

GEPHE SUMMARY

	Gephebase Gene		GepheID
benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT) (<a +benzoyl-coa:benzylalcohol="" 2-phenylethanol+benzoyltransferase+(bpbt)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+benzoyl-CoA:benzylalcohol/2-phenylethanol+benzoyltransferase+(BPBT)+"#gephebase-summary-title)		GP00001765	Main curator
		Courtier	
	Entry Status		
Published			

PHENOTYPIC CHANGE

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

Taxon A	Latin Name	Taxon B	Latin Name
Petunia integrifolia subsp. inflata (<a +petunia+integrifolia+subsp.+inflata+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Petunia+integrifolia+subsp.+inflata+"#gephebase-summary-title)		Petunia axillaris (<a +petunia+axillaris+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Petunia+axillaris+"#gephebase-summary-title)	
-	Common Name	-	Common Name
	Synonyms		Synonyms
Petunia inflata; Petunia inflata R.E.Fr., 1911; Petunia integrifolia subsp. inflata (R.E.Fr.) Wijsman, 1982		large white petunia; white moon petunia; Petunia axillaris (Lam.) Britton, Stern & Poggenb.; Petunia axillaris	
	Rank		Rank
subspecies		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunioidae; Petunia; Petunia integrifolia		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunioidae; 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		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)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Populus davidiana
BPBT		A0A172W606 (http://www.uniprot.org/uniprot/A0A172W606)	GenebankID or UniProtKB
	Synonyms		
-		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 ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null+No^#gephebase-summary-title))

Presumptive Null

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

Molecular Type

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

Aberration Type

Allele-specific expression in hybrids - de novo expression in *P. axillaris*

Molecular Details of the Mutation

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=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; Kuhlmeier 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 *Petunia* (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 *Capsella* (Brassicaceae) (see the accompanying paper) raises interesting questions about the possible causes of deep evolutionary conservation of the targets of evolutionary change.

Abstract

Copyright © 2016 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

1 (benzoic acid/salicylic acid carboxyl methyltransferase (BSMT)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=^212142^/and+Trait=Frangrance/or+Taxon ID=^33119^/and+Trait=Frangrance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=212142^/and+Trait=Frangrance/or+Taxon+ID=33119^/and+Trait=Frangrance/and+groupHaplotypes=true#gephebase-summary-title))

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS