

GEPHE SUMMARY

	Gephebase Gene		GepheID
RDO5 REDUCED DORMANCY5 (<a +rdo5+reduced+dormancy5+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+RDO5+REDUCED+DORMANCY5+"#gephebase-summary-title)		GP00001246	
	Entry Status	Arnoult	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Seed dormancy (<a +seed+dormancy+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 Boot-1			
	Ancestral State		
Data not curated		Taxonomic Status	
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Arabidopsis thaliana (<a +arabidopsis+thaliana+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Arabidopsis+thaliana+"#gephebase-summary-title)		Arabidopsis thaliana (<a +arabidopsis+thaliana+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Arabidopsis+thaliana+"#gephebase-summary-title)	
	Common Name		Common Name
thale cress		thale cress	
	Synonyms		Synonyms
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
	Parent		Parent
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Arabidopsis thaliana- Ler0		Arabidopsis thaliana Boot-1	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Arabidopsis thaliana
At4g11040		Q9T010 (http://www.uniprot.org/uniprot/Q9T010)	
	Synonyms		GenebankID or UniProtKB
RDO5; REDUCED DORMANCY 5; T22B4.20; T22B4_20; At4g11040; F8M12.14		826705 (https://www.ncbi.nlm.nih.gov/nuccore/826705)	
	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)			

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

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

G892A

Experimental Evidence

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

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

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 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

necessary for natural variation

