GEPHE SUMMARY

Gephebase Gene
cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^cytochrome b^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00002046
Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Xenobiotic resistance (fungicide; QoI; quinone outside inhibiting) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (fungicide; QoI; quinone outside inhibiting)^#gephebase-summary-title)
Trait State in Taxon A
sensitive
Trait State in Taxon B
resistant
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?
No

Taxon B

Latin Name
Schizosaccharomyces pombe (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Schizosaccharomyces pombe^#gephebase-summary-title)
Common Name
fission yeast
Synonyms
Schizosaccharomyces malidevorans; fission yeast; BCRC:21461; CBS 356; CBS:356; CCRC 21461; CCRC:21461; DBVPG 6277; DBVPG:6277; JCM 8274; JCM:8274; MUCL 30245; MUCL:30245; NRRL Y-12796; NRRL:Y:12796; Schizosaccharomyces pombeP
Rank
species
Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; Taphrinomycotina; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
Parent
Schizosaccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4895)
NCBI Taxonomy ID
4896 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4896)
is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
UQCRFS1
Synonyms
RIP1; RIS1; RISP; UQCR5
String
9606.ENSP00000306397 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000306397)
Sequence Similarities
-
GO - Molecular Function
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0051537 : 2 iron, 2 sulfur cluster binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051537)
GO:0008121 : ubiquinol-cytochrome-c reductase activity

UniProtKB Homo sapiens
P47985 (http://www.uniprot.org/uniprot/P47985)
GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0008121)

GO - Biological Process

GO:0006122 : mitochondrial electron transport, ubiquinol to cytochrome c
(https://www.ebi.ac.uk/QuickGO/term/GO:0006122)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0005743 : mitochondrial inner membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005743)
GO:0005751 : mitochondrial respiratory chain complex IV
(https://www.ebi.ac.uk/QuickGO/term/GO:0005751)
GO:0005750 : mitochondrial respiratory chain complex III
(https://www.ebi.ac.uk/QuickGO/term/GO:0005750)

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

N261D

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asn	Asp	261

Main Reference

The molecular basis for the natural resistance of the cytochrome bc1 complex from strobilurin-producing basidiomycetes to center Qp inhibitors. (1996)
(https://pubmed.ncbi.nlm.nih.gov/8631367)

Authors

Kraiczy P; Haase U; Gencic S; Flindt S; Anke T; Brandt U; Von Jagow G

Abstract

Mitochondria from the strobilurin A producing basidiomycetes Strobilurus tenacellus and Mycena galopoda exhibit natural resistance to (E)-beta-methoxyacrylate inhibitors of the ubiquinol oxidation center(center Qp) of the cytochrome bc1 complex. Isolated cytochrome bc1 complex from S. tenacellus was found to be highly similar to that of Saccharomyces cerevisiae with respect to subunit composition, as well as spectral characteristics and midpoint potentials of the heme centers. To understand the molecular basis of natural resistance, we determined the exon/intron organization and deduced the sequences of cytochromes b from S. tenacellus, M. galopoda and a third basidiomycete, Mycena viridimarginata, which produces no strobilurin A. Comparative sequence analysis of two regions of cytochrome b known to contribute to the formation of center Qp suggested that the generally lower sensitivity of all three basidiomycetes was due to the replacement of a small amino acid residue in position 127 by isoleucine. For M. galopoda replacement of Gly143 by alanine and Gly153 by serine, for S. tenacellus replacement of a small residue in position 254 by glutamine and Asn261 by aspartate was found to be the likely causes for resistance to (E)-beta-methoxyacrylates. The latter exchange is also found in Schizosaccharomyces pombe, which we found also to be naturally resistant to (E)-beta-methoxyacrylates.

Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, MKT1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Xenobiotic resistance/or+Taxon ID=^4896^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@MitochondrialGene - The Asn261Asp mutation has been found in other resistant taxa. Not clear if it is an interspecific or intraspecific change since a single strain of S. pombe was sequenced in this study. A alignment of many cyt b sequences from S. pombe would be required to check if the change is intra versus interspecific.