GEPHE SUMMARY

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

GepheID
GP00000951
Main curator
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
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
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)
Common Name
-
Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays
Rank
species
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
Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)
NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)
is Taxon A an Infraspecies?
Yes
Taxon A Description
Zea mays ssp. Mays

Taxon B

Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)
Common Name
-
Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays
Rank
species
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
Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)
NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)
is Taxon B an Infraspecies?
Yes
Taxon B Description
Zea mays ssp. mays

GENOTYPIC CHANGE

Generic Gene Name
RAP2-7
Synonyms
related to AP2.7; T17D12.11; T17D12_11; TARGET OF EARLY ACTIVATION TAGGED (EAT) 1; TOE1; At2g28550
String
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

UniProtKB Arabidopsis thaliana
Q9SK03 (http://www.uniprot.org/uniprot/Q9SK03)
GenebankID or UniProtKB
()

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; Svitashev 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)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE @DNAMethylation