

GEPHE SUMMARY

<p>RDO5 REDUCED DORMANCY5 (#https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=RDO5+REDUCED+DORMANCY5)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00001257</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology)</p> <p>Seed dormancy (#https://www.gephebase.org/search-criteria?/and+Trait=Seed+dormancy)</p> <p>Arabidopsis thaliana- Ler0</p> <p>Arabidopsis thaliana Sp_0</p> <p>Taxon A</p> <p>Intraspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Intraspecific)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Arabidopsis thaliana (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Arabidopsis+thaliana)</p> <p>thale cress</p> <p>thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress</p> <p>species</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis</p> <p>Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)</p> <p>3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)</p> <p>Yes</p> <p>Arabidopsis thaliana- Ler0</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p> <p>Taxon A Description</p>	<p>Arabidopsis thaliana (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Arabidopsis+thaliana)</p> <p>thale cress</p> <p>thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress</p> <p>species</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis</p> <p>Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)</p> <p>3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)</p> <p>Yes</p> <p>Arabidopsis thaliana Sp_0</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>
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GENOTYPIC CHANGE

<p>At4g11040</p> <p>RDO5; REDUCED DORMANCY 5; T22B4.20; T22B4_20; At4g11040; F8M12.14</p> <p>3702.AT4G11040.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G11040.1)</p> <p>Belongs to the PP2C family.</p> <p>GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)</p> <p>GO:0004721 : phosphoprotein phosphatase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004721)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>Q9T010 (http://www.uniprot.org/uniprot/Q9T010)</p> <p>826705 (https://www.ncbi.nlm.nih.gov/nuccore/826705)</p> <p>UniProtKB Arabidopsis thaliana</p> <p>GenebankID or UniProtKB</p>
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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](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion~#gephebase-summary-title))

Deletion Size

1-9 bp

Molecular Details of the Mutation

-4bp at position 11

Experimental Evidence

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

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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 paralogue), 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](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](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