

GEPHE SUMMARY

Gephebase Gene
desatF

Entry Status
Published

GepheID
GP00000220

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Pheromone production

Trait State in Taxon A
Drosophila takahashii and non-Sophophora species

Trait State in Taxon B
Drosophila (Sophophora) spp.

Ancestral State
Taxon A

Taxonomic Status
Interspecific

	Taxon A	Taxon B
Latin Name	<i>Drosophila takahashii</i>	<i>Drosophila</i>
Common Name	-	-
Synonyms	-	Drosophila (Drosophila); Drosophila (Drosophila) Fallen, 1823
Rank	species	subgenus
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; Acalytratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; takahashii 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; Acalytratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila
Parent	takahashii subgroup () - (Rank: species subgroup)	Drosophila (fruit flies) - (Rank: genus)
NCBI Taxonomy ID	29030	32281
is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies? No

GENOTYPIC CHANGE

Generic Gene Name
desatF

Synonyms
-

String
-

Sequence Similarities
Belongs to the fatty acid desaturase type 1 family.

GO - Molecular Function
GO:0016717 : oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water

GO - Biological Process
GO:0006633 : fatty acid biosynthetic process

GO - Cellular Component
GO:0016021 : integral component of membrane

Presumptive Null
No

UniProtKB Drosophila melanogaster
A7DZ97

GenebankID or UniProtKB
EDV51348

Molecular Type

Cis-regulatory

Aberration Type

Deletion

Deletion Size

1-9 bp

Molecular Details of the Mutation

Inactivation of DSX-binding site

Experimental Evidence

Candidate Gene

Main Reference

Rapid evolution of sex pheromone-producing enzyme expression in *Drosophila*. (2009)

Authors

Shirangi TR; Dufour HD; Williams TM; Carroll SB

Abstract

A wide range of organisms use sex pheromones to communicate with each other and to identify appropriate mating partners. While the evolution of chemical communication has been suggested to cause sexual isolation and speciation, the mechanisms that govern evolutionary transitions in sex pheromone production are poorly understood. Here, we decipher the molecular mechanisms underlying the rapid evolution in the expression of a gene involved in sex pheromone production in *Drosophilid* flies. Long-chain cuticular hydrocarbons (e.g., dienes) are produced female-specifically, notably via the activity of the desaturase DESAT-F, and are potent pheromones for male courtship behavior in *Drosophila melanogaster*. We show that across the genus *Drosophila*, the expression of this enzyme is correlated with long-chain diene production and has undergone an extraordinary number of evolutionary transitions, including six independent gene inactivations, three losses of expression without gene loss, and two transitions in sex-specificity. Furthermore, we show that evolutionary transitions from monomorphism to dimorphism (and its reversion) in *desatF* expression involved the gain (and the inactivation) of a binding-site for the sex-determination transcription factor, DOUBLESEX. In addition, we documented a surprising example of the gain of particular cis-regulatory motifs of the *desatF* locus via a set of small deletions. Together, our results suggest that frequent changes in the expression of pheromone-producing enzymes underlie evolutionary transitions in chemical communication, and reflect changing regimes of sexual selection, which may have contributed to speciation among *Drosophila*.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait