

## GEPHE SUMMARY

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> )	Gephebase Gene	GP00002488	GepheID
Published	Entry Status	Courtier	Main curator

## PHENOTYPIC CHANGE

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 Category		
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		
Aedes aegypti	Trait State in Taxon A		
Aedes aegypti - resistant from America and Brazil	Trait State in Taxon B		
Taxon A	Ancestral State		
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> )	Taxonomic Status		

Taxon A	Latin Name	Taxon B	Latin Name
Aedes aegypti ( <a +aedes+aegypti^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Aedes aegypti^#gephebase-summary-title</a> )	Aedes aegypti	Aedes aegypti ( <a +aedes+aegypti^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Aedes aegypti^#gephebase-summary-title</a> )	Aedes aegypti
yellow fever mosquito	Common Name	yellow fever mosquito	Common Name
Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)	Synonyms	Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)	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; Aedini; Aedes; Stegomyia	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; Aedini; Aedes; Stegomyia	Lineage
Stegomyia () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541</a> )	Parent	Stegomyia () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541</a> )	Parent
7159 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159</a> )	NCBI Taxonomy ID	7159 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159</a> )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

para	Generic Gene Name	P35500 ( <a href="http://www.uniprot.org/uniprot/P35500">http://www.uniprot.org/uniprot/P35500</a> )	UniProtKB Drosophila melanogaster
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]1; l(1)14Da; l(1)ESH548; lincRNA.S9469; Nav1; Occl; olfD; par; sbl; sbl-1; Shu; Shudderer	Synonyms	()	GenebankID or UniProtKB
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> )	String		
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.	Sequence Similarities		
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 - Molecular Function		
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 ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005248">https://www.ebi.ac.uk/QuickGO/term/GO:0005248</a> )			
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>)

Mutation #1

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

The 410L+1534C allele appears to have arisen by accumulation of the 410L mutation in an individual already having the 1534C allele or by a crossover event. The F1534C occurred independently in several populations of *Aedes aegypti*.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	TCA	TGA	-
Amino-acid	Phe	Cys	1534

Main Reference

Detection of a new pyrethroid resistance mutation (V410L) in the sodium channel of *Aedes aegypti*: a potential challenge for mosquito control. (2017)

(<https://pubmed.ncbi.nlm.nih.gov/28422157>)

Authors

Haddi K; TomÃ© HVV; Du Y; Valbon WR; Nomura Y; Martins GF; Dong K; Oliveira EE

Abstract

The yellow fever mosquito, *Aedes aegypti*, particularly in Neotropical regions, is the principal vector of dengue, yellow fever, Zika and Chikungunya viruses. Pyrethroids remain one of the most used insecticides to control *Aedes* mosquitoes, despite the development of pyrethroid resistance in many mosquito populations worldwide. Here, we report a Brazilian strain of *A. aegypti* with high levels (approximately 100-60,000 fold) of resistance to both type I and type II pyrethroids. We detected two mutations (V410L and F1534C) in the sodium channel from this resistant strain. This study is the first report of the V410L mutation in mosquitoes. Alone or in combination with the F1534C mutation, the V410L mutation drastically reduced the sensitivity of mosquito sodium channels expressed in *Xenopus* oocytes to both type I and type II pyrethroids. The V410L mutation presents a serious challenge for the control of *A. aegypti* and will compromise the use of pyrethroids for the control of *A. aegypti* in Brazil; therefore, early monitoring of the frequency of the V410L mutation will be a key resistance management strategy to preserve the effectiveness of pyrethroid insecticides.

Additional References

Evidence for both sequential mutations and recombination in the evolution of *kdr* alleles in *Aedes aegypti*. (2020) (<https://pubmed.ncbi.nlm.nih.gov/32302303>)

Mutation #2

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

The 410L+1534C allele appears to have arisen by accumulation of the 410L mutation in an individual already having the 1534C allele or by a crossover event. The F1534C occurred independently in several populations of *Aedes aegypti*.

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	Val	Leu	410

Main Reference

Detection of a new pyrethroid resistance mutation (V410L) in the sodium channel of *Aedes aegypti*: a potential challenge for mosquito control. (2017) (<https://pubmed.ncbi.nlm.nih.gov/28422157>)

Authors

Haddi K; TomÃ© HVV; Du Y; Valbon WR; Nomura Y; Martins GF; Dong K; Oliveira EE

Abstract

The yellow fever mosquito, *Aedes aegypti*, particularly in Neotropical regions, is the principal vector of dengue, yellow fever, Zika and Chikungunya viruses. Pyrethroids remain one of the most used insecticides to control *Aedes* mosquitoes, despite the development of pyrethroid resistance in many mosquito populations worldwide. Here, we report a Brazilian strain of *A. aegypti* with high levels (approximately 100-60,000 fold) of resistance to both type I and type II pyrethroids. We detected two mutations (V410L and F1534C) in the sodium channel from this resistant strain. This study is the first report of the V410L mutation in mosquitoes. Alone or in combination with the F1534C mutation, the V410L mutation drastically reduced the sensitivity of mosquito sodium channels expressed in *Xenopus* oocytes to both type I and type II pyrethroids. The V410L mutation presents a serious challenge for the control of *A. aegypti* and will compromise the use of pyrethroids for the control of *A. aegypti* in Brazil; therefore, early monitoring of the frequency of the V410L mutation will be a key resistance management strategy to preserve the effectiveness of pyrethroid insecticides.

Additional References

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RELATED GEPHE

Related Genes

4 (ABC4, CYP9J26, CYP9M6, resistance to dieldrin) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7159^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

7 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^7159^/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^7159^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7159^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7159^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS