

## GEPHE SUMMARY

### Gephebase Gene

RDO5 REDUCED DORMANCY5

### Entry Status

Published

### GepheID

GP00001259

### Main curator

Courtier

## PHENOTYPIC CHANGE

### Trait Category

Physiology

### Trait

Seed dormancy

### Trait State in Taxon A

Arabidopsis thaliana- Ler0

### Trait State in Taxon B

Arabidopsis thaliana- Kas-2

### 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- Kas-2

## GENOTYPIC CHANGE

### Generic Gene Name

At4g11040

### Synonyms

RDO5; REDUCED DORMANCY 5; T22B4.20; T22B4\_20; At4g11040; F8M12.14

### String

3702.AT4G11040.1

### Sequence Similarities

Belongs to the PP2C family.

### GO - Molecular Function

GO:0046872 : metal ion binding

GO:0004721 : phosphoprotein phosphatase activity

GO:0004722 : protein serine/threonine phosphatase activity

GO:0001691 : pseudophosphatase activity

### GO - Biological Process

GO:0010162 : seed dormancy process

GO:1902040 : positive regulation of seed dormancy process

### UniProtKB Arabidopsis thaliana

Q9T010

### GenebankID or UniProtKB

826705

GO - Cellular Component  
GO:0005634 : nucleus

Presumptive Null  
Yes

Molecular Type  
Coding

Aberration Type  
SNP

SNP Coding Change  
Nonsynonymous

#### Molecular Details of the Mutation

4 amino acid changes: N45K; G54R; T55K; E208A - the effect of each single amino acid change has not been tested

#### Experimental Evidence

Linkage Mapping

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

#### Main Reference

Sequence Polymorphisms at the REDUCED DORMANCY5 Pseudophosphatase Underlie Natural Variation in Arabidopsis Dormancy. (2016)

#### Authors

Xiang Y; Song B; NÄ©e G; Kramer K; Finkemeier I; Soppe WJ

#### Abstract

Seed dormancy controls the timing of germination, which regulates the adaptation of plants to their environment and influences agricultural production. The time of germination is under strong natural selection and shows variation within species due to local adaptation. The identification of genes underlying dormancy quantitative trait loci is a major scientific challenge, which is relevant for agricultural and ecological goals. In this study, we describe the identification of the DELAY OF GERMINATION18 (DOG18) quantitative trait locus, which was identified as a factor in natural variation for seed dormancy in Arabidopsis (*Arabidopsis thaliana*). DOG18 encodes a member of the clade A of the type 2C protein phosphatases family, which we previously identified as the REDUCED DORMANCY5 (RDO5) gene. DOG18/RDO5 shows a relatively high frequency of loss-of-function alleles in natural accessions restricted to northwestern Europe. The loss of dormancy in these loss-of-function alleles can be compensated for by genetic factors like DOG1 and DOG6, and by environmental factors such as low temperature. RDO5 does not have detectable phosphatase activity. Analysis of the phosphoproteome in dry and imbibed seeds revealed a general decrease in protein phosphorylation during seed imbibition that is enhanced in the *rdo5* mutant. We conclude that RDO5 acts as a pseudophosphatase that inhibits dephosphorylation during seed imbibition.

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#### Additional References

Natural variation for seed dormancy in Arabidopsis is regulated by additive genetic and molecular pathways. (2010)

## RELATED GEPHE

#### Related Genes

2 (D14 (KAI2 paralogs), DOG1 (DELAY OF GERMINATION 1))

#### Related Haplotypes

15

## EXTERNAL LINKS

## COMMENTS

@SeveralCandidateMutations ; Previously detected by QTL by 20145108 and as a mutant by 25415980