

## GEPHE SUMMARY

cadherin ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase= <sup>^</sup> cadherin <sup>^</sup> #gephebase-summary-title)	Gephebase Gene	GP00002055	GepheID
Published	Entry Status	Courtier	Main curator

## PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category= <sup>^</sup> Physiology <sup>^</sup> #gephebase-summary-title)	Trait Category		
Xenobiotic resistance (insecticide; Bt Cry1Ac) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=&lt;sup&gt;^&lt;/sup&gt;Xenobiotic resistance (insecticide; Bt Cry1Ac)&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (insecticide; Bt Cry1Ac)<sup>^</sup>#gephebase-summary-title</a> )	Trait		
Helicoverpa punctigera - Bt susceptible	Trait State in Taxon A		
Helicoverpa punctigera -Bt resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status= <sup>^</sup> Intraspecific <sup>^</sup> #gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Helicoverpa punctigera ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=&lt;sup&gt;^&lt;/sup&gt;Helicoverpa punctigera&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Helicoverpa punctigera<sup>^</sup>#gephebase-summary-title</a> )	Latin Name	Helicoverpa punctigera ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=&lt;sup&gt;^&lt;/sup&gt;Helicoverpa punctigera&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Helicoverpa punctigera<sup>^</sup>#gephebase-summary-title</a> )	Latin Name
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; 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; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; Obtectomera; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa	Lineage
Helicoverpa () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7112">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7112</a> )	Parent	Helicoverpa () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7112">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7112</a> )	Parent
27545 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27545">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27545</a> )	NCBI Taxonomy ID	27545 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27545">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27545</a> )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

BtR	Generic Gene Name	Q19KJ3 ( <a href="http://www.uniprot.org/uniprot/Q19KJ3">http://www.uniprot.org/uniprot/Q19KJ3</a> )	UniProtKB Helicoverpa armigera
-	Synonyms	0	GenebankID or UniProtKB
-	String		
-	Sequence Similarities		
GO:0005509 : calcium ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005509">https://www.ebi.ac.uk/QuickGO/term/GO:0005509</a> )	GO - Molecular Function		
GO:0007156 : homophilic cell adhesion via plasma membrane adhesion molecules ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0007156">https://www.ebi.ac.uk/QuickGO/term/GO:0007156</a> )	GO - Biological Process		
GO:0016021 : integral component of membrane ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016021">https://www.ebi.ac.uk/QuickGO/term/GO:0016021</a> )	GO - Cellular Component		

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

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))

Molecular Type

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))

Aberration Type

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

SNP Coding Change

-

Molecular Details of the Mutation

splice site GT mutated in GA so that splicing does not occur correctly and a 58bp insertion is found in the cDNA sequence of the cadherin gene. This insertion disrupts the coding sequence in cadherin domain 9 causing a downstream frameshift and a premature stop codon for the rest of the protein. This would result in a truncated protein of 1243 amino acids without the putative binding domain; the membrane anchoring domain; presumably retained inside the cell and not exposed to the Cry1Ac; or alternatively; exported into the gut where it would be degraded

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Isolating, characterising and identifying a Cry1Ac resistance mutation in field populations of *Helicoverpa punctigera*. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29422629>)

Authors

Walsh T; James B; Chakroun M; FerrÃ© J; Downes S

Abstract

Transgenic cotton expressing insecticidal proteins from *Bacillus thuringiensis* (Bt) has been grown in Australia for over 20 years and resistance remains the biggest threat. The native moth, *Helicoverpa punctigera* is a significant pest of cotton. A genotype causing resistance to Cry1Ac in *H. punctigera* was isolated from the field and a homozygous line established. The phenotype is recessive and homozygous individuals possess 113 fold resistance to Cry1Ac. Individuals that carry Cry1Ac resistance genes are rare in Australia with a frequency of 0.033 being detected in field populations. RNAseq, RT-PCR and DNA sequencing reveals a single nucleotide polymorphism at a splice site in the cadherin gene as the causal mutation, resulting in the partial transcription of the intron and a premature stop codon. Analysis of Cry1Ac binding to *H. punctigera* brush border membrane vesicles showed that it is unaffected by the disrupted cadherin gene. This suggests that the major Cry1Ac target is not cadherin but that this molecule plays a key role in resistance and therefore the mode of action. This work adds to our knowledge of resistance mechanisms in *H. punctigera* and the growing literature around the role of cadherin in the mode of action of Cry1 type Bt proteins.

Additional References

## RELATED GEPHE

Related Genes

1 (ABCA2) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=^27545^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^27545^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@Splicing @CodingInNonCodingRegion