

GEPHE SUMMARY

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

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	Latin Name	Taxon B	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)	
diamondback moth	Common Name	diamondback moth	Common Name
diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella	Synonyms	diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella	Synonyms
	Rank		Rank
species	Lineage	species	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	
Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)	Parent	Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)	Parent
51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)	NCBI Taxonomy ID	51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name		
para	Synonyms		
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]; I(1)14Da; I(1)ESHS48; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer	String	UniProtKB Drosophila melanogaster	
7227.FBpp0303597 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303597)	Sequence Similarities	P35500 (http://www.uniprot.org/uniprot/P35500)	GenebankID or UniProtKB
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.	GO - Molecular Function	ADH16760 (https://www.ncbi.nlm.nih.gov/nuccore/ADH16760)	
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

M918I+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

M918I+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, <i>Plutella xylostella</i> 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 <i>Musca domestica</i> . 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

Related Genes
 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 Haplotypes
 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))

EXTERNAL LINKS

COMMENTS