GEPHE SUMMARY

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

GepheID
GP00002436

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
tomato leafminer Tuta absoluta - susceptible

Trait State in Taxon B
tomato leafminer Tuta absoluta - Brazilian resistant strain BR-PSQ

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)
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

G4903 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	GAG	-
Amino-acid	Gly	Glu	4946

Main Reference

Ryanodine receptor point mutations confer diamide insecticide resistance in tomato leafminer, Tuta absoluta (Lepidoptera: Gelechiidae). (2017) (https://pubmed.ncbi.nlm.nih.gov/27845250)

Authors

Roditakis E; Steinbach D; Moritz G; Vasakis E; Stavrakaki M; Ilias A; GarcÃa-Vidal L; MartÃnez-Aguirre MDR; Bielza P; Morou E; Silva JE; Silva WM; Siqueira Î—AA; Iqbal S; Troczka BJ; Williamson MS; Bass C; Tsagkarakou A; Vontas J; Nauen R

Abstract

Insect ryanodine receptors (RyR) are the molecular target-site for the recently introduced diamide insecticides. Diamides are particularly active on Lepidoptera pests, including tomato leafminer, Tuta absoluta (Lepidoptera: Gelechiidae). High levels of diamide resistance were recently described in some European populations of T.Â absoluta, however, the mechanisms of resistance remained unknown. In this study the molecular basis of diamide resistance was investigated in a diamide resistant strain from Italy (IT-GELA-SD4), and additional resistant field populations collected in Greece, Spain and Brazil. The genetics of resistance was investigated by reciprocally crossing strain IT-GELA-SD4 with a susceptible strain and revealed an autosomal incompletely recessive mode of inheritance. To investigate the possible role of target-site mutations as known from diamondback moth (Plutella xylostella), we sequenced respective domains of the RyR gene of T.Â absoluta. Genotyping of individuals of IT-GELA-SD4 and field-collected strains showing different levels of diamide resistance revealed the presence of G4903E and I4746M RyR target-site mutations. These amino acid substitutions correspond to those recently described for diamide resistant diamondback moth, i.e. G4946E and I4790M. We also detected two novel mutations, G4903V and I4746T, in some of the resistant T.Â absoluta strains. Radioligand binding studies with thoracic membrane preparations of the IT-GELA-SD4 strain provided functional evidence that these mutations alter the affinity of the RyR to diamides. In combination with previous work on P.Â xylostella our study highlights the importance of position G4903 (G4946 in P.Â xylostella) of the insect RyR in defining sensitivity to diamides. The discovery of diamide resistance mutations in T.Â absoluta populations of diverse geographic origin has serious implications for the efficacy of diamides under applied conditions. The implementation of appropriate resistance management strategies is strongly advised to delay the further spread of resistance.

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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 - independent evolution of the same amino acid substitution (but different codon changes GGG>GAG and GGG>GAA) in different Brazilian Tuta absoluta field strains