

GEPHE SUMMARY

	Gephebase Gene		GepheID
Ugt86Dd (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Ugt86Dd~#gephebase-summary-title)		GP00001406	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait	
Xenobiotic resistance (nicotine ; larval stage) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (nicotine ; larval stage)~#gephebase-summary-title)			
	Trait State in Taxon A		
Drosophila melanogaster more resistant to nicotine		Trait State in Taxon B	
Drosophila melanogaster less resistant to nicotine			
	Ancestral State		
Taxon A		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila melanogaster~#gephebase-summary-title)		Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila melanogaster~#gephebase-summary-title)	
	Common Name		Common Name
fruit fly		fruit fly	
	Synonyms		Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
	Rank		Rank
species		species	
	Lineage		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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup		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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	
	Parent		Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)		7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
Ugt86Dd		Q9VGT8 (http://www.uniprot.org/uniprot/Q9VGT8)	
	Synonyms		GenebankID or UniProtKB
AC 006491D; CG6633; Dmel\CG6633; Dmel_CG6633		53507 (https://www.ncbi.nlm.nih.gov/nuccore/53507)	
	String		
7227.FBpp0112233 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 7227.FBpp0112233)			
	Sequence Similarities		
Belongs to the UDP-glycosyltransferase family.			
	GO - Molecular Function		
GO:0015020 : glucuronosyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015020)			
GO:0008194 : UDP-glycosyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008194)			

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0043231 : intracellular membrane-bounded organelle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043231>)

Presumptive Null

Yes ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes))

Molecular Type

Coding ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding))

Aberration Type

Deletion ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion))

Deletion Size

10-99 bp

Molecular Details of the Mutation

22-bp frameshift deletion in Ugt86Dd - CRISPR-induced deletions in Ugt86Dd lead to a large reduction in resistance

Experimental Evidence

Association Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping))

Main Reference

Fine-mapping nicotine resistance loci in *Drosophila* using a multiparent advanced generation inter-cross population. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25236448>)

Authors

Marriage TN; King EG; Long AD; Macdonald SJ

Abstract

Animals in nature are frequently challenged by toxic compounds, from those that occur naturally in plants as a defense against herbivory, to pesticides used to protect crops. On exposure to such xenobiotic substances, animals mount a transcriptional response, generating detoxification enzymes and transporters that metabolize and remove the toxin. Genetic variation in this response can lead to variation in the susceptibility of different genotypes to the toxic effects of a given xenobiotic. Here we use *Drosophila melanogaster* to dissect the genetic basis of larval resistance to nicotine, a common plant defense chemical and widely used addictive drug in humans. We identified quantitative trait loci (QTL) for the trait using the DSPR (*Drosophila* Synthetic Population Resource), a panel of multiparental advanced intercross lines. Mapped QTL collectively explain 68.4% of the broad-sense heritability for nicotine resistance. The two largest-effect loci-contributing 50.3 and 8.5% to the genetic variation-map to short regions encompassing members of classic detoxification gene families. The largest QTL resides over a cluster of ten UDP-glucuronosyltransferase (UGT) genes, while the next largest QTL harbors a pair of cytochrome P450 genes. Using RNAseq we measured gene expression in a pair of DSPR founders predicted to harbor different alleles at both QTL and showed that Ugt86Dd, Cyp28d1, and Cyp28d2 had significantly higher expression in the founder carrying the allele conferring greater resistance. These genes are very strong candidates to harbor causative, regulatory polymorphisms that explain a large fraction of the genetic variation in larval nicotine resistance in the DSPR.

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Additional References

Naturally Segregating Variation at Ugt86Dd Contributes to Nicotine Resistance in *Drosophila melanogaster*. (2017) (<https://pubmed.ncbi.nlm.nih.gov/28743761>)

RELATED GEPHE

Related Genes

19 (Acetylcholinesterase (Ace-2), alcohol dehydrogenase (Adh), Aldehyde dehydrogenase (Aldh), CG11699, Cyp12d1, Cyp28d1, Cyp28d1-Cyp28d2, cyp6d2, cyp6g1, glutamate-gated chloride channel (GluCl), GSS (glutathione synthetase), GSTE1-E10 cluster, kin of irre (kire), para (kdr), PHGPx, resistance to dieldrin, RnrS, SOD1, CHKov1)
(<https://www.gephebase.org/search-criteria?/or+Taxon+ID=~7227#/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

QTL mapping identified a cluster of 10 UDP-glucuronosyltransferase (UGT) genes. The candidate gene was identified according to induction of its expression in presence of nicotine. The effect of the deletion was tested using CRISPR in resistant lines. Despite this major effect of the deletion the allele appears to be very rare in wild-caught populations and likely explains only a small fraction of the natural variation for the trait.