GEPHE SUMMARY

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

GepheID
GP00002647

Entry Status
Published

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 albopictus

Trait State in Taxon B
Aedes albopictus - resistant from China

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

Common Name
Asian tiger mosquito

Synonyms
Stegomyia albopicta; Asian tiger mosquito; forest day mosquito; Aedes albopictus (Skuse, 1894)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; 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
7160 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7160)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
Asian tiger mosquito

Synonyms
Stegomyia albopicta; Asian tiger mosquito; forest day mosquito; Aedes albopictus (Skuse, 1894)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; 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
7160 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7160)

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)

UniProtKB Drosophila melanogaster
P35500 (http://www.uniprot.org/uniprot/P35500)

GenebankID or UniProtKB
()

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

I1532T

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	ACC	-
Amino-acid	Ile	Thr	1532

Main Reference

Knockdown Resistance (kdr) Mutations I1532T and F1534S Were Identified in Aedes albopictus Field Populations in Zhejiang Province, Central China. (2021)
(https://pubmed.ncbi.nlm.nih.gov/34268140)

Authors

Wu Y; Liu Q; Qi Y; Wu Y; Ni Q; Chen W; Wang J; Li T; Luo M; Hou J; Gong Z; Sun J

Abstract

Aedes albopictus is the only vector that can transmit the dengue virus in Zhejiang Province, central China, and it can develop insecticide resistance due to long-term exposure to pyrethroids. The presence of knockdown resistance (kdr) mutations is one of the mechanisms responsible for pyrethroid resistance, and has been reported in some Ae. albopictus populations in southern China. However, little is known about the DNA diversity of the voltage-gated sodium channel (VGSC) gene in Ae. albopictus populations in central China. Four Ae. albopictus field populations were collected, in Yiwu (YW), Quzhou (QZ), Wenzhou (WZ), and Jiaxing (JX) from Zhejiang Province, central China. The susceptibility of Ae. albopictus adults to three pyrethroids (beta-cypermethrin, deltamethrin, and permethrin) was tested using the WHO tube assay, and Kdr mutations were identified via PCR and sequencing. The relationship between kdr mutations and pyrethroid phenotypes was also analyzed. Of the four populations, none was sensitive to any pyrethroid tested, and the YW population showed the strongest pyrethroid resistance. Non-synonymous kdr mutations were detected in codons 1532 and 1534, domain III. At codon 1534, one mutant allele, TCC(S), was detected in the four populations with a frequency of 42.08%, while at codon 1532, one mutant allele, ACC(T), was detected in the JX and QZ populations, with frequencies of 4.22 and 3.03%, respectively. The F1534S mutant allele was positively correlated with both beta-cypermethrin and deltamethrin resistance phenotypes (OR > 1, P < 0.05), whereas the I1532T mutant allele was possibly negatively correlated with beta-cypermethrin, deltamethrin, and permethrin resistance phenotypes (OR < 1, P > 0.05). In conclusion, resistance and resistance mutations regarding to three pyrethroids are already present in the Ae. Albopictus populations from Zhejiang, central China, which prompts the need to use non-insecticide-based methods of insect control.

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Additional References

RELATED GEPHE

Related Genes

1 (resistance to dieldrin) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7160^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7160^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7160^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS