GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00002633

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Spodoptera exigua - susceptible

Trait State in Taxon B

Spodoptera exigua - 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

Spodoptera exigua (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Spodoptera exigua^#gephebase-summary-title)

Common Name

beet armyworm

Synonyms

beet armyworm; pigweed caterpillar; small mottled willow caterpillar; Spodoptera exigua (Hubner, 1808)

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; Obtectomera; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera

Parent

Spodoptera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7106)

NCBI Taxonomy ID

7107 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7107)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Spodoptera exigua (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Spodoptera exigua^#gephebase-summary-title)

Common Name

beet armyworm

Synonyms

beet armyworm; pigweed caterpillar; small mottled willow caterpillar; Spodoptera exigua (Hubner, 1808)

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; Obtectomera; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera

Parent

Spodoptera () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7106)

NCBI Taxonomy ID

7107 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7107)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

RyR

Synonyms

Ryr; CG10844; D-RyR; Dmel\CG10844; DmRyR; DRR; dry; DRY; dRyr; dRyR; dya; l(2)k00424; l(2)k04913; Rya-44F; Rya-r4; rya-r44F; Rya-r44F; Rya-R44F; Rya-r76CD; ryr; RYR; RyRs

String

7227.FBpp0293114 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0293114)

Sequence Similarities

Belongs to the ryanodine receptor (TC 1.A.3.1) family.

GO - Molecular Function

GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)
GO:0048763 : calcium-induced calcium release activity

UniProtKB Drosophila melanogaster

Q24498 (http://www.uniprot.org/uniprot/Q24498)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0048763)
GO:0005219 : ryanodine-sensitive calcium-release channel activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005219)

GO - Biological Process

GO:0006874 : cellular calcium ion homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0006874)
GO:0035206 : regulation of hemocyte proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035206)
GO:0006936 : muscle contraction (https://www.ebi.ac.uk/QuickGO/term/GO:0006936)
GO:0006816 : calcium ion transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006816)
GO:0060047 : heart contraction (https://www.ebi.ac.uk/QuickGO/term/GO:0060047)
GO:0072347 : response to anesthetic (https://www.ebi.ac.uk/QuickGO/term/GO:0072347)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0030659 : cytoplasmic vesicle membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0030659)
GO:0030018 : Z disc (https://www.ebi.ac.uk/QuickGO/term/GO:0030018)
GO:0042383 : sarcolemma (https://www.ebi.ac.uk/QuickGO/term/GO:0042383)
GO:0033017 : sarcoplasmic reticulum membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0033017)
GO:0005790 : smooth endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005790)

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

I4743M - corresponds to I4790M in PxRyR

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	Ile	Met	4790

Main Reference

Identification of the ryanodine receptor mutation I4743M and its contribution to diamide insecticide resistance in Spodoptera exigua (Lepidoptera: Noctuidae). (2020)
(https://pubmed.ncbi.nlm.nih.gov/31140744)

Authors

Zuo YY; Ma HH; Lu WJ; Wang XL; Wu SW; Nauen R; Wu YD; Yang YH

Abstract

Insect ryanodine receptors (RyRs) are the targets of diamide insecticides. Two point mutations G4946E and I4790M (numbering according to Plutella xylostella, PxRyR) in the transmembrane domain of the insect RyRs associated with diamide resistance have so far been identified in three lepidopteran pests, P. xylostella, Tuta absoluta and Chilo suppressalis. In this study, we identified one of the known RyR target site resistance mutations (I4790M) in a field-collected population of Spodoptera exigua. The field-collected WF population of S. exigua exhibited 154 fold resistance to chlorantraniliprole when compared with the susceptible WH-S strain. Sequencing the transmembrane domains of S. exigua RyR (SeRyR) revealed that the resistant WF strain was homozygous for the I4743M mutation (corresponding to I4790M in PxRyR), whereas the G4900E allele (corresponding to G4946E of PxRyR) was not detected. The 4743M allele was introgressed into the susceptible WH-S strain by crossing WF with WH-S, followed by three rounds of backcrossing with WH-S. The introgressed strain 4743M was homozygous for the mutant 4743M allele and shared about 94% of its genetic background with that of the recipient WH-S strain. Compared with WH-S, the near-isogenic 4743M strain showed moderate levels of resistance to chlorantraniliprole (21 fold), cyantraniliprole (25 fold) and flubendiamide (22 fold), suggesting that the I4743M mutation confers medium levels of resistance to all three diamides. Genetic analysis showed diamide resistance in the 4743M strain was inherited as an autosomal and recessive trait. Results from this study have direct implications for the design of appropriate resistance monitoring and management practices to sustainably control S. exigua.

Â© 2019 Institute of Zoology, Chinese Academy of Sciences.

Additional References

Investigation of the contribution of RyR target-site mutations in diamide resistance by CRISPR/Cas9 genome modification in Drosophila. (2017) (https://pubmed.ncbi.nlm.nih.gov/28669775)
Novel diamide resistance-linked mutation in Korean Spodoptera exigua and a LAMP assay based on a mutation-associated intronic InDel . (2021)
(https://pubmed.ncbi.nlm.nih.gov/00000000.000049)

RELATED GEPHE

Related Genes

4 (ABCC2, CYP321A8, CYP9A186, GSTe) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7107^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS