GEPHE SUMMARY

Gephebase Gene

ABCA2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ABCA2^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002467

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; Bt Cry2Ab) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide; Bt Cry2Ab)^#gephebase-summary-title)

Trait State in Taxon A

Trichoplusia ni -Bt susceptible

Trait State in Taxon B

Trichoplusia ni -Bt 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

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

Common Name

cabbage looper

Synonyms

cabbage looper; Trichoplusia ni (Hubner, 1803); Trichopluisa ni; Trichopulsia ni

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; Obtectomera; Noctuoidea; Noctuidae; Plusiinae; Trichoplusia

Parent

Trichoplusia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7110)

NCBI Taxonomy ID

7111 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7111)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

cabbage looper

Synonyms

cabbage looper; Trichoplusia ni (Hubner, 1803); Trichopluisa ni; Trichopulsia ni

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; Obtectomera; Noctuoidea; Noctuidae; Plusiinae; Trichoplusia

Parent

Trichoplusia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7110)

NCBI Taxonomy ID

7111 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7111)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

ABCA2

Synonyms

ABC2; IDPOGSA; KIAA1062

String

9606.ENSP00000344155 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000344155)

Sequence Similarities

Belongs to the ABC transporter superfamily. ABCA family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0042626 : ATPase activity, coupled to transmembrane movement of substances (https://www.ebi.ac.uk/QuickGO/term/GO:0042626)
GO:0000166 : nucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000166)
GO:0005319 : lipid transporter activity

UniProtKB Homo sapiens

Q9BZC7 (http://www.uniprot.org/uniprot/Q9BZC7)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0005319)
GO:0099038 : ceramide-translocating ATPase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0099038)
GO:0140359 : ABC-type transporter activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0140359)
GO:0061135 : endopeptidase regulator activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0061135)

GO - Biological Process

GO:0055085 : transmembrane transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0055085)
GO:0006357 : regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
GO:0042632 : cholesterol homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0042632)
GO:0090370 : negative regulation of cholesterol efflux
(https://www.ebi.ac.uk/QuickGO/term/GO:0090370)
GO:1902004 : positive regulation of amyloid-beta formation
(https://www.ebi.ac.uk/QuickGO/term/GO:1902004)
GO:0032805 : positive regulation of low-density lipoprotein particle receptor catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0032805)
GO:0007626 : locomotory behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007626)
GO:0006629 : lipid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006629)
GO:0006687 : glycosphingolipid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006687)
GO:0009410 : response to xenobiotic stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009410)
GO:0070723 : response to cholesterol
(https://www.ebi.ac.uk/QuickGO/term/GO:0070723)
GO:0006869 : lipid transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006869)
GO:0099040 : ceramide translocation
(https://www.ebi.ac.uk/QuickGO/term/GO:0099040)
GO:0150104 : transport across blood-brain barrier
(https://www.ebi.ac.uk/QuickGO/term/GO:0150104)
GO:0090156 : cellular sphingolipid homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0090156)
GO:0032289 : central nervous system myelin formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0032289)
GO:0001573 : ganglioside metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001573)
GO:0032384 : negative regulation of intracellular cholesterol transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0032384)
GO:1905598 : negative regulation of low-density lipoprotein receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:1905598)
GO:0071072 : negative regulation of phospholipid biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0071072)
GO:1905601 : negative regulation of receptor-mediated endocytosis involved in cholesterol transport (https://www.ebi.ac.uk/QuickGO/term/GO:1905601)
GO:0090155 : negative regulation of sphingolipid biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0090155)
GO:0045939 : negative regulation of steroid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0045939)
GO:0042986 : positive regulation of amyloid precursor protein biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042986)
GO:1902993 : positive regulation of amyloid precursor protein catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:1902993)
GO:0010872 : regulation of cholesterol esterification
(https://www.ebi.ac.uk/QuickGO/term/GO:0010872)
GO:0032383 : regulation of intracellular cholesterol transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0032383)
GO:1901873 : regulation of post-translational protein modification
(https://www.ebi.ac.uk/QuickGO/term/GO:1901873)
GO:0060049 : regulation of protein glycosylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0060049)
GO:1904375 : regulation of protein localization to cell periphery
(https://www.ebi.ac.uk/QuickGO/term/GO:1904375)
GO:2000008 : regulation of protein localization to cell surface
(https://www.ebi.ac.uk/QuickGO/term/GO:2000008)
GO:0019218 : regulation of steroid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0019218)
GO:0048545 : response to steroid hormone
(https://www.ebi.ac.uk/QuickGO/term/GO:0048545)
GO:0006684 : sphingomyelin metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006684)
GO:0046512 : sphingosine biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0046512)

GO - Cellular Component

GO:0016021 : integral component of membrane

(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005768 : endosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005768)
GO:0031410 : cytoplasmic vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0031410)
GO:0010008 : endosome membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0010008)
GO:0043231 : intracellular membrane-bounded organelle
(https://www.ebi.ac.uk/QuickGO/term/GO:0043231)
GO:0005764 : lysosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005764)
GO:0005765 : lysosomal membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005765)
GO:0005815 : microtubule organizing center
(https://www.ebi.ac.uk/QuickGO/term/GO:0005815)
GO:0043190 : ATP-binding cassette (ABC) transporter complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0043190)

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

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

insertion of a 2581-bp transposon Tntransib in ABCA2. This insertion disrupts splicing sites and leads to indels in the protein sequence. CRISPR ABCA2 mutants are highly resistant to Cry2Ab.

Experimental Evidence

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

Main Reference

Mutation of ABC transporter ABCA2 confers resistance to Bt toxin Cry2Ab in Trichoplusia ni. (2019) (https://pubmed.ncbi.nlm.nih.gov/31422154)

Authors

Yang X; Chen W; Song X; Ma X; Cotto-Rivera RO; Kain W; Chu H; Chen YR; Fei Z; Wang P

Abstract

Insecticidal proteins from Bacillus thuringiensis (Bt) are the primary recombinant proteins expressed in transgenic crops (Bt-crops) to confer insect resistance. Development of resistance to Bt toxins in insect populations threatens the sustainable application of Bt-crops in agriculture. The Bt toxin Cry2Ab is a major insecticidal protein used in current Bt-crops, and resistance to Cry2Ab has been selected in several insects, including the cabbage looper, Trichoplusia ni. In this study, the Cry2Ab resistance gene in T. ni was mapped to Chromosome 17 by genetic linkage analyses using a whole genome resequencing approach, and was then finely mapped using RNA-seq-based bulked segregant analysis (BSA) and amplicon sequencing (AmpSeq)-based fine linkage mapping to a locus containing two genes, ABCA1 and ABCA2. Mutations in ABCA1 and ABCA2 in Cry2Ab resistant T. ni were identified by both genomic DNA and cDNA sequencing. Analysis of the expression of ABCA1 and ABCA2 in T. ni larvae indicated that ABCA2 is abundantly expressed in the larval midgut, but ABCA1 is not a midgut-expressed gene. The mutation in ABCA2 in Cry2Ab resistant T. ni was identified to be an insertion of a transposon Tntransib in ABCA2. For confirmation of ABCA2 as the Cry2Ab-resistance gene, T. ni mutants with frameshift mutations in ABCA1 and ABCA2 were generated by CRISPR/Cas9 mutagenesis. Bioassays of the T. ni mutants with Cry2Ab verified that the mutations of ABCA1 did not change larval susceptibility to Cry2Ab, but the ABCA2 mutants were highly resistant to Cry2Ab. Genetic complementation test of the ABCA2 allele in Cry2Ab resistant T. ni with an ABCA2 mutant generated by CRISPR/Cas9 confirmed that the ABCA2 mutation in the Cry2Ab resistant strain confers the resistance. The results from this study confirmed that ABCA2 is essential for the toxicity of Cry2Ab in T. ni and mutation of ABCA2 confers the resistance to Cry2Ab in the resistant T. ni strain derived from a Bt resistant greenhouse population.

Additional References

RELATED GEPHE

Related Genes

1 (ABCC2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7111^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^ABCA2^/and+Taxon ID=^7111^/or+Gene Gephebase=^ABCA2^/and+Taxon ID=^7111^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

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