

GEPHE SUMMARY

	Gephebase Gene	GephelD
ENA1-2-5 cluster (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ENA1-2-5 cluster">#gephebase-summary-title)	GP00000266	Main curator
Published	Entry Status	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	Taxon B
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)
baker's yeast	Common Name	baker's yeast
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; Saccharomyces 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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	
Rank		Rank
species	Lineage	species
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
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

ENA1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P13587 (http://www.uniprot.org/uniprot/P13587)
HOR6; PMR2; PMR2A; YDR040C; YD6888.02C	Synonyms	GenebankID or UniProtKB Z54075 (https://www.ncbi.nlm.nih.gov/nuccore/Z54075)
4932.YDR040C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YDR040C)	String	
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IID subfamily.	Sequence Similarities	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) GO:0008556 : potassium-transporting ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008556) GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism (https://www.ebi.ac.uk/QuickGO/term/GO:0008553) GO:0008554 : sodium-exporting ATPase activity, phosphorylative mechanism	GO - Molecular Function	

GO:0055085 : transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)

GO:0006813 : potassium ion transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)

GO:0009651 : response to salt stress (<https://www.ebi.ac.uk/QuickGO/term/GO:0009651>)

GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)

GO:0042149 : cellular response to glucose starvation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042149>)

GO:0006972 : hyperosmotic response

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006972>)

GO:0009268 : response to pH (<https://www.ebi.ac.uk/QuickGO/term/GO:0009268>)

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>)

Presumptive Null

No ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No))

Molecular Type

Gene Amplification ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Gene+Amplification))

Aberration Type

Complex Change ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Complex+Change))

Molecular Details of the Mutation

uncharacterized expansion

Experimental Evidence

Association Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping))

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, PMA1, TRK1, MEP2) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4932/and+Trait=Salt+tolerance/and+groupHaplotypes=true))

Related Haplotypes

1 ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^ENA1-2-5+cluster/and+Taxon+ID=^4932/or+Gene+Gephebase=^ENA1-2-5+cluster/and+Taxon+ID=^4932)

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes ; Expansion is highly repeatable (see other independent study)