GEPHE SUMMARY

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

GepheID
GP00002536

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
Sensitive to Pyrethroids

Trait State in Taxon B
Resistant to Pyrethroids

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

Common Name
-

Synonyms
Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828

Rank
species

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

Parent
hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)

NCBI Taxonomy ID
74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
Anopheles (Anopheles) sinensis; Anopheles sinensis Wiedemann, 1828

Rank
species

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

Parent
hyrcanus group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 59131)

NCBI Taxonomy ID
74873 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 74873)

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

L1014C

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	TTG	TGT	-
Amino-acid	Leu	Cys	1014

Main Reference

The polymorphism and the geographical distribution of the knockdown resistance (kdr) of Anopheles sinensis in the Republic of Korea. (2012) (https://pubmed.ncbi.nlm.nih.gov/22554130)

Authors

Kang S; Jung J; Lee S; Hwang H; Kim W

Abstract

In the Republic of Korea (ROK), six sibling species of the Anopheles sinensis complex are considered the vector species of malaria, but data on their susceptibilities to malaria and vector capacities have been controversial. The intensive use of insecticides has contributed to the rapid development and spread of insecticide resistance in the An. sinensis complex. Knockdown resistance (kdr) to pyrethroids and DDT in the An. sinensis complex is associated with a mutation in codon 1014 of the voltage-gated sodium channel (VGSC) gene. Because the degree of insecticide resistance varies among mosquito species and populations, the detection of kdr mutations among the six sibling species of the An. sinensis complex is a prerequisite for establishing effective long-term vector control strategies in the ROK METHODS: In order to investigate species-specific kdr mutations, An. sinensis complex specimens have been collected from 22 sites in the ROK. Because of the difficulties with species identifications that are based only on morphological characteristics, molecular identification methods have been conducted on every specimen. Part of the IIS6 domain of the VGSC was polymerase chain reaction-amplified and directly sequenced.

The molecular analyses revealed that mutations existed at codon 1014 only in An. sinensis sensu stricto and no mutations were found in the other five Anopheles species. In An. sinensis s.s., one wild type (TTG L1014) and three mutant types (TTT L1014F, TTC L1014F, and TGT L1014C) of kdr alleles were detected. The TTC L1014F mutation was observed for the first time in this species.

The fact that the highly polymorphic kdr gene is only observed in An. sinensis s.s., out of the six Anopheles species and their geographical distribution suggest the need for future studies of insecticide resistance monitoring and investigations of species-specific resistance mechanisms in order to build successful malaria vector control programmes in the ROK.

Additional References

Molecular biology of insect sodium channels and pyrethroid resistance. (2014) (https://pubmed.ncbi.nlm.nih.gov/24704279)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

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)

EXTERNAL LINKS

COMMENTS

@Parallelism - Maybe the mutation was sequential from TTG L1014 to TTT L1014F to TGT L1014C.