

GEPHE SUMMARY

CPR (#gephebase-summary-title)	Gephebase Gene	GP00002398	Gepheid
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category			
Physiology (#gephebase-summary-title)	Trait		
Xenobiotic resistance (#gephebase-summary-title)	Trait State in Taxon A		
sensitive	Trait State in Taxon B		
resistant	Ancestral State		
Taxon A	Taxonomic Status		
Intraspecific (#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Tetranychus urticae (#gephebase-summary-title))		Tetranychus urticae (#gephebase-summary-title))	
two-spotted spider mite	Common Name	two-spotted spider mite	Common Name
two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836	Synonyms	two-spotted spider mite; red spider mite; twospotted mite; Tetranychus urticae Koch, 1836	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidea; Tetranychidae; Tetranychus	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidea; Tetranychidae; Tetranychus	Lineage
Tetranychus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32263)	Parent	Tetranychus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32263)	Parent
32264 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32264)	NCBI Taxonomy ID	32264 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32264)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Cpr	Generic Gene Name	UniProtKB Drosophila melanogaster
CCR; CG11567; cpr; CPR; DmCPR; Dmel\CG11567; DMR; NCPR; P450	Synonyms	GenebankID or UniProtKB
7227.FBpp0078880 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0078880)	String	Q27597 (http://www.uniprot.org/uniprot/Q27597)
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.	Sequence Similarities	Q27597 (https://www.ncbi.nlm.nih.gov/nuccore/Q27597)
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 - Molecular Function	

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=%22No%22#gephebase-summary-title>)

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Gene+Amplification%22#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22Insertion%22#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=%22Linkage+Mapping%22#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=%2232264%22/and+Trait=%22Xenobiotic+resistance%22/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

CPR is a NADPH cytochrome P450 reductase.

