

GEPHE SUMMARY

RAS2 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase='RAS2' #gephebase-summary-title)	Gephebase Gene	GP00000955	GephelD
	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
Low-glucose adaptation (experimental evolution) (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 (https://www.gephebase.org/search-criteria/?and+Taxonomic Status='Experimental Evolution' #gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
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	Common Name
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	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	Synonyms
Rank		Rank	
species	Lineage	species	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 Infraspecies?		is Taxon B an Infraspecies?	
No		No	

GENOTYPIC CHANGE

RAS2	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P01120 (http://www.uniprot.org/uniprot/P01120)	GenebankID or UniProtKB
CTN5; CYR3; GLC5; TSL7; ASC1; YNL098C; N2198	Synonyms	Z71374 (https://www.ncbi.nlm.nih.gov/nucore/Z71374)	
4932.YNL098C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YNL098C)	String		
Belongs to the small GTPase superfamily. Ras family.	Sequence Similarities		
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 - Molecular Function		
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165) GO:0032880 : regulation of protein localization	GO - Biological Process		

(<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>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Glu>Gln (C>G mutation)

Experimental Evidence

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

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RIM15, SLY41, TAF5) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4932^/and+Trait=Low-glucose+adaptation/and+groupHaplotypes=true))

Related Genes

2 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^RAS2^/and+Taxon+ID=^4932^/or+Gene+Gephebase=^RAS2^/and+Taxon+ID=^4932^))

Related Haplotypes

EXTERNAL LINKS

COMMENTS

PMID 25016004 includes nucleotidic changes