

GEPHE SUMMARY

	Gephebase Gene	GephelD
Brassinosteroid-deficient dwarf1 (brd1) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=Brassinosteroid-deficient dwarf1 (brd1)^#gephebase-summary-title)	GP00001628	Main curator
	Prigent	
	Entry Status	
Published		

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category=Morphology^#gephebase-summary-title)	Trait	
Plant size (height) (https://www.gephebase.org/search-criteria/?and+Trait=^Plant size (height)^#gephebase-summary-title)	Trait State in Taxon A	
Maize parental line B73	Trait State in Taxon B	
Maize alternative parent	Ancestral State	
Unknown	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=Intraspecific^#gephebase-summary-title)		
Taxon A		Taxon B
Zea mays (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)	Latin Name	Latin Name
-	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; Viridiplanteae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea		
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)	Parent	Parent
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)	NCBI Taxonomy ID	NCBI Taxonomy ID
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
Yes	Taxon A Description	Taxon B Description
Maize parental line B73	Maize alternative parent	

GENOTYPIC CHANGE

ZEAMMB73_Zm00001d033180	Generic Gene Name	UniProtKB Zea mays
	Synonyms	GenebankID or UniProtKB
ZEAMMB73_Zm00001d033180	String	
-	Sequence Similarities	
Belongs to the cytochrome P450 family.	GO - Molecular Function	
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)		
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)		
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)		
GO:0016705 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (https://www.ebi.ac.uk/QuickGO/term/GO:0016705)		

GO - Biological Process

GO:0007275 : multicellular organism development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)
 GO:0055114 : oxidation-reduction process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0055114>)
 GO:0016125 : sterol metabolic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016125>)
 GO:0010268 : brassinosteroid homeostasis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010268>)
 GO:0016132 : brassinosteroid biosynthetic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016132>)

GO - Cellular Component

-	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=^Unknown^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria/?and+Molecular+Type=^Unknown^#gephebase-summary-title)	Aberration Type
Unknown (https://www.gephebase.org/search-criteria/?and+Aberration+Type=^Unknown^#gephebase-summary-title)	Molecular Details of the Mutation
On chromosome 1 two C>T transitions reduce plant height in 18RIL families	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title)	Main Reference
The genetic architecture of maize height. (2014) (https://pubmed.ncbi.nlm.nih.gov/24514905)	Authors
Peiffer JA; Romay MC; Gore MA; Flint-Garcia SA; Zhang Z; Millard MJ; Gardner CA; McMullen MD; Holland JB; Bradbury PJ; Buckler ES	Abstract
Height is one of the most heritable and easily measured traits in maize (<i>Zea mays</i> L.). Given a pedigree or estimates of the genomic identity-by-state among related plants, height is also accurately predictable. But, mapping alleles explaining natural variation in maize height remains a formidable challenge. To address this challenge, we measured the plant height, ear height, flowering time, and node counts of plants grown in >64,500 plots across 13 environments. These plots contained >7300 inbreds representing most publicly available maize inbreds in the United States and families of the maize Nested Association Mapping (NAM) panel. Joint-linkage mapping of quantitative trait loci (QTL), fine mapping in near isogenic lines (NILs), genome-wide association studies (GWAS), and genomic best linear unbiased prediction (GBLUP) were performed. The heritability of maize height was estimated to be >90%. Mapping NAM family-nested QTL revealed the largest explained $2.1 \pm 0.9\%$ of height variation. The effects of two tropical alleles at this QTL were independently validated by fine mapping in NIL families. Several significant associations found by GWAS colocalized with established height loci, including brassinosteroid-deficient dwarf1, dwarf plant1, and semi-dwarf2. GBLUP explained >80% of height variation in the panels and outperformed bootstrap aggregation of family-nested QTL models in evaluations of prediction accuracy. These results revealed maize height was under strong genetic control and had a highly polygenic genetic architecture. They also showed that multiple models of genetic architecture differing in polygenicity and effect sizes can plausibly explain a population's variation in maize height, but they may vary in predictive efficacy.	Additional References

RELATED GEPHE

2 (Camta3, dwarf-8 (d8)) (https://www.gephebase.org/search-criteria/?or+Taxon+ID=^4577^/and+Trait=Plant+size/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS