

GEPHE SUMMARY

FMO1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=FMO1^#gephebase-summary-title)	Gephebase Gene	GP00000348	GephelD
	Entry Status	Martin	Main curator
Published			

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			
Taxonomic Status			
Data not curated			
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=Intergeneric or Higher^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Lepidoptera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Lepidoptera^#gephebase-summary-title)		Tyria jacobaeae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Tyria+jacobaeae^#gephebase-summary-title)	
butterflies and moths	Common Name	cinnabar moth	Common Name
butterflies and moths; moths	Synonyms	cinnabar moth; Tyria jacobaeae (Linnaeus, 1758)	Synonyms
order	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera	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	Lineage
Amphiesmenoptera () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 85604)	Parent	Tyria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 179665)	Parent
7088 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7088)	NCBI Taxonomy ID	179666 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 179666)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Fmo-1	Generic Gene Name	UniProtKB Drosophila melanogaster	
CG3006; Dmel\CG3006; DmFMO-1; Dmfm01; FMO-1; Dmel_CG3006	Synonyms	Q9W1E9 (http://www.uniprot.org/uniprot/Q9W1E9)	
7227.FBpp0072059 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0072059)	String	GenebankID or UniProtKB	
Belongs to the FMO family.	Sequence Similarities		
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)	GO - Molecular Function		
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)		Presumptive Null	
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)		Molecular Type	
GO:0043231 : intracellular membrane-bounded organelle (https://www.ebi.ac.uk/QuickGO/term/GO:0043231)		Aberration Type	
No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)		Molecular Details of the Mutation	
Gene Amplification (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Amplification%#gephebase-summary-title)		Experimental Evidence	
Complex Change (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Complex+Change%#gephebase-summary-title)		Main Reference	
Gene duplication		Authors	
Candidate Gene (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title)		Abstract	
Flavin-dependent monooxygenases as a detoxification mechanism in insects: new insights from the arctiids (lepidoptera). (2010) (https://pubmed.ncbi.nlm.nih.gov/20454663)		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 <i>Tyria jacobaeae</i> (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 <i>Bombyx mori</i> 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 <i>Grammia geneura</i> produced an N-oxygenizing enzyme that shows noticeably expanded substrate specificity compared with the related enzyme of the specialist <i>Tyria jacobaeae</i> . 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.	
Sehlmeyer S; Wang L; Langel D; Heckel DG; Mohagheghi H; Petschenka G; Ober D		Additional References	

RELATED GEPHE

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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

