GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00002438

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

tomato leafminer Tuta absoluta - susceptible

Trait State in Taxon B

tomato leafminer Tuta absoluta - resistant strain GR-IER-SD originating from Crete in Greece and obtained after four sequential selections of field populations with flubendiamide

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Gnorimoschema absoluta; Phthorimaea absoluta; Scrobipalpula absoluta; Scrobipalpuloides absoluta; Tuta absoluta (Meyrick, 1917)

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; Gelechioidea; Gelechiidae; Gelechiinae; Tuta

Parent

Tuta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702716)

NCBI Taxonomy ID

702717 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702717)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Gnorimoschema absoluta; Phthorimaea absoluta; Scrobipalpula absoluta; Scrobipalpuloides absoluta; Tuta absoluta (Meyrick, 1917)

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; Gelechioidea; Gelechiidae; Gelechiinae; Tuta

Parent

Tuta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702716)

NCBI Taxonomy ID

702717 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702717)

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)

UniProtKB Drosophila melanogaster

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

GenebankID or UniProtKB

()

GO:0048763 : calcium-induced calcium release activity (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

G4903V corresponds to the G4946E mutation site shown to confer diamide resistance in diamondback moth

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	GGG	GTG	-
Amino-acid	Gly	Val	4946

Main Reference

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)

Authors

Douris V; Papapostolou KM; Ilias A; Roditakis E; Kounadi S; Riga M; Nauen R; Vontas J

Abstract

Diamide insecticides are used widely against lepidopteran pests, acting as potent activators of insect Ryanodine Receptors (RyRs) and thus inducing muscle contraction and eventually death. However, resistant phenotypes have recently evolved in the field, associated with the emergence of target site resistance mutations (G4946E/V and I4790M). We investigated the frequency of the mutations found in a resistant population of Tuta absoluta from Greece (G4946V ~79% and I4790M ~21%) and the associated diamide resistance profile: there are very high levels of resistance against chlorantraniliprole (9329-fold) and flubendiamide (4969-fold), but moderate levels against cyantraniliprole (191-fold). To further investigate functionally the contribution of each mutation in the resistant phenotype, we used CRISPR/Cas9 to generate genome modified Drosophila carrying alternative allele combinations, and performed toxicity bioassays against all three diamides. Genome modified flies bearing the G4946V mutation exhibited high resistance ratios to flubendiamide (91.3-fold) and chlorantraniliprole (194.7-fold) when compared to cyantraniliprole (5.4-fold). Flies naturally wildtype for the I4790M mutation were moderately resistant to flubendiamide (15.3-fold) but significantly less resistant to chlorantraniliprole (7.5-fold), and cyantraniliprole (2.3-fold). These findings provide inÂ vivo functional genetic confirmation for the role and relative contribution of RyR mutations in diamide resistance and suggest that the mutations confer subtle differences on the relative binding affinities of the three diamides at an overlapping binding site on the RyR protein.

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)

RELATED GEPHE

Related Genes

2 (nAChR, para (kdr)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^702717^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

3 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^RYR^/and+Taxon ID=^702717^/or+Gene Gephebase=^RYR^/and+Taxon ID=^702717^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@Parallelism The two mutations found in GR-IER-SD have probably arisen independently since they are always found in different alleles and never in the same chromosome.