GEPHE SUMMARY

Gephebase Gene
Brassinosteroid-deficient dwarf1 (brd1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Brassinosteroid-deficient dwarf1 (brd1)^#gephebase-summary-title)

GepheID
GP00001628

Entry Status
Published

Main curator
Prigent

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

Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)

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; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Maize parental line B73

Taxon B

Latin Name
Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zea mays^#gephebase-summary-title)

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; Andropogonodae; Andropogoneae; Tripsacinae; Zea

Parent
Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4575)

NCBI Taxonomy ID
4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4577)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Maize alternative parent

GENOTYPIC CHANGE

Generic Gene Name
ZEAMMB73_Zm00001d033180

Synonyms
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)

UniProtKB Zea mays
A0A1D6KWT1 (http://www.uniprot.org/uniprot/A0A1D6KWT1)

GenebankID or UniProtKB
()

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 (Zea mays 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 Â± 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

Related Genes

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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS