

GEPHE SUMMARY

para (kdr) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase='para (kdr)'#gephebase-summary-title)	Gephebase Gene	GP00001699	GepheID
	Entry Status	admin	Main curator
Published			

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	Taxon B	Latin Name
Anopheles sinensis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Anopheles sinensis'#gephebase-summary-title)		Anopheles sinensis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Anopheles sinensis'#gephebase-summary-title)	
-	Common Name	-	Common Name
Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828	Synonyms	Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828	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; Anophelinae; Anopheles; Anopheles; Laticorn; Myzorrhynchus; hyrcanus group	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; Myzorrhynchus; hyrcanus group	Lineage
hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)	Parent	hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)	Parent
74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)	NCBI Taxonomy ID	74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Generic Gene Name			
para	Synonyms	P35500 (http://www.uniprot.org/uniprot/P35500)	UniProtKB Drosophila melanogaster
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]; I(1)14Da; I(1)ESHS48; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer	String	0	GenebankID or UniProtKB
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

(<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

L1014F; Haplotype H04

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

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](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

@Parallelism