

GEPHE SUMMARY

	Gephebase Gene	GephelD
desaturase 2 (desat2) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^desaturase 2 (desat2)^#gephebase-summary-title)	GP00000221	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category=^Physiology^#gephebase-summary-title)	Trait	
Pheromone production (https://www.gephebase.org/search-criteria/?and+Trait criteria=?and+Trait=^Pheromone production^#gephebase-summary-title)	Trait State in Taxon A	
Drosophila melanogaster - African and Caribbean - desat2[7-11HD-low] allele	Trait State in Taxon B	
Drosophila melanogaster - other areas - Desat2[5-9HD-low] allele	Ancestral State	
Taxon A	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)		
Taxon A		Taxon B
Drosophila melanogaster (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title)	Latin Name	Latin Name
fruit fly	Common Name	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Synonyms
species	Rank	Rank
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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	Parent	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
Desat2		
7-11HD; CG5925; desat; desat-2; desat2; desat2/Fad; Dmel\CG5925; ds2; Fad; desat 2; Dmel_CG5925	Synonyms	GenebankID or UniProtKB
7227.FBpp0082064 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0082064)	String	AB055100 (https://www.ncbi.nlm.nih.gov/nuccore/AB055100)
Belongs to the fatty acid desaturase type 1 family.	Sequence Similarities	
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)	GO - Molecular Function	
GO:0004768 : stearoyl-CoA 9-desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004768)		

GO - Biological Process

GO:0006636 : unsaturated fatty acid biosynthetic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006636>)

GO - Cellular Component

GO:0016021 : integral component of membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
 GO:0005789 : endoplasmic reticulum membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

Presumptive Null

No (<https://www.gepheebase.org/search-criteria?/and+Presumptive+Null=%No%#gepheebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gepheebase.org/search-criteria?/and+Molecular+Type=%Cis-regulatory%#gepheebase-summary-title>)

Aberration Type

Deletion (<https://www.gepheebase.org/search-criteria?/and+Aberration+Type=%Deletion%#gepheebase-summary-title>)

Deletion Size

10-99 bp

Molecular Details of the Mutation

16bp deletion about 150bp upstream of transcription start site

Experimental Evidence

Linkage Mapping (<https://www.gepheebase.org/search-criteria?/and+Experimental+Evidence=%Linkage+Mapping%#gepheebase-summary-title>)

Main Reference

The nucleotide changes governing cuticular hydrocarbon variation and their evolution in *Drosophila melanogaster*. (2001) (<https://pubmed.ncbi.nlm.nih.gov/11259658>)

Authors

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Abstract

The cuticular hydrocarbon (CH) pheromones in *Drosophila melanogaster* exhibit strong geographic variation. African and Caribbean populations have a high ratio of 5,9 heptacosadiene/7,11 heptacosadiene (the "High" CH type), whereas populations from all other areas have a low ratio ("Low" CH type). Based on previous genetic mapping, DNA markers were developed that localized the genetic basis of this CH polymorphism to within a 13-kb region. We then carried out a hierarchical search for diagnostic nucleotide sites starting with four lines, and increasing to 24 and 43 lines from a worldwide collection. Within the 13-kb region, only one variable site shows a complete concordance with the CH phenotype. This is a 16-bp deletion in the 5' region of a desaturase gene (*desat2*) that was recently suggested to be responsible for the CH polymorphism on the basis of its expression [Dallerac, R., Labeur, C., Jallon, J.-M., Knipple, D. C., Roelofs, W. L. & Wicker-Thomas, C. (2000) Proc. Natl. Acad. Sci. 97, 9449–9454]. The cosmopolitan Low type is derived from the ancestral High type, and DNA sequence variations suggest that the former spread worldwide with the aid of positive selection. Whether this CH variation could be a component of the sexual isolation between Zimbabwe and other cosmopolitan populations remains an interesting and unresolved question.

Additional References

A delta 9 desaturase gene with a different substrate specificity is responsible for the cuticular diene hydrocarbon polymorphism in *Drosophila melanogaster*. (2000)
 (<https://pubmed.ncbi.nlm.nih.gov/10920187>)

RELATED GEPHE

Related Genes

1 (*desatF*) (<https://www.gepheebase.org/search-criteria?/or+Taxon+ID=%7227%and+Trait=Pheromone+production/and+groupHaplotypes=true#gepheebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait - The cosmopolitan *desat2*[5-9HD-low] allele is derived from the ancestral *desat2*[7-11HD-low] allele and has spread worldwide. - <http://flybase.org/reports/FBal0095912.html> - <http://flybase.org/reports/FBal0147210.html> - <http://flybase.org/reports/FBal0230316>