

GEPHE SUMMARY

Gephebase Gene		GepheID
dwarf-8 (d8) (<a +dwarf-8+(d8)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+dwarf-8+(d8)+"#gephebase-summary-title)	GP00000241	
Entry Status		Main curator
Published		

PHENOTYPIC CHANGE

Trait Category	
Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)	
Trait	
Plant size (dwarfism) (<a +plant+size+(dwarfism)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)	
Taxon A	
Taxon B	
Latin Name	
Zea mays (<a +zea+mays+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 Intraspecies?	
No	

Taxon B	
Latin Name	
Zea mays (<a +zea+mays+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 Intraspecies?	
No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Zea mays
D8	Q9ST48 (http://www.uniprot.org/uniprot/Q9ST48)	
Synonyms		GenebankID or UniProtKB
-		AJ242530 (https://www.ncbi.nlm.nih.gov/nucleotide/AJ242530)
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		

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	
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence
‘Green revolution’ genes encode mutant gibberellin response modulators. (1999) (https://pubmed.ncbi.nlm.nih.gov/10421366)	Main Reference
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	Authors
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.	Abstract
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)	Additional References

RELATED GEPHE

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 Genes
No matches found.	Related Haplotypes

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.

