

## GEPHE SUMMARY

	Gephebase Gene	GephelD
FLM (MAF1) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FLM (MAF1)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FLM (MAF1)^#gephebase-summary-title</a> )	GP00000341	Main curator
Published	Entry Status	Martin

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title</a> )	Trait	
Flowering time ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Flowering time^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Flowering time^#gephebase-summary-title</a> )	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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title</a> )		
Taxon A		Taxon B
	Latin Name	Latin Name
Arabidopsis thaliana ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title</a> )		
thale cress	Common Name	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	Synonyms	
species	Rank	
	Lineage	
cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis		
Arabidopsis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701</a> )	Parent	
3702 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702</a> )	NCBI Taxonomy ID	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Arabidopsis thaliana- Col-3; Col-5	Taxon A Description	Taxon B Description

## GENOTYPIC CHANGE

AGL27	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	GenebankID or UniProtKB
AGAMOUS-like 27; AGL27; FLM; FLOWERING LOCUS M; MADS AFFECTING FLOWERING 1; FK1; MAF1; At1g77080; F22K20.15		AK175247 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AK175247">https://www.ncbi.nlm.nih.gov/nuccore/AK175247</a> )
3702.AT1G77080.4 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G77080.4">http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G77080.4</a> )	String	
-	Sequence Similarities	
GO:0046983 : protein dimerization activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046983">https://www.ebi.ac.uk/QuickGO/term/GO:0046983</a> )	GO - Molecular Function	
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.gephbase.org/search-criteria?/and+Presumptive Null=%27Yes%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Presumptive%20Null=%27Yes%27#gephbase-summary-title))

Molecular Type

Gene Loss ([https://www.gephbase.org/search-criteria?/and+Molecular Type=%27Gene Loss%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Molecular%20Type=%27Gene%20Loss%27#gephbase-summary-title))

Aberration Type

Complex Change ([https://www.gephbase.org/search-criteria?/and+Aberration Type=%27Complex Change%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Aberration%20Type=%27Complex%20Change%27#gephbase-summary-title))

Molecular Details of the Mutation

Deletion of entire gene

Experimental Evidence

Linkage Mapping ([https://www.gephbase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Experimental%20Evidence=%27Linkage%20Mapping%27#gephbase-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

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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.gephbase.org/search-criteria?/or+TaxonID=%273702%27/and+Trait=Flowering%20time/and+groupHaplotypes=true#gephbase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

