

GEPHE SUMMARY

	Gephebase Gene		GepheID
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	
Published	Entry Status	Courtier	Main curator

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	
	Latin Name		Latin Name
<i>Drosophila serrata</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Drosophila+serrata+^#gephebase-summary-title)		<i>Drosophila serrata</i> (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Drosophila+serrata+^#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
<i>Drosophila serrata</i> Malloch, 1927		<i>Drosophila serrata</i> Malloch, 1927	
	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; montium subgroup; <i>Drosophila serrata</i> species complex		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; <i>Drosophila serrata</i> species complex	
	Parent		Parent
<i>Drosophila serrata</i> species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=446045)		<i>Drosophila serrata</i> species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=446045)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7274 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7274)		7274 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7274)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB <i>Drosophila melanogaster</i>
Dmel\CG17560		Q9VES6 (http://www.uniprot.org/uniprot/Q9VES6)	
	Synonyms		GenebankID or UniProtKB
CT38785; Dmel\CG17560; CG17560; Dmel_CG17560		()	
	String		
7227.FBpp0082780 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0082780)			
	Sequence Similarities		
Belongs to the fatty acyl-CoA reductase family.			
	GO - Molecular Function		
GO:0102965 : alcohol-forming fatty acyl-CoA reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102965)			
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](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

Both alleles of DsFAR2-B appear to be functional. The distinction between the two alleles is 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](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=))

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; Freniu 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](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait