

## GEPHE SUMMARY

**Gephebase Gene**  
cytochrome b

**Entry Status**  
Published

**GepheID**  
GP00002044

**Main curator**  
Courtier

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Xenobiotic resistance (fungicide; QoI; quinone outside inhibiting)

**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

	Taxon A
<b>Latin Name</b>	<i>Mycena viridimarginata</i>
<b>Common Name</b>	-
<b>Synonyms</b>	-
<b>Rank</b>	species
<b>Lineage</b>	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena
<b>Parent</b>	Mycena () - (Rank: genus)
<b>NCBI Taxonomy ID</b>	41249
<b>is Taxon A an Intraspecies?</b>	No

	Taxon B
<b>Latin Name</b>	<i>Mycena galopus</i>
<b>Common Name</b>	-
<b>Synonyms</b>	Mycena galopoda
<b>Rank</b>	species
<b>Lineage</b>	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena
<b>Parent</b>	Mycena () - (Rank: genus)
<b>NCBI Taxonomy ID</b>	41248
<b>is Taxon B an Intraspecies?</b>	No

## GENOTYPIC CHANGE

**Generic Gene Name**  
UQCRFS1

**Synonyms**  
RIP1; RIS1; RISP; UQCR5

**String**  
9606.ENSP00000306397

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0046872 : metal ion binding  
GO:0051537 : 2 iron, 2 sulfur cluster binding  
GO:0008121 : ubiquinol-cytochrome-c reductase activity

**GO - Biological Process**  
GO:0006122 : mitochondrial electron transport, ubiquinol to cytochrome c

**GO - Cellular Component**  
GO:0016021 : integral component of membrane  
GO:0005739 : mitochondrion  
GO:0005743 : mitochondrial inner membrane  
GO:0005751 : mitochondrial respiratory chain complex IV  
GO:0005750 : mitochondrial respiratory chain complex III

**UniProtKB Homo sapiens**  
P47985

**GenebankID or UniProtKB**

**Mutation #1****Presumptive Null**

No

**Molecular Type**

Coding

**Aberration Type**

SNP

**SNP Coding Change**

Nonsynonymous

**Molecular Details of the Mutation**

Gly143Ala

**Experimental Evidence**

Candidate Gene

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

**Main Reference**

The molecular basis for the natural resistance of the cytochrome bc1 complex from strobilurin-producing basidiomycetes to center Qp inhibitors. (1996)

**Authors**

Kraiczky 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****Mutation #2****Presumptive Null**

No

**Molecular Type**

Coding

**Aberration Type**

SNP

**SNP Coding Change**

Nonsynonymous

**Molecular Details of the Mutation**

Ala153Ser

**Experimental Evidence**

Candidate Gene

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

**Main Reference**

The molecular basis for the natural resistance of the cytochrome bc1 complex from strobilurin-producing basidiomycetes to center Qp inhibitors. (1996)

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**Additional References**

## RELATED GEPHE

[Related Genes](#)

No matches found.

[Related Haplotypes](#)

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## EXTERNAL LINKS

## COMMENTS

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