GEPHE SUMMARY

Gephebase Gene

FMO2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FMO2^#gephebase-summary-title)

GepheID

GP00002065

Entry Status

Published

Main curator

Cao

PHENOTYPIC CHANGE

Trait Category

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

Trait

Xenobiotic resistance (insecticide) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide)^#gephebase-summary-title)

Trait State in Taxon A

Plutella xylostella -diamide (chlorantraniliprole) susceptible

Trait State in Taxon B

Plutella xylostella - diamide (chlorantraniliprole) resistant

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?

No

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?

No

GENOTYPIC CHANGE

Generic Gene Name

FMO2

Synonyms

FMO1B1

String

9606.ENSP00000209929 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000209929)

Sequence Similarities

Belongs to the FMO family.

GO - Molecular Function

GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)
GO:0050660 : flavin adenine dinucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050660)
GO:0004499 : N,N-dimethylaniline monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004499)
GO:0050661 : NADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050661)

UniProtKB Homo sapiens

Q99518 (http://www.uniprot.org/uniprot/Q99518)

GenebankID or UniProtKB Homo sapiens

Q99518 (https://www.ncbi.nlm.nih.gov/nuccore/Q99518)

GO - Biological Process

GO:0017144 : drug metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0017144)
GO:0006805 : xenobiotic metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006805)
GO:0006082 : organic acid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006082)
GO:0006739 : NADP metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006739)
GO:0070995 : NADPH oxidation (https://www.ebi.ac.uk/QuickGO/term/GO:0070995)
GO:0072592 : oxygen metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0072592)
GO:0009404 : toxin metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0009404)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005789 : endoplasmic reticulum membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005789)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

100-999 bp

Molecular Details of the Mutation

a putatative transposon (233bp) insertion in the HAW promoter sequence just 140 bp upstream of the start codon of PxFMO2 which was absent in the ROTH promoter, the boundaries of all copies of this element were found to be defined by 34 bp imperfect terminal inverted repeats, increase the expression of the gene PxFMO2 downstream

Experimental Evidence

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

Main Reference

A flavin-dependent monooxgenase confers resistance to chlorantraniliprole in the diamondback moth, Plutella xylostella. (2019) (https://pubmed.ncbi.nlm.nih.gov/31626952)

Authors

Mallott M; Hamm S; Troczka BJ; Randall E; Pym A; Grant C; Baxter S; Vogel H; Shelton AM; Field LM; Williamson MS; Paine M; Zimmer CT; Slater R; Elias J; Bass C

Abstract

The diamondback moth, Plutella xylostella, is a damaging pest of cruciferous crops, and has evolved resistance to many of the insecticides used for control, including members of the diamide class. Previous work on the molecular basis of resistance to diamides has documented mutations in the target-site, the ryanodine receptor, in resistant populations of P. xylostella worldwide. In contrast the role of metabolic resistance to this insecticide class is significantly less clear. Here we show that overexpression of a flavin-dependent monooxgenase (FMO) confers resistance to the diamide chlorantraniliprole in P. xylostella. Transcriptome profiling of diamide resistant strains, with and without target-site resistance, revealed constitutive over-expression of several transcripts encoding detoxification enzymes compared to susceptible strains. Two of these, CYP6BG1, and PxFMO2 were particularly highly overexpressed (33,000 and 14,700-fold, respectively) in a resistant strain (HAW) lacking target-site resistance. After 17 generations without diamide selection the resistance of the HAW strain fell by 52-fold and the expression of PxFMO2 byâ€¯>â€¯1300-fold, however, the expression of CYP6BG1 declined by only 3-fold. Generation of transgenic Drosophila melanogaster expressing these genes demonstrated that PxFMO2, but not CYP6BG1, confers resistance in vivo. Overexpression of PxFMO2 in the HAW strain is associated with mutations, including a putative transposable element insertion, in the promoter of this gene. These enhance the expression of a reporter gene when expressed in a lepidopteran cell line suggesting they are, at least in part, responsible for the overexpression of PxFMO2 in the resistant strain. Our results provide new evidence that insect FMOs can be recruited to provide resistance to synthetic insecticides.

Additional References

RELATED GEPHE

Related Genes

10 (ABCC2, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, glutamate-gated chloride channel (GluCl), MAP4K4, 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

@TE