

GEPHE SUMMARY

	Gephebase Gene		GepheID
Vanaso / disc losts (<a +vanaso+disc+losts"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">#gephebase-summary-title)		GP00001164	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Behavior (<a +behavior"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">#gephebase-summary-title)			
	Trait		
Olfactory behavior (<a +olfactory+behavior"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">#gephebase-summary-title)			
	Trait State in Taxon A		
Drosophila melanogaster - Oregon			
	Trait State in Taxon B		
Drosophila melanogaster - 2b			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Intraspecific (<a +intraspecific"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Drosophila melanogaster (<a +drosophila+melanogaster"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">#gephebase-summary-title)		Drosophila melanogaster (<a +drosophila+melanogaster"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">#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?
Yes		Yes	
	Taxon A Description		Taxon B Description
Drosophila melanogaster - Oregon		Drosophila melanogaster - 2b	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
dlt		Q8T626 (http://www.uniprot.org/uniprot/Q8T626)	
	Synonyms		GenebankID or UniProtKB
CG1977; CG32315; Dlt; DLT; Dmel\CG32315; dre1; l(3)04276; l(3)62Ba; l(3)dre1; Van; VA		AF487677 (https://www.ncbi.nlm.nih.gov/nuccore/AF487677)	
-			
	Sequence Similarities		
-			
	GO - Molecular Function		
-			
	GO - Biological Process		
GO:0042048 : olfactory behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0042048)			
GO:0042127 : regulation of cell proliferation			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042127>)
GO:0007560 : imaginal disc morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007560>)
GO:0001738 : morphogenesis of a polarized epithelium
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001738>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Vanaso is a candidate quantitative trait gene for Drosophila olfactory behavior. (2002) (<https://pubmed.ncbi.nlm.nih.gov/12454076>)

Authors

Fanara JJ; Robinson KO; Rollmann SM; Anholt RR; Mackay TF

Abstract

Most animals depend on olfaction for survival and procreation. Odor-guided behavior is a quantitative trait, with phenotypic variation due to multiple segregating quantitative trait loci (QTL). Despite its profound biological importance, the genetic basis of naturally occurring variation in olfactory behavior remains unexplored. Here, we mapped a single Drosophila QTL affecting variation in avoidance response to benzaldehyde, using a population of recombinant inbred lines. Deficiency complementation mapping resolved this region into one female- and one male-specific QTL. Subsequent quantitative complementation tests to all available mutations of positional candidate genes showed that the female-specific QTL failed to complement a P-element insertional mutation, l(3)04276. The P-element insertion was in the intron of a novel gene, Vanaso, which contains a putative guanylate binding protein domain, is highly polymorphic, and is expressed in the third antennal segment, the major olfactory organ of Drosophila. No expression was detected in the fly brain, suggesting that Vanaso plays a role in peripheral chemosensory processes rather than in central integration of olfactory information. QTL mapping followed by quantitative complementation tests to deficiencies and mutations is an effective strategy for gene discovery that allows characterization of effects of recessive lethal genes on adult phenotypes and here enabled identification of a candidate gene that contributes to sex-specific quantitative variation in olfactory behavior.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS