

GEPHE SUMMARY

| | | |
|--|----------------|--------------|
| | Gephebase Gene | GephelD |
| dihydroflavonol reductase (DFR) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=dihydroflavonol reductase (DFR) #gephebase-summary-title) | GP00000224 | Main curator |
| | Entry Status | Martin |
| Published | | |

PHENOTYPIC CHANGE

| | Trait Category | |
|--|-----------------------------|-----------------------------|
| Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=Morphology #gephebase-summary-title) | Trait | |
| Coloration (flowers) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (flowers) #gephebase-summary-title) | Trait State in Taxon A | |
| lochroma calycinum - blue morphs | Trait State in Taxon B | |
| lochroma calycinum - white morph | Ancestral State | |
| Taxon A | | Taxonomic Status |
| Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=Intraspecific #gephebase-summary-title) | | |
| Taxon A | Latin Name | Latin Name |
| lochroma calycinum (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^lochroma+calycinum #gephebase-summary-title) | | |
| - | Common Name | Common Name |
| lochroma calycinum Benth. | Synonyms | Synonyms |
| species | Rank | Rank |
| cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoidae; Physaleae; lochroma | Lineage | Lineage |
| lochroma () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=304104) | Parent | Parent |
| 362353 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=362353) | NCBI Taxonomy ID | NCBI Taxonomy ID |
| No | is Taxon A an Infraspecies? | is Taxon B an Infraspecies? |

GENOTYPIC CHANGE

| | | |
|---|--|--------------------------------|
| DFRA | Generic Gene Name | UniProtKB Arabidopsis thaliana |
| | Synonyms | GenebankID or UniProtKB |
| dihydroflavonol 4-reductase; DIHYDROFLAVONOL 4-REDUCTASE; DIHYDROKAEMPFEROL 4-REDUCTASE; M318; MJB21.18; MJB21_18; TT3; DFR; At5g42800 | P51102 (http://www.uniprot.org/uniprot/P51102) | |
| 3702.AT5G42800.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G42800.1) | String | |
| Belongs to the NAD(P)-dependent epimerase/dehydratase family. Dihydroflavonol-4-reductase subfamily. | Sequence Similarities | |
| GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491) GO:0050662 : coenzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050662) GO:0016616 : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0016616) | GO - Molecular Function | |

GO:0045552 : dihydrokaempferol 4-reductase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045552>)
GO:0047890 : flavanone 4-reductase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0047890>)

GO - Biological Process

GO:0009718 : anthocyanin-containing compound biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009718>)

GO - Cellular Component

GO:0042406 : extrinsic component of endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042406>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#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

10-99 bp

Molecular Details of the Mutation

33bp (11 a.a) deletion In coding sequence

Experimental Evidence

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

Main Reference

Genetic basis for a rare floral mutant in an Andean species of Solanaceae. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25667079>)

Authors

Coburn RA; Griffin RH; Smith SD

Abstract

White forms of typically pigmented flowers are one of the most common polymorphisms in flowering plants. Although the range of genetic changes that give rise to white phenotypes is well known from model systems, few studies have identified causative mutations in natural populations.

Here we combine genetic studies, in vitro enzyme assays, and biochemical analyses to identify the mechanism underlying the loss of anthocyanin pigment production in the naturally occurring white-flowered morph of *Iochroma calycinum* (Solanaceae).

Comparison of anthocyanin gene sequences revealed a putative loss-of-function mutation, an 11 amino-acid deletion in dihydroflavonol 4-reductase (DFR), in the white morph. Functional assays of Dfr alleles from blue and white morphs demonstrated that this deletion results in a loss of enzymatic activity, indicating that the deletion could be solely responsible for the lack of pigment production. Consistent with this hypothesis, quantitative PCR showed no significant differences in expression of anthocyanin genes between the morphs. Also, thin layer chromatography confirmed that the white morph continues to accumulate compounds upstream of the DFR enzyme.

Collectively, these experiments indicate that the structural mutation at Dfr underlies the rare white flower morph of *I. calycinum*. This study is one of only a few examples where a flower color polymorphism is due to a loss-of-function mutation in the coding region of an anthocyanin enzyme. The rarity of such mutations in nature suggests that negative consequences prevent fixation across populations.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS