

GEPHE SUMMARY

	Gephebase Gene		GepheID
CYP9M10 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~CYP9M10~#gephebase-summary-title)		GP00002116	
	Entry Status	Courtier	Main curator
Draft			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait	
Xenobiotic resistance (insecticide; pyrethroid) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic+resistance+(insecticide;+pyrethroid)~#gephebase-summary-title)		Trait State in Taxon A	
Culex pipiens quinquefasciatus - sensitive		Trait State in Taxon B	
Culex pipiens quinquefasciatus- resistant		Ancestral State	
Taxon A		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Culex quinquefasciatus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Culex+quinquefasciatus~#gephebase-summary-title)		Culex quinquefasciatus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Culex+quinquefasciatus~#gephebase-summary-title)	
	Common Name		Common Name
southern house mosquito		southern house mosquito	
	Synonyms		Synonyms
Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quinquifasiatus; Culex quiquefasciatus		Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quinquifasiatus; Culex quiquefasciatus	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Culicinae; Culicini; Culex; Culex; Culex pipiens complex		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Culicinae; Culicini; Culex; Culex; Culex pipiens complex	
	Parent		Parent
Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)		Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)		7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)	
	is Taxon A an Infrasppecies?		is Taxon B an Infrasppecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Culex quinquefasciatus
CYP9M10		D3KSB8 (http://www.uniprot.org/uniprot/D3KSB8)	
	Synonyms		GenebankID or UniProtKB
Cyp9m10; Cyp9m10v2		0	
-			
	String		
	Sequence Similarities		
Belongs to the cytochrome P450 family.			
	GO - Molecular Function		
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)			
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)			
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)			
GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (https://www.ebi.ac.uk/QuickGO/term/GO:0016705)			

GO - Biological Process

GO - Cellular Component

Mutation #1

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=))

Molecular Type

Gene Amplification ([https://www.gephebase.org/search-criteria?/and+Molecular Type=`Gene Amplification`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

Aberration Type

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

Insertion Size

100-1000 kb

Molecular Details of the Mutation

increased expression of the gene - identical tandem duplications of a 100-kb sequence containing the CYP9M10 locus

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=))

Main Reference

Genomic structures of Cyp9m10 in pyrethroid resistant and susceptible strains of *Culex quinquefasciatus*. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20600899>)

Authors

Itokawa K; Komagata O; Kasai S; Okamura Y; Masada M; Tomita T

Abstract

Development of insecticide resistance reduces the efficacy of controlling measures against the medical and agricultural insect pests. Cytochrome P450s are one of the major detoxification enzymes involved in insecticide metabolisms. Previously, we have reported that the P450 gene Cyp9m10 is about 260-fold overexpressed in a pyrethroid-resistant strain of *Culex quinquefasciatus* compared to a susceptible strain. In this study, we obtained direct evidence that the Cyp9m10 overexpression is caused by a cis-acting mutation. Additionally, a region of approximately 100 kb in length including the Cyp9m10 locus was specifically duplicated in the resistant strain. The two duplicated Cyp9m10 copies shared a completely identical sequence within the transcribed region and the flanking region up to the breakpoint located 1.1 kb upstream of the transcriptional start site. A Miniature Inverted-repeat Transposable Element (MITE)-like element was specifically inserted 0.2 kb upstream of both Cyp9m10 copies in the resistant strain. In backcross experiment, a haplotype containing the two duplicated Cyp9m10 copies was strongly associated with the pyrethroid resistance.

Copyright 2010 Elsevier Ltd. All rights reserved.

Additional References

Global spread and genetic variants of the two CYP9M10 haplotype forms associated with insecticide resistance in *Culex quinquefasciatus* Say. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23632895>)

Mutation #2

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=))

Molecular Type

Cis-regulatory ([https://www.gephebase.org/search-criteria?/and+Molecular Type=`Cis-regulatory`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

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=))

Molecular Details of the Mutation

G27A - increased expression of the gene

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=))

Main Reference

A single nucleotide change in a core promoter is involved in the progressive overexpression of the duplicated CYP9M10 haplotype lineage in *Culex quinquefasciatus*. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26494013>)

Authors

Itokawa K; Komagata O; Kasai S; Tomita T

Abstract

Although the importance of cis-acting mutations on detoxification enzyme genes for insecticide resistance is widely accepted, only a few of them have been determined as concrete mutations present in genomic DNA till date. The overexpression of a cytochrome P450 gene, CYP9M10, is associated with pyrethroid resistance in the southern house mosquito *Culex quinquefasciatus*. The haplotypes of CYP9M10 exhibiting overexpression (resistant haplotypes) belong to one specific phylogenetic lineage that shares high nucleotide sequence homology and the same insertion of a transposable element. Among the resistant haplotypes, allelic progression involving an additional cis-acting mutation and gene duplication evolved a CYP9M10 haplotype associated with extremely high transcription and strong pyrethroid resistance. Here we show that a single nucleotide substitution G-27A, which is located near the transcription start site of CYP9M10, is involved in the progression of the duplicated haplotype lineage. The deletion of a 7-bp AT-rich sequence that includes nucleotide -27 inhibited the initiation of transcription from the original transcriptional initiation site. The mutation was suspected to reside within a core promoter, TATA-box, of CYP9M10.

Copyright © 2015 The Authors. Published by Elsevier Ltd.. All rights reserved.

Additional References

RELATED GEPHE

Related Genes

5 (Cpm1, esterase B1 + esterase A, esterase B1 = esterase beta1, para (kdr), resistance to dieldrin) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=`7176`/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SelectiveSweep - There are only three segregating nucleotides within the region 2.2-kb upstream from the transcription start site: 2000T/G; 1176A/G and 27G/A. The G27A mutation apparently predates the duplication because they exist in both copies of duplicated haplotypes. @TE A Miniature Inverted-repeat Transposable Element (MITE)-like element was specifically inserted 0.2 kb upstream of both Cyp9m10 copies in the resistant strain