GEPHE SUMMARY

Gephebase Gene

ABCC2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ABCC2^#gephebase-summary-title)

GepheID

GP00002462

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

Trait State in Taxon A

Spodoptera frugiperda - susceptible

Trait State in Taxon B

Spodoptera frugiperda - individuals from Brazil resistant to transgenic maize expressing the Cry1F toxin

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

Common Name

fall armyworm

Synonyms

fall armyworm; Spodoptera frugiperda (Smith, 1797)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; 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

7108 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7108)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

fall armyworm

Synonyms

fall armyworm; Spodoptera frugiperda (Smith, 1797)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; 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

7108 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7108)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

MRP1

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0008514 : organic anion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008514)
GO:0140359 : ABC-type transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0140359)

GO - Biological Process

UniProtKB Drosophila melanogaster

H8YF43 (http://www.uniprot.org/uniprot/H8YF43)

GenebankID or UniProtKB

()

-

GO - Cellular Component

GO:0005887 : integral component of plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005887)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

two mutations in the extracellular loop 4 (ECL4) of ABCC2: a deletion of two amino acids (GY) at positions 788 and 789 and the change of a proline to either lysine or arginine at position 799. Expression of mutated ABCC2 in insect cells confirmed the role of these mutations in toxin binding.

Experimental Evidence

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

Main Reference

Molecular characterization of Cry1F resistance in fall armyworm, Spodoptera frugiperda from Brazil. (2020) (https://pubmed.ncbi.nlm.nih.gov/31740346)

Authors

Boaventura D; Ulrich J; Lueke B; Bolzan A; Okuma D; Gutbrod O; Geibel S; Zeng Q; Dourado PM; Martinelli S; Flagel L; Head G; Nauen R

Abstract

Fall armyworm, Spodoptera frugiperda (J.E. Smith) is a major lepidopteran pest of maize in Brazil and its control particularly relies on the use of genetically engineered crops expressing Bacillus thuringiensis (Bt) toxins such as Cry1F. However, control failures compromising the efficacy of this technology have been reported in many regions in Brazil, but the mechanism of Cry1F resistance in Brazilian fall armyworm populations remained elusive. Here we investigated the molecular mechanism of Cry1F resistance in two field-collected strains of S. frugiperda from Brazil exhibiting high levels of Cry1F resistance. We first rigorously evaluated several candidate reference genes for normalization of gene expression data across strains, larval instars and gut tissues, and identified ribosomal proteins L10, L17 and RPS3A to be most suitable. We then investigated the expression pattern of ten potential Bt toxin receptors/enzymes in both neonates and 2nd instar gut tissue of Cry1F resistant fall armyworm strains compared to a susceptible strain. Next we sequenced the ATP-dependent Binding Cassette subfamily C2 gene (ABCC2) and identified three mutated sites present in ABCC2 of both Cry1F resistant strains: two of them, a GY deletion (positions 788-789) and a P799Â K/R amino acid substitution, located in a conserved region of ABCC2 extracellular loop 4 (EC4) and another amino acid substitution, G1088D, but in a less conserved region. We further characterized the role of the novel mutations present in EC4 by functionally expressing both wild type and mutated ABCC2 transporters in insect cell lines, and confirmed a critical role of both sites for Cry1F binding by cell viability assays. Finally, we assessed the frequency of the mutant alleles by pooled population sequencing and pyrosequencing in 40 fall armyworm populations collected from maize fields in different regions in Brazil. We found that the GY deletion being present at high frequency. However we also observed many rare alleles which disrupt residues between sites 783-799, and their diversity and abundance in field collected populations lends further support to the importance of the EC4 domain for Cry1F toxicity.

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Additional References

RELATED GEPHE

Related Genes

2 (CYP9A, GSTe) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7108^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^ABCC2^/and+Taxon ID=^7108^/or+Gene Gephebase=^ABCC2^/and+Taxon ID=^7108^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS