

FLC (Flowering Locus C) (https://www.gephebase.org/search-criteria?and=Gene)	Gephebase Gene	GP00000335	GepheID
Gephebase~FLC (Flowering Locus C)^#gephebase-summary-title			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- flc-3	
	Trait State in Taxon B
Arabidopsis thaliana- Bur-0	
	Ancestral State
Data not curated	
	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	

GENOTYPIC CHANGE

FLC	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	Q9S7Q7 (http://www.uniprot.org/uniprot/Q9S7Q7)
AGAMOUS-like 25; AGL25; FLF; FLOWERING LOCUS C; FLOWERING LOCUS F; MADS BOX PROTEIN FLOWERING LOCUS F; REDUCED STEM BRANCHING 6; RSB6; T31P16.130; T31P16_130; At5g10140		GenebankID or UniProtKB
	String	AF116528 (https://www.ncbi.nlm.nih.gov/nucore/AF116528)
3702.AT5G10140.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT5G10140.1)		
	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: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:0042752 : regulation of circadian rhythm
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042752>)
GO:0009266 : response to temperature stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009266>)
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>)

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

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

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

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GA substitution disrupting Splice Site

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

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

FRIGIDA-independent variation in flowering time of natural Arabidopsis thaliana accessions. (2005) (<https://pubmed.ncbi.nlm.nih.gov/15911588>)

Werner JD; Borevitz JO; Uhlenhaut NH; Ecker JR; Chory J; Weigel D

FRIGIDA (FRI) and FLOWERING LOCUS C (FLC) are two genes that, unless plants are vernalized, greatly delay flowering time in Arabidopsis thaliana. Natural loss-of-function mutations in FRI cause the early flowering growth habits of many A. thaliana accessions. To quantify the variation among wild accessions due to FRI, and to identify additional genetic loci in wild accessions that influence flowering time, we surveyed the flowering times of 145 accessions in long-day photoperiods, with and without a 30-day vernalization treatment, and genotyped them for two common natural lesions in FRI. FRI is disrupted in at least 84 of the accessions, accounting for only approximately 40% of the flowering-time variation in long days. During efforts to dissect the causes for variation that are independent of known dysfunctional FRI alleles, we found new loss-of-function alleles in FLC, as well as late-flowering alleles that do not map to FRI or FLC. An FLC nonsense mutation was found in the early flowering Van-0 accession, which has otherwise functional FRI. In contrast, Lz-0 flowers late because of high levels of FLC expression, even though it has a deletion in FRI. Finally, eXtreme array mapping identified genomic regions linked to the vernalization-independent, late-flowering habit of Bur-0, which has an alternatively spliced FLC allele that behaves as a null allele.

Adaptive divergence in flowering time among natural populations of Arabidopsis thaliana: Estimates of selection and QTL mapping. (2017) (<https://pubmed.ncbi.nlm.nih.gov/27859214>)

RELATED GEPHE

12 (AGAMOUS-LIKE 50, Cryptochrome 2 (CRY2) EDI allele, EARLY FLOWERING 3(ELF3), FLM (MAF1), 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>)

6 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~FLC \(Flowering Locus C\)~/and+Taxon ID=~3702~/or+Gene Gephebase=~FLC \(Flowering Locus C\)~/and+Taxon ID=~3702~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~FLC (Flowering Locus C)~/and+Taxon ID=~3702~/or+Gene Gephebase=~FLC (Flowering Locus C)~/and+Taxon ID=~3702~#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

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