

GEPHE SUMMARY

	Gephebase Gene	GephelD
ODORANT1 [pseudo-replication between 2 ODO1 entries due to possible homology between alleles] (https://www.gephebase.org/search-criteria/?and+Gene)	GP00000750	
Gephebase=^ODORANT1 [pseudo-replication between 2 ODO1 entries due to possible homology between alleles]^#gephebase-summary-title)	Martin	Main curator
	Entry Status	
Published		

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait)		
Category=Physiology^#gephebase-summary-title)		
	Trait	
Fragrance (https://www.gephebase.org/search-criteria/?and+Trait=^Fragrance^#gephebase-summary-title)		
	Trait State in Taxon A	
Petunia axillaris (odorant)		
	Trait State in Taxon B	
Petunia exserta (scentless)		
	Ancestral State	
Data not curated		
	Taxonomic Status	
Interspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic)		
Status=^Interspecific^#gephebase-summary-title)		
Taxon A		Taxon B
	Latin Name	Latin Name
Petunia axillaris (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Petunia+axillaris^#gephebase-summary-title)		
	Common Name	Common Name
-		
	Synonyms	Synonyms
large white petunia; white moon petunia; Petunia axillaris (Lam.) Britton, Stern & Poggenb.; Petunia axillaris		
	Rank	Rank
species		
	Lineage	Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunioideae; Petunia		
	Parent	Parent
Petunia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4101)	Petunia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4101)	
	NCBI Taxonomy ID	NCBI Taxonomy ID
33119 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33119)	323115 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=323115)	
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
No	No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Petunia hybrida
ODO1		
	Synonyms	GenebankID or UniProtKB
-		
	String	
-		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		
	GO - Biological Process	
-		
	GO - Cellular Component	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)		
		Presumptive Null

Unknown ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%Unknown)

Molecular Type

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

Aberration Type

Unknown ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Aberration+Type=%Unknown)

Molecular Details of the Mutation

Not identified; but probably homologous to *P. hybrida* Mitchell x R27 promoter variation since these *P. hybrida* accessions are derived from a *P. axillaris* x *P. integrifolia* cross

Experimental Evidence

Linkage Mapping ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%Linkage+Mapping)

Main Reference

Pollinator choice in Petunia depends on two major genetic Loci for floral scent production. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21497087>)

Authors

Klahre U; Gurba A; Hermann K; Saxenhofer M; Bossolini E; Guerin PM; Kuhlemeier C

Abstract

Differences in floral traits, such as petal color, scent, morphology, or nectar quality and quantity, can lead to specific interactions with pollinators and may thereby cause reproductive isolation. Petunia provides an attractive model system to study the role of floral characters in reproductive isolation and speciation. The night-active hawkmoth pollinator *Manduca sexta* relies on olfactory cues provided by *Petunia axillaris*. In contrast, *Petunia exserta*, which displays a typical hummingbird pollination syndrome, is devoid of scent. The two species can easily be crossed in the laboratory, which makes it possible to study the genetic basis of the evolution of scent production and the importance of scent for pollinator behavior.

In an F2 population derived from an interspecific cross between *P. axillaris* and *P. exserta*, we identified two quantitative trait loci (QTL) that define the difference between the two species' ability to produce benzenoid volatiles. One of these loci was identified as the MYB transcription factor ODORANT1. Reciprocal introgressions of scent QTL were used for choice experiments under controlled conditions. These experiments demonstrated that the hawkmoth *M. sexta* prefers scented plants and that scent determines choice at a short distance. When exposed to conflicting cues of color versus scent, the insects display no preference, indicating that color and scent are equivalent cues.

Our results show that scent is an important flower trait that defines plant-pollinator interactions at the level of individual plants. The genetic basis underlying such a major phenotypic difference appears to be relatively simple and may enable rapid loss or gain of scent through hybridization.

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Additional References

RELATED GEPHE

Related Genes

3 (benzoic acid/salicylic acid carboxyl methyltransferase (BSMT), benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT), Cinnamate-CoA ligase 1 (CNL1)) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%33119/+and+Trait=Fragrance/or+Taxon+ID=%323115/+and+Trait=Fragrance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS