GEPHE SUMMARY

Gephebase Gene

AGAMOUS-Like6 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^AGAMOUS-Like6^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000053

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

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

Trait

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

Trait State in Taxon A

Arabidopsis thaliana - Ler

Trait State in Taxon B

Arabidopsis thaliana - C24 - reduced stem branching

Trait #2

Trait Category

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

Trait

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

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

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

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis thaliana - Ler

Taxon B

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

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

Parent

Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Arabidopsis thaliana - C24 - reduced stem branching

GENOTYPIC CHANGE

Generic Gene Name

AGL6

Synonyms

AGAMOUS-like 6; F17K2.18; REDUCED SHOOT BRANCHING 1; RSB1; At2g45650

String

3702.AT2G45650.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G45650.1)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0008134 : transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0000982 : transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000982)
GO:0044212 : transcription regulatory region DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0044212)

GO - Biological Process

GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)
GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0048437 : floral organ development (https://www.ebi.ac.uk/QuickGO/term/GO:0048437)
GO:0048481 : plant ovule development (https://www.ebi.ac.uk/QuickGO/term/GO:0048481)
GO:0009911 : positive regulation of flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009911)
GO:0010228 : vegetative to reproductive phase transition of meristem (https://www.ebi.ac.uk/QuickGO/term/GO:0010228)

GO - Cellular Component

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

UniProtKB Arabidopsis thaliana

P29386 (http://www.uniprot.org/uniprot/P29386)

GenebankID or UniProtKB

()

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

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Pro201Leu

Experimental Evidence

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

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

Main Reference

Epistatic natural allelic variation reveals a function of AGAMOUS-LIKE6 in axillary bud formation in Arabidopsis. (2012) (https://pubmed.ncbi.nlm.nih.gov/22730404)

Authors

Huang X; Effgen S; Meyer RC; Theres K; Koornneef M

Abstract

In the Arabidopsis multiparent recombinant inbred line mapping population, a limited number of plants were detected that lacked axillary buds in most of the axils of the cauline (stem) leaves, but formed such buds in almost all rosette axils. Genetic analysis showed that polymorphisms in at least three loci together constitute this phenotype, which only occurs in late-flowering plants. Early flowering is epistatic to two of these loci, called REDUCED SHOOT BRANCHING1 (RSB1) and RSB2, which themselves do not affect flowering time. Map-based cloning and confirmation by transformation with genes from the region where RSB1 was identified by fine-mapping showed that a specific allele of AGAMOUS-Like6 from accession C24 conferred reduced branching in the cauline leaves. Site-directed mutagenesis in the Columbia allele revealed the causal amino acid substitution, which behaved as dominant negative, as was concluded from a loss-of-function mutation that showed the same phenotype in the late-flowering genetic background. This causal allele occurs at a frequency of 15% in the resequenced Arabidopsis thaliana accessions and correlated with reduced stem branching only in late-flowering accessions. The data show the importance of natural variation and epistatic interactions in revealing gene function.

RELATED GEPHE

Related Genes

4 (ACS11, ERECTA, ICARUS1, phytochrome D (PHYD)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Plant architecture/or+Taxon ID=^3702^/and+Trait=Inflorescence architecture/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Epistasis Dominant-negative loss-of-function mutation ; Epistatic interaction with Early Flowering Locus ; use of the AMPRIL mapping population ; Functional Verification : Site-directed mutagenesis in Col background