

GEPHE SUMMARY

<p>AGAMOUS-Like6 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^AGAMOUS-Like6^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000053</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)	
Plant architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Plantarchitecture^#gephebase-summary-title)	Trait
Arabidopsis thaliana - Ler	Trait State in Taxon A
Arabidopsis thaliana - C24 - reduced stem branching	Trait State in Taxon B

Trait #2	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)	
Inflorescence architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Inflorescencearchitecture^#gephebase-summary-title)	Trait
-	Trait State in Taxon A
-	Trait State in Taxon B

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

	Taxon A
	Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Arabidopsisthaliana^#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 Intraspecies?
Yes	
	Taxon A Description
Arabidopsis thaliana - Ler	

	Taxon B
	Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=^Arabidopsisthaliana^#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 Intraspecies?
Yes	
	Taxon B Description
Arabidopsis thaliana - C24 - reduced stem branching	

GENOTYPIC CHANGE

AGL6	Generic Gene Name P29386 (http://www.uniprot.org/uniprot/P29386)	UniProtKB Arabidopsis thaliana
AGAMOUS-like 6; F17K2.18; REDUCED SHOOT BRANCHING 1; RSB1; At2g45650	Synonyms ()	GenebankID or UniProtKB
3702.AT2G45650.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT2G45650.1)	String	
-	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)	
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title)		Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title)		Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title)		Aberration Type
Nonsynonymous		SNP Coding Change
Pro201Leu		Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title)		Experimental Evidence

	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

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 Genes

No matches found.

Related Haplotypes

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