

	Gephebase Gene	GephelD
Cyp28d1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=Cyp28d1^#gephebase-summary-title)	GP00001407	
	Entry Status	Main curator
Published		

Physiology (#gephebase-summary-title)		Trait Category	
Xenobiotic resistance (nicotine ; larval stage) (#gephebase-summary-title)		Trait	
Drosophila melanogaster susceptible to nicotine		Trait State in Taxon A	
Drosophila melanogaster resistant to nicotine		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Drosophila melanogaster (#gephebase-summary-title)		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; Acalypratae; 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; Acalypratae; 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?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Strain ISO-1		Strain A4	

Generic Gene Name	UniProtKB Drosophila melanogaster
Cyp28d1	Q9VMT5 (http://www.uniprot.org/uniprot/Q9VMT5)
Synonyms	GenebankID or UniProtKB
28d1; CG10833; Dmel\CG10833	33749 (https://www.ncbi.nlm.nih.gov/nuccore/33749)
String	
7227.FBpp0078698 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0078698)	
Sequence Similarities	
Belongs to the cytochrome P450 family.	
GO - Molecular Function	
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)	

GO:0005506 : iron ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005506>)
GO:0004497 : monooxygenase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004497>)
GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or
reduction of molecular oxygen (<https://www.ebi.ac.uk/QuickGO/term/GO:0016705>)
GO - Biological Process

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GO - Cellular Component

GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)
GO:0031090 : organelle membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0031090>)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Null
Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Gene Amplification^#gephebase-summary-title)	Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)	Aberration Type
1-10 kb	Insertion Size
insertion of a partial 1.5kb Accord transposable element and a Cyp28d1 gene tandem duplication (CNV - 3754 bp) that may play complementary role in resistance levels	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	Experimental Evidence
Hidden genetic variation shapes the structure of functional elements in Drosophila. (2018) (https://pubmed.ncbi.nlm.nih.gov/29255259)	Main Reference
Chakraborty M; VanKuren NW; Zhao R; Zhang X; Kalsow S; Emerson JJ	Authors
Mutations that add, subtract, rearrange, or otherwise refashion genome structure often affect phenotypes, although the fragmented nature of most contemporary assemblies obscures them. To discover such mutations, we assembled the first new reference-quality genome of Drosophila melanogaster since its initial sequencing. By comparing this new genome to the existing D. melanogaster assembly, we created a structural variant map of unprecedented resolution and identified extensive genetic variation that has remained hidden until now. Many of these variants constitute candidates underlying phenotypic variation, including tandem duplications and a transposable element insertion that amplifies the expression of detoxification-related genes associated with nicotine resistance. The abundance of important genetic variation that still evades discovery highlights how crucial high-quality reference genomes are to deciphering phenotypes.	Abstract
Fine-mapping nicotine resistance loci in Drosophila using a multiparent advanced generation inter-cross population. (2014) (https://pubmed.ncbi.nlm.nih.gov/25236448) Structural variants exhibit widespread allelic heterogeneity and shape variation in complex traits. (2019) (https://pubmed.ncbi.nlm.nih.gov/31653862)	Additional References

RELATED GEPHE

19 (Acetylcholinesterase (Ace-2), alcohol dehydrogenase (Adh), Aldehyde dehydrogenase (Aldh), CG11699, Cyp12d1, 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, Ugt86Dd, CHKov1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Cyp28d1^/and+Taxon ID=^7227^/or+Gene Gephebase=^Cyp28d1^/and+Taxon ID=^7227^#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

The QTL harbors a pair of cytochrome P450 genes. According to gene expression Cyp28d1 is the best candidate but Cyp28d2 is also possible. @TE described with nicotine-dependent effect on gene expression in the follow-up article by Chakraborty et al.: Intergenic element between a gene copy is the 5â€™ end of Accord, a long terminal repeat (LTR) retrotransposon.; Insertion of Accord upstream of another gene called Cyp6g1 has been linked to upregulation of the encoded cytochrome P450 enzyme suggesting that the retrotransposon may be responsible for the upregulated expression of the Cyp28d gene