

GEPHE SUMMARY

Gephebase Gene
Cauliflower (BoCAL)

Entry Status
Published

GepheID
GP00000173

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Inflorescence morphology

Trait State in Taxon A
Brassica oleracea - wild-type

Trait State in Taxon B
Brassica oleracea var. botrytis (cauliflower)

Ancestral State
Taxon A

Taxonomic Status
Domesticated

Taxon A

Latin Name
Brassica oleracea

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; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica

Parent
Brassica () - (Rank: genus)

NCBI Taxonomy ID
3712

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Brassica oleracea var. *botrytis*

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; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica; Brassica oleracea

Parent
Brassica oleracea (wild cabbage) - (Rank: species)

NCBI Taxonomy ID
3715

is Taxon B an Intraspecies?
Yes

Taxon B Description
Brassica oleracea var. botrytis

GENOTYPIC CHANGE

Generic Gene Name
CAL

Synonyms
AGAMOUS-like 10; AGL10; CAL1; CAULIFLOWER; F28B23.25; F28B23_25; MADS5; At1g26310; F28B23.24

String
3702.AT1G26310.1

Sequence Similarities
-

GO - Molecular Function
GO:0046983 : protein dimerization activity
GO:0003700 : DNA-binding transcription factor activity
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
GO:0043565 : sequence-specific DNA binding
GO:0008134 : transcription factor binding
GO:0000982 : transcription factor activity, RNA polymerase II proximal promoter sequence-

UniProtKB Arabidopsis thaliana
Q39081

GenebankID or UniProtKB
AAS67313

specific DNA binding

GO:0044212 : transcription regulatory region DNA binding

GO - Biological Process

GO:0007275 : multicellular organism development

GO:0045944 : positive regulation of transcription by RNA polymerase II

GO:0030154 : cell differentiation

GO:0009911 : positive regulation of flower development

GO:0010582 : floral meristem determinacy

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

Yes

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsense

Molecular Details of the Mutation

GAG>TAG; E151*; protein truncated after only 150 of the 255 amino acids of the wild-type protein

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Molecular basis of the cauliflower phenotype in Arabidopsis. (1995)

Authors

Kempin SA; Savidge B; Yanofsky MF

Abstract

Genetic studies demonstrate that two Arabidopsis genes, CAULIFLOWER and APETALA1, encode partially redundant activities involved in the formation of floral meristems, the first step in the development of flowers. Isolation of the CAULIFLOWER gene from Arabidopsis reveals that it is closely related in sequence to APETALA1. Like APETALA1, CAULIFLOWER is expressed in young flower primordia and encodes a MADS-domain, indicating that it may function as a transcription factor. Analysis of the cultivated garden variety of cauliflower (*Brassica oleracea* var. botrytis) reveals that its CAULIFLOWER gene homolog is not functional, suggesting a molecular basis for one of the oldest recognized flower abnormalities.

Additional References

Variation and selection at the CAULIFLOWER floral homeotic gene accompanying the evolution of domesticated *Brassica oleracea*. (2000)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

COMMENTS