GEPHE SUMMARY

Gephebase Gene
Camta3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Camta3^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00001629

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 from NCRPIS diversity panel

Trait State in Taxon B
Maize from NCRPIS diversity panel

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 from NCRPIS diversity panel

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 from NCRPIS diversity panel

GENOTYPIC CHANGE

Generic Gene Name
CAMTA3

Synonyms
CALMODULIN-BINDING TRANSCRIPTION ACTIVATOR 3; CAMTA3; signal responsive 1; T26C19.4; T26C19_4; CMTA3; SARD3; SR1; At2g22300

String
3702.AT2G22300.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G22300.1)

Sequence Similarities
Belongs to the CAMTA family.

GO - Molecular Function
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)

UniProtKB Arabidopsis thaliana
Q8GSA7 (http://www.uniprot.org/uniprot/Q8GSA7)

GenebankID or UniProtKB
()

GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001077)
GO:0005516 : calmodulin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005516)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0042742 : defense response to bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0042742)
GO:0009409 : response to cold (https://www.ebi.ac.uk/QuickGO/term/GO:0009409)
GO:0050832 : defense response to fungus (https://www.ebi.ac.uk/QuickGO/term/GO:0050832)
GO:0070417 : cellular response to cold (https://www.ebi.ac.uk/QuickGO/term/GO:0070417)
GO:0010150 : leaf senescence (https://www.ebi.ac.uk/QuickGO/term/GO:0010150)
GO:1900367 : positive regulation of defense response to insect (https://www.ebi.ac.uk/QuickGO/term/GO:1900367)

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

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

C>T transition on chromosome 3

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association 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 (Brassinosteroid-deficient dwarf1 (brd1), 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