

GEPHE SUMMARY

cytochrome b (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] cytochrome b [^] #gephebase-summary-title)	Gephebase Gene	GP00002042	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; Qol; quinone outside inhibiting; famoxadone) (https://www.gephebase.org/search-criteria?/and+Trait = [^] Xenobiotic resistance (fungicide; Qol; quinone outside inhibiting; famoxadone) [^] #gephebase-summary-title)	Trait		
sensitive	Trait State in Taxon A		
resistant - clade II	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	
Plasmopara viticola (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Plasmopara viticola [^] #gephebase-summary-title)	Latin Name	Plasmopara viticola (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Plasmopara viticola [^] #gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Peronosporaceae; Plasmopara	Lineage	cellular organisms; Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Peronosporaceae; Plasmopara	Lineage
Plasmopara () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4780)	Parent	Plasmopara () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4780)	Parent
143451 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=143451) is Taxon A an Infrasppecies?	NCBI Taxonomy ID	143451 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=143451) is Taxon B an Infrasppecies?	NCBI Taxonomy ID
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.ENSPP00000306397 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000306397)	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>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP^#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Gly143Ala G1256C

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	GGN	GCN	1256
Amino-acid	Gly	Ala	143

Main Reference

At least two origins of fungicide resistance in grapevine downy mildew populations. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17586672>)

Authors

Chen WJ; Delmotte F; Richard-Cervera S; Douence L; Greif C; Corio-Costet MF

Abstract

Quinone outside inhibiting (QoI) fungicides represent one of the most widely used groups of fungicides used to control agriculturally important fungal pathogens. They inhibit the cytochrome bc1 complex of mitochondrial respiration. Soon after their introduction onto the market in 1996, QoI fungicide-resistant isolates were detected in field plant pathogen populations of a large range of species. However, there is still little understanding of the processes driving the development of QoI fungicide resistance in plant pathogens. In particular, it is unknown whether fungicide resistance occurs independently in isolated populations or if it appears once and then spreads globally by migration. Here, we provide the first case study of the evolutionary processes that lead to the emergence of QoI fungicide resistance in the plant pathogen *Plasmopara viticola*. Sequence analysis of the complete cytochrome b gene showed that all resistant isolates carried a mutation resulting in the replacement of glycine by alanine at codon 143 (G143A). Phylogenetic analysis of a large mitochondrial DNA fragment including the cytochrome b gene (2,281 bp) across a wide range of European *P. viticola* isolates allowed the detection of four major haplotypes belonging to two distinct clades, each of which contains a different QoI fungicide resistance allele. This is the first demonstration that a selected substitution conferring resistance to a fungicide has occurred several times in a plant-pathogen system. Finally, a high population structure was found when the frequency of QoI fungicide resistance haplotypes was assessed in 17 French vineyards, indicating that pathogen populations might be under strong directional selection for local adaptation to fungicide pressure.

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=~143451^/or+Gene Gephebase=~cytochrome b^/and+Taxon ID=~143451^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~cytochrome+b^/and+Taxon+ID=~143451^/or+Gene+Gephebase=~cytochrome+b^/and+Taxon+ID=~143451^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@MitochondrialGene @Parallelism - phylogenetic reconstruction shows that the same mutation G>C Gly>Ala occurred independently in two different haplotypes

