Ger	ohebase Gene
Cinnamate-CoA ligase 1 (CNL1) (https://www.gephebase.org/search-criteria?/and+Gene	
Gephebase=^Cinnamate-CoA ligase 1 (CNL1)^#gephebase-summary-title)	
	Entry Status

Published

# PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title) Trait
rrait Fragrance (https://www.gephebase.org/search-criteria?/and+Trait=^Fragrance^#gephebase- summary-title)
Trait State in Taxon A Petunia axillaris pollinated by nocturnal hawkmoths
Trait State in Taxon B Petunia exserta pollinated by hummingbirds
Ancestral State
Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)
Taxon A
Latin Name
Petunia axillaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Petunia axillaris^#gephebase-summary-title)
Common Name
- Synonyms
large white petunia; white moon petunia; Petunia axillaris (Lam.) Britton, Stern & Poggenb.; Petunia axilliaris
Rank
Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Iamiids; Solanales; Solanaceae; Petunioideae: Petunia
Parent
Petunia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4101 )
NCBI Taxonomy ID 33119
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33119 )
is Taxon A an Infraspecies? No

GP00001391

Courtier

GephelD

Main curator

Taxon B

Latin Name

Petunia exserta		
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Petunia		
exserta^#gephebase-summary-title)		
	Common Name	
-		
	Synonyms	
Petunia exserta Stehmann, 1987		
	Rank	
species		
	Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; I	Embryophyta;	
Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangios	permae;	
eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Sola	anaceae;	
Petunioideae; Petunia		
	Parent	
Petunia () - (Rank: genus)		
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4101 )		
N	CBI Taxonomy ID	
323115		
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 323115 )		
is Taxon	B an Infraspecies?	
No		

## GENOTYPIC CHANGE

	eneric Gene Name
CNL	Synonyms
-	String
- Sec	quence Similarities
GO:0016874 : ligase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0	Aolecular Function 0016874) Biological Process
- GO - Ce	ellular Component

UniProtKB Populus davidiana A0A172W603 (http://www.uniprot.org/uniprot/A0A172W603) GenebankID or UniProtKB

0

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive	e Null=^Yes^#gephebase-sumn	nary-title)	
Coding (https://www.gephebase.org/search-criteria?/and+Molecul	lar Type=^Coding^#gephebase	e-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration	Type=^SNP^#gephebase-sum	nmary-title)	Aberration Type
Nonsense			SNP Coding Change
nonsense mutation in the fourth exon which is predicted to shorten synthetase/ligase and peroxisomal targeting domains are truncated		This leaves the conserved AMP binding inta	Molecular Details of the Mutation ct but both the AMP-dependent
Linkage Mapping (https://www.gephebase.org/search-criteria?/and		kage Mapping^#gephebase-summary-title)	Experimental Evidence
	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-
Gain and Loss of Floral Scent Production through Changes in Struc Amrad A: Moser M: Mandel T: de Vries M: Schuurink RC: Freitas	-	Mediated Speciation. (2016) (https://pubmec	Main Reference I.ncbi.nlm.nih.gov/27916524) Authors
Amrad A; Moser M; Mandel I ; de Vries M; Schuurink KC; Freitas	L; Kuniemeier C		Abstract
The interactions of plants with their pollinators are thought to be a multiple floral traits controlled by multiple genes. Surprisingly, such changes in one such trait, floral scent emission, in the genus Petunia pollination was due to de novo expression of the genes encoding benzoyltransferase (BPBT) together with moderately increased transfunction as well as a reduction in the expression of the MYB transcr gene in the hummingbird-adapted species is inactive due to a stop happened relatively early in the transition toward hummingbird polloss of scent during the transition from outcrossing to selfing in Capevolutionary conservation of the targets of evolutionary change.	a complex genetic shifts have ha a (Solanaceae). The increase in benzoic acid/salicylic acid carb nscript levels for most enzymes ription factor ODO1 explain the codon, but also appears to have ollination, and probably precede	appened numerous times during evolution. He the quantity and complexity of the volatiles of oxyl methyltransferase (BSMT) and benzoyl- of the phenylpropanoid/benzenoid pathway. e loss of scent during the transition from mo e undergone further degradation over time. T ed the loss of UV-absorbing flavonols. The di	ere we report on the genetic basis of the luring the shift from bee to hawkmoth CoA:benzylalcohol/2-phenylethanol Loss of cinnamate-CoA ligase (CNL) th to hummingbird pollination. The CNL 'herefore, we propose that loss of scent scovery that CNL is also involved in the

Mutation #2			
			Presumptive Null
Yes (https://www.gephebase.org/search-criteria?/and+Presun	nptive Null=^Yes^#gephebase-summ	nary-title)	
Coding (https://www.gephebase.org/search-criteria?/and+Mo	olocular Typo=^Coding^#gophobass	summan-title)	Molecular Type
Cound (https://www.gepnebase.org/search-chtena:/and+wt	necular Type- County #gephebase	-summary-tite)	Aberration Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberr	ration Type=^SNP^#gephebase-sum	mary-title)	, , , , , , , , , , , , , , , , , , ,
			SNP Coding Change
Nonsynonymous			Molecular Details of the Mutation
two amino acids making up the peroxisomal targeting signal a	ire changed in the P. exserta sequenc	e (ARL to TRI) and are expected to lead to	
···· - ····· - ···· - ·· - ··· - ··· - ··· - ··· - ··· - ··· - ··· - ··· - ··· - ··· - ··· - ·· - ··· - · - ·· - ·· - ·· - ·· - ·· - · - ·· - ·· - · - ·· - ·· - ·· - · - ·· - · - ·· - · · · ·		- (	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria	a?/and+Experimental Evidence=^Link	kage Mapping^#gephebase-summary-title)	1
	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Gain and Loss of Floral Scent Production through Changes in Structural Genes during Pollinator-Mediated Speciation. (2016) (https://pubmed.ncbi.nlm.nih.gov/27916524)

Amrad A; Moser M; Mandel T; de Vries M; Schuurink RC; Freitas L; Kuhlemeier C

Abstract

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.

Mutation #3	
Presumptive Null	
Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)	
Molecular Type Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	
Aberration Type	
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	
Molecular Details of the Mutation	
analysis of allele-specific expression in hybrids shows that CNL1 expression is highly reduced in P. exserta due to cis-regulatory mutation(s) in CNL1	
Experimental Evidence Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	
Linkage Mapping (https://www.gephebase.org/search-chtena:/and+cxperimental_chdenceLinkage Mapping #gephebase-summary-itte/	
Gain and Loss of Floral Scent Production through Changes in Structural Genes during Pollinator-Mediated Speciation. (2016) (https://pubmed.ncbi.nlm.nih.gov/27916524)	
Authors	
Amrad A; Moser M; Mandel T; de Vries M; Schuurink RC; Freitas L; Kuhlemeier C	
Abstract	
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 genesÄ 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.	

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RELATED GEPHE

#### **Related Genes**

Related Haplotypes

Additional References

3 (benzoic acid/salicylic acid carboxyl methyltransferase (BSMT), benzoyl-CoA:benzylalcohol/2-phenylethanol benzoyltransferase (BPBT), ODORANT1 [pseudo-replication between 2 ODO1 entries due to possible homology between alleles]) (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)

No matches found.

## **EXTERNAL LINKS**

### COMMENTS

@SeveralMutationsWithEffect The loss of function of CNL1 abolished methylbenzoate emission - 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. The authors propose that loss of scent happened relatively early in the transition toward hummingbird pollination and probably preceded the loss of UV-absorbing flavonols.