GEPHE SUMMARY

Gephebase Gene

PMA1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PMA1^#gephebase-summary-title)

GepheID

GP00000904

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Salt tolerance (experimental evolution)^#gephebase-summary-title)

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 (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#gephebase-summary-title)

Taxon A

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

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; Saccaromyces 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) (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)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

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; Saccaromyces 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) (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)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

PMA1

Synonyms

KTI10; YGL008C

String

4932.YGL008C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YGL008C)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P05030 (http://www.uniprot.org/uniprot/P05030)

Sequence Similarities

Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIIA subfamily.

GenebankID or UniProtKB

X03534 (https://www.ncbi.nlm.nih.gov/nuccore/X03534)

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

Gly294Val

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