

GEPHE SUMMARY

ABCA2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ABCA2^#gephebase-summary-title)	Gephebase Gene	GP00000002	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category		
Xenobiotic resistance (insecticide; Bt Cry2Ab toxin) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(insecticide;+Bt+Cry2Ab+toxin)^#gephebase-summary-title)	Trait		
Helicoverpa armigera - Bt-Cry2Ab susceptible	Trait State in Taxon A		
Helicoverpa armigera - Bt-Cry2Ab resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Helicoverpa armigera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Helicoverpa+armigera^#gephebase-summary-title)	Latin Name	Helicoverpa armigera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Helicoverpa+armigera^#gephebase-summary-title)	Latin Name
cotton bollworm	Common Name	cotton bollworm	Common Name
Heliothis (Helicoverpa) armigera; Heliothis armigera; cotton bollworm; American bollworm; corn ear worm; scarce bordered straw; tobacco budworm; Helicoverpa armigera (Hubner, 1808)	Synonyms	Heliothis (Helicoverpa) armigera; Heliothis armigera; cotton bollworm; American bollworm; corn ear worm; scarce bordered straw; tobacco budworm; Helicoverpa armigera (Hubner, 1808)	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa	Lineage
Helicoverpa () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7112)	Parent	Helicoverpa () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7112)	Parent
29058 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29058)	NCBI Taxonomy ID	29058 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29058)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

ABCA2	Generic Gene Name	A0A0S0G7V0 (http://www.uniprot.org/uniprot/A0A0S0G7V0)	UniProtKB Helicoverpa armigera
-	Synonyms		GenebankID or UniProtKB
-	String		
-	Sequence Similarities		
-	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 - Biological Process		

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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))

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))

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

10-99 bp

65bp indel in exon16 inducing a frameshift

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

Insect Resistance to *Bacillus thuringiensis* Toxin Cry2Ab Is Conferred by Mutations in an ABC Transporter Subfamily A Protein. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26583651>)

Tay WT; Mahon RJ; Heckel DG; Walsh TK; Downes S; James WJ; Lee SF; Reineke A; Williams AK; Gordon KH

The use of conventional chemical insecticides and bacterial toxins to control lepidopteran pests of global agriculture has imposed significant selection pressure leading to the rapid evolution of insecticide resistance. Transgenic crops (e.g., cotton) expressing the Bt Cry toxins are now used world wide to control these pests, including the highly polyphagous and invasive cotton bollworm *Helicoverpa armigera*. Since 2004, the Cry2Ab toxin has become widely used for controlling *H. armigera*, often used in combination with Cry1Ac to delay resistance evolution. Isolation of *H. armigera* and *H. punctigera* individuals heterozygous for Cry2Ab resistance in 2002 and 2004, respectively, allowed aspects of Cry2Ab resistance (level, fitness costs, genetic dominance, complementation tests) to be characterised in both species. However, the gene identity and genetic changes conferring this resistance were unknown, as was the detailed Cry2Ab mode of action. No cross-resistance to Cry1Ac was observed in mutant lines. Biphasic linkage analysis of a Cry2Ab-resistant *H. armigera* family followed by exon-primed intron-crossing (EPIC) marker mapping and candidate gene sequencing identified three independent resistance-associated INDEL mutations in an ATP-Binding Cassette (ABC) transporter gene we named HaABCA2. A deletion mutation was also identified in the *H. punctigera* homolog from the resistant line. All mutations truncate the ABCA2 protein. Isolation of further Cry2Ab resistance alleles in the same gene from field *H. armigera* populations indicates unequal resistance allele frequencies and the potential for Bt resistance evolution. Identification of the gene involved in resistance as an ABC transporter of the A subfamily adds to the body of evidence on the crucial role this gene family plays in the mode of action of the Bt Cry toxins. The structural differences between the ABCA2, and that of the C subfamily required for Cry1Ac toxicity, indicate differences in the detailed mode-of-action of the two Bt Cry toxins.

Presumptive Null

Molecular Type

Aberration Type

Indel Size

Molecular Details of the Mutation

Experimental Evidence

Main Reference

Authors

Abstract

Additional References

RELATED GEPHE

6 (Aminopeptidase N (APN), cadherin, CYP337B3, Ha_BtR, para (kdr), tetraspanin) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~29058^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~29058^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Genes

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~ABCA2^/and+Taxon ID=~29058^/or+Gene Gephebase=~ABCA2^/and+Taxon ID=~29058^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~ABCA2^/and+Taxon+ID=~29058^/or+Gene+Gephebase=~ABCA2^/and+Taxon+ID=~29058^#gephebase-summary-title))

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Parallelism - intraspecific and interspecific