

GEPHE SUMMARY

| | | | |
|---|----------------|------------|--------------|
| cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] cytochrome b [^] #gephebase-summary-title) | Gephebase Gene | GP00002044 | 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; QoI; quinone outside inhibiting) (https://www.gephebase.org/search-criteria?/and+Trait = [^] Xenobiotic resistance (fungicide; QoI; quinone outside inhibiting) [^] #gephebase-summary-title) | Trait | | |
| sensitive | Trait State in Taxon A | | |
| resistant to its own toxin and to myxothiazol and (E)-p-methoxyacrylate-stilben | 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 | |
| | Latin Name | | Latin Name |
| Mycena viridimarginata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Mycena viridimarginata [^] #gephebase-summary-title) | | Mycena galopus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Mycena galopus [^] #gephebase-summary-title) | |
| - | Common Name | - | Common Name |
| - | Synonyms | | Synonyms |
| species | Rank | Mycena galopoda | Rank |
| cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena | Lineage | species | Lineage |
| Mycena () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41247) | Parent | cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Mycenaceae; Mycena | Parent |
| 41249 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41249) | NCBI Taxonomy ID | Mycena () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41247) | NCBI Taxonomy ID |
| | is Taxon A an Intraspecies? | 41248 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=41248) | is Taxon B an Intraspecies? |
| No | | No | |

GENOTYPIC CHANGE

| | | | |
|---|-------------------------|--|-------------------------|
| UQCRFS1 | Generic Gene Name | P47985 (http://www.uniprot.org/uniprot/P47985) | UniProtKB Homo sapiens |
| RIP1; RIS1; RISP; UQCR5 | Synonyms | () | 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:0006122 : mitochondrial electron transport, ubiquinol to cytochrome c (https://www.ebi.ac.uk/QuickGO/term/GO:0006122) | GO - Biological Process | | |

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)

Mutation #1 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
 Gly143Ala Experimental Evidence
 Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

| | 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)
 (https://pubmed.ncbi.nlm.nih.gov/8631367)

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 (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
 Ala153Ser 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 | 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)
 (https://pubmed.ncbi.nlm.nih.gov/8631367)

Authors

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Additional References

RELATED GEPHE

No matches found.

Related Genes

Related Haplotypes

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>)

EXTERNAL LINKS

COMMENTS

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