GEPHE SUMMARY

Gephebase Gene

Reduced height-D1 (RhtD1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Reduced height-D1 (RhtD1)^#gephebase-summary-title)

GepheID

GP00000966

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

Triticum aestivum

Trait State in Taxon B

Triticum aestivum -dwarf

Ancestral State

Data not curated

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Triticum aestivum^#gephebase-summary-title)

Common Name

bread wheat

Synonyms

Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivam; Triticum aestivum8

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum

Parent

Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4564)

NCBI Taxonomy ID

4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4565)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Triticum aestivum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Triticum aestivum^#gephebase-summary-title)

Common Name

bread wheat

Synonyms

Triticum aestivum subsp. aestivum; Triticum vulgare; bread wheat; Canadian hard winter wheat; common wheat; wheat; Triticum aestivum L.; Triticum vulgare L.; Triticum vulgare Vill., nom. illeg.; Tricum aestivum; Triticum aestivam; Triticum aestivum8

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum

Parent

Triticum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4564)

NCBI Taxonomy ID

4565 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4565)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Triticum aestivum -dwarf

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

UniProtKB Zea mays

Q9ST48 (http://www.uniprot.org/uniprot/Q9ST48)

GenebankID or UniProtKB

()

(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

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

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

E61*; GGA>TGA

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

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

RELATED GEPHE

Related Genes

1 (Reduced height-B1 (RhtB1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4565^/and+Trait=Plant size/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Various mutant alleles (gai in Arabidopsis; D8 in maize, and Rht1 in sunflowers) resembles the phenotypic effect of Rht1 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.