

GEPHE SUMMARY

Gephebase Gene

bHLH2

Entry Status

Published

GepheID

GP00002091

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Morphology

Trait

Coloration (flowers; seeds)

Trait State in Taxon A

Ipomoea tricolor - bright blue flowers and dark-brown seeds

Trait State in Taxon B

Ipomoea tricolor - pale blue flowers with a few fine blue spots and ivory seeds with tiny dark brown spots

Ancestral State

Taxon A

Taxonomic Status

Domesticated

Taxon A

Latin Name

Ipomoea tricolor

Common Name

-

Synonyms

Ipomoea rubro-caerulea; *Ipomoea rubrocaerulea*; *Pharbitis rubro-caerulea*; *Pharbitis rubrocaeruleus*; *campanilla*; *flying-saucers*; *pearly-gates*; *yaxcelil*; *Ipomoea rubrocaerulea* Hook., 1834; *Ipomoea tricolor* Cav., 1795; *Pharbitis rubrocaeruleus* (Hook.) Planch., 1854

Rank

species

Lineage

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

Parent

Ipomoea () - (Rank: genus)

NCBI Taxonomy ID

89664

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Ipomoea tricolor

Common Name

-

Synonyms

Ipomoea rubro-caerulea; *Ipomoea rubrocaerulea*; *Pharbitis rubro-caerulea*; *Pharbitis rubrocaeruleus*; *campanilla*; *flying-saucers*; *pearly-gates*; *yaxcelil*; *Ipomoea rubrocaerulea* Hook., 1834; *Ipomoea tricolor* Cav., 1795; *Pharbitis rubrocaeruleus* (Hook.) Planch., 1854

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species

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

Parent

Ipomoea () - (Rank: genus)

NCBI Taxonomy ID

89664

is Taxon B an Intraspecies?

No

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

1-10 kb

Molecular Details of the Mutation

intragenic tandem duplication of 3.3 kbp of the bHLH2 gene. Each of the tandem repeats is flanked by a 3-bp sequence AAT; indicating that the 3-bp microhomology is used to generate the tandem duplication. The transcripts in the pale-blue flower buds of the mutant contain an internal 583-bp tandem duplication that results in the production of a truncated polypeptide lacking the bHLH domain. The mRNA accumulation of most of the structural genes encoding enzymes for anthocyanin biosynthesis in the flower buds of the mutant was significantly reduced. The transcripts identical to the wild-type mRNAs for the transcriptional activator were present abundantly in blue spots of the variegated flowers whereas the transcripts containing the 583-bp tandem duplication were predominant in the pale-blue background of the same flowers. The flower and seed variegations studied here are likely to be caused by somatic homologous recombination between an intragenic tandem duplication in the gene encoding a bHLH transcriptional activator for anthocyanin biosynthesis.

Experimental Evidence

Candidate Gene

Main Reference

An intragenic tandem duplication in a transcriptional regulatory gene for anthocyanin biosynthesis confers pale-colored flowers and seeds with fine spots in *Ipomoea tricolor*. (2004)

Authors

Park KI; Choi JD; Hoshino A; Morita Y; Iida S

Abstract

While the wild-type morning glory (*Ipomoea tricolor*) displays bright-blue flowers and dark-brown seeds, its spontaneous mutant, Blue Star, carrying the mutable ivory seed-variegated (*ivs-v*) allele, exhibits pale-blue flowers with a few fine blue spots and ivory seeds with tiny dark-brown spots. The mutable allele is caused by an intragenic tandem duplication of 3.3 kbp within a gene for transcriptional activator containing a basic helix-loop-helix (bHLH) DNA-binding motif. Each of the tandem repeats is flanked by a 3-bp sequence AAT, indicating that the 3-bp microhomology is used to generate the tandem duplication. The transcripts in the pale-blue flower buds of the mutant contain an internal 583-bp tandem duplication that results in the production of a truncated polypeptide lacking the bHLH domain. The mRNA accumulation of most of the structural genes encoding enzymes for anthocyanin biosynthesis in the flower buds of the mutant was significantly reduced. The transcripts identical to the wild-type mRNAs for the transcriptional activator were present abundantly in blue spots of the variegated flowers, whereas the transcripts containing the 583-bp tandem duplication were predominant in the pale-blue background of the same flowers. The flower and seed variegations studied here are likely to be caused by somatic homologous recombination between an intragenic tandem duplication in the gene encoding a bHLH transcriptional activator for anthocyanin biosynthesis, whereas various flower variegations are reported to be caused by excision of DNA transposons inserted into pigmentation genes.

Additional References

RELATED GEPHE

Related Genes

1 (flavonoid 3'-hydroxylase (F3'H))

Related Haplotypes

No matches found.

COMMENTS