

	Gephebase Gene	GepheID
FLC-2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=FLC-2^#gephebase-summary-title)	GP00000339	Main curator
Published	Entry Status: Martin	

	Trait Category				
Physiology (#https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology #gephebase-summary-title)					
	Trait				
Flowering time (#https://www.gephebase.org/search-criteria?/and+Trait=~Floweringtime #gephebase-summary-title)					
	Trait State in Taxon A				
Brassica oleracea; annual					
	Trait State in Taxon B				
Brassica oleracea; biennial					
	Ancestral State				
Taxon A					
	Taxonomic Status				
Domesticated (#https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated #gephebase-summary-title)					
Taxon A			Taxon B		
	Latin Name			Latin Name	
Brassica oleracea (#https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~BrassicaoLERACEA #gephebase-summary-title)			Brassica oleracea (#https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~BrassicaoLERACEA #gephebase-summary-title)		
	Common Name			Common Name	
wild cabbage			wild cabbage		
	Synonyms			Synonyms	
wild cabbage; Brassica oleracea L., 1753			wild cabbage; Brassica oleracea L., 1753		
	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; Brassiceae; Brassica			cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica		
	Parent			Parent	
Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)			Brassica () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3705)		
	NCBI Taxonomy ID			NCBI Taxonomy ID	
3712 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3712)			3712 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3712)		
	is Taxon A an Intraspecies?			is Taxon B an Intraspecies?	
No			No		

FLC	Generic Gene Name	UniProtKB Arabidopsis thaliana
	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		Q9S7Q7 (http://www.uniprot.org/uniprot/Q9S7Q7) AHY82602 (https://www.ncbi.nlm.nih.gov/nuccore/AHY82602)
	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>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes~#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title))

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

1bp deletion resulting in frameshift

Experimental Evidence

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

Main Reference

Mapping and characterization of FLC homologs and QTL analysis of flowering time in Brassica oleracea. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17136371>)

Authors

Okazaki K; Sakamoto K; Kikuchi R; Saito A; Togashi E; Kuginuki Y; Matsumoto S; Hirai M

Abstract

The FLC gene product is an inhibitor of flowering in Arabidopsis. FLC homologs in Brassica species are thought to control vernalization. We cloned four FLC homologs (BoFLCs) from Brassica oleracea. Three of these, BoFLC1, BoFLC3 and BoFLC5, have been previously characterized. The fourth novel sequence displayed 98% sequence homology to the previously identified gene BoFLC4, but also showed 91% homology to BrFLC2 from Brassica rapa. Phylogenetic analysis showed that this clone belongs to the FLC2 clade. Therefore, we designated this gene BoFLC2. Based on the segregation of RFLP, SRAP, CAPS, SSR and AFLP loci, a detailed linkage map of B. oleracea was constructed in the F(2) progeny obtained from a cross of B. oleracea cv. Green Comet (broccoli; non-vernalization type) and B. oleracea cv. Reiho (cabbage; vernalization type), which covered 540 cM, 9 major linkage groups. Six quantitative trait loci (QTL) controlling flowering time were detected. BoFLC1, BoFLC3 and BoFLC5 were not linked to the QTLs controlling flowering time. However, the largest QTL effect was located in the region where BoFLC2 was mapped. Genotyping of F(2)plants at the BoFLC2 locus showed that most of the early flowering plants were homozygotes of BoFLC-GC, whereas most of the late- and non-flowering plants were homozygotes of BoFLC-Rei. The BoFLC2 homologs present in plants of the non-vernalization type were non-functional, due to a frameshift in exon 4. Moreover, duplications and deletions of BoFLC2 were detected in broccoli and a rapid cycling line, respectively. These results suggest that BoFLC2 contributes to the control of flowering time in B. oleracea.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

