GEPHE SUMMARY

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

GepheID
GP00000832

Entry Status
Published

Main curator
Martin

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
Haematobia irritans

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

Common Name
horn fly

Synonyms
Lyperosia irritans; horn fly; Haematobia irritans (Linnaeus, 1758); Haematobia iritans

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calyptratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Haematobia

Parent
Haematobia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7367)

NCBI Taxonomy ID
7368 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7368)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
horn fly

Synonyms
Lyperosia irritans; horn fly; Haematobia irritans (Linnaeus, 1758); Haematobia iritans

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calyptratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Haematobia

Parent
Haematobia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7367)

NCBI Taxonomy ID
7368 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7368)

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
AAC12796 (https://www.ncbi.nlm.nih.gov/nuccore/AAC12796)

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

L150F (=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

Toxicological and molecular characterization of pyrethroid-resistant horn flies, Haematobia irritans: identification of kdr and super-kdr point mutations. (1997 Aug-Sep)
(https://pubmed.ncbi.nlm.nih.gov/9443375)

Authors

Guerrero FD; Jamroz RC; Kammlah D; Kunz SE

Abstract

Two pyrethroid-resistant strains of horn flies were found to be 17- and 688-fold more resistant to permethrin and 17- and 11,300-fold more resistant to cyhalothrin than a susceptible control strain. Synergism experiments with piperonyl butoxide showed that both target site insensitivity and metabolic resistance mechanisms were present in the Super Resistant strain. Using the reverse transcriptase-polymerase chain reaction (RT-PCR), a 0.9 kb fragment of the putative sodium channel gene from susceptible and resistant flies was cloned and sequenced. Two sequence variants were detected, presumably arising from alternative splicing of transcripts. The amino acid sequences deduced from the resistant and susceptible fly gene fragments were identical except for three amino acid substitutions, two of which have been associated with resistance in house flies. A leucine to phenylalanine substitution associated with knockdown resistance (kdr) was found in both resistant strains. A methionine to threonine substitution associated with super-kdr was found in the Super Resistant strain. Translation of poly(A)+ RNA followed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) detected translation products whose concentrations increased in association with pyrethroid resistance. Random-amplified polymorphic DNA (RAPD)-PCR of genomic DNA with over 260 DNA oligomers yielded one resistance-associated marker, designated HF-77, which was not detected in any susceptible flies but was present in 16% of the resistant individuals.

Additional References

The L1014F point mutation in the house fly Vssc1 sodium channel confers knockdown resistance to pyrethroids. (1997) (https://pubmed.ncbi.nlm.nih.gov/9474777)

RELATED GEPHE

Related Genes

2 (Acetylcholinesterase (Ace-2), resistance to dieldrin) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7368^/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=^7368^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^7368^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS