

## GEPHE SUMMARY

	Gephebase Gene	GephelD
para (kdr) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene Gephebase='para (kdr)'#gephebase-summary-title">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 href="https://www.gephebase.org/search-criteria?/and+Trait Category='Physiology'#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait Category='Physiology'#gephebase-summary-title</a> )	Trait
Xenobiotic resistance (insecticide) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait='Xenobiotic resistance (insecticide)'#gephebase-summary-title">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 href="https://www.gephebase.org/search-criteria?/and+Taxonomic Status='Intraspecific'#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic Status='Intraspecific'#gephebase-summary-title</a> )	

Taxon A	Latin Name	Taxon B	Latin Name
Culex quinquefasciatus ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Culex quinquefasciatus'#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Culex quinquefasciatus'#gephebase-summary-title</a> )	Common Name	Culex quinquefasciatus ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Culex quinquefasciatus'#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Culex quinquefasciatus'#gephebase-summary-title</a> )	Common Name
southern house mosquito	Synonyms	southern house mosquito	Synonyms
Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quiquefasciatus	Rank	Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quiquefasciatus	Rank
species	Lineage	species	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	Parent	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
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	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
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> )	
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
para	Synonyms	GenebankID or UniProtKB
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 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> )	P35500 ( <a href="http://www.uniprot.org/uniprot/P35500">http://www.uniprot.org/uniprot/P35500</a> ) 0	
	String	
	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=%22No%22#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%22Coding%22#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%22SNP%22#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=%22Candidate+Gene%22#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=%227176%22+and+Trait=Xenobiotic+resistance+and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria/?or+Gene+Gephebase=%22para+\(kdr\)%22+and+Taxon+ID=%227176%22+or+Gene+Gephebase=%22para+\(kdr\)%22+and+Taxon+ID=%227176%22#gephebase-summary-title](https://www.gephebase.org/search-criteria/?or+Gene+Gephebase=%22para+(kdr)%22+and+Taxon+ID=%227176%22+or+Gene+Gephebase=%22para+(kdr)%22+and+Taxon+ID=%227176%22#gephebase-summary-title))

## EXTERNAL LINKS

## COMMENTS