

GEPHE SUMMARY

cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+cytochrome+b+gephebase-summary-title)	Gephebase Gene	GP00002046	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+gephebase-summary-title)	Trait Category		
Xenobiotic resistance (fungicide; Qol; quinone outside inhibiting) (https://www.gephebase.org/search-criteria?/and+Trait+Xenobiotic+resistance+(fungicide;+Qol;+quinone+outside+inhibiting)+gephebase-summary-title)	Trait		
sensitive	Trait State in Taxon A		
resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Interspecific+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	Schizosaccharomyces pombe (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Schizosaccharomyces+pombe+gephebase-summary-title)	Latin Name
baker's yeast	Common Name	fission yeast	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; Saccharomyces cerevisiae; Saccharomyces cerevisiae	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	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; Taphrinomycotina; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	Parent	Schizosaccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4895)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID	4896 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4896)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

UQCRFS1	Generic Gene Name	P47985 (http://www.uniprot.org/uniprot/P47985)	UniProtKB Homo sapiens
RIP1; RIS1; RISP; UQCR5	Synonyms	0	GenebankID or UniProtKB
9606.ENSP00000306397 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000306397)	String		
-	Sequence Similarities		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)	GO - Molecular Function		
GO:0051537 : 2 iron, 2 sulfur cluster binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051537)			
GO:0008121 : ubiquinol-cytochrome-c reductase activity			

(<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

Kraczy 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.

