GEPHE SUMMARY

Gephebase Gene
RTA1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RTA1^#gephebase-summary-title)

GepheID
GP00001312

Entry Status
Published

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
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#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
RTA1

Synonyms
YGR213C

String
4932.YGR213C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YGR213C)

Sequence Similarities
Belongs to the lipid-translocating exporter (LTE) (TC 9.A.26.1) family.

GO - Molecular Function
-

GO - Biological Process
-

GO - Cellular Component

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P53047 (http://www.uniprot.org/uniprot/P53047)

GenebankID or UniProtKB
()

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0000324 : fungal-type vacuole (https://www.ebi.ac.uk/QuickGO/term/GO:0000324)

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

unknown

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, GPX2, 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