

GEPHE SUMMARY

	Gephebase Gene	GephelD
cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="cytochrome b">#gephebase-summary-title)	GP00002044	Main curator
	Entry Status	Courtier
Published		

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology">#gephebase-summary-title)	Trait
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 State in Taxon A
sensitive	Trait State in Taxon B
resistant to its own toxin and to myxothiazol and (E)-p-methoxyacrylate-stilben	Ancestral State
Taxon A	Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Interspecific">#gephebase-summary-title)	

Taxon A		Taxon B	
Latin Name		Latin Name	
Mycena viridimarginata (#gephebase-summary-title)		Mycena galopus (#gephebase-summary-title)	
	Common Name		Common Name
-	Synonyms	-	Synonyms
-	Rank	-	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena	
	Parent		Parent
Mycena () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41247)		Mycena () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41247)	
41249 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41249)	NCBI Taxonomy ID	41248 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41248)	NCBI Taxonomy ID
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No	No		

GENOTYPIC CHANGE

UQCRLS1	Generic Gene Name	UniProtKB Homo sapiens
RIP1; RIS1; RISP; UQCRL5	Synonyms	GenebankID or UniProtKB
9606.ENSP00000306397 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000306397)	String	0
	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 (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 : mitochondrial (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>)

Mutation #1

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Coding%#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%SNP%#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Gly143Ala	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title)	Experimental Evidence

Taxon A	Taxon B	Position	
Codon	GGN	GCN	-
Amino-acid	Gly	Ala	143

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)	Main Reference
Kraiczy P; Haase U; Gencic S; Flindt S; Anke T; Brandt U; Von Jagow G	Authors
Mitochondria from the strobilurin A producing basidiomycetes <i>Strobilurus tenacellus</i> and <i>Mycena galopoda</i> exhibit natural resistance to (E)-beta-methoxyacrylate inhibitors of the ubiquinol oxidation center(Qp) of the cytochrome bc1 complex. Isolated cytochrome bc1 complex from <i>S. tenacellus</i> was found to be highly similar to that of <i>Saccharomyces cerevisiae</i> 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 <i>S. tenacellus</i> , <i>M. galopoda</i> and a third basidiomycete, <i>Mycena viridimarginata</i> , 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 <i>M. galopoda</i> replacement of Gly143 by alanine and Gly153 by serine, for <i>S. tenacellus</i> 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 <i>Schizosaccharomyces pombe</i> , which we found also to be naturally resistant to (E)-beta-methoxyacrylates.	Abstract
	Additional References

Mutation #2

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Coding%#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%SNP%#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Ala153Ser	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title)	Experimental Evidence

Taxon A	Taxon B	Position	
Codon	-	-	-
Amino-acid	Ala	Ser	153

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)	Main Reference
Kraiczy P; Haase U; Gencic S; Flindt S; Anke T; Brandt U; Von Jagow G	Authors
	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

No matches found.

Related Genes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%cytochrome b%/and+Taxon ID=%41249%/or+Gene Gephebase=%cytochrome b%/and+Taxon ID=%41248%#gephebase-summary-title>)

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@MitochondrialGene @SeveralMutationsWithEffect - The two mutations have been found in other resistant taxa.