GEPHE SUMMARY

Gephebase Gene
Reduced height-1 (Rht1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Reduced height-1 (Rht1)^#gephebase-summary-title)

GepheID
GP00001728

Entry Status
Published

Main curator
Courtier

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

Latin Name
Helianthus annuus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Helianthus annuus^#gephebase-summary-title)

Common Name
common sunflower

Synonyms
common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annus; Helianthus annuus8

Rank
species

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

Parent
Helianthus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4231)

NCBI Taxonomy ID
4232 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4232)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Helianthus annuus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Helianthus annuus^#gephebase-summary-title)

Common Name
common sunflower

Synonyms
common sunflower; Helianthus annuus L.; Helianthus annua; Helianthus annus; Helianthus annuus8

Rank
species

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

Parent
Helianthus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4231)

NCBI Taxonomy ID
4232 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4232)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Sunflower (Helianthus annuus L. var. macrocarpus Ckll.) var. DDR

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)

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

GenebankID or UniProtKB
()

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

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 motifâ€"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)

	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.