

GEPHE SUMMARY

	Gephebase Gene	GephelD
para (kdr) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase='para (kdr)'#gephebase-summary-title)	GP00002531	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

	Trait Category		
	Trait		
	Trait State in Taxon A		
Anopheles culicifacies	Trait State in Taxon B		
Anopheles culicifacies - resistant	Ancestral State		
Taxon A	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status='Intraspecific'#gephebase-summary-title)			
Taxon A	Latin Name		Latin Name
Anopheles culicifacies (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms='Anopheles culicifacies'#gephebase-summary-title)			
	Common Name		Common Name
-	Synonyms		Synonyms
Anopheles culicifacies Giles, 1901		Anopheles culicifacies Giles, 1901	
species	Rank		Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Myzomyia; culicifacies species complex	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Myzomyia; culicifacies species complex	Lineage
culicifacies species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 63408)	Parent	culicifacies species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 63408)	Parent
139723 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 139723)	NCBI Taxonomy ID	139723 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 139723)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
para	P35500 (http://www.uniprot.org/uniprot/P35500)	GenebankID or UniProtKB
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	0	
	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)		

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

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

PCR-based methods for the detection of L1014 kdr mutation in *Anopheles culicifacies* sensu lato. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19594947>)

Main Reference

Singh OP; Bali P; Hemingway J; Subbarao SK; Dash AP; Adak T

Authors

An *Anopheles culicifacies* s.l., a major malaria vector in India, has developed widespread resistance to DDT and is becoming resistant to pyrethroids-the only insecticide class recommended for the impregnation of bed nets. Knock-down resistance due to a point mutation in the voltage gated sodium channel at L1014 residue (kdr) is a common mechanism of resistance to DDT and pyrethroids. The selection of this resistance may pose a serious threat to the success of the pyrethroid-impregnated bed net programme. This study reports the presence of kdr mutation (L1014F) in a field population of An. culicifacies s.l. and three new PCR-based methods for kdr genotyping.

The IIS4-IIS5 linker to IIS6 segments of the para type voltage gated sodium channel gene of DDT and pyrethroid resistant An. culicifacies s.l. population from the Surat district of India was sequenced. This revealed the presence of an A-to-T substitution at position 1014 leading to a leucine-phenylalanine mutation (L1014F) in a few individuals. Three molecular methods viz. Allele Specific PCR (AS-PCR), an Amplification Refractory Mutation System (ARMS) and Primer Introduced Restriction Analysis-PCR (PIRA-PCR) were developed and tested for kdr genotyping. The specificity of the three assays was validated following DNA sequencing of the samples genotyped.

The genotyping of this An. culicifacies s.l. population by the three PCR based assays provided consistent result and were in agreement with DNA sequencing result. A low frequency of the kdr allele mostly in heterozygous condition was observed in the resistant population. Frequencies of the different genotypes were in Hardy-Weinberg equilibrium.

The Leu-Phe mutation, which generates the kdr phenotype in many insects, was detected in a pyrethroid and DDT resistant An. culicifacies s.l. population. Three PCR-based methods were developed for kdr genotyping. All the three assays were specific. The ARMS method was refractory to non-specific amplification in non-stringent amplification conditions. The PIRA-PCR assay is able to detect both the codons for the phenylalanine mutation at kdr locus, i.e., TTT and TTC, in a single assay, although the latter codon was not found in the population genotyped.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%para+\(kdr\)%/and+Taxon+ID=%139723%/or+Gene+Gephebase=%para+\(kdr\)%/and+Taxon+ID=%139723%#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%para+(kdr)%/and+Taxon+ID=%139723%/or+Gene+Gephebase=%para+(kdr)%/and+Taxon+ID=%139723%#gephebase-summary-title))

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