

IRA2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="IRA2" #gephebase-summary-title)	Gephebase Gene	GP00000505	GepheID
Published	Entry Status	Martin	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait Category	
Growth rate (environment-dependent) (https://www.gephebase.org/search-criteria?/and+Trait=^Growth rate (environment-dependent)^#gephebase-summary-title)		Trait	
Saccharomyces cerevisiae - S288c strain		Trait State in Taxon A	
Saccharomyces cerevisiae - RM strain		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
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		baker's yeast	
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	
species		species	
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	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
NCBI Taxonomy ID 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		NCBI Taxonomy ID 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	
Saccharomyces cerevisiae - S288c strain		Saccharomyces cerevisiae - RM strain	

IRA2	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) P19158 (http://www.uniprot.org/uniprot/P19158)
CCS1; GLC4; YOL081W; O0985	Synonyms	GenebankID or UniProtKB CAA99093 (https://www.ncbi.nlm.nih.gov/nuccore/CAA99093)
4932.YOL081W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YOL081W)	String	
-	Sequence Similarities	
GO:0005096 : GTPase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005096)	GO - Molecular Function	
GO:0043547 : positive regulation of GTPase activity	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0043547>)
GO:0070417 : cellular response to cold
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070417>)
GO:0070301 : cellular response to hydrogen peroxide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070301>)
GO:0034599 : cellular response to oxidative stress
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034599>)
GO:0007193 : adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007193>)
GO:0071248 : cellular response to metal ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071248>)
GO:0046580 : negative regulation of Ras protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046580>)

GO - Cellular Component

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
Unknown (#gephebase-summary-title)	
	Molecular Type
Coding (#gephebase-summary-title)	
	Aberration Type
Unknown (#gephebase-summary-title)	
	Molecular Details of the Mutation
unknown	
	Experimental Evidence
Linkage Mapping (#gephebase-summary-title)	
	Main Reference
Gene-environment interaction in yeast gene expression. (2008) (https://pubmed.ncbi.nlm.nih.gov/18416601)	
	Authors
Smith EN; Kruglyak L	

Abstract

The effects of genetic variants on phenotypic traits often depend on environmental and physiological conditions, but such gene-environment interactions are poorly understood. Recently developed approaches that treat transcript abundances of thousands of genes as quantitative traits offer the opportunity to broadly characterize the architecture of gene-environment interactions. We examined the genetic and molecular basis of variation in gene expression between two yeast strains (BY and RM) grown in two different conditions (glucose and ethanol as carbon sources). We observed that most transcripts vary by strain and condition, with 2,996, 3,448, and 2,037 transcripts showing significant strain, condition, and strain-condition interaction effects, respectively. We expression profiled over 100 segregants derived from a cross between BY and RM in both growth conditions, and identified 1,555 linkages for 1,382 transcripts that show significant gene-environment interaction. At the locus level, local linkages, which usually correspond to polymorphisms in cis-regulatory elements, tend to be more stable across conditions, such that they are more likely to show the same effect or the same direction of effect across conditions. Distant linkages, which usually correspond to polymorphisms influencing trans-acting factors, are more condition-dependent, and often show effects in different directions in the two conditions. We characterized a locus that influences expression of many growth-related transcripts, and showed that the majority of the variation is explained by polymorphism in the gene IRA2. The RM allele of IRA2 appears to inhibit Ras/PKA signaling more strongly than the BY allele, and has undergone a change in selective pressure. Our results provide a broad overview of the genetic architecture of gene-environment interactions, as well as a detailed molecular example, and lead to key insights into how the effects of different classes of regulatory variants are modulated by the environment. These observations will guide the design of studies aimed at understanding the genetic basis of complex traits.

Additional References

RELATED GEPHE

	Related Genes
6 (Allantoin permease DAL4, Allantoinase DAL1, Proline specific permease PUT4, Aquaporin (AQY1), Aquaporin (AQY2), BMH1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932#/and+Trait=Growth rate/and+groupHaplotypes=true#gephebase-summary-title)	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

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