

FLM (MAF1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=*FLM (MAF1)^#gephebase-summary-title)	Gephebase Gene	GepheID
	GP00000341	Main curator
Published	Entry Status	Martin

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	
	Trait
Flowering time (https://www.gephebase.org/search-criteria?/and+Trait=^Flowering+time^#gephebase-summary-title)	
	Trait State in Taxon A
Arabidopsis thaliana- Col-3; Col-5	
	Trait State in Taxon B
Arabidopsis thaliana- Nd-1	
	Ancestral State
Data not curated	
	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	

GENOTYPIC CHANGE

AGL27	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	Q9AT76 (http://www.uniprot.org/uniprot/Q9AT76)
AGAMOUS-like 27; AGL27; FLM; FLOWERING LOCUS M; MADS AFFECTING FLOWERING 1; FK1; MAF1; At1g77080; F22K20.15		GenebankID or UniProtKB
	String	AK175247 (https://www.ncbi.nlm.nih.gov/nuccore/AK175247)
3702.AT1G77080.4 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT1G77080.4)		
	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: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:0006355 : regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0009908 : flower development (<https://www.ebi.ac.uk/QuickGO/term/GO:0009908>)
GO:0009910 : negative regulation of flower development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009910>)
GO:0009909 : regulation of flower development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009909>)
GO:0048573 : photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048573>)
GO:0010048 : vernalization response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010048>)

GO - Cellular Component

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

Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title>)

Molecular Type

Gene Loss (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Loss~#gephebase-summary-title>)

Aberration Type

Complex Change (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Complex Change~#gephebase-summary-title>)

Molecular Details of the Mutation

Deletion of entire gene

Experimental Evidence

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

Main Reference

Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. (2005) (<https://pubmed.ncbi.nlm.nih.gov/15695584>)

Authors

Werner JD; Borevitz JO; Warthmann N; Trainer GT; Ecker JR; Chory J; Weigel D

Abstract

Much of the flowering time variation in wild strains of *Arabidopsis thaliana* is due to allelic variation at two epistatically acting loci, FRIGIDA (FRI) and FLOWERING LOCUS C (FLC). FLC encodes a MADS (MCM1/AGAMOUS/DEFICIENS/SRF1) domain transcription factor that directly represses a series of flowering-promoting genes. FRI and FLC, however, do not explain all of the observed variation, especially when plants are grown in short days. To identify loci that act in addition to FRI and FLC in controlling flowering of natural accessions, we have analyzed a recombinant inbred line population derived from crosses of accession Niederzenz (Nd) to Columbia, both of which contain natural FRI lesions. Quantitative trait locus mapping and genomic DNA analysis by microarray hybridization were used to identify candidate genes affecting variation in flowering behavior. In both long and short days, the quantitative trait locus of largest effect, termed FLOWERING 1 (FLW1), was found to be associated with a Nd-specific deletion of FLOWERING LOCUS M (FLM), which encodes a floral repressor closely related to FLC. Analysis of near isogenic lines and quantitative transgenic complementation experiments confirmed that the FLM deletion is, in large part, responsible for the early flowering of the Nd accession.

Additional References

RELATED GEPHE

Related Genes

12 (AGAMOUS-LIKE 50, Cryptochrome 2 (CRY2) EDI allele, EARLY FLOWERING 3(ELF3), FLC (Flowering Locus C), Flowering locus T (FT), Frigida (FRI), Frigida like 1 (FRL1), Frigida like 2 (FRL2), MADS AFFECTING FLOWERING 2 (MAF2), SVP (SHORT VEGETATIVE PHASE), VIN3, HUA2) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

