

GEPHE SUMMARY

	Gephebase Gene		GepheID
Brassinosteroid-deficient dwarf1 (brd1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Brassinosteroid-deficient+dwarf1+(brd1)^#gephebase-summary-title)		GP00001628	Main curator
	Entry Status	Prigent	
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	
	Latin Name		Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Zea+mays^#gephebase-summary-title)		Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Zea+mays^#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Zea mays var. japonica; maize; Zea mays L.; Zea mays mays		Zea mays var. japonica; maize; Zea mays L.; Zea mays mays	
	Rank		Rank
species		species	
	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		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		Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)		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)		4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Maize parental line B73		Maize alternative parent	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Zea mays
ZEAMMB73_Zm00001d033180		A0A1D6KWT1 (http://www.uniprot.org/uniprot/A0A1D6KWT1)	GenebankID or UniProtKB
	Synonyms		
ZEAMMB73_Zm00001d033180		0	
	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

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<p>Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)</p> <p>Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)</p> <p>Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)</p> <p>On chromosome 1 two C>T transitions reduce plant height in 18RIL families</p> <p>Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)</p> <p>The genetic architecture of maize height. (2014) (https://pubmed.ncbi.nlm.nih.gov/24514905)</p> <p>Peiffer JA; Romay MC; Gore MA; Flint-Garcia SA; Zhang Z; Millard MJ; Gardner CA; McMullen MD; Holland JB; Bradbury PJ; Buckler ES</p> <p>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 publically 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 Å± 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.</p>	<p>Presumptive Null</p> <p>Molecular Type</p> <p>Aberration Type</p> <p>Molecular Details of the Mutation</p> <p>Experimental Evidence</p> <p>Main Reference</p> <p>Authors</p> <p>Abstract</p> <p>Additional References</p>
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RELATED GEPHE

<p>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)</p> <p>No matches found.</p>	<p>Related Genes</p> <p>Related Haplotypes</p>
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EXTERNAL LINKS

COMMENTS