

## GEPHE SUMMARY

**Gephebase Gene**  
APSR

**Entry Status**  
Published

**GepheID**  
GP00000100

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Sulfate content (shoot)

**Trait State in Taxon A**  
Arabidopsis thaliana- Bay-0

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

**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- Bay-0

### 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- Shahdara

## GENOTYPIC CHANGE

**Generic Gene Name**  
APR2

**Synonyms**  
3'-PHOSPHOADENOSINE-5'-PHOSPHOSULFATE (PAPS) REDUCTASE HOMOLOG 43; 5'adenylylphosphosulfate reductase 2; ADENOSINE-5'-PHOSPHOSULFATE REDUCTASE; APS REDUCTASE; APSR; ATAPR2; F19K23.11; F19K23\_11; PRH; PRH43; At1g62180

**String**  
3702.AT1G62180.1

**Sequence Similarities**  
Belongs to the APS reductase family.

**GO - Molecular Function**  
GO:0033741 : adenylyl-sulfate reductase (glutathione) activity  
GO:0009973 : adenylyl-sulfate reductase activity  
GO:0004604 : phosphoadenylyl-sulfate reductase (thioredoxin) activity

**GO - Biological Process**

**UniProtKB Arabidopsis thaliana**  
P92981

**GenebankID or UniProtKB**  
AF016283

GO:0045454 : cell redox homeostasis  
GO:0019344 : cysteine biosynthetic process  
GO:0000103 : sulfate assimilation  
GO:0019379 : sulfate assimilation, phosphoadenylyl sulfate reduction by phosphoadenylyl-sulfate reductase (thioredoxin)

GO - Cellular Component  
GO:0009507 : chloroplast  
GO:0009570 : chloroplast stroma

#### Presumptive Null

Yes

#### Molecular Type

Coding

#### Aberration Type

SNP

#### SNP Coding Change

Nonsynonymous

#### Molecular Details of the Mutation

A399E

#### Experimental Evidence

Linkage Mapping

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

#### Main Reference

Natural variation for sulfate content in *Arabidopsis thaliana* is highly controlled by *APR2*. (2007)

#### Authors

Loudet O; Saliba-Colombani V; Camilleri C; Calenge F; Gaudon V; Koprivova A; North KA; Kopriva S; Daniel-Vedele F

#### Abstract

Most agronomic traits of importance, whether physiological (such as nutrient use efficiency) or developmental (such as flowering time), are controlled simultaneously by multiple genes and their interactions with the environment. Here, we show that variation in sulfate content between wild *Arabidopsis thaliana* accessions Bay-0 and Shahdara is controlled by a major quantitative trait locus that results in a strong interaction with nitrogen availability in the soil. Combining genetic and biochemical results and using a candidate gene approach, we have cloned the underlying gene, showing how a single-amino acid substitution in a key enzyme of the assimilatory sulfate reduction pathway, adenosine 5'-phosphosulfate reductase, is responsible for a decrease in enzyme activity, leading to sulfate accumulation in the plant. This work illustrates the potential of natural variation as a source of new alleles of known genes, which can aid in the study of gene function and metabolic pathway regulation. Our new insights on sulfate assimilation may have an impact on sulfur fertilizer use and stress defense improvement.

#### Additional References

## RELATED GEPHE

#### Related Genes

No matches found.

#### Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@GxE

