GEPHE SUMMARY

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

GepheID
GP00000821

Entry Status
Published

Main curator
Martin

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)

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

L1014F

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	TTT	-
Amino-acid	Leu	Phe	1014

Main Reference

First report on co-occurrence knockdown resistance mutations and susceptibility to beta-cypermethrin in Anopheles sinensis from Jiangsu Province, China. (2012)
(https://pubmed.ncbi.nlm.nih.gov/22272229)

Authors

Tan WL; Wang ZM; Li CX; Chu HL; Xu Y; Dong YD; Wang ZC; Chen DY; Liu H; Liu DP; Liu N; Sun J; Zhao T

Abstract

The increasing prevalence of insecticide resistance in Anopheles sinensis, a major vector of malaria in Jiangsu province in eastern China, threatens to compromise the successful use of insecticides in malaria control strategies. It is therefore vital to understand the insecticide resistance status of An. sinensis in the region. This study examined the nucleotide diversity of the para-sodium channel and knockdown resistance (kdr) in five field populations of adult An. sinensis mosquitoes collected in Jiangsu province, identifying the L1014F and L1014C substitutions for the first time. Competitive polymerase chain reaction (PCR) amplification of specific allele (cPASA) and polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP) for resistance diagnosis were developed and validated. Comparing the results with direct sequencing revealed that the PCR-RFLP method was more sensitive and specific whereas the cPASA method was more convenient and suitable. The significant positive correlation between kdr allele frequency and bioassay-based resistance phenotype demonstrates that the frequency of L1014F and L1014C substitutions in the kdr gene provides a useful molecular marker for monitoring beta-cypermethrin resistance in natural populations of An. sinensis. Our results point to the L1014F substitution as the key mutation associated with beta-cypermethrin resistance. The high resistance and mutation frequency detected in the five populations also suggest cross-resistance with other pyrethroids may occur in An. sinensis, highlighting the need for further surveys to map insecticide resistance in China and the adoption of a rational management of insecticide application for resistance management and mosquito vector control.

Additional References

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

F1014C

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	TTT	TGT	-
Amino-acid	Phe	Cys	1014

Main Reference

First report on co-occurrence knockdown resistance mutations and susceptibility to beta-cypermethrin in Anopheles sinensis from Jiangsu Province, China. (2012) (https://pubmed.ncbi.nlm.nih.gov/22272229)

Authors

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Additional References

Landscape genetic structure and evolutionary genetics of insecticide resistance gene mutations in Anopheles sinensis. (2016) (https://pubmed.ncbi.nlm.nih.gov/27108406)

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

@TwoNucleotideChangesInSameCodon @SuccessiveMutationsAtSameCodon - The intermediate sequence carrying only the first mutation is present within the population.