

GEPHE SUMMARY

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

Gephebase Gene GP00002507

Entry Status Courtier

Published

GephelD Main curator

PHENOTYPIC CHANGE

Physiology ([https://www.gephebase.org/search-criteria?/and+Trait Category="+Physiology+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Trait+Category=))

Trait Category

Xenobiotic resistance (insecticide) ([https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic resistance \(insecticide\)+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Trait=))

Trait

Frankliniella occidentalis

Trait State in Taxon A

Frankliniella occidentalis - resistant

Trait State in Taxon B

Taxon A

Ancestral State

Intraspecific ([https://www.gephebase.org/search-criteria?/and+Taxonomic Status="+Intraspecific+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=))

Taxonomic Status

Taxon A

Frankliniella occidentalis

([https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Frankliniella occidentalis+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=))

Latin Name

Common Name

western flower thrips

Synonyms

Euthrips occidentalis; Frankliniella brunnescens; Frankliniella californica; Frankliniella occidentalis brunnescens; western flower thrips; Frankliniella occidentalis (Pergande, 1895); Frankliniella occidentalis brunnescens Priesner, 1932

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Paraneoptera; Thysanoptera; Terebrantia; Thripidae; Thripidae; Thripinae; Frankliniella

Parent

Frankliniella () - (Rank: genus)

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=45059>)

NCBI Taxonomy ID

133901

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=133901>)

is Taxon A an Infrasppecies?

No

Taxon B

Frankliniella occidentalis

([https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Frankliniella occidentalis+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=))

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(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=45059>)

NCBI Taxonomy ID

133901

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=133901>)

is Taxon B an Infrasppecies?

No

GENOTYPIC CHANGE

para

Generic Gene Name

Synonyms

bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]1; l(1)14Da; l(1)ESH548; 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

T929C

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	Thr	Cys	929

Main Reference

High nucleotide diversity in the para-like voltage-sensitive sodium channel gene sequence in the western flower thrips (Thysanoptera: Thripidae). (2002)

(<https://pubmed.ncbi.nlm.nih.gov/12216829>)

Authors

Forcioli D; Frey B; Frey JE

Abstract

In a search for a pyrethroid resistance diagnostic marker, a partial sequence of the para-like sodium channel gene was obtained from 78 diploid females of the arrhenotokous insect pest species *Frankliniella occidentalis* (Pergande), the western flower thrips. Although all the insects analyzed came from a single laboratory population, nine different haplotypes were obtained. Two haplotypes did have the well-known L to F *kdr* mutation, but only one of these could be statistically linked to pyrethroid resistance in our population. This haplotype did not have the super*kdr* mutation, but did have a unique mutation a few amino acids downstream, at a position already linked to resistance in *Plutella*. Although this para-like locus seemed to have a role in pyrethroid resistance in our population, other resistance mechanisms were also probably involved. The fact that our laboratory population, open to migration, contained a high genetic diversity for this selected gene shows that "pest tourism" is a major factor for resistance dynamics in this greenhouse pest. This, with the possible occurrence of an original resistance mutation, might preclude the use of very specific approaches for resistance monitoring in the field in this species.

Additional References

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

RELATED GEPHE

Related Genes

2 (Chitin synthase 1 (CHS1), nAChR) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^133901^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

3 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^133901^/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^133901^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^133901^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^133901^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

Mutation hotspot with four different amino acid changes observed in different individuals.