

PMA1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~PMA1~#gephebase-summary-title)	Gephebase Gene	GP00000903	GepheID
Published	Entry Status	Martin	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category
Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Salt tolerance (experimental evolution)^#gephebase-summary-title)	Trait
<i>Saccharomyces cerevisiae</i>	Trait State in Taxon A
<i>Saccharomyces cerevisiae</i> - 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

GENOTYPIC CHANGE	
PMA1	Generic Gene Name UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)
KT110; YGL008C	Synonyms P05030 (http://www.uniprot.org/uniprot/P05030)
4932.YGL008C	String X03534 (https://www.ncbi.nlm.nih.gov/nucore/X03534)
(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:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	GO - Molecular Function 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

Val157Phe

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.

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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

