## GEPHE SUMMARY

Gephebase Gene
CYP392A16 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CYP392A16^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00002471
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) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide)^#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 | Taxon B |
|---|---|---|
| Latin Name | Tetranychus urticae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Tetranychus urticae^#gephebase-summary-title) | Tetranychus urticae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Tetranychus urticae^#gephebase-summary-title) |
| Common Name | two-spotted spider mite | two-spotted spider mite |
| Synonyms | two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836 | two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836 |
| Rank | species | species |
| Lineage | cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidea; Tetranychidae; Tetranychus | 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 ) | 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 ) | 32264 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32264 ) |
| is Taxon A an Infraspecies? / is Taxon B an Infraspecies? | No | No |

## GENOTYPIC CHANGE

Generic Gene Name
Ace
Synonyms
AcChE; ace; ACE; ace-2; ache; AchE; AChE; CG17907; CHE; dAChE; dmAChE; DmAChE; Dmel\CG17907; Dm_ace; FBgn0000024; l(3)26; l(3)87Ed
String
7227.FBpp0289713 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0289713 )
Sequence Similarities
Belongs to the type-B carboxylesterase/lipase family.
GO - Molecular Function
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0003990 : acetylcholinesterase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003990)
GO:0004104 : cholinesterase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004104)
GO:0043199 : sulfate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043199)

UniProtKB Drosophila melanogaster
P07140 (http://www.uniprot.org/uniprot/P07140)
GenebankID or UniProtKB
()

GO - Biological Process

GO:0006581 : acetylcholine catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006581)
GO:0001507 : acetylcholine catabolic process in synaptic cleft (https://www.ebi.ac.uk/QuickGO/term/GO:0001507)
GO:0007268 : chemical synaptic transmission (https://www.ebi.ac.uk/QuickGO/term/GO:0007268)
GO:0042426 : choline catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0042426)
GO:0042331 : phototaxis (https://www.ebi.ac.uk/QuickGO/term/GO:0042331)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0031225 : anchored component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0031225)
GO:0030054 : cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0030054)
GO:0043083 : synaptic cleft (https://www.ebi.ac.uk/QuickGO/term/GO:0043083)

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

several non-synonymous SNP - exact causing amino acid change(s) unknown. Functional analysis of the putative promoter region from the resistant and susceptible parental strains revealed a higher reporter gene expression confirming the presence of cis-acting regulatory mechanisms.

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 | - | - | - |

Main Reference

Sequence of a cDNA encoding acetylcholinesterase from susceptible and resistant two-spotted spider mite, Tetranychus urticae. (2003) (https://pubmed.ncbi.nlm.nih.gov/12706630)

Authors

Anazawa Y; Tomita T; Aiki Y; Kozaki T; Kono Y

Abstract

Acetylcholinesterase (AChE) from two-spotted spider mites, Tetranychus urticae was compared between an organophosphate susceptible (TKD) and a resistant (NCN) strain. The AChE of TKD had lower affinity to acetylthiocholine and propionylthiocholine than that of NCN, and the inhibition of AChE by DDVP, ambenonium, eserine and n-methyl-eserine showed that NCN was more insensitive than TKD. AChE cDNA sequence was determined, and the 687 amino acids of primary structure were deduced. There were six replacements of amino acid residues in TKD and two in NCN. #F331(439)C was the only substitution unique to NCN, however, this mutation existed homozygously in only two out of nine mites. This residue is one of the gorge lining components, and #F331(439)C might act an important role in the sensitivity of AChE to the inhibitors.

Additional References

Over-expression in cis of the midgut P450 CYP392A16 contributes to abamectin resistance in Tetranychus urticae. (2022) (https://pubmed.ncbi.nlm.nih.gov/34995778)

## RELATED GEPHE

Related Genes

8 (Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CPR, CYP392E8, cytochrome b, glutamate-gated chloride channel (GluCl), para (kdr), PSST) (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