

GEPHE SUMMARY

	Gephebase Gene	GephelD
grassy tillers1 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^grassy tillers1^#gephebase-summary-title)	GP00000414	Main curator
	Entry Status	Martin
Published		

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category=^Morphology^#gephebase-summary-title)	Trait	
Plant architecture (number of ears) (https://www.gephebase.org/search-criteria/?and+Trait=^Plant architecture (number of ears)^#gephebase-summary-title)	Trait State in Taxon A	
Zea mays ssp. mexicana (teosinthe)	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		Taxon B
Zea mays	Latin Name	Latin Name
(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	Synonyms
	Rank	Rank
	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		
Zea () - (Rank: genus)	Parent	Parent
(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. mexicana (teosinthe)	Zea mays ssp. mays	

GENOTYPIC CHANGE

gt1	Generic Gene Name	UniProtKB Zea mays subsp. mays
-	Synonyms	GenebankID or UniProtKB
-	String	
-	Sequence Similarities	
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)	GO - Molecular Function	
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)		
GO:0048450 : floral organ structural organization (https://www.ebi.ac.uk/QuickGO/term/GO:0048450)	GO - Biological Process	

GO:2000032 : regulation of secondary shoot formation
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000032>)

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

unknown but narrow 2.7kb interval

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title>)

Main Reference

From many, one: genetic control of prolificacy during maize domestication. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23825971>)

Authors

Wills DM; Whipple CJ; Takuno S; Kursel LE; Shannon LM; Ross-Ibarra J; Doebley JF

Abstract

A reduction in number and an increase in size of inflorescences is a common aspect of plant domestication. When maize was domesticated from teosinte, the number and arrangement of ears changed dramatically. Teosinte has long lateral branches that bear multiple small ears at their nodes and tassels at their tips. Maize has much shorter lateral branches that are tipped by a single large ear with no additional ears at the branch nodes. To investigate the genetic basis of this difference in prolificacy (the number of ears on a plant), we performed a genome-wide QTL scan. A large effect QTL for prolificacy (*prol1.1*) was detected on the short arm of chromosome 1 in a location that has previously been shown to influence multiple domestication traits. We fine-mapped *prol1.1* to a 2.7 kb "causative region" upstream of the *grassy tillers1 (gt1)* gene, which encodes a homeodomain leucine zipper transcription factor. Tissue *in situ* hybridizations reveal that the maize allele of *prol1.1* is associated with up-regulation of *gt1* expression in the nodal plexus. Given that maize does not initiate secondary ear buds, the expression of *gt1* in the nodal plexus in maize may suppress their initiation. Population genetic analyses indicate positive selection on the maize allele of *prol1.1*, causing a partial sweep that fixed the maize allele throughout most of domesticated maize. This work shows how a subtle cis-regulatory change in tissue specific gene expression altered plant architecture in a way that improved the harvestability of maize.

Additional References

RELATED GEPHE

Related Genes

2 (Barren inflorescence2 (BIF2), teosinte branched 1 (tb1)) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4577^/and+Trait=Plant+architecture/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS