

GEPHE SUMMARY

	Gephebase Gene		GepheID
Cinnamate-CoA ligase 1 (CNL1) (<a +cinnamate-coa+ligase+1+(cnl1)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=">https://www.gephebase.org/search-criteria?/and+GeneGephebase="+Cinnamate-CoA+ligase+1+(CNL1)+"#gephebase-summary-title)	GP00001391		
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TraitCategory=">https://www.gephebase.org/search-criteria?/and+TraitCategory="+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 axillaris pollinated by nocturnal hawkmoths		Trait State in Taxon B	
Petunia exserta pollinated by hummingbirds			
	Ancestral State		
Taxon A		Taxonomic Status	
Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=">https://www.gephebase.org/search-criteria?/and+TaxonomicStatus="+Interspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
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)		Petunia exserta (<a +petunia+exserta+"#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+exserta+"#gephebase-summary-title)	
-	Common Name	-	Common Name
	Synonyms		Synonyms
large white petunia; white moon petunia; Petunia axillaris (Lam.) Britton, Stern & Poggenb.; Petunia axillaris		Petunia exserta Stehmann, 1987	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunioideae; Petunia		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; 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 Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Populus davidiana
CNL		A0A172W603 (http://www.uniprot.org/uniprot/A0A172W603)	
	Synonyms		GenebankID or UniProtKB
-			
	String		
-			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0016874 : ligase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016874)			
	GO - Biological Process		
-			
	GO - Cellular Component		
-			
Mutation #1			Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

nonsense mutation in the fourth exon which is predicted to shorten the protein by 171 amino acids. This leaves the conserved AMP binding intact but both the AMP-dependent synthetase/ligase and peroxisomal targeting domains are truncated or absent

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title>)

	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>)

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 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.

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Additional References

Mutation #2

Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

two amino acids making up the peroxisomal targeting signal are changed in the P. exserta sequence (ARL to TRI) and are expected to lead to a loss-of function

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title>)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

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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>)

Main Reference

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Authors

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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), 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=Frangrance/or+Taxon ID=~323115~/and+Trait=Frangrance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

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.