## GEPHE SUMMARY

Gephebase Gene

Chitin synthase 1 (CHS1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Chitin synthase 1 (CHS1)^#gephebase-summary-title)

GepheID

GP00001600

Entry Status

Published

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

Trait State in Taxon A

Plutella xylostella BCS-S and Japan reference strains susceptible

Trait State in Taxon B

Plutella xylostella Sudlon-Tfm strain sampled in a Philippine cabbage field selected with triflumuron under laboratory conditions resistant to diverse BPU and also etoxazole (>178-fold)

Ancestral State

Unknown

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

Plutella xylostella BCS-S and Japan reference strains susceptible

### 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

Plutella xylostella Sudlon-Tfm strain sampled in a Philippine cabbage field selected with triflumuron under laboratory conditions resistant to diverse BPU and also etoxazole (>178-fold)

## GENOTYPIC CHANGE

Generic Gene Name

CHS1

Synonyms

CHS1; PxCHS1B

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0016758 : transferase activity, transferring hexosyl groups (https://www.ebi.ac.uk/QuickGO/term/GO:0016758)

UniProtKB Plutella xylostella

A3KCN0 (http://www.uniprot.org/uniprot/A3KCN0)

GenebankID or UniProtKB

KX420690 (https://www.ncbi.nlm.nih.gov/nuccore/KX420690)

GO - Biological Process

-

GO - Cellular Component

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

Presumptive Null

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

Molecular Type

Coding (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)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

T>G p.I1042M (I1056 in D. melanogaster) located in the C-terminal transmembrane domain

Experimental Evidence

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

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

Main Reference

Resistance mutation conserved between insects and mites unravels the benzoylurea insecticide mode of action on chitin biosynthesis. (2016) (https://pubmed.ncbi.nlm.nih.gov/27930336)

Authors

Douris V; Steinbach D; Panteleri R; Livadaras I; Pickett JA; Van Leeuwen T; Nauen R; Vontas J

Abstract

Despite the major role of chitin biosynthesis inhibitors such as benzoylureas (BPUs) in the control of pests in agricultural and public health for almost four decades, their molecular mode of action (MoA) has in most cases remained elusive. BPUs interfere with chitin biosynthesis and were thought to interact with sulfonylurea receptors that mediate chitin vesicle transport. Here, we uncover a mutation (I1042M) in the chitin synthase 1 (CHS1) gene of BPU-resistant Plutella xylostella at the same position as the I1017F mutation reported in spider mites that confers etoxazole resistance. Using a genome-editing CRISPR/Cas9 approach coupled with homology-directed repair (HDR) in Drosophila melanogaster, we introduced both substitutions (I1056M/F) in the corresponding fly CHS1 gene (kkv). Homozygous lines bearing either of these mutations were highly resistant to etoxazole and all tested BPUs, as well as buprofezin-an important hemipteran chitin biosynthesis inhibitor. This provides compelling evidence that BPUs, etoxazole, and buprofezin share in fact the same molecular MoA and directly interact with CHS. This finding has immediate effects on resistance management strategies of major agricultural pests but also on mosquito vectors of serious human diseases such as Dengue and Zika, as diflubenzuron, the standard BPU, is one of the few effective larvicides in use. The study elaborates on how genome editing can directly, rapidly, and convincingly elucidate the MoA of bioactive molecules, especially when target sites are complex and hard to reconstitute in vitro.

Additional References

## RELATED GEPHE

Related Genes

10 (ABCC2, Acetylcholinesterase (Ace-1), CYP6BG1, FMO2, 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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Chitin synthase 1 (CHS1)^/and+Taxon ID=^51655^/or+Gene Gephebase=^Chitin synthase 1 (CHS1)^/and+Taxon ID=^51655^#gephebase-summary-title)

## EXTERNAL LINKS

## COMMENTS

The mutation was present at low frequency (3%) in the Sudlon strain before selection and fixed in selected Sudlon-Tfm strain. It is homozygous in 7% of Japan strain and also present in field populations in China and India. Selected strain showed significant longer larval and pupal development time indicative of possible fitness costs associated with benzoylurea resistance. Transgenic flies with the same mutation is highly resistant to etoxazole and all tested benzoylureas as well as buprofezin