

GEPHE SUMMARY

| | | | |
|---|----------------|------------|--------------|
| nAChR (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~nAChR^#gephebase-summary-title) | Gephebase Gene | GP00002650 | GepheID |
| Published | Entry Status | Courtier | Main curator |

PHENOTYPIC CHANGE

| | | | |
|---|-----------------------------|---|-----------------------------|
| Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title) | Trait Category | | |
| Xenobiotic resistance (insecticide; spinosad) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (insecticide; spinosad)^#gephebase-summary-title) | Trait | | |
| Bactrocera dorsalis- sensitive | Trait State in Taxon A | | |
| Bactrocera dorsalis- resistant | Trait State in Taxon B | | |
| Taxon A | Ancestral State | | |
| Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title) | Taxonomic Status | | |
| | Taxon A | Taxon B | |
| Bactrocera dorsalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Bactrocera dorsalis^#gephebase-summary-title) | Latin Name | Bactrocera dorsalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Bactrocera dorsalis^#gephebase-summary-title) | Latin Name |
| oriental fruit fly | Common Name | oriental fruit fly | Common Name |
| Bactrocera (Bactrocera) dorsalis; Bactrocera (Bactrocera) invadens; Bactrocera invadens; Bactrocera papayae; Bactrocera philippinensis; oriental fruit fly; Philippines fruit fly; papaya fruit fly; Bactrocera dorsalis (Hendel, 1912); Bactrocera invadens Drew, Tsuruta & White, 2005; Bactrocera philippinensis Drew & Hancock, 1994 | Synonyms | Bactrocera (Bactrocera) dorsalis; Bactrocera (Bactrocera) invadens; Bactrocera invadens; Bactrocera papayae; Bactrocera philippinensis; oriental fruit fly; Philippines fruit fly; papaya fruit fly; Bactrocera dorsalis (Hendel, 1912); Bactrocera invadens Drew, Tsuruta & White, 2005; Bactrocera philippinensis Drew & Hancock, 1994 | Synonyms |
| species | Rank | species | Rank |
| 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; Acalypratae; Tephritoidea; Tephritidae; Dacinae; Dacini; Bactrocera; Bactrocera; Bactrocera dorsalis complex | 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; Acalypratae; Tephritoidea; Tephritidae; Dacinae; Dacini; Bactrocera; Bactrocera; Bactrocera dorsalis complex | Lineage |
| Bactrocera dorsalis complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=98805) | Parent | Bactrocera dorsalis complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=98805) | Parent |
| 27457 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=27457) | NCBI Taxonomy ID | 27457 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=27457) | NCBI Taxonomy ID |
| No | is Taxon A an Intraspecies? | No | is Taxon B an Intraspecies? |

GENOTYPIC CHANGE

| | | | |
|--|-------------------------|--|-------------------------|
| CHRNA6 | Generic Gene Name | Q15825 (http://www.uniprot.org/uniprot/Q15825) | UniProtKB Homo sapiens |
| CHNRA6 | Synonyms | () | GenebankID or UniProtKB |
| 9606.ENSP00000276410 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000276410) | String | | |
| 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. | Sequence Similarities | | |
| GO:0015464 : acetylcholine receptor activity | GO - Molecular Function | | |

(<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 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](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](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding^#gephebase-summary-title))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown^#gephebase-summary-title))

Molecular Details of the Mutation

Mutation in *Bd1±6* intron 2 (A change to T) just before the truncated/mis-splicing region and in same location with a mutation previously reported in the *Pxy1±6* gene. Small deletions and insertions leading to premature stop codons in exon 7.

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene^#gephebase-summary-title))

Main Reference

Truncated transcripts of nicotinic acetylcholine subunit gene *Bd1±6* are associated with spinosad resistance in *Bactrocera dorsalis*. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22898623>)

Authors

Hsu JC; Feng HT; Wu WJ; Geib SM; Mao CH; Vontas J

Abstract

Spinosad-resistance mechanisms of *Bactrocera dorsalis*, one of the most important agricultural pests worldwide, were investigated. Resistance levels to spinosad in a *B. dorsalis* strain from Taiwan were more than 2000-fold, but showed no cross resistance to imidacloprid or fipronil. Combined biochemical and synergistic data indicated that target-site insensitivity is the major resistance component. The gene encoding the nAChR subunit alpha 6 (*Bd1±6*), the putative molecular target of spinosad, was isolated using PCR and RACE techniques. The full-length cDNA of *Bd1±6* from spinosad-susceptible strains had an open reading frame of 1467 bp and codes for a typical nAChR subunit. Two isoforms of exon 3 (3a and 3b) and exon 8 (8a and 8b), and four full-length splicing variants were found in the susceptible strain. All transcripts from the spinosad-resistant strain were truncated and coded for apparently non-functional *Bd1±6*. Genetic linkage analysis further associated spinosad-resistance phenotype with the truncated *Bd1±6* forms. This finding is consistent with a previous study in *Plutella xylostella*. Small deletions and insertions and consequent premature stop codons in exon 7 were associated with the truncated transcripts at the cDNA level. Analysis of genomic DNA sequences (intron 2 and exons 3-6) failed to detect exon 5 in resistant flies. In addition, a mutation in *Bd1±6* intron 2, just before the truncated/mis-splicing region and in same location with a mutation previously reported in the *Pxy1±6* gene, was identified in the resistant flies. RNA editing was investigated but was not found to be associated with resistance. While the demonstration of truncated transcripts causing resistance was outlined, the mechanism responsible for generating truncated transcripts remains unknown.

Copyright © 2012 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

Related Genes

1 (Acetylcholinesterase (Ace)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~27457^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~27457^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Splicing