

GEPHE SUMMARY

Rap2.7 (vgt1) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase^Rap2.7(vgt1)^#gephebase-summary-title)	Gephebase Gene	GP00000951	GephelD
	Entry Status	Martin	Main curator
Published			

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
Zea mays ssp. Mays	Trait State in Taxon B
Zea mays ssp. mays	Ancestral State
Data not curated	Taxonomic Status

Domesticated (<https://www.gephebase.org/search-criteria/?and+Taxonomic Status^Domesticated^#gephebase-summary-title>)

Taxon A	Latin Name	Taxon B	Latin Name
Zea mays (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms^Zea mays^#gephebase-summary-title)		Zea mays (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms^Zea mays^#gephebase-summary-title)	
-	Common Name	-	Common Name
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms	Zea mays var. japonica; maize; Zea mays L.; Zea mays mays species	Synonyms
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea	Rank
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Lineage	Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Lineage
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	Parent	4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	Parent
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Zea mays ssp. Mays	Taxon A Description	Zea mays ssp. mays	Taxon B Description

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
RAP2.7	Synonyms	Q9SK03 (http://www.uniprot.org/uniprot/Q9SK03)	GenebankID or UniProtKB
related to AP2.7; T17D12.11; T17D12_11; TARGET OF EARLY ACTIVATION TAGGED (EAT) 1; TOE1; At2g28550	String	0	
3702.AT2G28550.3 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G28550.3)	Sequence Similarities		
Belongs to the AP2/ERF transcription factor family. AP2 subfamily.	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			
	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>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

2kb-sequence located 70kb upstream of the Vg1 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>)

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; Svitashov 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

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

Related Genes

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE @DNAMethylation