

GEPHE SUMMARY

	Gephbase Gene	GephelD
para (kdr) (https://www.gephebase.org/search-criteria?/and+Gene Gephbase='para (kdr)'#gephebase-summary-title)	GP00002524	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category='Physiology'#gephebase-summary-title)	Trait
Xenobiotic resistance (insecticide) (https://www.gephebase.org/search-criteria?/and+Trait='Xenobiotic resistance (insecticide)'#gephebase-summary-title)	Trait State in Taxon A
Culex quinquefasciatus	Trait State in Taxon B
Culex quinquefasciatus - resistant	Ancestral State
Taxon A	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status='Intraspecific'#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	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)	
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

	Generic Gene Name	UniProtKB Drosophila melanogaster
para	Synonyms	P35500 (http://www.uniprot.org/uniprot/P35500)
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]; I(1)14Da; I(1)ESHS48; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer	String	GenebankID or UniProtKB
7227.FBpp0303597 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303597)	Sequence Similarities	0
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.	GO - Molecular Function	
GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)		
GO:0005244 : voltage-gated ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005244)		
GO:0005248 : voltage-gated sodium channel activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005248>)

GO:0005272 : sodium channel activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005272>)

GO - Biological Process

GO:0045433 : male courtship behavior, veined wing generated song production

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045433>)

GO:0001666 : response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0001666>)

GO:0009612 : response to mechanical stimulus

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009612>)

GO:0034765 : regulation of ion transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0034765>)

GO:0035725 : sodium ion transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035725>)

GO:0007638 : mechanosensory behavior

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007638>)

GO:0060078 : regulation of postsynaptic membrane potential

(<https://www.ebi.ac.uk/QuickGO/term/GO:0060078>)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

GO:0001518 : voltage-gated sodium channel complex

(<https://www.ebi.ac.uk/QuickGO/term/GO:0001518>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L1014F

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Resistance in the mosquito, *Culex quinquefasciatus*, and possible mechanisms for resistance. (2005) (<https://pubmed.ncbi.nlm.nih.gov/16032654>)

Main Reference

Xu Q; Liu H; Zhang L; Liu N

Authors

Abstract

Two mosquito strains of *Culex quinquefasciatus* (Say), MAmCq(G0) and HAmCq(G0), were collected from Mobile and Huntsville, Alabama, respectively. MAmCq(G0) and HAmCq(G0) were further selected in the laboratory with permethrin for one and three generations, respectively. The levels of resistance to permethrin in MAmCq(G1) (after one-generation selection) and HAmCq(G3) (after three-generation selection) increased rapidly. Resistance to permethrin in MAmCq(G1) and HAmCq(G3) was partially suppressed by piperonyl butoxide (PBO), S,S,S-tributylphosphorothioate (DEF) and diethyl maleate (DEM), inhibitors of cytochrome P450 monooxygenases, hydrolases and glutathione S-transferases (GST), respectively, suggesting these three enzyme families are important in conferring permethrin resistance in both strains. A substitution of leucine to phenylalanine (L to F) resulting from a single nucleotide polymorphism (SNP), termed the kdr mutation, in the para-homologous sodium channel gene has been reported as a very common mutation associated with pyrethroid resistance of insects. A 341-bp sodium channel gene fragment, where the kdr mutation resides, was generated by PCR from genomic DNAs of *Cx. quinquefasciatus* strains. We found that the kdr mutation was present in both permethrin-selected and unselected HAmCq and MAmCq mosquito populations, suggesting that the kdr mutation plays the role in permethrin resistance. There was no significant change in the frequency and heterozygosity of the A to T SNP for the kdr allele between permethrin-selected and unselected MAmCq and HAmCq mosquitoes, indicating that other mechanisms are involved in the evolution of resistance in mosquitoes selected by permethrin in the laboratory.

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Additional References

Molecular biology of insect sodium channels and pyrethroid resistance. (2014) (<https://pubmed.ncbi.nlm.nih.gov/24704279>)

RELATED GEPHE

Related Genes

4 (Cpm1, esterase B1 + esterase A, esterase B1 = esterase beta1, resistance to dieldrin) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7176^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^para+\(kdr\)^/and+Taxon+ID=^7176^/or+Gene+Gephebase=^para+\(kdr\)^/and+Taxon+ID=^7176^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^para+(kdr)^/and+Taxon+ID=^7176^/or+Gene+Gephebase=^para+(kdr)^/and+Taxon+ID=^7176^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS