

GEPHE SUMMARY

FRM2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+^FRM2^#gephebase-summary-title)	Gephebase Gene	GP00001311	GepheID
Published	Entry Status	Arnoult	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+^Physiology^#gephebase-summary-title)	Trait Category		
Xenobiotic resistance (citrinin) (https://www.gephebase.org/search-criteria?/and+Trait+^Xenobiotic+resistance+(citrinin)^#gephebase-summary-title)	Trait		
Saccharomyces cerevisiae S288c	Trait State in Taxon A		
Saccharomyces paradoxus CBS432	Trait State in Taxon B		
Taxon A	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)	Latin Name	Saccharomyces paradoxus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Saccharomyces+paradoxus^#gephebase-summary-title)	Latin Name
baker's yeast	Common Name	-	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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Synonyms	AS 2.2401; AS:2.2401; BCRC:22587; CBS 432; CBS:432; CCRC 22587; CCRC:22587; CLIB 228; CLIB:228; DBVPG 6411; DBVPG:6411; IFO 10609; IFO:10609; IGC 4570; IGC:4570; MUCL 31498; MUCL:31498; NCYC 2600; NCYC:2600; NRRL Y-17217; NRRL:Y:17217; PYCC 4570; PYCC:4570	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID	27291 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=27291)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Saccharomyces cerevisiae S288c	Taxon A Description	Saccharomyces paradoxus CBS432	Taxon B Description

GENOTYPIC CHANGE

FRM2	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P37261 (http://www.uniprot.org/uniprot/P37261)
YCLX08C; YCL026C-A; YCLX8C	Synonyms	GenebankID or UniProtKB
4932.YCL026C-A (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YCL026C-A)	String	()
-	Sequence Similarities	
GO:0016657 : oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0016657)	GO - Molecular Function	
	GO - Biological Process	

GO:0006631 : fatty acid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006631>)
GO:0034599 : cellular response to oxidative stress
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034599>)
GO:0045922 : negative regulation of fatty acid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045922>)

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>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

mutations within 1kb in promotor region

Experimental Evidence

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

Main Reference

Dissecting the Genetic Basis of a Complex cis-Regulatory Adaptation. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26713447>)

Authors

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Abstract

Although single genes underlying several evolutionary adaptations have been identified, the genetic basis of complex, polygenic adaptations has been far more challenging to pinpoint. Here we report that the budding yeast *Saccharomyces paradoxus* has recently evolved resistance to citrinin, a naturally occurring mycotoxin. Applying a genome-wide test for selection on cis-regulation, we identified five genes involved in the citrinin response that are constitutively up-regulated in *S. paradoxus*. Four of these genes are necessary for resistance, and are also sufficient to increase the resistance of a sensitive strain when over-expressed. Moreover, cis-regulatory divergence in the promoters of these genes contributes to resistance, while exacting a cost in the absence of citrinin. Our results demonstrate how the subtle effects of individual regulatory elements can be combined, via natural selection, into a complex adaptation. Our approach can be applied to dissect the genetic basis of polygenic adaptations in a wide range of species.

Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, TSA2, CIS1, GPX2, RTA1, cytochrome b, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Xenobiotic resistance/or+Taxon ID=^27291^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

A total of 4 genes involved in resistance to citrinin found in this study