

GEPHE SUMMARY

Gephebase Gene
Acetylcholinesterase (Ace)

Entry Status
Published

GepheID
GP00000040

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Xenobiotic resistance (insecticide)

Trait State in Taxon A
Musca domestica - sensitive

Trait State in Taxon B
Musca domestica- resistant 49R

Ancestral State
Taxon A

Taxonomic Status
Intraspecific

Taxon A

Latin Name
Musca domestica

Common Name
house fly

Synonyms
house fly; Musca domestica Linnaeus, 1758

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calyptratae; Muscoidea; Muscidae; Muscinae; Muscini; Musca; Musca

Parent
Musca () - (Rank: subgenus)

NCBI Taxonomy ID
7370

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Musca domestica

Common Name
house fly

Synonyms
house fly; Musca domestica Linnaeus, 1758

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calyptratae; Muscoidea; Muscidae; Muscinae; Muscini; Musca; Musca

Parent
Musca () - (Rank: subgenus)

NCBI Taxonomy ID
7370

is Taxon B an Intraspecies?
Yes

Taxon B Description
Musca domestica- resistant 49R

GENOTYPIC CHANGE

Generic Gene Name
Ace

Synonyms
AcChE; ace; ACE; ace-2; ache; AchE; AChE; CG17907; CHE; dAChE; dmAChE; DmAChE; Dmel\CG17907; Dm_ace; FBgn0000024; I(3)26; I(3)87Ed

String
7227.FBpp0289713

Sequence Similarities
Belongs to the type-B carboxylesterase/lipase family.

GO - Molecular Function
GO:0042803 : protein homodimerization activity
GO:0003990 : acetylcholinesterase activity
GO:0004104 : cholinesterase activity
GO:0043199 : sulfate binding

GO - Biological Process
GO:0006581 : acetylcholine catabolic process

UniProtKB Drosophila melanogaster
P07140

GenebankID or UniProtKB
ACM68725

GO:0001507 : acetylcholine catabolic process in synaptic cleft
GO:0007268 : chemical synaptic transmission
GO:0042426 : choline catabolic process
GO:0042331 : phototaxis

GO - Cellular Component
GO:0005886 : plasma membrane
GO:0005737 : cytoplasm
GO:0031225 : anchored component of membrane
GO:0030054 : cell junction
GO:0043083 : synaptic cleft

Presumptive Null
No

Molecular Type
Coding

Aberration Type
SNP

SNP Coding Change
Nonsynonymous

Molecular Details of the Mutation
Gly365Ala

Experimental Evidence
Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Identification and characterization of mutations in housefly (*Musca domestica*) acetylcholinesterase involved in insecticide resistance. (2001)

Authors

Walsh SB; Dolden TA; Moores GD; Kristensen M; Lewis T; Devonshire AL; Williamson MS

Abstract

Acetylcholinesterase (AChE) insensitive to organophosphate and carbamate insecticides has been identified as a major resistance mechanism in numerous arthropod species. However, the associated genetic changes have been reported in the AChE genes from only three insect species; their role in conferring insecticide insensitivity has been confirmed, using functional expression, only for those in *Drosophila melanogaster*. The housefly, *Musca domestica*, was one of the first insects shown to have this mechanism; here we report the occurrence of five mutations (Val-180-->Leu, Gly-262-->Ala, Gly-262-->Val, Phe-327-->Tyr and Gly-365-->Ala) in the AChE gene of this species that, either singly or in combination, confer different spectra of insecticide resistance. The baculovirus expression of wild-type and mutated housefly AChE proteins has confirmed that the mutations each confer relatively modest levels of insecticide insensitivity except the novel Gly-262-->Val mutation, which results in much stronger resistance (up to 100-fold) to certain compounds. In all cases the effects of mutation combinations are additive. The mutations introduce amino acid substitutions that are larger than the corresponding wild-type residues and are located within the active site of the enzyme, close to the catalytic triad. The likely influence of these substitutions on the accessibility of the different types of inhibitor and the orientation of key catalytic residues are discussed in the light of the three-dimensional structures of the AChE protein from *Torpedo californica* and *D. melanogaster*.

Additional References

RELATED GEPHE

Related Genes

4 (CYP6D1, esterase isozyme E7 = E3, para (kdr), resistance to dieldrin)

Related Haplotypes

4

EXTERNAL LINKS

COMMENTS

