

GEPHE SUMMARY

	Gephebase Gene	GepheID
para (kdr) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^para (kdr)^#gephebase-summary-title)	GP00000848	
	Entry Status	Martin
Published		Main curator

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	
Plutella xylostella		Trait State in Taxon B	
Plutella xylostella - resistant		Ancestral State	
Data not curated		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Plutella xylostella (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plutella xylostella^#gephebase-summary-title)		Plutella xylostella (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plutella xylostella^#gephebase-summary-title)	
	Common Name		Common Name
diamondback moth		diamondback moth	
	Synonyms		Synonyms
diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella		diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Yponomeutoidea; Plutellidae; Plutella		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Yponomeutoidea; Plutellidae; Plutella	
	Parent		Parent
Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)		Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)		51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)	
	is Taxon A an Infrappecies?		is Taxon B an Infrappecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
para	P35500 (http://www.uniprot.org/uniprot/P35500)	
	Synonyms	GenebankID or UniProtKB
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	ADH16760 (https://www.ncbi.nlm.nih.gov/nuccore/ADH16760)	
	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)		
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)

Mutation #1

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

M918L+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	Met	Leu	918

Main Reference

Alternatively spliced sodium channel transcripts expressed in field strains of the diamondback moth. (2008) (https://pubmed.ncbi.nlm.nih.gov/18692135)

Authors

Sonoda S; Igaki C; Tsumuki H

Abstract

The frequencies of the L1014F and T929I mutations, both of which are involved in nerve insensitive resistance to pyrethroids, were examined in field and laboratory strains of the diamondback moth, *Plutella xylostella* at DNA and RNA levels. Results showed that the resistance allele frequencies at the L1014F and T929I sites in the field strains were respectively, 82.8-100% and 72.9-94.4%. No posttranscriptional regulation of the L1014F mutation was observed. The examined insects were classifiable into four groups according to the expression patterns of mutually exclusive exons 18a and 18b. Most insects in the field strains expressed transcripts containing exon 18b more abundantly than those containing exon 18a, although both transcripts were expressed with similar proportions in all insects of the laboratory strains. Some other insects expressed a chimeric transcript comprising parts of exons 18a and 18b. Deduced amino acid sequences of the chimeric transcript encoded amino substitution from Met to Ile at the site corresponding to the super-kdr mutation (M918T) in *Musca domestica*. The frequencies of the M918I mutation in the field strains were 5.0-19.4%. Analyses of the genomic organization revealed that the chimeric sequences are encoded in the genome.

Additional References

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

Mutation #2

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

M918L+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	Leu	Phe	1014

Alternatively spliced sodium channel transcripts expressed in field strains of the diamondback moth. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18692135>)

Main Reference

Sonoda S; Igaki C; Tsumuki H

Authors

The frequencies of the L1014F and T929I mutations, both of which are involved in nerve insensitive resistance to pyrethroids, were examined in field and laboratory strains of the diamondback moth, *Plutella xylostella* at DNA and RNA levels. Results showed that the resistance allele frequencies at the L1014F and T929I sites in the field strains were respectively, 82.8-100% and 72.9-94.4%. No posttranscriptional regulation of the L1014F mutation was observed. The examined insects were classifiable into four groups according to the expression patterns of mutually exclusive exons 18a and 18b. Most insects in the field strains expressed transcripts containing exon 18b more abundantly than those containing exon 18a, although both transcripts were expressed with similar proportions in all insects of the laboratory strains. Some other insects expressed a chimeric transcript comprising parts of exons 18a and 18b. Deduced amino acid sequences of the chimeric transcript encoded amino substitution from Met to Ile at the site corresponding to the super-kdr mutation (M918T) in *Musca domestica*. The frequencies of the M918I mutation in the field strains were 5.0-19.4%. Analyses of the genomic organization revealed that the chimeric sequences are encoded in the genome.

Abstract

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

Additional References

RELATED GEPHE

10 (ABCC2, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), MAP4K4, nAChR, resistance to dieldrin, RYR)
(<https://www.gephebase.org/search-criteria?/or+Taxon ID=~51655~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

4 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~para \(kdr\)^/and+Taxon ID=~51655~/or+Gene Gephebase=~para \(kdr\)^/and+Taxon ID=~51655~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~para (kdr)^/and+Taxon ID=~51655~/or+Gene Gephebase=~para (kdr)^/and+Taxon ID=~51655~#gephebase-summary-title))

Related Haplotypes

EXTERNAL LINKS

COMMENTS