GEPHE SUMMARY

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

GepheID
GP00002531

Entry Status
Published

Main curator
Courtier

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
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
Anopheles culicifacies (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles culicifacies^#gephebase-summary-title)

Common Name
-

Synonyms
Anopheles culicifacies Giles, 1901

Rank
species

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

Parent
culicifacies species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 63408)

NCBI Taxonomy ID
139723 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 139723)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Anopheles culicifacies (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles culicifacies^#gephebase-summary-title)

Common Name
-

Synonyms
Anopheles culicifacies Giles, 1901

Rank
species

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

Parent
culicifacies species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 63408)

NCBI Taxonomy ID
139723 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 139723)

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)

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	-	-	-

Main Reference

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

Authors

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

Abstract

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)

EXTERNAL LINKS

COMMENTS