GEPHE SUMMARY

Gephebase Gene
TSA2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^TSA2^#gephebase-summary-title)

GepheID
GP00001831

Entry Status
Published

Main curator
Duveau

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Sensitive

Trait State in Taxon B
Tolerant

Ancestral State
Taxon A

Taxonomic Status
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#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?
No

Taxon B

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 B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
TSA2

Synonyms
YDR453C; D9461.38

String
4932.YDR453C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YDR453C)

Sequence Similarities
Belongs to the peroxiredoxin family. AhpC/Prx1 subfamily.

GO - Molecular Function
GO:0051920 : peroxiredoxin activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051920)
GO:0008379 : thioredoxin peroxidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008379)

GO - Biological Process
GO:0006457 : protein folding (https://www.ebi.ac.uk/QuickGO/term/GO:0006457)
GO:0045454 : cell redox homeostasis

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) Q04120 (http://www.uniprot.org/uniprot/Q04120)

GenebankID or UniProtKB
Saccharomyces cerevisiae (strain ATCC 204508 / S288c) Q04120 (https://www.ncbi.nlm.nih.gov/nuccore/Q04120)

(https://www.ebi.ac.uk/QuickGO/term/GO:0045454)
GO:0034599 : cellular response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0034599)
GO:0006979 : response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0006979)
GO:0042744 : hydrogen peroxide catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042744)
GO:0050821 : protein stabilization (https://www.ebi.ac.uk/QuickGO/term/GO:0050821)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Chromosome 4 whole duplication. Using a genetic mapping strategy that involves systematically deleting segments of a duplicated chromosome; the authors show that the chromosome IVâ€™s duplication effect is largely due to the generation of a second copy of the stress-inducible cytoplasmic thioredoxin peroxidase TSA2.

Experimental Evidence

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

Main Reference

The Stress-Inducible Peroxidase TSA2 Underlies a Conditionally Beneficial Chromosomal Duplication in Saccharomyces cerevisiae. (2017) (https://pubmed.ncbi.nlm.nih.gov/28743806)

Authors

Linder RA; Greco JP; Seidl F; Matsui T; Ehrenreich IM

Abstract

AIthough chromosomal duplications are often deleterious, in some cases they enhance cells' abilities to tolerate specific genetic or environmental challenges. Identifying the genes that confer these conditionally beneficial effects to particular chromosomal duplications can improve our understanding of the genetic and molecular mechanisms that enable certain aneuploidies to persist in cell populations and contribute to disease and evolution. Here, we perform a screen for spontaneous mutations that improve the tolerance of haploid Saccharomyces cerevisiae to hydrogen peroxide. Chromosome IV duplication is the most frequent mutation, as well as the only change in chromosomal copy number seen in the screen. Using a genetic mapping strategy that involves systematically deleting segments of a duplicated chromosome, we show that the chromosome IV's duplication effect is largely due to the generation of a second copy of the stress-inducible cytoplasmic thioredoxin peroxidase TSA2 Our findings add to a growing body of literature that shows the conditionally beneficial effects of chromosomal duplication are typically mediated by a small number of genes that enhance tolerance to specific stresses when their copy numbers are increased.

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Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Fitness @GeneDuplication ; @& Experimental Evidence should be "Gene editing".