

GEPHE SUMMARY

	Gephebase Gene		GepheID
ENA1-2-5 cluster (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="ENA1-2-5 cluster"#gephebase-summary-title)		GP00000266	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)			
	Trait		
Salt tolerance (experimental evolution) (<a (experimental="" evolution)"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=" salt="" tolerance="">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		Taxon B
	Latin Name		Latin Name
Saccharomyces cerevisiae (<a cerevisiae"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" saccharomyces="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces cerevisiae"#gephebase-summary-title)		Saccharomyces cerevisiae (<a cerevisiae"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" saccharomyces="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces cerevisiae"#gephebase-summary-title)	
	Common Name		Common Name
baker's yeast		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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes 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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
	Rank		Rank
species		species	
	Lineage		Lineage
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	
	Parent		Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
ENA1		P13587 (http://www.uniprot.org/uniprot/P13587)	
	Synonyms		GenebankID or UniProtKB
HOR6; PMR2; PMR2A; YDR040C; YD6888.02C		Z54075 (https://www.ncbi.nlm.nih.gov/nuccore/Z54075)	
	String		
4932.YDR040C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YDR040C)			
	Sequence Similarities		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IID subfamily.			
	GO - Molecular Function		
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			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008554>)

GO - Biological Process

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

uncharacterized expansion

Experimental Evidence

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

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

Related Haplotypes

1 ([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"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

EXTERNAL LINKS

COMMENTS

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