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
GP00000336

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- Ler0

Trait State in Taxon B
Arabidopsis thaliana- LI-0

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- Ler0

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- 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 (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
AF116527 (https://www.ncbi.nlm.nih.gov/nuccore/AF116527)

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

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

50bp deletion in 5′UTR

Experimental Evidence

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

Main Reference

Novel natural alleles at FLC and LVR loci account for enhanced vernalization responses in Arabidopsis thaliana. (2012) (https://pubmed.ncbi.nlm.nih.gov/22494398)

Authors

SÃinchez-Bermejo E; MÃ©ndez-Vigo B; PicÃ³ FX; MartÃnez-Zapater JM; Alonso-Blanco C

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 Ll-0 accession of Arabidopsis thaliana. Quantitative trait locus (QTL) mapping for several flowering initiation traits in relation to vernalization, in a new Ler Ã— Ll-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 Ll-0, we carried out genetic association analyses using a regional collection of wild genotypes. FLC-Ll-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) (https://pubmed.ncbi.nlm.nih.gov/27859214)

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

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