

GEPHE SUMMARY

Gephebase Gene
Ha_BtR

Entry Status
Published

GepheID
GP00000432

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
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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 a LTR retrotransposon

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](#)

EXTERNAL LINKS

COMMENTS

@TE Parallelism: repeated loss-of-function