

GEPHE SUMMARY

	Gephebase Gene		GepheID
Reduced height-1 (Rht1) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00001728	
Gephebase="Reduced height-1 (Rht1)"#gephebase-summary-title)			Main curator
	Entry Status	Courtier	
Published			

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		
normal height			
	Trait State in Taxon B		
dwarf			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic)			
Status="Domesticated"#gephebase-summary-title)			
	Taxon A	Taxon B	
	Latin Name		Latin Name
Helianthus annuus		Helianthus annuus	
(<a helianthus"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Helianthus)		(<a helianthus"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Helianthus)	
annuus"#gephebase-summary-title)		annuus"#gephebase-summary-title)	
	Common Name		Common Name
common sunflower		common sunflower	
	Synonyms		Synonyms
common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annuus; Helianthus annuus8		common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annuus; Helianthus annuus8	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Heliantheae; Helianthus		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Heliantheae; Helianthus	
	Parent		Parent
Helianthus () - (Rank: genus)		Helianthus () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4231)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4231)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4232		4232	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4232)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4232)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
			Sunflower (Helianthus annuus L. var. macrocarpus Ckll.) var. DDR

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Zea mays
D8		Q9ST48 (http://www.uniprot.org/uniprot/Q9ST48)	
	Synonyms		GenebankID or UniProtKB
-		0	
	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](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type+=^SNP^#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

T-to-C transition corresponding to nucleotide positions 143 - the SNP at position 143 converts a leucine residue in a proline within the conserved DELLA motif. This amino acid position corresponds to amino acid position 57 in the full-length amino acid sequence encoded by the *L. sativa* DELLA1 nucleotide sequence of GenBank Accession No. BAG71200.1

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	143
Amino-acid	Pro	Leu	57

Main Reference

Phenotypic characterization, genetic mapping and candidate gene analysis of a source conferring reduced plant height in sunflower. (2013) (<https://pubmed.ncbi.nlm.nih.gov/22972203>)

Authors

Ramos ML; Altieri E; Bulos M; Sala CA

Abstract

Reduced height germplasm has the potential to increase stem strength, standability, and also yields potential of the sunflower crop (*Helianthus annuus* L. var. *macrocarpus* Ckll.). In this study, we report on the inheritance, mapping, phenotypic and molecular characterization of a reduced plant height trait in inbred lines derived from the source DDR. This trait is controlled by a semidominant allele, *Rht1*, which maps on linkage group 12 of the sunflower public consensus map. Phenotypic effects of this allele include shorter height and internode length, insensibility to exogenous gibberellin application, normal skotomorphogenetic response, and reduced seed set under self-pollination conditions. This later effect presumably is related to the reduced pollen viability observed in all DDR-derived lines studied. *Rht1* completely cosegregated with a haplotype of the *HaDella1* gene sequence. This haplotype consists of a point mutation converting a leucine residue in a proline within the conserved DELLA domain. Taken together, the phenotypic, genetic, and molecular results reported here indicate that *Rht1* in sunflower likely encodes an altered DELLA protein. If the DELPA motif of the *HaDella1* sequence in the *Rht1*-encoded protein determines by itself the observed reduction in height is a matter that remains to be investigated.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Various mutant alleles (gai in Arabidopsis; D8 in maize, and Rht-B1b/Rht-D1b in wheat) 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.