

## GEPHE SUMMARY

	Gephebase Gene		GepheID
Rap2.7 (vgt1) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Rap2.7+(vgt1)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Rap2.7+(vgt1)^#gephebase-summary-title</a> )		GP00000951	
	Entry Status	Martin	Main curator
Published			

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology^#gephebase-summary-title</a> )			
	Trait		
Flowering time ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Flowering+time^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Flowering+time^#gephebase-summary-title</a> )			
	Trait State in Taxon A		
Zea mays ssp. Mays			
	Trait State in Taxon B		
Zea mays ssp. mays			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated^#gephebase-summary-title</a> )			
Taxon A		Taxon B	
	Latin Name		Latin Name
Zea mays ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Zea+mays^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Zea+mays^#gephebase-summary-title</a> )		Zea mays ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Zea+mays^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Zea+mays^#gephebase-summary-title</a> )	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays		Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	
	Parent		Parent
Zea () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575</a> )		Zea () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4577 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577</a> )		4577 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Zea mays ssp. Mays		Zea mays ssp. mays	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
RAP2-7		Q9SK03 ( <a href="http://www.uniprot.org/uniprot/Q9SK03">http://www.uniprot.org/uniprot/Q9SK03</a> )	
	Synonyms		GenebankID or UniProtKB
related to AP2.7; T17D12.11; T17D12_11; TARGET OF EARLY ACTIVATION TAGGED (EAT) 1; TOE1; At2g28550		()	
	String		
3702.AT2G28550.3 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G28550.3">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G28550.3</a> )			
	Sequence Similarities		
Belongs to the AP2/ERF transcription factor family. AP2 subfamily.			
	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003700">https://www.ebi.ac.uk/QuickGO/term/GO:0003700</a> )			
GO:0003677 : DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003677">https://www.ebi.ac.uk/QuickGO/term/GO:0003677</a> )			
	GO - Biological Process		

GO:0009873 : ethylene-activated signaling pathway  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009873>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

2kb-sequence located 70kb upstream of the Vgt1 transcription start site - insertion of a miniature transposon (MITE) belonging to the Tourist family

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=))

Main Reference

Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17595297>)

Authors

Salvi S; Sponza G; Morgante M; Tomes D; Niu X; Fengler KA; Meeley R; Ananiev EV; Svitashv S; Bruggemann E; Li B; Hainey CF; Radovic S; Zaina G; Rafalski JA; Tingey SV; Miao GH; Phillips RL; Tuberosa R

Abstract

Flowering time is a fundamental trait of maize adaptation to different agricultural environments. Although a large body of information is available on the map position of quantitative trait loci for flowering time, little is known about the molecular basis of quantitative trait loci. Through positional cloning and association mapping, we resolved the major flowering-time quantitative trait locus, Vegetative to generative transition 1 (Vgt1), to an approximately 2-kb noncoding region positioned 70 kb upstream of an Ap2-like transcription factor that we have shown to be involved in flowering-time control. Vgt1 functions as a cis-acting regulatory element as indicated by the correlation of the Vgt1 alleles with the transcript expression levels of the downstream gene. Additionally, within Vgt1, we identified evolutionarily conserved noncoding sequences across the maize-sorghum-rice lineages. Our results support the notion that changes in distant cis-acting regulatory regions are a key component of plant genetic adaptation throughout breeding and evolution.

Additional References

The genetic architecture of maize flowering time. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19661422>)

## RELATED GEPHE

Related Genes

2 (zfl2, ZmCCT) ([https://www.gephebase.org/search-criteria?/or+Taxon ID="+4577+"/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@TE @DNAMethylation