

GEPHE SUMMARY

	Gephebase Gene		GepheID
Rds2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Rds2~#gephebase-summary-title)		GP00000964	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)			
	Trait		
Oxidative stress resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Oxidative stress resistance~#gephebase-summary-title)			
	Trait State in Taxon A		
Saccharomyces cerevisiae - clinical strain			
	Trait State in Taxon B		
Saccharomyces cerevisiae - laboratory strain			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		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)	
	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; Saccaromyces 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; Saccaromyces 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?
Yes		Yes	
	Taxon A Description		Taxon B Description
Saccharomyces cerevisiae - clinical strain		Saccharomyces cerevisiae - laboratory strain	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
RDS2		P19541 (http://www.uniprot.org/uniprot/P19541)	
	Synonyms		GenebankID or UniProtKB
YPL133C; LPI12C		KZV07383 (https://www.ncbi.nlm.nih.gov/nuccore/KZV07383)	
	String		
4932.YPL133C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YPL133C)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)			
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)			
GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA			

polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0045722 : positive regulation of gluconeogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045722>)
GO:0015976 : carbon utilization (<https://www.ebi.ac.uk/QuickGO/term/GO:0015976>)
GO:0071555 : cell wall organization (<https://www.ebi.ac.uk/QuickGO/term/GO:0071555>)
GO:0071466 : cellular response to xenobiotic stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071466>)
GO:0061415 : negative regulation of transcription from RNA polymerase II promoter by a nonfermentable carbon source (<https://www.ebi.ac.uk/QuickGO/term/GO:0061415>)
GO:0035948 : positive regulation of gluconeogenesis by positive regulation of transcription from RNA polymerase II promoter (<https://www.ebi.ac.uk/QuickGO/term/GO:0035948>)
GO:0061414 : positive regulation of transcription from RNA polymerase II promoter by a nonfermentable carbon source (<https://www.ebi.ac.uk/QuickGO/term/GO:0061414>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

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

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

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

Nonsynonymous

H251D

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

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

Oxidative stress survival in a clinical *Saccharomyces cerevisiae* isolate is influenced by a major quantitative trait nucleotide. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21515583>)

Diezmann S; Dietrich FS

One of the major challenges in characterizing eukaryotic genetic diversity is the mapping of phenotypes that are the cumulative effect of multiple alleles. We have investigated tolerance of oxidative stress in the yeast *Saccharomyces cerevisiae*, a trait showing phenotypic variation in the population. Initial crosses identified that this is a quantitative trait. Microorganisms experience oxidative stress in many environments, including during infection of higher eukaryotes. Natural variation in oxidative stress tolerance is an important aspect of response to oxidative stress exerted by the human immune system and an important trait in microbial pathogens. A clinical isolate of the usually benign yeast *S. cerevisiae* was found to survive oxidative stress significantly better than the laboratory strain. We investigated the genetic basis of increased peroxide survival by crossing those strains, phenotyping 1500 segregants, and genotyping of high-survival segregants by hybridization of bulk and single segregant DNA to microarrays. This effort has led to the identification of an allele of the transcription factor *Rds2* as contributing to stress response. *Rds2* has not previously been associated with the survival of oxidative stress. The identification of its role in the oxidative stress response here is an example of a specific trait that appears to be beneficial to *Saccharomyces cerevisiae* when growing as a pathogen. Understanding the role of this fungal-specific transcription factor in pathogenicity will be important in deciphering how fungi infect and colonize the human host and could eventually lead to a novel drug target.

RELATED GEPHE

No matches found.

No matches found.

EXTERNAL LINKS

COMMENTS

