

GEPHE SUMMARY

	Gephebase Gene		GepheID
FLC (Flowering Locus C) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00000331	
Gephebase="^FLC (Flowering Locus C)"#gephebase-summary-title)			Main curator
Published	Entry Status	Martin	

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait)		
Category="^Physiology"#gephebase-summary-title)	Trait	
Flowering time (<a flowering"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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- Lov-1		
	Ancestral State	
Data not curated		
	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)		
Status="^Intraspecific"#gephebase-summary-title)		

Taxon A	Latin Name	Taxon B	Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="^Arabidopsis thaliana"#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="^Arabidopsis thaliana"#gephebase-summary-title)	
Common Name		Common Name	
thale cress		thale cress	
Synonyms		Synonyms	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Parent		Parent	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Col0		Arabidopsis thaliana- Lov-1	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
FLC		Q9S7Q7 (http://www.uniprot.org/uniprot/Q9S7Q7)
	Synonyms	GenebankID or UniProtKB
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		AL356332 (https://www.ncbi.nlm.nih.gov/nucore/AL356332)
	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)		

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)

Mutation #1

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

Presumptive Null

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

Molecular Type

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

Aberration Type

SNP _121 associated with lower Histone H3K27 methylation

Molecular Details of the Mutation

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

Experimental Evidence

Quantitative modulation of polycomb silencing underlies natural variation in vernalization. (2012) (https://pubmed.ncbi.nlm.nih.gov/22798408)

Main Reference

Coustham V; Li P; Strange A; Lister C; Song J; Dean C

Authors

Arabidopsis thaliana accessions have adapted to growth in a wide range of climates. Variation in flowering and alignment of vernalization response with winter length are central to this adaptation. Vernalization involves the epigenetic silencing of the floral repressor FLC via a conserved Polycomb (PRC2) mechanism involving trimethylation of Lys(27) on histone H3 (H3K27me3). We found that variation for response to winter length maps to cis polymorphism within FLC. A rare combination of four polymorphisms localized around the nucleation region of a PHD-Polycomb complex determines a need for longer cold. Chromatin immunoprecipitation experiments indicate that these polymorphisms influence the accumulation of H3K27me3 in Arabidopsis accession Lov-1, both at the nucleation site and over the gene body. Quantitative modulation of chromatin silencing through cis variation may be a general mechanism contributing to evolutionary change.

Abstract

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)

Additional References

Mutation #2

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

Presumptive Null

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

Molecular Type

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

Aberration Type

SNP +598 associated with lower Histone H3K27 methylation

Molecular Details of the Mutation

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

Experimental Evidence

Quantitative modulation of polycomb silencing underlies natural variation in vernalization. (2012) (https://pubmed.ncbi.nlm.nih.gov/22798408)

Main Reference

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Abstract

H3K27me3 in Arabidopsis accession Lov-1, both at the nucleation site and over the gene body. Quantitative modulation of chromatin silencing through cis variation may be a general mechanism contributing to evolutionary change.

Additional References

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(<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+TaxonID=^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+TaxonID=^3702^/or+Gene+Gephebase=^FLC+\(Flowering+Locus+C\)^/and+TaxonID=^3702^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^FLC+(Flowering+Locus+C)^/and+TaxonID=^3702^/or+Gene+Gephebase=^FLC+(Flowering+Locus+C)^/and+TaxonID=^3702^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect Polymorphism affects epigenetic silencing via Polycomb binding