

GEPHE SUMMARY

Gephebase Gene
cytochrome b

Entry Status
Published

GepheID
GP00002043

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Xenobiotic resistance (fungicide; myxothiazol)

Trait State in Taxon A
sensitive

Trait State in Taxon B
resistant

Ancestral State
Taxon A

Taxonomic Status
Intraspecific

Taxon A

Latin Name
Chlamydomonas reinhardtii

Common Name
-

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
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas

Parent
Chlamydomonas () - (Rank: genus)

NCBI Taxonomy ID
3055

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Chlamydomonas reinhardtii

Common Name
-

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

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Parent
Chlamydomonas () - (Rank: genus)

NCBI Taxonomy ID
3055

is Taxon B an Intraspecies?
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

UniProtKB Homo sapiens
P47985

GenebankID or UniProtKB

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

F129L

Experimental Evidence

Candidate Gene

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

Main ReferenceMitochondrial genetics of *Chlamydomonas reinhardtii*: resistance mutations marking the cytochrome b gene. (1991)**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****Related Genes**

No matches found.

Related Haplotypes

No matches found.

COMMENTS

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