

GEPHE SUMMARY

para (kdr) (#gephebase-summary-title)	Gephebase Gene	GP00001691	GepheID
Published	Entry Status	admin	Main curator

PHENOTYPIC CHANGE

Physiology (#gephebase-summary-title)	Trait Category		
Xenobiotic resistance (insecticide) (#gephebase-summary-title)	Trait		
Sensitive to Pyrethroids	Trait State in Taxon A		
Resistant to Pyrethroids	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (#gephebase-summary-title)	Taxonomic Status		
Taxon A	Latin Name	Taxon B	Latin Name
Anopheles sinensis (#gephebase-summary-title)		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

para	Generic Gene Name	UniProtKB Drosophila melanogaster
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]; l(1)14Da; l(1)ESHS48; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer	Synonyms	GenebankID or UniProtKB
7227.FBpp0303597 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303597)	String	0
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.	Sequence Similarities	
GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)	GO - Molecular Function	
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=%22No%22#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Coding%22#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22SNP%22#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L1014S; Haplotype H04

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Candidate+Gene%22#gephebase-summary-title>)

		Taxon A	Taxon B	Position
Codon	TTG	TCG	-	
Amino-acid	Leu	Ser	1014	

Main Reference

Knockdown resistance in *Anopheles vagus*, *An. sinensis*, *An. paraliae* and *An. peditaeniatus* populations of the Mekong region. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20646327>)

Authors

Verhaeghen K; Van Bortel W; Trung HD; Sochantha T; Keokenchanh K; Coosemans M

Abstract

In the Mekong region (Vietnam, Cambodia and Laos), a large investigation was conducted to assess the susceptibility of *Anopheles* species against DDT and pyrethroids. In this study, the resistance status of the potential malaria vectors *An. vagus*, *An. sinensis*, *An. paraliae* and *An. peditaeniatus* was assessed.

Bioassays were performed on field collected unfed female mosquitoes using the standard WHO susceptibility tests. In addition, the DIIS6 region of the para-type sodium channel gene was amplified and sequenced and four allele-specific PCR assays were developed to assess the kdr frequencies.

In Southern Vietnam all species were DDT and pyrethroid resistant, which might suggest the presence of a kdr resistance mechanism. Sequence-analysis of the DIIS6 region of the para-type sodium channel gene revealed the presence of a L1014S kdr mutation in *An. vagus*, *An. sinensis* and *An. paraliae*. In *An. peditaeniatus*, a low frequency L1014S kdr mutation was found in combination with a high frequency L1014F kdr mutation. For pyrethroids and DDT, no genotypic differentiation was found between survivors and non-survivors for any of these species. In the two widespread species, *An. vagus* and *An. sinensis*, kdr was found only in southern Vietnam and in Cambodia near the Vietnamese border.

Different levels of resistance were measured in Laos, Cambodia and Vietnam. The kdr mutation in different *Anopheles* species seems to occur in the same geographical area. These species breed in open agricultural lands where malaria endemicity is low or absent and vector control programs less intensive. It is therefore likely that the selection pressure occurred on the larval stages by insecticides used for agricultural purposes.

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

No matches found.

Related Genes

6 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%22para+\(kdr\)%22/and+Taxon+ID=%2274873%22/or+Gene+Gephebase=%22para+\(kdr\)%22/and+Taxon+ID=%2274873%22#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%22para+(kdr)%22/and+Taxon+ID=%2274873%22/or+Gene+Gephebase=%22para+(kdr)%22/and+Taxon+ID=%2274873%22#gephebase-summary-title))

Related Haplotypes

EXTERNAL LINKS

COMMENTS

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