GEPHE SUMMARY

Gephebase Gene

RDO5 REDUCED DORMANCY5 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RDO5 REDUCED DORMANCY5^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001251

Main curator

Arnoult

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Arabidopsis thaliana- Ler0

Trait State in Taxon B

Arabidopsis thaliana TueWa1-2

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 TueWa1-2

GENOTYPIC CHANGE

Generic Gene Name

At4g11040

Synonyms

RDO5; REDUCED DORMANCY 5; T22B4.20; T22B4_20; At4g11040; F8M12.14

String

3702.AT4G11040.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT4G11040.1)

Sequence Similarities

Belongs to the PP2C family.

GO - Molecular Function

GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0004721 : phosphoprotein phosphatase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004721)

UniProtKB Arabidopsis thaliana

Q9T010 (http://www.uniprot.org/uniprot/Q9T010)

GenebankID or UniProtKB

826705 (https://www.ncbi.nlm.nih.gov/nuccore/826705)

GO:0004722 : protein serine/threonine phosphatase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004722)
GO:0001691 : pseudophosphatase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0001691)

GO - Biological Process

GO:0010162 : seed dormancy process
(https://www.ebi.ac.uk/QuickGO/term/GO:0010162)
GO:1902040 : positive regulation of seed dormancy process
(https://www.ebi.ac.uk/QuickGO/term/GO:1902040)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

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

10-99 bp

Molecular Details of the Mutation

-13bp at position 1440

Experimental Evidence

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

Main Reference

Sequence Polymorphisms at the REDUCED DORMANCY5 Pseudophosphatase Underlie Natural Variation in Arabidopsis Dormancy. (2016) (https://pubmed.ncbi.nlm.nih.gov/27288362)

Authors

Xiang Y; Song B; NÃ©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) (https://pubmed.ncbi.nlm.nih.gov/20145108)

RELATED GEPHE

Related Genes

2 (D14 (KAI2 paralog), DOG1 (DELAY OF GERMINATION 1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Seed dormancy/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

15 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^RDO5 REDUCED DORMANCY5^/and+Taxon ID=^3702^/or+Gene Gephebase=^RDO5 REDUCED DORMANCY5^/and+Taxon ID=^3702^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

predicted phenotypic effect