GEPHE SUMMARY

Gephebase Gene

FMO1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FMO1^#gephebase-summary-title)

GepheID

GP00000348

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Xenobiotic resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance^#gephebase-summary-title)

Trait State in Taxon A

Other lepidopterans

Trait State in Taxon B

Tyria jacobaeae and other arctiidae

Trait #2

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Host plant specialization (https://www.gephebase.org/search-criteria?/and+Trait=^Host plant specialization^#gephebase-summary-title)

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Data not curated

Taxonomic Status

Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#gephebase-summary-title)

Taxon A

Latin Name

Lepidoptera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Lepidoptera^#gephebase-summary-title)

Common Name

butterflies and moths

Synonyms

butterflies and moths; moths

Rank

order

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera

Parent

Amphiesmenoptera () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 85604)

NCBI Taxonomy ID

7088 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7088)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Tyria jacobaeae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Tyria jacobaeae^#gephebase-summary-title)

Common Name

cinnabar moth

Synonyms

cinnabar moth; Tyria jacobaeae (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; Noctuoidea; Erebidae; Arctiinae; Arctiini; Tyria

Parent

Tyria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 179665)

NCBI Taxonomy ID

179666 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 179666)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

Fmo-1

Synonyms

CG3006; Dmel\CG3006; DmFMO-1; Dmfmo1; FMO-1; Dmel_CG3006

String

7227.FBpp0072059 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0072059)

Sequence Similarities

Belongs to the FMO family.

GO - Molecular Function

GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)
GO:0050660 : flavin adenine dinucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050660)
GO:0004499 : N,N-dimethylaniline monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004499)
GO:0050661 : NADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050661)

GO - Biological Process

-

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0043231 : intracellular membrane-bounded organelle (https://www.ebi.ac.uk/QuickGO/term/GO:0043231)

UniProtKB Drosophila melanogaster

Q9W1E9 (http://www.uniprot.org/uniprot/Q9W1E9)

GenebankID or UniProtKB

()

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

Complex Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Complex Change^#gephebase-summary-title)

Molecular Details of the Mutation

Gene duplication

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Flavin-dependent monooxygenases as a detoxification mechanism in insects: new insights from the arctiids (lepidoptera). (2010) (https://pubmed.ncbi.nlm.nih.gov/20454663)

Authors

Sehlmeyer S; Wang L; Langel D; Heckel DG; Mohagheghi H; Petschenka G; Ober D

Abstract

Insects experience a wide array of chemical pressures from plant allelochemicals and pesticides and have developed several effective counterstrategies to cope with such toxins. Among these, cytochrome P450 monooxygenases are crucial in plant-insect interactions. Flavin-dependent monooxygenases (FMOs) seem not to play a central role in xenobiotic detoxification in insects, in contrast to mammals. However, the previously identified senecionine N-oxygenase of the arctiid moth Tyria jacobaeae (Lepidoptera) indicates that FMOs have been recruited during the adaptation of this insect to plants that accumulate toxic pyrrolizidine alkaloids. Identification of related FMO-like sequences of various arctiids and other Lepidoptera and their combination with expressed sequence tag (EST) data and sequences emerging from the Bombyx mori genome project show that FMOs in Lepidoptera form a gene family with three members (FMO1 to FMO3). Phylogenetic analyses suggest that FMO3 is only distantly related to lepidopteran FMO1 and FMO2 that originated from a more recent gene duplication event. Within the FMO1 gene cluster, an additional gene duplication early in the arctiid lineage provided the basis for the evolution of the highly specific biochemical, physiological, and behavioral adaptations of these butterflies to pyrrolizidine-alkaloid-producing plants. The genes encoding pyrrolizidine-alkaloid-N-oxygenizing enzymes (PNOs) are transcribed in the fat body and the head of the larvae. An N-terminal signal peptide mediates the transport of the soluble proteins into the hemolymph where PNOs efficiently convert pro-toxic pyrrolizidine alkaloids into their non-toxic N-oxide derivatives. Heterologous expression of a PNO of the generalist arctiid Grammia geneura produced an N-oxygenizing enzyme that shows noticeably expanded substrate specificity compared with the related enzyme of the specialist Tyria jacobaeae. The data about the evolution of FMOs within lepidopteran insects and the functional characterization of a further member of this enzyme family shed light on this almost uncharacterized detoxification system in insects.

Additional References

RELATED GEPHE

Related Genes

25 (ABCA2, Aminopeptidase N (APN), cadherin, CYP337B3, Ha_BtR, para (kdr), tetraspanin, ABCC2, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), MAP4K4, nAChR, resistance to dieldrin, RYR, CYP321A8, CYP9A186, GSTe, CYP9A, CYP6AB3, Na/K-ATPase alpha-subunit, CYP6B1, CYP6B4) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7088^/and+Trait=Xenobiotic resistance/or+Taxon ID=^7088^/and+Trait=Host plant specialization/or+Taxon ID=^179666^/and+Trait=Xenobiotic resistance/or+Taxon ID=^179666^/and+Trait=Host plant specialization/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS