

GEPHE SUMMARY

Gephebase Gene
FLC (Flowering Locus C)

Entry Status
Published

GepheID
GP00000332

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Flowering time

Trait State in Taxon A
Arabidopsis thaliana- Col0

Trait State in Taxon B
Arabidopsis thaliana- Ler0

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- Col0

Taxon B

Latin Name
Arabidopsis thaliana

Common Name
thale cress

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Parent
Arabidopsis () - (Rank: genus)

NCBI Taxonomy ID
3702

is Taxon B an Intraspecies?
Yes

Taxon B Description
Arabidopsis thaliana- Ler0

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
AF116528

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

Insertion

Insertion Size

1-10 kb

Molecular Details of the Mutation

TE insertion in intron 1; a region required for normal FLC regulation. The transposable element renders FLC-Ler subject to repressive chromatin modifications mediated by short interfering RNAs generated from homologous transposable elements in the genome.

Experimental Evidence

Candidate Gene

Main Reference

Attenuation of FLOWERING LOCUS C activity as a mechanism for the evolution of summer-annual flowering behavior in Arabidopsis. (2003)

Authors

Michaels SD; He Y; Scortecci KC; Amasino RM

Abstract

Plant species have evolved a wide variety of flowering habits, each adapted to maximize reproductive success in their local environment. Even within a species, accessions from different environments can exhibit markedly different flowering behavior. In Arabidopsis, some accessions are rapid-cycling summer annuals, whereas others accessions are late flowering and vernalization responsive and thus behave as winter annuals. Two genes, FLOWERING LOCUS C (FLC) and FRIGIDA (FRI), interact synergistically to confer the winter-annual habit. Previous work has shown that many summer-annual accessions contain null mutations in the FRI gene; thus it appears that these summer-annual accessions have arisen from winter-annual ancestors by losing FRI function. In this work we demonstrate that naturally occurring allelic variation in FLC has provided another route to the evolution of summer-annual flowering behavior in Arabidopsis. We have identified two summer-annual accessions, Da (1)-12 and Shakh dara, that contain functional alleles of FRI, but are early flowering because of weak alleles of FLC. We have also determined that the weak allele of FLC found in Landsberg erecta is naturally occurring. Unlike accessions that have arisen because of loss-of-function mutations in FRI, the FLC alleles from Da (1)-12, Shakh dara, and Landsberg erecta are not nulls; however, they exhibit lower steady-state mRNA levels than strong alleles of FLC. Sequence analysis indicates that these weak alleles of FLC have arisen independently at least twice during the course of evolution.

Additional References

Analysis of the molecular basis of flowering time variation in Arabidopsis accessions. (2003)

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

siRNAs targeting an intronic transposon in the regulation of natural flowering behavior in Arabidopsis. (2004)

RELATED GEPHE

Related Genes

12 (AGAMOUS-LIKE 50, Cryptochrome 2 (CRY2) ED1 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

EXTERNAL LINKS

COMMENTS

@GxE @TE @Epigenetics

