

GEPHE SUMMARY

<p>Camta3 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Camta3~#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001629</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)</p> <p>Plant size (height) (https://www.gephebase.org/search-criteria?/and+Trait=~Plant+size+(height)~#gephebase-summary-title)</p> <p>Maize from NCRPIS diversity panel</p> <p>Maize from NCRPIS diversity panel</p> <p>Unknown</p> <p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays~#gephebase-summary-title)</p> <p>Common Name</p> <p>-</p> <p>Synonyms</p> <p>Zea mays var. japonica; maize; Zea mays L.; Zea mays mays</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea</p> <p>Parent</p> <p>Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)</p> <p>NCBI Taxonomy ID</p> <p>4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Maize from NCRPIS diversity panel</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Zea mays (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Zea+mays~#gephebase-summary-title)</p> <p>Common Name</p> <p>-</p> <p>Synonyms</p> <p>Zea mays var. japonica; maize; Zea mays L.; Zea mays mays</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea</p> <p>Parent</p> <p>Zea () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4575)</p> <p>NCBI Taxonomy ID</p> <p>4577 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4577)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Maize from NCRPIS diversity panel</p>
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GENOTYPIC CHANGE

<p>CAMTA3</p> <p>CALMODULIN-BINDING TRANSCRIPTION ACTIVATOR 3; CAMTA3; signal responsive 1; T26C19.4; T26C19_4; CMTA3; SARD3; SR1; At2g22300</p> <p>3702.AT2G22300.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G22300.1)</p> <p>Belongs to the CAMTA family.</p> <p>GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)</p> <p>GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>Q8GSA7 (http://www.uniprot.org/uniprot/Q8GSA7)</p> <p>()</p> <p>UniProtKB Arabidopsis thaliana</p> <p>GenebankID or UniProtKB</p>
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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 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

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

