GEPHE SUMMARY

Gephebase Gene
RAD5 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RAD5^#gephebase-summary-title)

GepheID
GP00000950

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Saccharomyces cerevisiae - S288c strain

Trait State in Taxon B
Saccharomyces cerevisiae - RM strain

Ancestral State
Data not curated

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 strain

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?
Yes

Taxon B Description
Saccharomyces cerevisiae - RM strain

GENOTYPIC CHANGE

Generic Gene Name
RAD5

Synonyms
REV2; SNM2; YLR032W

String
4932.YLR032W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YLR032W)

Sequence Similarities
Belongs to the SNF2/RAD54 helicase family.

GO - Molecular Function
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)
GO:0000403 : Y-form DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000403)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P32849 (http://www.uniprot.org/uniprot/P32849)

GenebankID or UniProtKB
M96644 (https://www.ncbi.nlm.nih.gov/nuccore/M96644)

GO:0008094 : DNA-dependent ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008094)
GO:0000400 : four-way junction DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000400)
GO:0009378 : four-way junction helicase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0009378)

GO - Biological Process

GO:0000209 : protein polyubiquitination (https://www.ebi.ac.uk/QuickGO/term/GO:0000209)
GO:0006302 : double-strand break repair (https://www.ebi.ac.uk/QuickGO/term/GO:0006302)
GO:0042275 : error-free postreplication DNA repair (https://www.ebi.ac.uk/QuickGO/term/GO:0042275)
GO:0070987 : error-free translesion synthesis (https://www.ebi.ac.uk/QuickGO/term/GO:0070987)
GO:0042276 : error-prone translesion synthesis (https://www.ebi.ac.uk/QuickGO/term/GO:0042276)
GO:0010994 : free ubiquitin chain polymerization (https://www.ebi.ac.uk/QuickGO/term/GO:0010994)
GO:0006301 : postreplication repair (https://www.ebi.ac.uk/QuickGO/term/GO:0006301)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0000790 : nuclear chromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000790)
GO:0000781 : chromosome, telomeric region (https://www.ebi.ac.uk/QuickGO/term/GO:0000781)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

I791S

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Identification and dissection of a complex DNA repair sensitivity phenotype in Baker's yeast. (2008) (https://pubmed.ncbi.nlm.nih.gov/18617998)

Authors

Demogines A; Smith E; Kruglyak L; Alani E

Abstract

Complex traits typically involve the contribution of multiple gene variants. In this study, we took advantage of a high-density genotyping analysis of the BY (S288c) and RM strains of Saccharomyces cerevisiae and of 123 derived spore progeny to identify the genetic loci that underlie a complex DNA repair sensitivity phenotype. This was accomplished by screening hybrid yeast progeny for sensitivity to a variety of DNA damaging agents. Both the BY and RM strains are resistant to the ultraviolet light-mimetic agent 4-nitroquinoline 1-oxide (4-NQO); however, hybrid progeny from a BYxRM cross displayed varying sensitivities to the drug. We mapped a major quantitative trait locus (QTL), RAD5, and identified the exact polymorphism within this locus responsible for 4-NQO sensitivity. By using a backcrossing strategy along with array-assisted bulk segregant analysis, we identified one other locus, MKT1, and a QTL on Chromosome VII that also link to the hybrid 4-NQO-sensitive phenotype but confer more minor effects. This work suggests an additive model for sensitivity to 4-NQO and provides a strategy for mapping both major and minor QTL that confer background-specific phenotypes. It also provides tools for understanding the effect of genetic background on sensitivity to genotoxic agents.

Additional References

Dissection of genetically complex traits with extremely large pools of yeast segregants. (2010) (https://pubmed.ncbi.nlm.nih.gov/20393561)

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, SWS2, TSA2, 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