

GEPHE SUMMARY

Gephebase Gene
PMA1

Entry Status
Published

GepheID
GP00000908

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Salt tolerance (experimental evolution)

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

Taxon A

Latin Name
Saccharomyces cerevisiae

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; Saccharomyces 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)

NCBI Taxonomy ID
4932

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Saccharomyces cerevisiae

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; Saccharomyces 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)

NCBI Taxonomy ID
4932

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
PMA1

Synonyms
KTI10; YGL008C

String
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
GO:0046872 : metal ion binding
GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism

GO - Biological Process
GO:0055085 : transmembrane transport
GO:0006885 : regulation of pH
GO:1902906 : proteasome storage granule assembly
GO:0120029 : proton export across plasma membrane

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P05030

GenebankID or UniProtKB
X03554

GO:1902600 : proton transmembrane transport
GO:0051453 : regulation of intracellular pH

GO - Cellular Component

GO:0016021 : integral component of membrane
GO:0005886 : plasma membrane
GO:0045121 : membrane raft

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Iso564Thr

Experimental Evidence

Association Mapping

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

Main Reference

The underlying structure of adaptation under strong selection in 12 experimental yeast populations. (2014)

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)

Related Haplotypes

10

COMMENTS

PMID 25016004 includes nucleotidic changes