GEPHE SUMMARY

Gephebase Gene

FLC (Flowering Locus C) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FLC (Flowering Locus C)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000332

Main curator

Martin

PHENOTYPIC CHANGE

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- Col0

Trait State in Taxon B

Arabidopsis thaliana- Ler0

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis thaliana- Col0

Taxon B

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID

3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?

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 (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)

UniProtKB Arabidopsis thaliana

Q9S7Q7 (http://www.uniprot.org/uniprot/Q9S7Q7)

GenebankID or UniProtKB

AF116528 (https://www.ncbi.nlm.nih.gov/nuccore/AF116528)

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)

Presumptive Null

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

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)

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 (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Attenuation of FLOWERING LOCUS C activity as a mechanism for the evolution of summer-annual flowering behavior in Arabidopsis. (2003) (https://pubmed.ncbi.nlm.nih.gov/12904584)

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 Shakhdara, 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, Shakhdara, 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) (https://pubmed.ncbi.nlm.nih.gov/12805638)
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)
siRNAs targeting an intronic transposon in the regulation of natural flowering behavior in Arabidopsis. (2004) (https://pubmed.ncbi.nlm.nih.gov/15545622)

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) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

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)

EXTERNAL LINKS

COMMENTS

@GxE @TE @Epigenetics