GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002651

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; spinosad) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide; spinosad)^#gephebase-summary-title)

Trait State in Taxon A

Plutella xylostella - sensitive

Trait State in Taxon B

Plutella xylostella - 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

Plutella xylostella (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plutella xylostella^#gephebase-summary-title)

Common Name

diamondback moth

Synonyms

diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella

Rank

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

Parent

Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)

NCBI Taxonomy ID

51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Plutella xylostella (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plutella xylostella^#gephebase-summary-title)

Common Name

diamondback moth

Synonyms

diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella

Rank

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

Parent

Plutella () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51654)

NCBI Taxonomy ID

51655 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 51655)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

CHRNA6

Synonyms

CHNRA6

String

9606.ENSP00000276410 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000276410)

Sequence Similarities

Belongs to the ligand-gated ion channel (TC 1.A.9) family. Acetylcholine receptor (TC 1.A.9.1) subfamily. Alpha-6/CHRNA6 sub-subfamily.

GO - Molecular Function

GO:0015464 : acetylcholine receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015464)

GO:0022848 : acetylcholine-gated cation-selective channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0022848)

GO:1904315 : transmitter-gated ion channel activity involved in regulation of postsynaptic

UniProtKB Homo sapiens

Q15825 (http://www.uniprot.org/uniprot/Q15825)

GenebankID or UniProtKB

()

membrane potential (https://www.ebi.ac.uk/QuickGO/term/GO:1904315)
GO:0005231 : excitatory extracellular ligand-gated ion channel activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005231)
GO:0030594 : neurotransmitter receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0030594)

GO - Biological Process

GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0007268 : chemical synaptic transmission
(https://www.ebi.ac.uk/QuickGO/term/GO:0007268)
GO:0034220 : ion transmembrane transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0034220)
GO:0050877 : nervous system process
(https://www.ebi.ac.uk/QuickGO/term/GO:0050877)
GO:0042391 : regulation of membrane potential
(https://www.ebi.ac.uk/QuickGO/term/GO:0042391)
GO:0014059 : regulation of dopamine secretion
(https://www.ebi.ac.uk/QuickGO/term/GO:0014059)
GO:0051899 : membrane depolarization
(https://www.ebi.ac.uk/QuickGO/term/GO:0051899)
GO:2000300 : regulation of synaptic vesicle exocytosis
(https://www.ebi.ac.uk/QuickGO/term/GO:2000300)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0043005 : neuron projection (https://www.ebi.ac.uk/QuickGO/term/GO:0043005)
GO:0045202 : synapse (https://www.ebi.ac.uk/QuickGO/term/GO:0045202)
GO:0005892 : acetylcholine-gated channel complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005892)
GO:0099055 : integral component of postsynaptic membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0099055)
GO:0099056 : integral component of presynaptic membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0099056)
GO:0070161 : anchoring junction (https://www.ebi.ac.uk/QuickGO/term/GO:0070161)
GO:0098691 : dopaminergic synapse (https://www.ebi.ac.uk/QuickGO/term/GO:0098691)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#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

-

Molecular Details of the Mutation

A mutation within the ninth intron splice junction of Pxalpha6 results in mis-splicing of transcripts and produce a predicted protein truncated between the third and fourth transmembrane domains.

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Mis-spliced transcripts of nicotinic acetylcholine receptor alpha6 are associated with field evolved spinosad resistance in Plutella xylostella (L.). (2010)
(https://pubmed.ncbi.nlm.nih.gov/20062520)

Authors

Baxter SW; Chen M; Dawson A; Zhao JZ; Vogel H; Shelton AM; Heckel DG; Jiggins CD

Abstract

The evolution of insecticide resistance is a global constraint to agricultural production. Spinosad is a new, low-environmental-risk insecticide that primarily targets nicotinic acetylcholine receptors (nAChR) and is effective against a wide range of pest species. However, after only a few years of application, field evolved resistance emerged in the diamondback moth, Plutella xylostella, an important pest of brassica crops worldwide. Spinosad resistance in a Hawaiian population results from a single incompletely recessive and autosomal gene, and here we use AFLP linkage mapping to identify the chromosome controlling resistance in a backcross family. Recombinational mapping with more than 700 backcross progeny positioned a putative spinosad target, nAChR alpha 6 (Pxalpha6), at the resistance locus, PxSpinR. A mutation within the ninth intron splice junction of Pxalpha6 results in mis-splicing of transcripts, which produce a predicted protein truncated between the third and fourth transmembrane domains. Additional resistance-associated Pxalpha6 transcripts that excluded the mutation containing exon were detected, and these were also predicted to produce truncated proteins. Identification of the locus of resistance in this important crop pest will facilitate field monitoring of the spread of resistance and offer insights into the genetic basis of spinosad resistance in other species.

Additional References

RELATED GEPHE

Related Genes

10 (ABCC2, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), MAP4K4, para (kdr), 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

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^nAChR^/and+Taxon ID=^51655^/or+Gene Gephebase=^nAChR^/and+Taxon ID=^51655^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

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