

## GEPHE SUMMARY

**Gephebase Gene**  
FLC (Flowering Locus C)

**Entry Status**  
Published

**GepheID**  
GP00000336

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Flowering time

**Trait State in Taxon A**  
Arabidopsis thaliana- Ler0

**Trait State in Taxon B**  
Arabidopsis thaliana- LI-0

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Intraspecific

### Taxon A

**Latin Name**  
*Arabidopsis thaliana*

**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)

**NCBI Taxonomy ID**  
3702

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Arabidopsis thaliana- Ler0

### Taxon B

**Latin Name**  
*Arabidopsis thaliana*

**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)

**NCBI Taxonomy ID**  
3702

**is Taxon B an Intraspecies?**  
Yes

**Taxon B Description**  
Arabidopsis thaliana- LI-0

## GENOTYPIC CHANGE

**Generic Gene Name**  
FLC

**Synonyms**  
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

**String**  
3702.AT5G10140.1

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0046983 : protein dimerization activity  
GO:0003700 : DNA-binding transcription factor activity  
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding  
GO:0043565 : sequence-specific DNA binding  
GO:0008134 : transcription factor binding

**UniProtKB Arabidopsis thaliana**  
Q9S7Q7

**GenebankID or UniProtKB**  
AF116527

GO:0000982 : transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding

GO:0044212 : transcription regulatory region DNA binding

#### GO - Biological Process

GO:0007275 : multicellular organism development

GO:0045944 : positive regulation of transcription by RNA polymerase II

GO:0030154 : cell differentiation

GO:0009908 : flower development

GO:0009910 : negative regulation of flower development

GO:0042752 : regulation of circadian rhythm

GO:0009266 : response to temperature stimulus

GO:0010048 : vernalization response

#### GO - Cellular Component

GO:0005634 : nucleus

#### Presumptive Null

No

#### Molecular Type

Cis-regulatory

#### Aberration Type

Deletion

#### Deletion Size

10-99 bp

#### Molecular Details of the Mutation

50bp deletion in 5'UTR

#### Experimental Evidence

Linkage Mapping

#### Main Reference

Novel natural alleles at FLC and LVR loci account for enhanced vernalization responses in *Arabidopsis thaliana*. (2012)

#### Authors

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#### Abstract

Vernalization, the induction of flowering by low winter temperatures, is likely to be involved in plant climatic adaptation. However, the genetic, molecular and ecological bases underlying the quantitative variation that tunes vernalization sensitivity to natural environments are largely unknown. To address these questions, we have studied the enhanced vernalization response shown by the LI-0 accession of *Arabidopsis thaliana*. Quantitative trait locus (QTL) mapping for several flowering initiation traits in relation to vernalization, in a new Ler Ã— LI-0 recombinant inbred line (RIL) population, identified large effect alleles at FRI, FLC and HUA2, together with two small effect loci named as Llagostera vernalization response (LVR) 1 and 2. Phenotypic analyses of near isogenic lines validated LVR1 effect on flowering vernalization responses. To further characterize the FLC allele from LI-0, we carried out genetic association analyses using a regional collection of wild genotypes. FLC-LI-0 appeared as a low-frequency allele that is distinguished by polymorphism Del(-57), a 50-bp-deletion in the 5'-UTR. Del(-57) was significantly associated with enhanced vernalization responses and FLC RNA expression, as well as with altitude and minimum temperatures. These results are consistent with Del(-57) acting as a novel cis-regulatory FLC polymorphism that may confer climatic adaptation by increasing vernalization sensitivity.

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#### Additional References

Adaptive divergence in flowering time among natural populations of *Arabidopsis thaliana*: Estimates of selection and QTL mapping. (2017)

## RELATED GEPHE

#### Related Genes

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)

#### Related Haplotypes

6

## COMMENTS

@GxE