GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00002635

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 (METI-I acaricide) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (METI-I acaricide)^#gephebase-summary-title)

Trait State in Taxon A

Tetranychus urticae - sensitive

Trait State in Taxon B

Tetranychus urticae - 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

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

Common Name

two-spotted spider mite

Synonyms

two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidea; Tetranychidae; Tetranychus

Parent

Tetranychus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32263)

NCBI Taxonomy ID

32264 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32264)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

two-spotted spider mite

Synonyms

two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidea; Tetranychidae; Tetranychus

Parent

Tetranychus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32263)

NCBI Taxonomy ID

32264 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32264)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

ND-20

Synonyms

20 kDa; CG9172; Dmel\CG9172; Dmel_CG9172; dNDUFS7; dNDUFS7A; ND20; NUKM; PSST

String

7227.FBpp0073949 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0073949)

Sequence Similarities

Belongs to the complex I 20 kDa subunit family.

GO - Molecular Function

GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0048038 : quinone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0048038)
GO:0051539 : 4 iron, 4 sulfur cluster binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051539)
GO:0008137 : NADH dehydrogenase (ubiquinone) activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008137)

UniProtKB Drosophila melanogaster

Q9VXK7 (http://www.uniprot.org/uniprot/Q9VXK7)

GenebankID or UniProtKB

()

GO - Biological Process

GO:0000302 : response to reactive oxygen species
(https://www.ebi.ac.uk/QuickGO/term/GO:0000302)
GO:0008340 : determination of adult lifespan
(https://www.ebi.ac.uk/QuickGO/term/GO:0008340)
GO:2000331 : regulation of terminal button organization
(https://www.ebi.ac.uk/QuickGO/term/GO:2000331)
GO:0009060 : aerobic respiration (https://www.ebi.ac.uk/QuickGO/term/GO:0009060)
GO:0015990 : electron transport coupled proton transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0015990)
GO:0032981 : mitochondrial respiratory chain complex I assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0032981)

GO - Cellular Component

GO:0005747 : mitochondrial respiratory chain complex I
(https://www.ebi.ac.uk/QuickGO/term/GO:0005747)

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

H92R

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	His	Arg	92

Main Reference

A mutation in the PSST homologue of complex I (NADH:ubiquinone oxidoreductase) from Tetranychus urticae is associated with resistance to METI acaricides. (2017)
(https://pubmed.ncbi.nlm.nih.gov/27919778)

Authors

Bajda S; Dermauw W; Panteleri R; Sugimoto N; Douris V; Tirry L; Osakabe M; Vontas J; Van Leeuwen T

Abstract

The acaricidal compounds pyridaben, tebufenpyrad and fenpyroximate are frequently used in the control of phytophagous mites such as Tetranychus urticae, and are referred to as Mitochondrial Electron Transport Inhibitors, acting at the quinone binding pocket of complex I (METI-I acaricides). Because of their very frequent use, resistance evolved fast more than 20 years ago, and is currently wide-spread. Increased activity of P450 monooxygenases has been often associated with resistance, but target-site based resistance mechanisms were never reported. Here, we report the discovery of a mutation (H92R) in the PSST homologue of complex I in METI-I resistant T.Â urticae strains. The position of the mutation was studied using the high-resolution crystal structure of Thermus thermophilus, and was located in a stretch of amino acids previously photo-affinity labeled by fenpyroximate. Selection experiments with a strain segregating for the mutant allele, together with marker-assisted back-crossing of the mutation in a susceptible background, confirmed the involvement of the mutation in METI-I resistance. Additionally, an independent genetic mapping approach; QTL analysis identified the genomic region of pyridaben resistance, which included the PSST gene. Last, we used CRISPR-Cas9 genome editing tools to introduce the mutation in the Drosophila PSST homologue.

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Additional References

RELATED GEPHE

Related Genes

8 (Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CPR, CYP392A16, CYP392E8, cytochrome b, glutamate-gated chloride channel (GluCl), para (kdr))
(https://www.gephebase.org/search-criteria?/or+Taxon ID=^32264^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS