GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002530

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

L1014S

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

Presence of two alternative kdr-like mutations, L1014F and L1014S, and a novel mutation, V1010L, in the voltage gated Na+ channel of Anopheles culicifacies from Orissa, India. (2010)
(https://pubmed.ncbi.nlm.nih.gov/20509922)

Authors

Singh OP; Dykes CL; Das MK; Pradhan S; Bhatt RM; Agrawal OP; Adak T

Abstract

Knockdown resistance in insects resulting from mutation(s) in the voltage gated Na+ channel (VGSC) is one of the mechanisms of resistance against DDT and pyrethroids. Recently a point mutation leading to Leu-to-Phe substitution in the VGSC at residue 1014, a most common kdr mutation in insects, was reported in Anopheles culicifacies-a major malaria vector in the Indian subcontinent. This study reports the presence of two additional amino acid substitutions in the VGSC of an An. culicifacies population from Malkangiri district of Orissa, India.

Anopheles culicifacies sensu lato (s.l.) samples, collected from a population of Malkangiri district of Orissa (India), were sequenced for part of the second transmembrane segment of VGSC and analyzed for the presence of non-synonymous mutations. A new primer introduced restriction analysis-PCR (PIRA-PCR) was developed for the detection of the new mutation L1014S. The An. culicifacies population was genotyped for the presence of L1014F substitution by an amplification refractory mutation system (ARMS) and for L1014S substitutions by using a new PIRA-PCR developed in this study. The results were validated through DNA sequencing.

DNA sequencing of An. culicifacies individuals collected from district Malkangiri revealed the presence of three amino acid substitutions in the IIS6 transmembrane segments of VGSC, each one resulting from a single point mutation. Two alternative point mutations, 3042A>T transversion or 3041T>C transition, were found at residue L1014 leading to Leu (TTA)-to-Phe (TTT) or -Ser (TCA) changes, respectively. A third and novel substitution, Val (GTG)-to-Leu (TTG or CTG), was identified at residue V1010 resulting from either of the two transversions-3028G>T or 3028G>C. The L1014S substitution co-existed with V1010L in all the samples analyzed irrespective of the type of point mutation associated with the latter. The PIRA-PCR strategy developed for the identification of the new mutation L1014S was found specific as evident from DNA sequencing results of respective samples. Since L1014S was found tightly linked to V1010L, no separate assay was developed for the latter mutation. Screening of population using PIRA-PCR assays for 1014S and ARMS for 1014F alleles revealed the presence of all the three amino acid substitutions in low frequency.

This is the first report of the presence of L1014S (homologous to the kdr-e in An. gambiae) and a novel mutation V1010L (resulting from G-to-T or -C transversions) in the VGSC of An. culicifacies in addition to the previously described mutation L1014F. The V1010L substitution was tightly linked to L1014S substitution. A new PIRA-PCR strategy was developed for the detection of L1014S mutation and the linked V1010L mutation.

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