

GEPHE SUMMARY

	Gephebase Gene	GephelD
teosinte branched 1 (tb1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="teosinte branched 1 (tb1)"#gephebase-summary-title)	GP00001116	
Published	Entry Status	Main curator

PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Plant architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Plant architecture^#gephebase-summary-title)	Trait State in Taxon A
Zea mays ssp. parviflora and mexicana (teosinthe)	Trait State in Taxon B
Zea mays ssp. mays	

Trait #2	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait
Inflorescence architecture (https://www.gephebase.org/search-criteria?/and+Trait=^Inflorescence+architecture #gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

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

GENOTYPIC CHANGE

TB1	Generic Gene Name	UniProtKB Zea mays
tb1; Z178A11.18	Synonyms	GenebankID or UniProtKB
4577.AC233950.1_FGP002 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4577.AC233950.1_FGP002)	String	
-	Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	GO - Molecular Function	
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)	GO - Biological Process	
GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)	GO - Cellular Component	
GO:2000032 : regulation of secondary shoot formation (https://www.ebi.ac.uk/QuickGO/term/GO:2000032)		
GO:0048831 : regulation of shoot system development (https://www.ebi.ac.uk/QuickGO/term/GO:0048831)		
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)		Presumptive Null
No (https://www.gephbase.org/search-criteria/?and+Presumptive+Null=%No%#gephbase-summary-title)		Molecular Type
Cis-regulatory (https://www.gephbase.org/search-criteria/?and+Molecular+Type=%Cis-regulatory%#gephbase-summary-title)		Aberration Type
Insertion (https://www.gephbase.org/search-criteria/?and+Aberration+Type=%Insertion%#gephbase-summary-title)		Insertion Size
1-10 kb		Molecular Details of the Mutation
Hopscotch TE insertion		Experimental Evidence
Linkage Mapping (https://www.gephbase.org/search-criteria/?and+Experimental+Evidence=%Linkage+Mapping%#gephbase-summary-title)		Main Reference
A distant upstream enhancer at the maize domestication gene tb1 has pleiotropic effects on plant and inflorescent architecture. (2006) (https://pubmed.ncbi.nlm.nih.gov/16642024)		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 (<i>Zea mays</i> ssp. <i>mays</i>) from its wild ancestors, the teosintes (<i>Z. mays</i> ssp. <i>parviflora</i> and <i>mexicana</i>). We used a fine mapping approach to show that intergenic sequences approximately 58–69 kb 5' to the tb1 cDNA confer pleiotropic effects on <i>Z. mays</i> 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) (https://pubmed.ncbi.nlm.nih.gov/21946354)		
Evidence for a natural allelic series at the maize domestication locus teosinte branched1. (2012) (https://pubmed.ncbi.nlm.nih.gov/22505628)		

RELATED GEPHE

2 (Barren inflorescence2 (BIF2), grassy tillers1) (<https://www.gephbase.org/search-criteria/?or+Taxon+ID=%4577%and+Trait=Plant+architecture/or+Taxon+ID=%4577%and+Trait=Inflorescence+architecture/and+groupHaplotypes=true#gephbase-summary-title>)

Related Genes

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Pleiotropy

