

GEPHE SUMMARY

Gephebase Gene
bHLH2

Entry Status
Published

GepheID
GP00002092

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (flowers)

Trait State in Taxon A
Petunia axillaris

Trait State in Taxon B
Petunia axillaris - white flowers with red and pink revertant spots

Ancestral State
Taxon A

Taxonomic Status
Domesticated

Taxon A

Latin Name
Petunia axillaris

Common Name
-

Synonyms
large white petunia; white moon petunia; *Petunia axillaris* (Lam.) Britton, Stern & Poggenb.;
Petunia axillaris

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)

NCBI Taxonomy ID
33119

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Petunia axillaris

Common Name
-

Synonyms
large white petunia; white moon petunia; *Petunia axillaris* (Lam.) Britton, Stern & Poggenb.;
Petunia axillaris

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)

NCBI Taxonomy ID
33119

is Taxon B an Intraspecies?
Yes

Taxon B Description
petunia line W138

GENOTYPIC CHANGE

Generic Gene Name
BHLH2

Synonyms
AtEGL3; ATMYC-2; EGL1; ENHANCER OF GLABRA 3; F24D7.16; F24D7_16; EGL3;
EN30; MYC146; At1g63650

String
3702.AT1G63650.3

Sequence Similarities
-

GO - Molecular Function
GO:0046983 : protein dimerization activity
GO:0003700 : DNA-binding transcription factor activity
GO:0003677 : DNA binding

GO - Biological Process
GO:0007275 : multicellular organism development
GO:0006355 : regulation of transcription, DNA-templated

UniProtKB Arabidopsis thaliana
Q9CAD0

GenebankID or UniProtKB

GO:0009867 : jasmonic acid mediated signaling pathway

GO:0009957 : epidermal cell fate specification

GO:0010026 : trichome differentiation

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

Yes

Molecular Type

Coding

Aberration Type

Insertion

Insertion Size

-

Molecular Details of the Mutation

insertion of a dTph1 transposon in the AN1 gene

Experimental Evidence

Candidate Gene

Main Reference

ANTHOCYANIN1 of petunia controls pigment synthesis, vacuolar pH, and seed coat development by genetically distinct mechanisms. (2002)

Authors

Spelt C; Quattrocchio F; Mol J; Koes R

Abstract

ANTHOCYANIN1 (AN1) of petunia is a transcription factor of the basic helix-loop-helix (bHLH) family that is required for the synthesis of anthocyanin pigments. Here, we show that AN1 controls additional aspects of cell differentiation: the acidification of vacuoles in petal cells, and the size and morphology of cells in the seed coat epidermis. We identified an1 alleles, formerly known as ph6, that sustain anthocyanin synthesis but not vacuolar acidification and seed coat morphogenesis. These alleles express truncated proteins lacking the C-terminal half of AN1, including the bHLH domain, at an approximately 30-fold higher level than wild-type AN1. An allelic series in which one, two, or three amino acids were inserted into the bHLH domain indicated that this domain is required for both anthocyanin synthesis and vacuolar acidification. These findings show that AN1 controls more aspects of epidermal cell differentiation than previously thought through partially separable domains.

Additional References

RELATED GEPHE

Related Genes

3 (anthocyanin2 (an2), MYB-FL, WDR1)

Related Haplotypes

No matches found.

COMMENTS

@TE - bHLH2 is also named anthocyanin1 (an1).