

GEPHE SUMMARY

| | | | |
|--|----------------|------------|--------------|
| CIS1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=CIS1#gephebase-summary-title) | Gephebase Gene | GP00001313 | 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

| | | |
|--|-------------------------|--|
| ATG31 | Generic Gene Name | UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) Q12421 (http://www.uniprot.org/uniprot/Q12421) |
| CIS1; YDR022C; PZD196; YD9335.08c | Synonyms | GenebankID or UniProtKB |
| 4932.YDR022C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YDR022C) | String | () |
| - | Sequence Similarities | |
| - | GO - Molecular Function | |
| - | GO - Biological Process | |
| GO:0015031 : protein transport (https://www.ebi.ac.uk/QuickGO/term/GO:0015031) | | |
| GO:0006914 : autophagy (https://www.ebi.ac.uk/QuickGO/term/GO:0006914) | | |

GO:0000422 : autophagy of mitochondrion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000422>)
GO:0007059 : chromosome segregation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007059>)
GO:0000741 : karyogamy (<https://www.ebi.ac.uk/QuickGO/term/GO:0000741>)
GO:0044805 : late nucleophagy (<https://www.ebi.ac.uk/QuickGO/term/GO:0044805>)
GO:0034727 : piecemeal microautophagy of the nucleus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034727>)

GO - Cellular Component

GO:1990316 : Atg1/ULK1 kinase complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990316>)
GO:0005874 : microtubule (<https://www.ebi.ac.uk/QuickGO/term/GO:0005874>)
GO:0000407 : phagophore assembly site
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000407>)

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, FRM2, 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