

GEPHE SUMMARY

	Gephebase Gene		GepheID
RAS1 (<a +ras1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=">https://www.gephebase.org/search-criteria?/and+GeneGephebase="+RAS1+"#gephebase-summary-title)		GP00000952	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TraitCategory=">https://www.gephebase.org/search-criteria?/and+TraitCategory="+Physiology+"#gephebase-summary-title)			
	Trait		
Low-glucose adaptation (experimental evolution) (<a +low-glucose+adaptation+(experimental+evolution)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Low-glucose+adaptation+(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 (<a +experimental+evolution+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=">https://www.gephebase.org/search-criteria?/and+TaxonomicStatus="+Experimental+Evolution+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Saccharomyces cerevisiae (<a +saccharomyces+cerevisiae+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Saccharomyces+cerevisiae+"#gephebase-summary-title)		Saccharomyces cerevisiae (<a +saccharomyces+cerevisiae+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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)
RAS2		P01120 (http://www.uniprot.org/uniprot/P01120)	
	Synonyms		GenebankID or UniProtKB
CTN5; CYR3; GLC5; TSL7; ASC1; YNL098C; N2198		Z71374 (https://www.ncbi.nlm.nih.gov/nuccore/Z71374)	
	String		
4932.YNL098C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YNL098C)			
	Sequence Similarities		
Belongs to the small GTPase superfamily. Ras family.			
	GO - Molecular Function		
GO:0005525 : GTP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005525)			
GO:0003924 : GTPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003924)			
	GO - Biological Process		
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)			
GO:0032880 : regulation of protein localization			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0032880>)
GO:0016236 : macroautophagy (<https://www.ebi.ac.uk/QuickGO/term/GO:0016236>)
GO:0007190 : activation of adenylate cyclase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007190>)
GO:0030437 : ascospore formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030437>)
GO:0045762 : positive regulation of adenylate cyclase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045762>)
GO:2000222 : positive regulation of pseudohyphal growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000222>)
GO:0000411 : positive regulation of transcription by galactose
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000411>)
GO:0032258 : protein localization by the Cvt pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032258>)
GO:0097271 : protein localization to bud neck
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097271>)
GO:0010603 : regulation of cytoplasmic mRNA processing body assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010603>)
GO:0001302 : replicative cell aging (<https://www.ebi.ac.uk/QuickGO/term/GO:0001302>)
GO - Cellular Component
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

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

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title>) Molecular Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title>) Aberration Type

Nonsynonymous SNP Coding Change

Glu>Ala (A>C mutation) Molecular Details of the Mutation

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

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

The underlying structure of adaptation under strong selection in 12 experimental yeast populations. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25016004>) Main Reference

Kohn LM; Anderson JB Authors

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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RELATED GEPHE

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS2, RIM15, SLY41, TAF5) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title>) Related Genes

No matches found. Related Haplotypes

EXTERNAL LINKS

COMMENTS

Same mutation replicated in two experimental populations but not included here as a second entry in case of contamination issue. PMID 25016004 includes nucleotidic changes