GEPHE SUMMARY

Gephebase Gene
dwarf-8 (d8) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^dwarf-8 (d8)^#gephebase-summary-title)

GepheID
GP00000241

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Plant size (dwarfism) (https://www.gephebase.org/search-criteria?/and+Trait=^Plant size (dwarfism)^#gephebase-summary-title)

Trait State in Taxon A
Zea mays

Trait State in Taxon B
Zea mays

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#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?
No

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?
No

GENOTYPIC CHANGE

Generic Gene Name
D8

Synonyms
-

String
4577.GRMZM2G144744_P01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4577.GRMZM2G144744_P01)

Sequence Similarities
Belongs to the GRAS family. DELLA subfamily.

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)
GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)

GO - Biological Process

UniProtKB Zea mays
Q9ST48 (http://www.uniprot.org/uniprot/Q9ST48)

GenebankID or UniProtKB
AJ242530 (https://www.ncbi.nlm.nih.gov/nuccore/AJ242530)

GO:0009740 : gibberellic acid mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0009740)
GO:2000377 : regulation of reactive oxygen species metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:2000377)
GO:0009737 : response to abscisic acid
(https://www.ebi.ac.uk/QuickGO/term/GO:0009737)
GO:2000033 : regulation of seed dormancy process
(https://www.ebi.ac.uk/QuickGO/term/GO:2000033)
GO:0042538 : hyperosmotic salinity response
(https://www.ebi.ac.uk/QuickGO/term/GO:0042538)
GO:0009867 : jasmonic acid mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0009867)
GO:0009938 : negative regulation of gibberellic acid mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0009938)
GO:0010187 : negative regulation of seed germination
(https://www.ebi.ac.uk/QuickGO/term/GO:0010187)
GO:0009723 : response to ethylene (https://www.ebi.ac.uk/QuickGO/term/GO:0009723)
GO:0009863 : salicylic acid mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0009863)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

100-999 bp

Molecular Details of the Mutation

330bp deletion to V84

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

'Green revolution' genes encode mutant gibberellin response modulators. (1999) (https://pubmed.ncbi.nlm.nih.gov/10421366)

Authors

Peng J; Richards DE; Hartley NM; Murphy GP; Devos KM; Flintham JE; Beales J; Fish LJ; Worland AJ; Pelica F; Sudhakar D; Christou P; Snape JW; Gale MD; Harberd NP

Abstract

World wheat grain yields increased substantially in the 1960s and 1970s because farmers rapidly adopted the new varieties and cultivation methods of the so-called 'green revolution'. The new varieties are shorter, increase grain yield at the expense of straw biomass, and are more resistant to damage by wind and rain. These wheats are short because they respond abnormally to the plant growth hormone gibberellin. This reduced response to gibberellin is conferred by mutant dwarfing alleles at one of two Reduced height-1 (Rht-B1 and Rht-D1) loci. Here we show that Rht-B1/Rht-D1 and maize dwarf-8 (d8) are orthologues of the Arabidopsis Gibberellin Insensitive (GAI) gene. These genes encode proteins that resemble nuclear transcription factors and contain an SH2-like domain, indicating that phosphotyrosine may participate in gibberellin signalling. Six different orthologous dwarfing mutant alleles encode proteins that are altered in a conserved amino-terminal gibberellin signalling domain. Transgenic rice plants containing a mutant GAI allele give reduced responses to gibberellin and are dwarfed, indicating that mutant GAI orthologues could be used to increase yield in a wide range of crop species.

Additional References

Maize adaptation to temperate climate: relationship between population structure and polymorphism in the Dwarf8 gene. (2006) (https://pubmed.ncbi.nlm.nih.gov/16415370)
Dwarf8 polymorphisms associate with variation in flowering time. (2001) (https://pubmed.ncbi.nlm.nih.gov/11431702)

RELATED GEPHE

Related Genes

2 (Brassinosteroid-deficient dwarf1 (brd1), Camta3) (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

Various mutant alleles (gai in Arabidopsis; Rht1 in sunflowers, and Rht-B1b/Rht-D1b in wheat) resembles the phenotypic effect of d8 described here: they act in a genetically dominant fashion and encode active (altered function) mutant products that decrease GA response and thus confer reduced height.