saccharomyces cerevisiae - after 500 generations of selective pressure	Trait State in Taxon B		
Taxon A	Ancestral State		
Experimental Evolution (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Experimental Evolution ^#gephebase-summary-title)	Taxonomic Status		
Taxon A		Taxon B	
Saccharomyces cerevisiae	Latin Name	Saccharomyces cerevisiae	Latin Name
(#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)	
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; Saccharomyes 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; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus)	Parent	Saccharomyces () - (Rank: genus)	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID
4932		4932	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon A an Infrapopulation?	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon B an Infrapopulation?
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>)

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

Pro535Thr

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

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.

Copyright Â© 2014, American Society for Microbiology. All Rights Reserved.

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

