

GEPHE SUMMARY

cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] cytochrome b [^] #gephebase-summary-title)	Gephebase Gene	GP00002043	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; myxothiazol) (<a href="https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (fungicide; myxothiazol)<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=[^]Xenobiotic resistance (fungicide; myxothiazol)[^]#gephebase-summary-title)	Trait		
sensitive	Trait State in Taxon A		
resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Intraspecific [^] #gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Chlamydomonas reinhardtii (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Chlamydomonas reinhardtii<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Chlamydomonas reinhardtii[^]#gephebase-summary-title)	Latin Name	Chlamydomonas reinhardtii (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Chlamydomonas reinhardtii<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Chlamydomonas reinhardtii[^]#gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
	Synonyms		Synonyms
Chlamydomonas smithii; Chlamydomonas reinhardtii P.A.Dangeard; Chlamydomonas smithii R.W.Howshaw & H.Ettl; SAG 53.72; SAG 54.72; SAG:53.72; SAG:54.72; UTEX 90; UTEX:90; Chlamydomonas reihhardtii; Chlamydonas reinhardtii	Rank	Chlamydomonas smithii; Chlamydomonas reinhardtii P.A.Dangeard; Chlamydomonas smithii R.W.Howshaw & H.Ettl; SAG 53.72; SAG 54.72; SAG:53.72; SAG:54.72; UTEX 90; UTEX:90; Chlamydomonas reihhardtii; Chlamydonas reinhardtii	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas	Parent	cellular organisms; Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas	Parent
Chlamydomonas () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3052)	NCBI Taxonomy ID	Chlamydomonas () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3052)	NCBI Taxonomy ID
3055 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3055)	is Taxon A an Intraspecies?	3055 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3055)	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 - 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 : 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 ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null+No))

Molecular Type

Coding ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type+Coding))

Aberration Type

SNP ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type+SNP))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

F129L

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Phe	Lys	129

Main Reference

Mitochondrial genetics of *Chlamydomonas reinhardtii*: resistance mutations marking the cytochrome b gene. (1991) (<https://pubmed.ncbi.nlm.nih.gov/2004707>)

Authors

Bennoun P; Delosme M; KÄ¼ck U

Abstract

We describe the genetic and molecular analysis of the first non-Mendelian mutants of *Chlamydomonas reinhardtii* resistant to myxothiazol, an inhibitor of the respiratory cytochrome bc1 complex. Using a set of seven oligonucleotide probes, restriction fragments containing the mitochondrial cytochrome b (cyt b) gene from *C. reinhardtii* were isolated from a mitochondrial DNA library. This gene is located adjacent to the gene for subunit 4 of the mitochondrial NADH-dehydrogenase (ND4), near one end of the 15.8-kb linear mitochondrial genome of *C. reinhardtii*. The algal cytochrome b apoprotein contains 381 amino-acid residues and exhibits a sequence similarity of about 59% with other plant cytochrome b proteins. The cyt b gene from four myxothiazol resistant mutants of *C. reinhardtii* was amplified for DNA sequence analysis. In comparison to the wild-type strain, all mutants contain an identical point mutation in the cyt b gene, leading to a change of a phenylalanine codon to a leucine codon at amino acid position 129 of the cytochrome b protein. Segregation analysis in tetrads from reciprocal crosses of mutants with wild type shows a strict uniparental inheritance of this mutation from the mating type minus parent (UP-). However, mitochondrial markers from both parents are recovered in vegetative diploids in variable proportions from one experiment to the next for a given cross. On the average, a strong bias is seen for markers inherited from the mating type minus parent.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@MitochondrialGene

