GEPHE SUMMARY

Gephebase Gene

para (kdr) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^para (kdr)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002488

Main curator

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

Aedes aegypti

Trait State in Taxon B

Aedes aegypti - resistant from America and Brazil

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Aedes aegypti (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Aedes aegypti^#gephebase-summary-title)

Common Name

yellow fever mosquito

Synonyms

Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)

Rank

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; Aedini; Aedes; Stegomyia

Parent

Stegomyia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 53541)

NCBI Taxonomy ID

7159 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7159)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Aedes aegypti (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Aedes aegypti^#gephebase-summary-title)

Common Name

yellow fever mosquito

Synonyms

Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)

Rank

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; Aedini; Aedes; Stegomyia

Parent

Stegomyia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 53541)

NCBI Taxonomy ID

7159 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7159)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

para

Synonyms

bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]1; l(1)14Da; l(1)ESHS48; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer

String

7227.FBpp0303597 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303597)

Sequence Similarities

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

UniProtKB Drosophila melanogaster

P35500 (http://www.uniprot.org/uniprot/P35500)

GenebankID or UniProtKB

()

(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

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

RELATED GEPHE

Related Genes

4 (ABCB4, 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)

EXTERNAL LINKS

COMMENTS