

GEPHE SUMMARY

	Gephebase Gene		GepheID
FLC-2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^FLC-2^#gephebase-summary-title)	GP00000340		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 (https://www.gephebase.org/search-criteria?/and+Trait=^Flowering+time^#gephebase-summary-title)	Trait State in Taxon A		
Brassica rapa	Trait State in Taxon B		
Brassica rapa	Ancestral State		
Data not curated	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Brassica rapa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Brassica+rapa^#gephebase-summary-title)	Common Name		Common Name
field mustard	Synonyms		Synonyms
field mustard; Brassica rapa L.; Brassica rapa L., 1753	Rank		Rank
species	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Brassicaceae; Brassica	Parent		Parent
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)	NCBI Taxonomy ID		NCBI Taxonomy ID
3711 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3711)	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No			No

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
FLC	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	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>)

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title>)

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

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title>)

unknown

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

BrFLC2 (FLOWERING LOCUS C) as a candidate gene for a vernalization response QTL in Brassica rapa. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20231331>)

Zhao J; Kulkarni V; Liu N; Del Carpio DP; Bucher J; Bonnema G

Flowering time is an important agronomic trait, and wide variation exists among Brassica rapa. In Arabidopsis, FLOWERING LOCUS C (FLC) plays an important role in modulating flowering time and the response to vernalization. Brassica rapa contains several paralogues of FLC at syntenic regions. BrFLC2 maps under a major flowering time and vernalization response quantitative trait locus (QTL) at the top of A02. Here the effects of vernalization on flowering time in a double haploid (DH) population and on BrFLC2 expression in selected lines of a DH population in B. rapa are described. The effect of the major flowering time QTL on the top of A02 where BrFLC2 maps clearly decreases upon vernalization, which points to a role for BrFLC2 underlying the QTL. In all developmental stages and tissues (seedlings, cotyledons, and leaves), BrFLC2 transcript levels are higher in late flowering pools of DH lines than in pools of early flowering DH lines. BrFLC2 expression diminished after different durations of seedling vernalization in both early and late DH lines. The reduction of BrFLC2 expression upon seedling vernalization of both early and late flowering DH lines was strongest at the seedling stage and diminished in subsequent growth stages, which suggests that the commitment to flowering is already set at very early developmental stages. Taken together, these data support the hypothesis that BrFLC2 is a candidate gene for the flowering time and vernalization response QTL in B. rapa.

RELATED GEPHE

1 (FLC-1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3711~/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS

