

## GEPHE SUMMARY

	Gephebase Gene		GepheID
para (kdr) ( <a +para+(kdr)^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+para+(kdr)^#gephebase-summary-title</a> )		GP00002489	Main curator
Published	Entry Status	Courtier	

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a +physiology^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology^#gephebase-summary-title</a> )			
	Trait		
Xenobiotic resistance (insecticide) ( <a +xenobiotic+resistance+(insecticide)^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic+resistance+(insecticide)^#gephebase-summary-title</a> )			
	Trait State in Taxon A		
Culex quinquefasciatus			
	Trait State in Taxon B		
Culex quinquefasciatus - resistant			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific ( <a +intraspecific^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific^#gephebase-summary-title</a> )			
Taxon A		Taxon B	
	Latin Name		Latin Name
Culex quinquefasciatus ( <a +culex+quinquefasciatus^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Culex+quinquefasciatus^#gephebase-summary-title</a> )		Culex quinquefasciatus ( <a +culex+quinquefasciatus^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Culex+quinquefasciatus^#gephebase-summary-title</a> )	
	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) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105</a> )		Culex pipiens complex () - (Rank: no rank) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7176 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7176">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7176</a> )		7176 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7176">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7176</a> )	
	is Taxon A an Infrasppecies?		is Taxon B an Infrasppecies?
No		No	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
para		P35500 ( <a href="http://www.uniprot.org/uniprot/P35500">http://www.uniprot.org/uniprot/P35500</a> )	GenebankID or UniProtKB
	Synonyms		
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]1; l(1)14Da; l(1)ESH548; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer		()	
	String		
7227.FBpp0303597 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597</a> )			
	Sequence Similarities		
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.			
	GO - Molecular Function		
GO:0005509 : calcium ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005509">https://www.ebi.ac.uk/QuickGO/term/GO:0005509</a> )			
GO:0005244 : voltage-gated ion channel activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005244">https://www.ebi.ac.uk/QuickGO/term/GO:0005244</a> )			
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 (<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>)

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

3 nonsynonymous A(109)S L(982)F and W(1573)R and 6 synonymous L(852) G(891) A(1241) D(1245) P(1249) and G(1733)) mutations were identified. The co-existence of all 9 mutations and their homozygosity were found to be important factors for high levels of resistance.

Experimental Evidence

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

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

Main Reference

Evolutionary adaptation of the amino acid and codon usage of the mosquito sodium channel following insecticide selection in the field mosquitoes. (2012)

(<https://pubmed.ncbi.nlm.nih.gov/23082181>)

Authors

Xu Q; Zhang L; Li T; Zhang L; He L; Dong K; Liu N

Abstract

Target site insensitivity resulting from point mutations within the voltage-gated sodium channel of the insect nervous system is known to be of primary importance in the development of resistance to pyrethroid insecticides. This study shifts current research paradigms by conducting, for the first time, a global analysis of all the naturally occurring mutations, both nonsynonymous and synonymous mutations, as well as mutation combinations in the entire mosquito sodium channel of *Culex quinquefasciatus* and analyzing their evolutionary and heritable feature and roles in insecticide resistance. Through a systematic analysis of comparing nucleotide polymorphisms in the entire sodium channel cDNAs of individuals between susceptible and resistant mosquito strains, between field parental mosquitoes and their permethrin selected offspring, and among different mosquito groups categorized by their levels of tolerance to specific permethrin concentrations within and among the mosquito strains of the field parental strains and their permethrin selected offspring, 3 nonsynonymous (A(109)S, L(982)F, and W(1573)R) and 6 synonymous (L(852), G(891), A(1241), D(1245), P(1249), and G(1733)) mutations were identified. The co-existence of all 9 mutations, both nonsynonymous and synonymous, and their homozygosity were found to be important factors for high levels of resistance. Our study, for the first time, provide a strong case demonstrating the co-existence of both nonsynonymous and synonymous mutations in the sodium channel of resistant mosquitoes in response to insecticide resistance and the inheritance of these mutations in the offspring of field mosquito strains following insecticide selection.

Additional References

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