GEPHE SUMMARY

Gephebase Gene

GPX2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^GPX2^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001310

Main curator

Arnoult

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Xenobiotic resistance (citrinin) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (citrinin)^#gephebase-summary-title)

Trait State in Taxon A

Saccharomyces cerevisiae S288c

Trait State in Taxon B

Saccharomyces paradoxus CBS432

Ancestral State

Taxon A

Taxonomic Status

Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

Common Name

baker's yeast

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

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

Parent

Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Saccharomyces cerevisiae S288c

Taxon B

Latin Name

Saccharomyces paradoxus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces paradoxus^#gephebase-summary-title)

Common Name

-

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

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

Parent

Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

27291 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27291)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Saccharomyces paradoxus CBS432

GENOTYPIC CHANGE

Generic Gene Name

GPX2

Synonyms

AMI1; YBR244W; YBR1632

String

4932.YBR244W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBR244W)

Sequence Similarities

Belongs to the glutathione peroxidase family.

GO - Molecular Function

GO:0004602 : glutathione peroxidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004602)
GO:0051920 : peroxiredoxin activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051920)
GO:0047066 : phospholipid-hydroperoxide glutathione peroxidase activity

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P38143 (http://www.uniprot.org/uniprot/P38143)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0047066)

GO - Biological Process

GO:0034599 : cellular response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0034599)

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)
GO:0031315 : extrinsic component of mitochondrial outer membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0031315)
GO:0031314 : extrinsic component of mitochondrial inner membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0031314)

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

Naranjo S; Smith JD; Artieri CG; Zhang M; Zhou Y; Palmer ME; Fraser HB

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, FRM2, 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