## GEPHE SUMMARY

Gephebase Gene
MYB1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MYB1^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00002089

Main curator
Courtier

## PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (flowers; seeds; stems) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (flowers; seeds; stems)^#gephebase-summary-title)

Trait State in Taxon A
Ipomoea nil - bright blue flowers with colored stems and dark-brown seeds

Trait State in Taxon B
Ipomoea nil - recessive c-1 mutant - white flowers with red stems and colored seeds

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

### Taxon A

Latin Name
Ipomoea nil (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Ipomoea nil^#gephebase-summary-title)

Common Name
Japanese morning glory

Synonyms
Convolvulus nil; Pharbitis nil; Japanese morning glory; qian niu; Convolvulus nil L., 1762; Ipomoea nil (L.) Roth, 1797; Pharbitis nil (L.) Choisy, 1834

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Convolvulaceae; Ipomoeeae; Ipomoea

Parent
Ipomoea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4119 )

NCBI Taxonomy ID
35883 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35883 )

is Taxon A an Infraspecies?
No

### Taxon B

Latin Name
Ipomoea nil (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Ipomoea nil^#gephebase-summary-title)

Common Name
Japanese morning glory

Synonyms
Convolvulus nil; Pharbitis nil; Japanese morning glory; qian niu; Convolvulus nil L., 1762; Ipomoea nil (L.) Roth, 1797; Pharbitis nil (L.) Choisy, 1834

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Convolvulaceae; Ipomoeeae; Ipomoea

Parent
Ipomoea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4119 )

NCBI Taxonomy ID
35883 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35883 )

is Taxon B an Infraspecies?
No

## GENOTYPIC CHANGE

Generic Gene Name
myb1

Synonyms
-

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

GO - Biological Process
-

GO - Cellular Component
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

UniProtKB Ipomoea purpurea
Q4QS21 (http://www.uniprot.org/uniprot/Q4QS21)

GenebankID or UniProtKB
()

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

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

frameshift mutation caused by a 2 bp deletion

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Isolation of cDNAs for R2R3-MYB, bHLH and WDR transcriptional regulators and identification of c and ca mutations conferring white flowers in the Japanese morning glory. (2006) (https://pubmed.ncbi.nlm.nih.gov/16446312)

Authors

Morita Y; Saitoh M; Hoshino A; Nitasaka E; Iida S

Abstract

The transcriptional regulators for anthocyanin biosynthesis include members of proteins containing an R2R3-MYB domain, a bHLH (basic helix-loop-helix) domain and conserved WD40 repeats (WDRs). Spacial and temporal expression of the structural genes encoding the enzymes for anthocyanin biosynthesis is thought to be determined by combinations of the R2R3-MYB, bHLH and WDR factors and their interactions. While the wild-type Japanese morning glory (Ipomoea nil) exhibits blue flowers with colored stems and dark-brown seeds, the c mutants display white flowers with red stems and colored seeds, and the ca mutants exhibit white flowers with green stems and ivory seeds. Here, we characterize the tissue-specific expression of three MYB genes, three bHLH genes and two WDR genes in I. nil. We also show that the recessive c-1 and ca alleles are frameshift mutations caused by a 2 bp deletion and 7 bp insertions in the genes for the R2R3-MYB and WDR transcriptional regulators designated as InMYB1 and InWDR1, respectively. In addition to defects in flower, stem and seed pigmentations, the ca mutants were found to show reduced trichome formation in seeds but to produce leaf and stem trichomes and root hairs normally. Except for the gene for chalcone synthase E in the ca mutant, all structural genes tested were coordinately reduced in both c-1 and ca mutant flower limbs. However, slight but significant expression of the genes for chalcone synthase D, chalcone isomerase and flavanone 3-hydroxylase in the pathway for flavonol biosynthesis was detectable in c-1 and ca mutants, whereas no such residual expression could be observed in other genes involved in the later anthocyanin biosynthesis pathway. The biological roles of the C-1 and Ca genes in I. nil epidermal traits and their evolutionary implications are also discussed.

Additional References

## RELATED GEPHE

Related Genes

2 (flavonoid 3′-hydroxylase (F3′H), WDR1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^35883^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

MYB1 is also named R2R3-MYB and is is closely related to the petunia (Petunia hybrida) AN2 gene.