

GEPHE SUMMARY

Gephebase Gene
CYP6B4

Entry Status
Published

GephelD
GP00000206

Main curator
Martin

PHENOTYPIC CHANGE

Trait #1
Trait Category
Physiology
Trait
Xenobiotic resistance
Trait State in Taxon A
Other butterflies
Trait State in Taxon B
Papilio glaucus and *Papilio canadensis*

Trait #2
Trait Category
Physiology
Trait
Host plant specialization
Trait State in Taxon A
-
Trait State in Taxon B
-

Ancestral State
Data not curated

Taxonomic Status
Intergeneric or Higher

Taxon A

Latin Name
Nymphalidae
Common Name
brushfoots
Synonyms
brushfoots; brush-footed butterflies
Rank
family
Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea

Parent
Papilionoidea (butterflies) - (Rank: superfamily)

NCBI Taxonomy ID
33415

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Papilio glaucus
Common Name
eastern tiger swallowtail
Synonyms
Pterourus glaucus; eastern tiger swallowtail; tiger swallowtail; *Papilio glaucus* Linnaeus, 1758
Rank
species
Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; *Papilio*

Parent
Papilio () - (Rank: genus)

NCBI Taxonomy ID
45779

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
CYP6B4

UniProtKB *Papilio glaucus*
Q27902

Synonyms	GenebankID or UniProtKB U65489														
String	-														
Sequence Similarities	Belongs to the cytochrome P450 family.														
GO - Molecular Function	GO:0020037 : heme binding GO:0005506 : iron ion binding GO:0070330 : aromatase activity														
GO - Biological Process	-														
GO - Cellular Component	GO:0005789 : endoplasmic reticulum membrane GO:0031090 : organelle membrane														
Presumptive Null	No														
Molecular Type	Coding														
Aberration Type	SNP														
SNP Coding Change	Nonsynonymous														
Molecular Details of the Mutation	Lys484Ser and probably other a.a. substitutions														
Experimental Evidence	Candidate Gene														
<table border="1"> <thead> <tr> <th></th> <th>Taxon A</th> <th>Taxon B</th> <th>Position</th> </tr> </thead> <tbody> <tr> <td>Codon</td> <td>-</td> <td>-</td> <td>-</td> </tr> <tr> <td>Amino-acid</td> <td>Lys</td> <td>Ser</td> <td>484</td> </tr> </tbody> </table>					Taxon A	Taxon B	Position	Codon	-	-	-	Amino-acid	Lys	Ser	484
	Taxon A	Taxon B	Position												
Codon	-	-	-												
Amino-acid	Lys	Ser	484												
Main Reference															
Cytochrome P450s in Papilio multicaudatus and the transition from oligophagy to polyphagy in the Papilionidae. (2007)															
Authors	Mao W; Schuler MA; Berenbaum MR														
Abstract	Although substrate-specific CYP6B1 and CYP6B3 enzymes in Papilio polyxenes contribute to specialization on furanocoumarin-containing host plants, CYP6B4 and CYP6B17 enzymes in the polyphagous Papilio glaucus and Papilio canadensis have a broader range of substrates. Papilio multicaudatus, an oligophage with one furanocoumarin-containing host, is putatively ancestral to polyphagous Papilio species. Furanocoumarin-inducible CYP6B33-CYP6B37 and CYP6AB6 were characterized from this species. Heterologous expression of CYP6B33 revealed furanocoumarin metabolism resembling that of CYP6B4-CYP6B17 enzymes from P. glaucus and P. canadensis. Molecular models of CYP6B33 and CYP6B4 indicate that seven conserved aromatic side chains stabilize their hydrophobic catalytic sites and that a Lys484-Ser484 substitution enlarges the CYP6B4 active site pocket to increase the predicted distance between the substrate and reactive oxygen relative to CYP6B1. Loss of specialization in this lineage may have resulted from relatively few mutational changes, allowing acquisition of broader catalytic activities without loss of ancestral furanocoumarin-metabolizing activities.														
Additional References															

RELATED GEPHE

Related Genes
[2 \(CYP6B1, Na/K-ATPase alpha-subunit\)](#)
 Related Haplotypes
 No matches found.

EXTERNAL LINKS

COMMENTS

