

GEPHE SUMMARY

	Gephebase Gene	GephelD
fatty acyl-CoA reductase FAR2-B (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^fatty acyl-CoA reductase FAR2-B^#gephebase-summary-title)	GP00002395	Main curator
	Entry Status	Courtier
Published		

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait	
Pheromone production (cuticular hydrocarbons) (https://www.gephebase.org/search-criteria?/and+Trait=^Pheromone+production+(cuticular+hydrocarbons)^#gephebase-summary-title)	Trait State in Taxon A	
short-chain cuticular hydrocarbons	Trait State in Taxon B	
long-chain cuticular hydrocarbons	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)		
Taxon A		Taxon B
Drosophila serrata (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+serrata^#gephebase-summary-title)	Latin Name	Latin Name
-	Common Name	Common Name
Drosophila serrata Malloch, 1927	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; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; montium subgroup; Drosophila serrata species complex	Lineage	Lineage
Drosophila serrata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=446045)	Parent	Parent
7274 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7274)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Dmel\CG17560	Generic Gene Name	UniProtKB Drosophila melanogaster
CT38785; Dmel\CG17560; CG17560; Dmel_CG17560	Synonyms	GenebankID or UniProtKB
7227.FBpp0082780 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0082780)	String	0
Belongs to the fatty acyl-CoA reductase family.	Sequence Similarities	
GO:0102965 : alcohol-forming fatty acyl-CoA reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102965)	GO - Molecular Function	
GO:0080019 : fatty acyl-CoA reductase (alcohol-forming) activity (https://www.ebi.ac.uk/QuickGO/term/GO:0080019)		

GO - Biological Process

GO:0035336 : long-chain fatty-acyl-CoA metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035336>)

GO:0006629 : lipid metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006629>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)GO:0005777 : peroxisome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005777>)

GO:0043231 : intracellular membrane-bounded organelle

(<https://www.ebi.ac.uk/QuickGO/term/GO:0043231>)

Presumptive Null

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

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

Both alleles of DsFAR2-B appear to be functional. The distinction between the two alleles iss a large number of non-synonymous substitutions.

Experimental Evidence

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

Main Reference

Natural variation at a single gene generates sexual antagonism across fitness components in Drosophila. (2022) (<https://pubmed.ncbi.nlm.nih.gov/35700732>)

Authors

Rusuwa BB; Chung H; Allen SL; Frentiu FD; Chenoweth SF

Abstract

Mutations with conflicting fitness effects in males and females accumulate in sexual populations, reducing their adaptive capacity. Although quantitative genetic studies indicate that sexually antagonistic polymorphisms are common, their molecular basis and population genetic properties remain poorly understood. Here, we show in fruit flies how natural variation at a single gene generates sexual antagonism through phenotypic effects on cuticular hydrocarbon (CHC) traits that function as both mate signals and protectors against abiotic stress across a latitudinal gradient. Tropical populations of *Drosophila serrata* have polymorphic CHCs producing sexual antagonism through opposing but sex-limited effects on these two fitness-related functions. We dissected this polymorphism to a single fatty-acyl CoA reductase gene, DsFAR2-B, that is expressed in oenocyte cells where CHCs are synthesized. RNAi-mediated disruption of the DsFAR2-B ortholog in *D. melanogaster* oenocytes affected CHCs in a similar way to that seen in *D. serrata*. Population genomic analysis revealed that balancing selection likely operates at the DsFAR2-B locus in the wild. Our study provides insights into the genetic basis of sexual antagonism in nature and connects sexually varying antagonistic selection on phenotypes with balancing selection on genotypes that maintains molecular variation.

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Additional References

RELATED GEPHE

Related Genes

1 (fatty acid synthase) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7274^/and+Trait=Pheromone production/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait