

## GEPHE SUMMARY

**Gephebase Gene**  
CYP6B1

**Entry Status**  
Published

**GepheID**  
GP00000205

**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 polyxenes

**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**  
Interspecific

### 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; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea

**Parent**  
Papilionoidea (butterflies) - (Rank: superfamily)

**NCBI Taxonomy ID**  
33415

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Papilio polyxenes*

**Common Name**  
black swallowtail

**Synonyms**  
black swallowtail; American swallowtail; eastern black swallowtail; *Papilio polyxenes* Fabricius, 1775

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio

**Parent**  
Papilio () - (Rank: genus)

**NCBI Taxonomy ID**  
7146

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
CYP6B1

**UniProtKB** *Papilio polyxenes*  
Q04552

**Synonyms**

-

**GenebankID or UniProtKB**

U05037

**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**

Ile484Phe and probably other a.a. substitutions

**Experimental Evidence**[Candidate Gene](#)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ile	Phe	484

**Main Reference**[Diversification of furanocoumarin-metabolizing cytochrome P450 monooxygenases in two papilionids: Specificity and substrate encounter rate. \(2003\)](#)**Authors**

Li W; Schuler MA; Berenbaum MR

**Abstract**

Diversification of cytochrome P450 monooxygenases (P450s) is thought to result from antagonistic interactions between plants and their herbivorous enemies. However, little direct evidence demonstrates the relationship between selection by plant toxins and adaptive changes in herbivore P450s. Here we show that the furanocoumarin-metabolic activity of CYP6B proteins in two species of swallowtail caterpillars is associated with the probability of encountering host plant furanocoumarins. Catalytic activity was compared in two closely related CYP6B4 and CYP6B17 groups in the polyphagous congeners *Papilio glaucus* and *Papilio canadensis*. Generally, P450s from *P. glaucus*, which feeds occasionally on furanocoumarin-containing host plants, display higher activities against furanocoumarins than those from *P. canadensis*, which normally does not encounter furanocoumarins. These P450s in turn catalyze a larger range of furanocoumarins at lower efficiency than CYP6B1, a P450 from *Papilio polyxenes*, which feeds exclusively on furanocoumarin-containing host plants. Reconstruction of the ancestral CYP6B sequences using maximum likelihood predictions and comparisons of the sequence and geometry of their active sites to those of contemporary CYP6B proteins indicate that host plant diversity is directly related to P450 activity and inversely related to substrate specificity. These predictions suggest that, along the lineage leading to *Papilio* P450s, the ancestral, highly versatile CYP6B protein presumed to exist in a polyphagous species evolved through time into a more efficient and specialized CYP6B1-like protein in *Papilio* species with continual exposure to furanocoumarins. Further diversification of *Papilio* CYP6Bs has likely involved interspersed events of positive selection in oligophagous species and relaxation of functional constraints in polyphagous species.

**Additional References****RELATED GEPHE****Related Genes**

2 (CYP6B4, Na/K-ATPase alpha-subunit)

**Related Haplotypes**

No matches found.

**EXTERNAL LINKS****COMMENTS**

