

GEPHE SUMMARY

	Gephebase Gene	GephelD
benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT)^#gephebase-summary-title)	GP00001765	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	
Fragrance (https://www.gephebase.org/search-criteria?/and+Trait=^Fragrance^#gephebase-summary-title)	
Petunia inflata (less odorant; bee pollinated)	Trait State in Taxon A
Petunia axillaris (very odorant; increase of phenylpropanoids and benzenoids; hawkmoth pollinated)	Trait State in Taxon B
	Ancestral State
Taxon A	Taxonomic Status

	Taxon A	Taxon B
	Latin Name	Latin Name
	Common Name	Common Name
Petunia integrifolia subsp. inflata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Petunia integrifolia subsp. inflata^#gephebase-summary-title)	Petunia axillaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Petunia axillaris^#gephebase-summary-title)	
-	-	
Petunia inflata; Petunia inflata R.E.Fr., 1911; Petunia integrifolia subsp. inflata (R.E.Fr.) Wijisman, 1982	Synonyms	Synonyms
		large white petunia; white moon petunia; Petunia axillaris (Lam.) Britton, Stern & Pogggenb.; Petunia axillaris
subspecies	Rank	Rank
	Lineage	Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunoideae; Petunia; Petunia integrifolia		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunoideae; Petunia
	Parent	Parent
Petunia integrifolia () - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4103)	Petunia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4101)	NCBI Taxonomy ID
212142 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 212142)	33119 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33119)	NCBI Taxonomy ID
		is Taxon B an Infraspecies?
No	No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Populus davidiana
BPBT	A0A172W606 (http://www.uniprot.org/uniprot/A0A172W606)	
	Synonyms	GenebankID or UniProtKB
-	0	
	String	
-		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0016747 : transferase activity, transferring acyl groups other than amino-acyl groups (https://www.ebi.ac.uk/QuickGO/term/GO:0016747)		
	GO - Biological Process	
-		
	GO - Cellular Component	
-		

No (#gephebase-summary-title)	Presumptive Null
Cis-regulatory (#gephebase-summary-title)	Molecular Type
Unknown (#gephebase-summary-title)	Aberration Type
Allele-specific expression in hybrids - de novo expression in <i>P. axillaris</i>	Molecular Details of the Mutation
Linkage Mapping (#gephebase-summary-title)	Experimental Evidence
Gain and Loss of Floral Scent Production through Changes in Structural Genes during Pollinator-Mediated Speciation. (2016) (https://pubmed.ncbi.nlm.nih.gov/27916524)	Main Reference
Amrad A; Moser M; Mandel T; de Vries M; Schuurink RC; Freitas L; Kuhlemeier C	Authors
The interactions of plants with their pollinators are thought to be a driving force in the evolution of angiosperms. Adaptation to a new pollinator involves coordinated changes in multiple floral traits controlled by multiple genes. Surprisingly, such complex genetic shifts have happened numerous times during evolution. Here we report on the genetic basis of the changes in one such trait, floral scent emission, in the genus <i>Petunia</i> (Solanaceae). The increase in the quantity and complexity of the volatiles during the shift from bee to hawkmoth pollination was due to de novo expression of the genes encoding benzoic acid/salicylic acid carboxyl methyltransferase (BSMT) and benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT) together with moderately increased transcript levels for most enzymes of the phenylpropanoid/benzenoid pathway. Loss of cinnamate-CoA ligase (CNL) function as well as a reduction in the expression of the MYB transcription factor ODO1 explain the loss of scent during the transition from moth to hummingbird pollination. The CNL gene in the hummingbird-adapted species is inactive due to a stop codon, but also appears to have undergone further degradation over time. Therefore, we propose that loss of scent happened relatively early in the transition toward hummingbird pollination, and probably preceded the loss of UV-absorbing flavonols. The discovery that CNL is also involved in the loss of scent during the transition from outcrossing to selfing in <i>Capsella</i> (Brassicaceae) (see the accompanying paper) raises interesting questions about the possible causes of deep evolutionary conservation of the targets of evolutionary change.	Abstract
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RELATED GEPHE

1 (benzoic acid/salicylic acid carboxyl methyltransferase (BSMT)) (#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS