

## GEPHE SUMMARY

	Gephebase Gene		GepheID
para (kdr) ( <a +para+(kdr)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+para+(kdr)+"#gephebase-summary-title</a> )		GP00001695	Main curator
	Entry Status	admin	
Published			

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title</a> )		
	Trait	
Xenobiotic resistance (insecticide) ( <a +xenobiotic+resistance+(insecticide)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic+resistance+(insecticide)+"#gephebase-summary-title</a> )		
	Trait State in Taxon A	
Sensitive to Pyrethroids		
	Trait State in Taxon B	
Resistant to Pyrethroids		
	Ancestral State	
Taxon A		
	Taxonomic Status	
Intraspecific ( <a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title</a> )		

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

## GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
para		P35500 ( <a href="http://www.uniprot.org/uniprot/P35500">http://www.uniprot.org/uniprot/P35500</a> )
	Synonyms	GenebankID or UniProtKB
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 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597</a> )		
	Sequence Similarities	
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.		
	GO - Molecular Function	
GO:0005509 : calcium ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005509">https://www.ebi.ac.uk/QuickGO/term/GO:0005509</a> )		
GO:0005244 : voltage-gated ion channel activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005244">https://www.ebi.ac.uk/QuickGO/term/GO:0005244</a> )		
GO:0005248 : voltage-gated sodium channel activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005248">https://www.ebi.ac.uk/QuickGO/term/GO:0005248</a> )		

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>)

- No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title>) Presumptive Null
- Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title>) Molecular Type
- SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title>) Aberration Type
- Nonsynonymous SNP Coding Change
- L1014S Molecular Details of the Mutation
- Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title>) Experimental Evidence

	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 DIIIS6 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 DIIIS6 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=~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)) Related Haplotypes

EXTERNAL LINKS

## COMMENTS

@Parallelism