

GEPHE SUMMARY

CYP9M10 (#gephebase-summary-title)	Gephebase Gene	GP00002116	GephelD
Draft	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category			
Physiology (#gephebase-summary-title)	Trait		
Xenobiotic resistance (insecticide; pyrethroid) (<a and+taxonomicstatus='Intraspecific"' href="https://www.gephebase.org/search-criteria?/and+Trait=Xenobiotic+resistance+(insecticide;+pyrethroid)#gephebase-summary-title)</td><td>Trait State in Taxon A</td><td></td><td></td></tr> <tr> <td>Culex pipiens quinquefasciatus - sensitive</td><td>Trait State in Taxon B</td><td></td><td></td></tr> <tr> <td>Culex pipiens quinquefasciatus- resistant</td><td>Ancestral State</td><td></td><td></td></tr> <tr> <td>Taxon A</td><td>Taxonomic Status</td><td></td><td></td></tr> <tr> <td>Intraspecific (#gephebase-summary-title)			
Taxon A		Taxon B	
Culex quinquefasciatus (#gephebase-summary-title)	Latin Name	Culex quinquefasciatus (#gephebase-summary-title)	Latin Name
southern house mosquito	Common Name	southern house mosquito	Common Name
Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquefasciatus; Culex quinquefasciatus; Culex quiquefasciatus	Synonyms	Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquefasciatus; Culex quinquefasciatus; Culex quiquefasciatus	Synonyms
species	Rank	species	Rank
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	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	Lineage
Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)	Parent	Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)	Parent
7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)	NCBI Taxonomy ID	7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

CYP9M10	Generic Gene Name	UniProtKB Culex quinquefasciatus
Cyp9m10; Cyp9m10v2	Synonyms	GenebankID or UniProtKB
-	String	0
Belongs to the cytochrome P450 family.	Sequence Similarities	
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 - Molecular Function	

Mutation #1

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Gene Amplification (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Amplification%#gephebase-summary-title)	Molecular Type
Insertion (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Insertion%#gephebase-summary-title)	Aberration Type
100-1000 kb	Insertion Size
increased expression of the gene - identical tandem duplications of a 100-kb sequence containing the CYP9M10 locus	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title)	Experimental Evidence
Genomic structures of Cyp9m10 in pyrethroid resistant and susceptible strains of <i>Culex quinquefasciatus</i> . (2010) (https://pubmed.ncbi.nlm.nih.gov/20600899)	Main Reference
Itokawa K; Komagata O; Kasai S; Okamura Y; Masada M; Tomita T	Authors
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 <i>Culex quinquefasciatus</i> 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.	Abstract
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 <i>Culex quinquefasciatus</i> Say. (2013) (https://pubmed.ncbi.nlm.nih.gov/23632895)	

Mutation #2

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Cis-regulatory%#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%SNP%#gephebase-summary-title)	Aberration Type
G27A - increased expression of the gene	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title)	Experimental Evidence
A single nucleotide change in a core promoter is involved in the progressive overexpression of the duplicated CYP9M10 haplotype lineage in <i>Culex quinquefasciatus</i> . (2015) (https://pubmed.ncbi.nlm.nih.gov/26494013)	Main Reference
Itokawa K; Komagata O; Kasai S; Tomita T	Authors
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 <i>Culex quinquefasciatus</i> . 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 A-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.	Abstract
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RELATED GEPHE

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)	Related Genes
No matches found.	Related Haplotypes

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