## GEPHE SUMMARY

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

GepheID
GP00002395
Main curator
Courtier

## 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 | Drosophila serrata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila serrata^#gephebase-summary-title) | Drosophila serrata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila serrata^#gephebase-summary-title) |
| Common Name | - | - |
| Synonyms | Drosophila serrata Malloch, 1927 | Drosophila serrata Malloch, 1927 |
| Rank | species | species |
| 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; Drosophila serrata 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; Drosophila serrata species complex |
| Parent | Drosophila serrata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 446045 ) | Drosophila serrata species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 446045 ) |
| 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 Infraspecies? / is Taxon B an Infraspecies? | No | No |

## GENOTYPIC CHANGE

Generic Gene Name
Dmel\CG17560
Synonyms
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)

UniProtKB Drosophila melanogaster
Q9VES6 (http://www.uniprot.org/uniprot/Q9VES6)
GenebankID or UniProtKB
()

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.Â melanogaster oenocytes affected CHCs in a similar way to that seen in D.Â 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.

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