

GEPHE SUMMARY

CPR (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~CPR^#gephebase-summary-title)	Gephebase Gene	GP00002398	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)		Trait Category	
Xenobiotic resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobioticresistance^#gephebase-summary-title)		Trait	
sensitive		Trait State in Taxon A	
resistant		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Tetranychus urticae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Tetranychusurticae^#gephebase-summary-title)		Tetranychus urticae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Tetranychusurticae^#gephebase-summary-title)	
two-spotted spider mite		two-spotted spider mite	
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	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidae; Tetranychidae; Tetranychus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidae; Tetranychidae; Tetranychus	
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)	
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 Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

Cpr	Generic Gene Name	UniProtKB Drosophila melanogaster
	Synonyms	Q27597 (http://www.uniprot.org/uniprot/Q27597)
	String	GenebankID or UniProtKB
CCR; CG11567; cpr; CPR; DmCPR; Dmel\CG11567; DMR; NCPR; P450		
7227.FBpp0078880 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0078880)		
Sequence Similarities		
Belongs to the NADPH--cytochrome P450 reductase family.;In the N-terminal section; belongs to the flavodoxin family.;In the C-terminal section; belongs to the flavoprotein pyridine nucleotide cytochrome reductase family.		
GO - Molecular Function		
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)		
GO:0050660 : flavin adenine dinucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050660)		
GO:0050661 : NADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050661)		
GO:0010181 : FMN binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010181)		

GO:0003958 : NADPH-hemoprotein reductase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003958>)

GO - Biological Process

GO:0009725 : response to hormone (<https://www.ebi.ac.uk/QuickGO/term/GO:0009725>)

GO:0006723 : cuticle hydrocarbon biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006723>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

GO:0005789 : endoplasmic reticulum membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

GO:0012505 : endomembrane system

(<https://www.ebi.ac.uk/QuickGO/term/GO:0012505>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Amplification~#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title>)

Insertion Size

1-10 kb

Molecular Details of the Mutation

Pyflubumide resistant populations are estimated to harbor three CPR copies by two methods, whereas susceptible populations have a single CPR copy.

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

Main Reference

High-resolution genetic mapping reveals cis-regulatory and copy number variation in loci associated with cytochrome P450-mediated detoxification in a generalist arthropod pest. (2021)
(<https://pubmed.ncbi.nlm.nih.gov/34153029>)

Authors

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Abstract

Chemical control strategies are driving the evolution of pesticide resistance in pest populations. Understanding the genetic mechanisms of these evolutionary processes is of crucial importance to develop sustainable resistance management strategies. The acaricide pyflubumide is one of the most recently developed mitochondrial complex II inhibitors with a new mode of action that specifically targets spider mite pests. In this study, we characterize the molecular basis of pyflubumide resistance in a highly resistant population of the spider mite *Tetranychus urticae*. Classical genetic crosses indicated that pyflubumide resistance was incompletely recessive and controlled by more than one gene. To identify resistance loci, we crossed the resistant population to a highly susceptible *T. urticae* inbred strain and propagated resulting populations with and without pyflubumide exposure for multiple generations in an experimental evolution set-up. High-resolution genetic mapping by a bulked segregant analysis approach led to the identification of three quantitative trait loci (QTL) linked to pyflubumide resistance. Two QTLs were found on the first chromosome and centered on the cytochrome P450 CYP392A16 and a cluster of CYP392E6-8 genes. Comparative transcriptomics revealed a consistent overexpression of CYP392A16 and CYP392E8 in the experimental populations that were selected for pyflubumide resistance. We further corroborated the involvement of CYP392A16 in resistance by in vitro functional expression and metabolism studies. Collectively, these experiments uncovered that CYP392A16 N-demethylates the toxic carboxamide form of pyflubumide to a non-toxic compound. A third QTL coincided with cytochrome P450 reductase (CPR), a vital component of cytochrome P450 metabolism. We show here that the resistant population harbors three gene copies of CPR and that this copy number variation is associated with higher mRNA abundance. Together, we provide evidence for detoxification of pyflubumide by cytochrome P450s that is likely synergized by gene amplification of CPR.

Additional References

RELATED GEPHE

Related Genes

8 (Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP392A16, 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

CPR is a NADPH cytochrome P450 reductase.

