GEPHE SUMMARY

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

GepheID
GP00002540

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
Sensitive to Pyrethroids

Trait State in Taxon B
Resistant to Pyrethroids

Ancestral State
Taxon A

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

Taxon A

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

Common Name
-

Synonyms
Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828

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; Anophelinae; Anopheles; Anopheles; Laticorn; Myzorhynchus; hyrcanus group

Parent
hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)

NCBI Taxonomy ID
74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828

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; Anophelinae; Anopheles; Anopheles; Laticorn; Myzorhynchus; hyrcanus group

Parent
hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)

NCBI Taxonomy ID
74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)

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

L1014W

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	TTG	TGG	-
Amino-acid	Leu	Trp	1014

Main Reference

First detection of multiple knockdown resistance (kdr)-like mutations in voltage-gated sodium channel using three new genotyping methods in Anopheles sinensis from Guangxi Province, China. (2012) (https://pubmed.ncbi.nlm.nih.gov/23025181)

Authors

Tan WL; Li CX; Wang ZM; Liu MD; Dong YD; Feng XY; Wu ZM; Guo XX; Xing D; Zhang YM; Wang ZC; Zhao TY

Abstract

To investigate knockdown resistance (kdr)-like mutations associated with pyrethroid resistance in Anopheles sinensis (Wiedemann, 1828), from Guangxi province, southwest China, a segment of a sodium channel gene was sequenced and genotyped using three new genotyping assays. Direct sequencing revealed the presence of TTG-to-TCG and TG-to-TTT mutations at allele position L1014, which led to L1014S and L1014F substitutions in a few individual and two novel substitutions of N1013S and L1014W in two DNA templates. A low frequency of the kdr allele mostly in the heterozygous state of L1014S and L1014F was observed in this mosquito population. In this study, the genotyping of An. sinensis using three polymerase chain reaction-based methods generated consistent results, which agreed with the results of DNA sequencing. In total, 52 mosquitoes were genotyped using a direct sequencing assay. The number of mosquitoes and their genotypes were as follows: L/L = 24, L/S = 19, L/F = 8, and F/W = 1. The allelic frequency of L1014, 1014S, and 1014F were 72, 18, and 9%, respectively.

Additional References

Molecular biology of insect sodium channels and pyrethroid resistance. (2014) (https://pubmed.ncbi.nlm.nih.gov/24704279)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

6 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^74873^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^74873^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS