GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00000939

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Brassica oleracea var botrytis

Trait State in Taxon B
Brassica oleracea var botrytis -Purple

Ancestral State
Data not curated

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

Taxon A

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

Common Name
wild cabbage

Synonyms
wild cabbage; Brassica oleracea L., 1753

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica

Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3705)

NCBI Taxonomy ID
3712 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3712)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Brassica oleracea var botrytis

Taxon B

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

Common Name
-

Synonyms
Brassica oleracea subsp. botrytis; cauliflower; Brassica oleracea var. botrytis L.; Brassica oleracea botrytis

Rank
varietas

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica; Brassica oleracea

Parent
Brassica oleracea (wild cabbage) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3712)

NCBI Taxonomy ID
3715 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3715)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Brassica oleracea var botrytis -Purple

GENOTYPIC CHANGE

Generic Gene Name
MYB2

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 Brassica oleracea var. botrytis
E5D8F5 (http://www.uniprot.org/uniprot/E5D8F5)

GenebankID or UniProtKB
GU219987 (https://www.ncbi.nlm.nih.gov/nuccore/GU219987)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#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

unknown

Experimental Evidence

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

Main Reference

The purple cauliflower arises from activation of a MYB transcription factor. (2010) (https://pubmed.ncbi.nlm.nih.gov/20855520)

Authors

Chiu LW; Zhou X; Burke S; Wu X; Prior RL; Li L

Abstract

Anthocyanins are responsible for the color of many flowers, fruits, and vegetables. An interesting and unique Purple (Pr) gene mutation in cauliflower (Brassica oleracea var botrytis) confers an abnormal pattern of anthocyanin accumulation, giving the striking mutant phenotype of intense purple color in curds and a few other tissues. To unravel the nature of the Pr mutation in cauliflower, we isolated the Pr gene via a combination of candidate gene analysis and fine mapping. Pr encoded a R2R3 MYB transcription factor that exhibited tissue-specific expression, consistent with an abnormal anthocyanin accumulation pattern in the mutant. Transgenic Arabidopsis (Arabidopsis thaliana) and cauliflower plants expressing the Pr-D allele recapitulated the mutant phenotype, confirming the isolation of the Pr gene. Up-regulation of Pr specifically activated a basic helix-loop-helix transcription factor and a subset of anthocyanin structural genes encoding flavonoid 3′-hydroxylase, dihydroflavonol 4-reductase, and leucoanthocyanidin dioxygenase to confer ectopic accumulation of pigments in the purple cauliflower. Our results indicate that the genetic variation including a Harbinger DNA transposon insertion in the upstream regulatory region of the Pr-D allele is responsible for the up-regulation of the Pr gene in inducing phenotypic change in the plant. The successful isolation of Pr provides important information on the regulatory control of anthocyanin biosynthesis in Brassica vegetables, and offers a genetic resource for development of new varieties with enhanced health-promoting properties and visual appeal.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS