

## GEPHE SUMMARY

**Gephebase Gene**  
Ha\_BtR

**Entry Status**  
Published

**GepheID**  
GP00000433

**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 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