

## GEPHE SUMMARY

desatF ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase="desatF">#gephebase-summary-title)	Gephebase Gene	GP00000220	GephelD
	Entry Status	Martin	Main curator
Published			

## PHENOTYPIC CHANGE

Trait Category			
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category="Physiology">#gephebase-summary-title)	Trait		
Pheromone production ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Pheromone+production">#gephebase-summary-title)</a>	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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status="Interspecific">#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Drosophila takahashii ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+takahashii">#gephebase-summary-title</a> )	Drosophila ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila</a> #gephebase-summary-title)		
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
-	Rank	-	Rank
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; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; takahashii subgroup	Drosophila (fruit flies) - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32354">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32354</a> )	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; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila	Parent
takahashii subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 29030">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 29030</a> )	NCBI Taxonomy ID 32281 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32281">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32281</a> )		NCBI Taxonomy ID 32281 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32281">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32281</a> )
	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?
No			

## GENOTYPIC CHANGE

Generic Gene Name			
desatF	Synonyms	A7DZ97 ( <a href="http://www.uniprot.org/uniprot/A7DZ97">http://www.uniprot.org/uniprot/A7DZ97</a> )	UniProtKB Drosophila melanogaster
-	String	EDV51348 ( <a href="https://www.ncbi.nlm.nih.gov/nucore/EDV51348">https://www.ncbi.nlm.nih.gov/nucore/EDV51348</a> )	GenebankID or UniProtKB
-	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 ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016717">https://www.ebi.ac.uk/QuickGO/term/GO:0016717</a> )	GO - Biological Process		
GO:0006633 : fatty acid biosynthetic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0006633">https://www.ebi.ac.uk/QuickGO/term/GO:0006633</a> )	GO - Cellular Component		

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

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

Inactivation of DSX-binding site

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria/?/and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title>)

Main Reference

Rapid evolution of sex pheromone-producing enzyme expression in Drosophila. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19652700>)

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