

GEPHE SUMMARY

	Gephebase Gene		GepheID
PHO84 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^PHO84^#gephebase-summary-title)		GP00000865	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobioticresistance^#gephebase-summary-title)			
	Trait State in Taxon A		
Saccharomyces cerevisiae - S288c strain			
	Trait State in Taxon B		
Saccharomyces cerevisiae - RM 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+TaxonandSynonyms=^Saccharomycescerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Saccharomycescerevisiae^#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 - S288c strain		Saccharomyces cerevisiae - RM strain	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
PHO84		P25297 (http://www.uniprot.org/uniprot/P25297)	
	Synonyms		GenebankID or UniProtKB
YML123C; YM7056.03C		D90346 (https://www.ncbi.nlm.nih.gov/nuccore/D90346)	
	String		
4932.YML123C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YML123C)			
	Sequence Similarities		
Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family.			
	GO - Molecular Function		
GO:0005384 : manganese ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005384)			
GO:0005315 : inorganic phosphate transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005315)			

GO:0097079 : selenite:proton symporter activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097079>)

GO - Biological Process

GO:0006828 : manganese ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006828>)
GO:0006817 : phosphate ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006817>)
GO:0097080 : plasma membrane selenite transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097080>)
GO:0006797 : polyphosphate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006797>)
GO:1904728 : positive regulation of replicative senescence
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904728>)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L259P

Experimental Evidence

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

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

Main Reference

Genetic basis of individual differences in the response to small-molecule drugs in yeast. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17334364>)

Authors

Perlstein EO; Ruderfer DM; Roberts DC; Schreiber SL; Kruglyak L

Abstract

Individual response to small-molecule drugs is variable; a drug that provides a cure for some may confer no therapeutic benefit or trigger an adverse reaction in others. To begin to understand such differences systematically, we treated 104 genotyped segregants from a cross between two yeast strains with a collection of 100 diverse small molecules. We used linkage analysis to identify 124 distinct linkages between genetic markers and response to 83 compounds. The linked markers clustered at eight genomic locations, or quantitative-trait locus ‘hotspots’, that contain one or more polymorphisms that affect response to multiple small molecules. We also experimentally verified that a deficiency in leucine biosynthesis caused by a deletion of LEU2 underlies sensitivity to niguldipine, which is structurally related to therapeutic calcium channel blockers, and that a natural coding-region polymorphism in the inorganic phosphate transporter PHO84 underlies sensitivity to two polychlorinated phenols that uncouple oxidative phosphorylation. Our results provide a step toward a systematic understanding of small-molecule drug action in genetically distinct individuals.

Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, RAD5, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

