

GEPHE SUMMARY

Gephebase Gene
teosinte branched 1 (tb1)

Entry Status
Published

GepheID
GP00001116

Main curator
Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category
Morphology

Trait
Plant architecture

Trait State in Taxon A
Zea mays ssp. parviglumis and mexicana (teosinthe)

Trait State in Taxon B
Zea mays ssp. mays

Trait #2

Trait Category
Morphology

Trait
Inflorescence architecture

Trait State in Taxon A
-

Trait State in Taxon B
-

Ancestral State
Taxon A

Taxonomic Status
Domesticated

Taxon A

Latin Name
Zea mays

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; Andropogonodeae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus)

NCBI Taxonomy ID
4577

is Taxon A an Intraspecies?
Yes

Taxon A Description
Zea mays ssp. parviglumis and mexicana (teosinthe)

Taxon B

Latin Name
Zea mays

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; Andropogonodeae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus)

NCBI Taxonomy ID
4577

is Taxon B an Intraspecies?
Yes

Taxon B Description
Zea mays ssp. mays

GENOTYPIC CHANGE

Generic Gene Name

UniProtKB Zea mays

TB1

Q93W12

Synonyms

tb1; Z178A11.18

GenebankID or UniProtKB

U94494

String

4577.AC233950.1_FGP002

Sequence Similarities

-

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity

GO:0043565 : sequence-specific DNA binding

GO - Biological Process

GO:0007275 : multicellular organism development

GO:2000032 : regulation of secondary shoot formation

GO:0048831 : regulation of shoot system development

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

No

Molecular Type

Cis-regulatory

Aberration Type

Insertion

Insertion Size

1-10 kb

Molecular Details of the Mutation

Hopscotch TE insertion

Experimental Evidence

Linkage Mapping

Main Reference

A distant upstream enhancer at the maize domestication gene tb1 has pleiotropic effects on plant and inflorescent architecture. (2006)

Authors

Clark RM; Wagler TN; Quijada P; Doebley J

Abstract

Although quantitative trait locus (QTL) mapping has been successful in describing the genetic architecture of complex traits, the molecular basis of quantitative variation is less well understood, especially in plants such as maize that have large genome sizes. Regulatory changes at the teosinte branched1 (tb1) gene have been proposed to underlie QTLs of large effect for morphological differences that distinguish maize (*Zea mays* ssp. *mays*) from its wild ancestors, the teosintes (*Z. mays* ssp. *parviglumis* and *mexicana*). We used a fine mapping approach to show that intergenic sequences approximately 58-69 kb 5' to the tb1 cDNA confer pleiotropic effects on *Z. mays* morphology. Moreover, using an allele-specific expression assay, we found that sequences >41 kb upstream of tb1 act in cis to alter tb1 transcription. Our findings show that the large stretches of noncoding DNA that comprise the majority of many plant genomes can be a source of variation affecting gene expression and quantitative phenotypes.

Additional References

Identification of a functional transposon insertion in the maize domestication gene tb1. (2011)

Evidence for a natural allelic series at the maize domestication locus teosinte branched1. (2012)

RELATED GEPHE

Related Genes

2 (Barren inflorescence2 (BIF2), grassy tillers1)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Pleiotropy

