

## GEPHE SUMMARY

**Gephebase Gene**  
GLABROUS1

**Entry Status**  
Published

**GepheID**  
GP00001241

**Main curator**  
Arnout

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

**Trait**  
Trichome density (leaf)

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

**Trait State in Taxon B**  
Arabidopsis thaliana Mir-0; Br-0 - Glabrous

**Ancestral State**  
Taxon A

**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- Colo

### 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 Mir-0; Br-0

## GENOTYPIC CHANGE

**Generic Gene Name**  
GL1

**Synonyms**  
ATGL1; ATMYB0; GL1; GLABRA 1; myb domain protein 0; TRICHOME DIFFERENTIATION PROTEIN GL1; MYB0; At3g27920; K16N12.17

**String**  
3702.AT3G27920.1

**Sequence Similarities**  
-

**GO - Molecular Function**  
GO:0003700 : DNA-binding transcription factor activity  
GO:0043565 : sequence-specific DNA binding  
GO:0044212 : transcription regulatory region DNA binding  
GO:0003677 : DNA binding

**GO - Biological Process**  
GO:0030154 : cell differentiation

**UniProtKB Arabidopsis thaliana**  
P27900

**GenebankID or UniProtKB**  
ABD65321

GO:0009740 : gibberellic acid mediated signaling pathway  
GO:0001708 : cell fate specification  
GO:0009867 : jasmonic acid mediated signaling pathway  
GO:0010026 : trichome differentiation  
GO:0032880 : regulation of protein localization  
GO:2000039 : regulation of trichome morphogenesis  
GO:0048629 : trichome patterning

GO - Cellular Component  
GO:0005634 : nucleus

Presumptive Null  
Yes

Molecular Type  
Coding

Aberration Type  
Deletion

Deletion Size  
1-9 bp

Molecular Details of the Mutation  
-1bp at position 203 causing premature stop

Experimental Evidence  
Candidate Gene

Main Reference  
Trichome distribution in *Arabidopsis thaliana* and its close relative *Arabidopsis lyrata*: molecular analysis of the candidate gene *GLABROUS1*. (2001)

Authors  
Hauser MT; Harr B; Schläpffer C

Abstract  
GLABROUS1 (GL1) belongs to the large family of MYB transcription factors and is known to play a central role in trichome initiation. We studied trichome distribution and the molecular variation of GL1 in 28 *A. thaliana* accessions. Trichome density on rosette leaves was highly variable among those accessions. On the molecular level, we detected substantial sequence variation in a 3-kb fragment which included the complete coding region of the GL1 locus ( $\pi = 0.01$ ). Phylogenetic analysis of GL1 indicates the presence of two diverged clades among 28 accessions. Using ANOVA, we show that the phenotypic variation in trichome density cannot be explained by the sequence divergence between the two phylogenetic lineages. Sequence analysis of wild-type *Arabidopsis thaliana* and *Arabidopsis lyrata* accessions indicates that all amino acid substitutions are located outside of the conserved helix-turn-helix DNA-binding domains R2 and R3. Using plants of *A. thaliana* and *A. lyrata* with either naturally occurring or ethyl methane sulfonate--induced glabrous phenotypes, we demonstrate that the last 14 C-terminal amino acids of the GL1 gene have no major impact on the initiation of trichomes.

Additional References  
Trichome distribution in *Arabidopsis thaliana* and its close relative *Arabidopsis lyrata*: molecular analysis of the candidate gene *GLABROUS1*. (2001)

## RELATED GEPHE

Related Genes  
2 (AtMYC1, ETC2)  
Related Haplotypes  
4

## COMMENTS

Based on previous mappings showing the involvement of GL1 locus on trichome density; complementation test with glabrous mutant