

## GEPHE SUMMARY

**Gephebase Gene**  
Beta-glucosidase6 (BGLU6)

**Entry Status**  
Published

**GepheID**  
GP00001265

**Main curator**  
Arnout

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Resistance to UV irradiation (flavonol glycosylation)

**Trait State in Taxon A**  
Arabidopsis thaliana- Ler0

**Trait State in Taxon B**  
Arabidopsis thaliana- Cvi

**Ancestral State**  
Data not curated

**Taxonomic Status**  
Intraspecific

**Taxon A**

**Latin Name**  
*Arabidopsis thaliana*

**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)

**NCBI Taxonomy ID**  
3702

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Arabidopsis thaliana- Ler0

**Taxon B**

**Latin Name**  
*Arabidopsis thaliana*

**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)

**NCBI Taxonomy ID**  
3702

**is Taxon B an Intraspecies?**  
Yes

**Taxon B Description**  
Arabidopsis thaliana- Cvi

## GENOTYPIC CHANGE

**Generic Gene Name**  
BGLU6

**Synonyms**  
beta glucosidase 6; T13D8.16; T13D8\_16; At1g60270

**String**  
3702.AT1G60270.1

**Sequence Similarities**  
Belongs to the glycosyl hydrolase 1 family.

**GO - Molecular Function**  
GO:0008422 : beta-glucosidase activity  
GO:0102483 : scopolin beta-glucosidase activity

**GO - Biological Process**  
GO:0005975 : carbohydrate metabolic process

**GO - Cellular Component**  
-

**UniProtKB Arabidopsis thaliana**  
Q682B4

**GenebankID or UniProtKB**  
3767579

#### Presumptive Null

Yes

#### Molecular Type

Coding

#### Aberration Type

SNP

#### SNP Coding Change

Nonsense

#### Molecular Details of the Mutation

GAG to stop codon TAG at position 913

#### Experimental Evidence

Linkage Mapping

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

#### Main Reference

Natural variation in flavonol accumulation in Arabidopsis is determined by the flavonol glucosyltransferase BGLU6. (2016)

#### Authors

Ishihara H; Tohge T; Viehöver 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 flavonol 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 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 glycosyltransferases 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 F3GG7R. 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: 6-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)

## RELATED GEPHE

#### Related Genes

No matches found.

#### Related Haplotypes

4

## EXTERNAL LINKS

## COMMENTS

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