GEPHE SUMMARY

Gephebase Gene

MAP4K4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MAP4K4^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001673

Main curator

Prigent

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)

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

Generic Gene Name

MAP4K4

Synonyms

HGK; NIK; MEKKK4; FLH21957; HEL-S-31; KIAA0687

String

9606.ENSP00000314363 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000314363)

Sequence Similarities

Belongs to the protein kinase superfamily. STE Ser/Thr protein kinase family. STE20 subfamily.

UniProtKB Homo sapiens

O95819 (http://www.uniprot.org/uniprot/O95819)

GenebankID or UniProtKB

()

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.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-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.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-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

RELATED GEPHE

Related Genes

10 (ABCC2, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), nAChR, para (kdr), resistance to dieldrin, RYR) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^51655^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

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