GEPHE SUMMARY

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

GepheID
GP00001391

Entry Status
Published

Main curator
Courtier

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 pollinated by nocturnal hawkmoths

Trait State in Taxon B
Petunia exserta pollinated by hummingbirds

Ancestral State
Taxon A

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
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; 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

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; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Petunioideae; Petunia

Parent
Petunia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4101)

NCBI Taxonomy ID
323115 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 323115)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
CNL

Synonyms
-

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
-

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

GenebankID or UniProtKB
()

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 genesÂ 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 lossÂ 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 inÂ 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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Additional References

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=Fragrance/or+Taxon ID=^323115^/and+Trait=Fragrance/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.