GEPHE SUMMARY

Gephebase Gene
Beta-glucosidase6 (BGLU6) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Beta-glucosidase6 (BGLU6)^#gephebase-summary-title)

GepheID
GP00001266

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

Trait
Resistance to UV irradiation (flavonol glycosylation) (https://www.gephebase.org/search-criteria?/and+Trait=^Resistance to UV irradiation (flavonol glycosylation)^#gephebase-summary-title)

Trait State in Taxon A
Arabidopsis thaliana- Ler0

Trait State in Taxon B
Arabidopsis thaliana- Bor-4; Se-0; Uod-1; and Zdr-1

Ancestral State
Taxon A

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

Taxon A

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

Common Name
thale cress

Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Arabidopsis thaliana- Ler0

Taxon B

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

Common Name
thale cress

Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)

NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Arabidopsis thaliana- Bor-4; Se-0; Uod-1; and Zdr-1

GENOTYPIC CHANGE

Generic Gene Name
BGLU6

Synonyms
beta glucosidase 6; T13D8.16; T13D8_16; At1g60270

String
3702.AT1G60270.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G60270.1)

Sequence Similarities
Belongs to the glycosyl hydrolase 1 family.

GO - Molecular Function
GO:0008422 : beta-glucosidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008422)
GO:0102483 : scopolin beta-glucosidase activity

UniProtKB Arabidopsis thaliana
Q682B4 (http://www.uniprot.org/uniprot/Q682B4)

GenebankID or UniProtKB
3767579 (https://www.ncbi.nlm.nih.gov/nuccore/3767579)

(https://www.ebi.ac.uk/QuickGO/term/GO:0102483)

GO - Biological Process

GO:0005975 : carbohydrate metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0005975)

GO - Cellular Component

-

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

1-9 bp

Molecular Details of the Mutation

A deletion of one nucleotide in the seventh exon (BGLU6 CDS position 678) results in a premature stop codon in the accessions Bor-4, Se-0, Uod-1, and Zdr-1. premature stop codon

Experimental Evidence

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

Main Reference

Natural variation in flavonol accumulation in Arabidopsis is determined by the flavonol glucosyltransferase BGLU6. (2016) (https://pubmed.ncbi.nlm.nih.gov/26717955)

Authors

Ishihara H; Tohge T; ViehÃ¶ver P; Fernie AR; Weisshaar B; Stracke R

Abstract

Flavonols are colourless secondary metabolites, primarily regarded as UV-protection pigments that are deposited in plants in their glycosylated forms. The glycosylation of flavonols is mainly catalysed by UDP-sugar-dependent glycosyltransferases (UGTs). Although the structures of flavonol glycosides accumulating in Arabidopsis thaliana are known, many genes involved in the ï¬,avonol glycosylation pathway are yet to be discovered. The flavonol glycoside profiles of seedlings from 81 naturally occurring A. thaliana accessions were screened using high performance thin layer chromatography. A qualitative variation in flavonol 3-O-gentiobioside 7-O-rhamnoside (F3GG7R) content was identified. Ler Ã— Col-0 recombinant inbred line mapping and whole genome association mapping led to the identification of a glycoside hydrolase family 1-type gene, At1g60270/BGLU6, that encodes a homolog of acyl-glucose-dependent glucosyltransferases involved in the glycosylation of anthocyanins, possibly localized in the cytoplasm, and that is co-expressed with genes linked to phenylpropanoid biosynthesis. A causal single nucleotide polymorphism introducing a premature stop codon in non-producer accessions was found to be absent in the producers. Several other naturally occurring loss-of-function alleles were also identified. Two independent bglu6 T-DNA insertion mutants from the producer accessions showed loss of F3GG7R. Furthermore, bglu6 mutant lines complemented with the genomic Ler BGLU6 gene confirmed that BGLU6 is essential for production of F3GGR7. We have thus identified an accession-specific gene that causes a qualitative difference in flavonol glycoside accumulation in A. thaliana strains. This gene encodes a flavonol 3-O-glucoside: 6â€³-O-glucosyltransferase that does not belong to the large canonical family of flavonol glycosyltransferases that use UDP-conjugates as the activated sugar donor substrate.

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Additional References

The genetics of plant metabolism. (2006) (https://pubmed.ncbi.nlm.nih.gov/16751770)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

4 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Beta-glucosidase6 (BGLU6)^/and+Taxon ID=^3702^/or+Gene Gephebase=^Beta-glucosidase6 (BGLU6)^/and+Taxon ID=^3702^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Vast gene region previously detected in two QTL papers; QTL + mapping