

GEPHE SUMMARY

Gephebase Gene

Ha_BtR

Entry Status

Published

GepheID

GP00000430

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology

Trait

Xenobiotic resistance (insecticide; Bt Cry1Ac toxin)

Trait State in Taxon A

Helicoverpa armigera - Bt-Cry1Ac susceptible

Trait State in Taxon B

Helicoverpa armigera - Bt-Cry1Ac resistant

Ancestral State

Taxon A

Taxonomic Status

Intraspecific

Taxon A

Latin Name

Helicoverpa armigera

Common Name

cotton bollworm

Synonyms

Heliothis (*Helicoverpa*) *armigera*; *Heliothis armigera*; cotton bollworm; American bollworm; corn ear worm; scarce bordered straw; tobacco budworm; *Helicoverpa armigera* (Hubner, 1808)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Noctuoidea; Noctuidae; Heliothinae; *Helicoverpa*

Parent

Helicoverpa () - (Rank: genus)

NCBI Taxonomy ID

29058

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Helicoverpa armigera

Common Name

cotton bollworm

Synonyms

Heliothis (*Helicoverpa*) *armigera*; *Heliothis armigera*; cotton bollworm; American bollworm; corn ear worm; scarce bordered straw; tobacco budworm; *Helicoverpa armigera* (Hubner, 1808)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Noctuoidea; Noctuidae; Heliothinae; *Helicoverpa*

Parent

Helicoverpa () - (Rank: genus)

NCBI Taxonomy ID

29058

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

ABCA2

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0005524 : ATP binding

GO:0042626 : ATPase activity, coupled to transmembrane movement of substances

GO - Biological Process

-

GO - Cellular Component

GO:0016021 : integral component of membrane

Presumptive Null

UniProtKB *Helicoverpa armigera*

A0A0S0G7V0

GenebankID or UniProtKB

Yes

Molecular Type

Coding

Aberration Type

Insertion

Insertion Size

1-10 kb

Molecular Details of the Mutation

Insertion of an incomplete RNA transposon (1498bp)

Experimental Evidence

Candidate Gene

Main Reference

[Diverse cadherin mutations conferring resistance to Bacillus thuringiensis toxin Cry1Ac in Helicoverpa armigera. \(2010\)](#)

Authors

Zhao J; Jin L; Yang Y; Wu Y

Abstract

Transgenic cotton expressing Bacillus thuringiensis (Bt) toxins has been widely adopted to control some key lepidopteran pests including the bollworm *Helicoverpa armigera*. Evolution of resistance to Bt cotton by target pests is a major threat to the continued success of Bt cotton. Previous results revealed 3 null alleles (r1-r3) of a cadherin gene (Ha_BtR) conferring Cry1Ac resistance in *H. armigera*. An F(1) screen of 123 single-pair families was conducted between a Cry1Ac-resistant strain (the SCD-r1 strain, homozygous for the r1 allele of Ha_BtR) and field-derived insects from Jiangpu population (Jiangsu province, China) in 2008. Five new null alleles of Ha_BtR (r4-r8) were identified in six candidate single-pair families. These null alleles were created through either an insertion or a point mutation. Interestingly, intact alleles of Ha_BtR were found in two field-derived insects from another two candidate single-pair families. It suggests that these two field-derived insects may carry novel resistance alleles of Ha_BtR, with missense mutations resulting in a non-functional cadherin protein, or a major dominant mutation at a locus other than cadherin. The resistance allele frequency of Ha_BtR was detected at an appreciable level (0.024) in the Jiangpu population of *H. armigera* in 2008. Together with previous findings, a total of eight different resistance alleles of Ha_BtR were identified from three Chinese strains of *H. armigera*. Mutational diversity of Ha_BtR could impair DNA screening for Bt resistance allele frequency in the field, and an F(1) screen should be used routinely for monitoring cadherin-based resistance allele frequencies in *H. armigera*.

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Additional References

[Identification and molecular detection of a deletion mutation responsible for a truncated cadherin of Helicoverpa armigera. \(2006\)](#)

RELATED GEPHE

Related Genes

2 (ABCA2, BTR1- Cadherin-like protein)

Related Haplotypes

7

COMMENTS

@TE Parallelism: repeated loss-of-function