

GEPHE SUMMARY

	Gephebase Gene	GephelD
MAP4K4 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase="MAP4K4">#gephebase-summary-title)	GP00001673	Main curator
	Entry Status	Prigent
Published		

PHENOTYPIC CHANGE

Trait Category
 Physiology (<https://www.gephebase.org/search-criteria/?and+Trait>
Category="Physiology">#gephebase-summary-title)

Trait

Xenobiotic resistance (insecticide; Bt Cry1Ac toxin) ([https://www.gephebase.org/search-criteria/?and+Trait-^Xenobiotic+resistance+\(insecticide;+Bt+Cry1Ac+toxin\)^#gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Trait-^Xenobiotic+resistance+(insecticide;+Bt+Cry1Ac+toxin)^#gephebase-summary-title))

Trait State in Taxon A

Bt-susceptible

Trait State in Taxon B

Bt-resistant strains collected from Florida (DBM1Ac-R >3500-fold resistance) Shenzhen (SZ-R 458-fold CryAc resistance) Shanghai (SH-R 1890-fold Bt var. kurstaki resistance) and NIL-R (>3900-fold Cry1Ac resistance and >2800-fold Btk resistance)

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (<https://www.gephebase.org/search-criteria/?and+Taxonomic>
Status="Intraspecific">#gephebase-summary-title)

Taxon A

Latin Name

Plutella xylostella
(<https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Plutella+xylostella^#gephebase-summary-title>)

Common Name

diamondback moth

Synonyms

diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Yponomeutoidea; Plutellidae; Plutella

Parent

Plutella () - (Rank: genus)

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=51654>)

NCBI Taxonomy ID

51655

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=51655>)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Diamondback moth Bt susceptible strain DBM1Ac-S

Taxon B

Latin Name

Plutella xylostella
(<https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Plutella+xylostella^#gephebase-summary-title>)

Common Name

diamondback moth

Synonyms

diamondback moth; cabbage moth; Plutella xylostella (Linnaeus, 1758); Putella xylostella

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Yponomeutoidea; Plutellidae; Plutella

Parent

Plutella () - (Rank: genus)

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=51654>)

NCBI Taxonomy ID

51655

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=51655>)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Diamondback moth strains collected from Florida (DBM1Ac-R >3500-fold resistance) Shenzhen (SZ-R 458-fold CryAc resistance) Shanghai (SH-R 1890-fold Bt var. kurstaki resistance) and NIL-R (>3900-fold Cry1Ac resistance and >2800-fold Btk resistance)

GENOTYPIC CHANGE

MAP4K4	Generic Gene Name	UniProtKB Homo sapiens
HKG; NIK; MEKK4; FLH21957; HEL-S-31; KIAA0687	Synonyms	GenebankID or UniProtKB
9606.ENSP00000314363 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000314363)	String	0
	Sequence Similarities	
Belongs to the protein kinase superfamily. STE Ser/Thr protein kinase family. STE20 subfamily.		

GO - Molecular Function

GO:0005524 : ATP binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005524>)
GO:0004674 : protein serine/threonine kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004674>)
GO:0008017 : microtubule binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0008017>)
GO:0004111 : creatine kinase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0004111>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0000165 : MAPK cascade (<https://www.ebi.ac.uk/QuickGO/term/GO:0000165>)
GO:0006468 : protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006468>)
GO:0043547 : positive regulation of GTPase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043547>)
GO:0001953 : negative regulation of cell-matrix adhesion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001953>)
GO:0030335 : positive regulation of cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030335>)
GO:0035556 : intracellular signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)
GO:0046328 : regulation of JNK cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046328>)
GO:0048812 : neuron projection morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048812>)
GO:0032147 : activation of protein kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032147>)
GO:0051894 : positive regulation of focal adhesion assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051894>)
GO:0061179 : negative regulation of insulin secretion involved in cellular response to glucose stimulus (<https://www.ebi.ac.uk/QuickGO/term/GO:0061179>)
GO:0070571 : negative regulation of neuron projection regeneration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070571>)
GO:1903393 : positive regulation of adherens junction organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:1903393>)
GO:0032014 : positive regulation of ARF protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032014>)
GO:0051549 : positive regulation of keratinocyte migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051549>)
GO:0023014 : signal transduction by protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0023014>)
GO:0031098 : stress-activated protein kinase signaling cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031098>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005925 : focal adhesion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005925>)

Presumptive Null

No (<https://www.gephbase.org/search-criteria?/and+Presumptive+Null=%27No%27#gephbase-summary-title>)

Molecular Type

Unknown (<https://www.gephbase.org/search-criteria?/and+Molecular+Type=%27Unknown%27#gephbase-summary-title>)

Aberration Type

Unknown (<https://www.gephbase.org/search-criteria?/and+Aberration+Type=%27Unknown%27#gephbase-summary-title>)

Molecular Details of the Mutation

MAP4K4 constitutively up-regulated leading to up-regulated PxABCC1 and down-regulated PxABCC2 and PxABCC3 and reduction of membrane-bound ALP (mALP) expression responsible for reduced Cry1Ac toxin binding to midgut proteins

Experimental Evidence

Linkage Mapping (<https://www.gephbase.org/search-criteria?/and+Experimental+Evidence=%27Linkage+Mapping%27#gephbase-summary-title>)

Main Reference

MAPK signaling pathway alters expression of midgut ALP and ABCC genes and causes resistance to *Bacillus thuringiensis* Cry1Ac toxin in diamondback moth. (2015)
(<https://pubmed.ncbi.nlm.nih.gov/25875245>)

Authors

Guo Z; Kang S; Chen D; Wu Q; Wang S; Xie W; Zhu X; Baxter SW; Zhou X; Jurat-Fuentes JL; Zhang Y

Abstract

Insecticidal crystal toxins derived from the soil bacterium *Bacillus thuringiensis* (Bt) are widely used as biopesticide sprays or expressed in transgenic crops to control insect pests. However, large-scale use of Bt has led to field-evolved resistance in several lepidopteran pests. Resistance to Bt Cry1Ac toxin in the diamondback moth, *Plutella xylostella* (L.), was previously mapped to a multigenic resistance locus (BtR-1). Here, we assembled the 3.15 Mb BtR-1 locus and found high-level resistance to Cry1Ac and Bt biopesticide in four independent *P. xylostella* strains were all associated with differential expression of a midgut membrane-bound alkaline phosphatase (ALP) outside this locus and a suite of ATP-binding cassette transporter subfamily C (ABCC) genes inside this locus. The interplay between these resistance genes is controlled by a previously uncharacterized trans-regulatory mechanism via the mitogen-activated protein kinase (MAPK) signaling pathway. Molecular, biochemical, and functional analyses have established ALP as a functional Cry1Ac receptor. Phenotypic association experiments revealed that the recessive Cry1Ac resistance was tightly linked to down-regulation of ALP, ABCC2 and ABCC3, whereas it was not linked to up-regulation of ABCC1. Silencing of ABCC2 and ABCC3 in susceptible larvae reduced their susceptibility to Cry1Ac but did not affect the expression of ALP, whereas suppression of MAP4K4, a constitutively transcriptionally-activated MAPK upstream gene within the BtR-1 locus, led to a transient recovery of gene expression thereby restoring the susceptibility in resistant larvae. These results highlight a crucial role for ALP and ABCC genes in field-evolved resistance to Cry1Ac and reveal a novel trans-regulatory signaling mechanism responsible for modulating the expression of these pivotal genes in *P. xylostella*.

Additional References

No matches found.

EXTERNAL LINKS

COMMENTS

Possible Supergene since the mapped interval contains toxin receptors in addition to the upstream regulator. RNAi evidence seems to validate the MAPK gene