GEPHE SUMMARY

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

GepheID
GP00002524

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
Culex quinquefasciatus

Trait State in Taxon B
Culex quinquefasciatus - 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
Culex quinquefasciatus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Culex quinquefasciatus^#gephebase-summary-title)

Common Name
southern house mosquito

Synonyms
Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quinquifasiatus; Culex quiquefasciatus

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; Culicinae; Culicini; Culex; Culex; Culex pipiens complex

Parent
Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)

NCBI Taxonomy ID
7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
southern house mosquito

Synonyms
Culex fatigans; Culex pipiens fatigans; Culex pipiens quinquefasciatus; southern house mosquito; Culex fatigan; Culex pipiens quiquefasciatus; Culex quinquifasciatus; Culex quinquifasiatus; Culex quiquefasciatus

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; Culicinae; Culicini; Culex; Culex; Culex pipiens complex

Parent
Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 518105)

NCBI Taxonomy ID
7176 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7176)

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

UniProtKB Drosophila melanogaster
P35500 (http://www.uniprot.org/uniprot/P35500)

GenebankID or UniProtKB
()

(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	-	-	-

Main Reference

Resistance in the mosquito, Culex quinquefasciatus, and possible mechanisms for resistance. (2005) (https://pubmed.ncbi.nlm.nih.gov/16032654)

Authors

Xu Q; Liu H; Zhang L; Liu N

Abstract

Two mosquito strains of Culex quinquefasciatus (Say), MAmCq(G0) and HAmCq(G0), were collected from Mobile and Huntsville, Alabama, respectively. MAmCq(G0) and HAmCq(G0) were further selected in the laboratory with permethrin for one and three generations, respectively. The levels of resistance to permethrin in MAmCq(G1) (after one-generation selection) and HAmCq(G3) (after three-generation selection) increased rapidly. Resistance to permethrin in MAmCq(G1) and HAmCq(G3) was partially suppressed by piperonyl butoxide (PBO), S,S,S-tributylphosphorotrithioate (DEF) and diethyl maleate (DEM), inhibitors of cytochrome P450 monooxygenases, hydrolases and glutathione S-transferases (GST), respectively, suggesting these three enzyme families are important in conferring permethrin resistance in both strains. A substitution of leucine to phenylalanine (L to F) resulting from a single nucleotide polymorphism (SNP), termed the kdr mutation, in the para-homologous sodium channel gene has been reported as a very common mutation associated with pyrethroid resistance of insects. A 341-bp sodium channel gene fragment, where the kdr mutation resides, was generated by PCR from genomic DNAs of Cx. quinquefasciatus strains. We found that the kdr mutation was present in both permethrin-selected and unselected HAmCq and MAmCq mosquito populations, suggesting that the kdr mutation plays the role in permethrin resistance. There was no significant change in the frequency and heterozygosity of the A to T SNP for the kdr allele between permethrin-selected and unselected MAmCq and HAmCq mosquitoes, indicating that other mechanisms are involved in the evolution of resistance in mosquitoes selected by permethrin in the laboratory.

Copyright 2005 Society of Chemical Industry.

Additional References

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

RELATED GEPHE

Related Genes

4 (Cpm1, esterase B1 + esterase A, esterase B1 = esterase beta1, resistance to dieldrin) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7176^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7176^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7176^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS