

GEPHE SUMMARY

	Gephebase Gene	GepheID
Phosphate transporter PHO1 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^Phosphate transporter PHO1^#gephebase-summary-title)	GP00001284	
Published	Entry Status	Main curator

PHENOTYPIC CHANGE

	Trait Category
Morphology (https://www.gephebase.org/search-criteria/?and+Trait Category=Morphology^#gephebase-summary-title)	Trait
Root growth (allometry of lateral roots) (https://www.gephebase.org/search-criteria/?and+Trait=^Root+growth+(allometry+of+lateral+roots)^#gephebase-summary-title)	Trait State in Taxon A
Arabidopsis thaliana- 69 accessions	Trait State in Taxon B
Arabidopsis thaliana- 69 accessions	Ancestral State
Unknown	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis+thaliana^#gephebase-summary-title)	Common 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	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	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis		cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent	Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	NCBI Taxonomy ID	3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	NCBI Taxonomy ID
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
PHO1		
ARABIDOPSIS PHOSPHATE 1; ATPHO1; phosphate 1; At3g23430; MLM24.26	String	GenebankID or UniProtKB
3702.AT3G23430.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT3G23430.1)	Sequence Similarities	821924 (https://www.ncbi.nlm.nih.gov/nucore/821924)
Belongs to the SYG1 (TC 2.A.94) family.	GO - Molecular Function	
GO:0000822 : inositol hexakisphosphate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000822)		
GO:0015114 : phosphate ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015114)		
GO:0016036 : cellular response to phosphate starvation	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016036>)

GO:0048016 : inositol phosphate-mediated signaling

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048016>)

GO:0006817 : phosphate ion transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006817>)

GO:0006799 : polyphosphate biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006799>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)

GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)

GO:0005789 : endoplasmic reticulum membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

GO:0005802 : trans-Golgi network (<https://www.ebi.ac.uk/QuickGO/term/GO:0005802>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

histidine to tyrosine @position 8388425 in chromosome III

Experimental Evidence

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

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

Main Reference

Integration of responses within and across *Arabidopsis* natural accessions uncovers loci controlling root systems architecture. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23980140>)

Authors

Rosas U; Cibrian-Jaramillo A; Ristova D; Banta JA; Gifford ML; Fan AH; Zhou RW; Kim GJ; Krout G; Birnbaum KD; Purugganan MD; Coruzzi GM

Abstract

Phenotypic plasticity is presumed to be involved in adaptive change toward species diversification. We thus examined how candidate genes underlying natural variation across populations might also mediate plasticity within an individual. Our implementation of an integrative “plasticity space” approach revealed that the root plasticity of a single *Arabidopsis* accession exposed to distinct environments broadly recapitulates the natural variation “space.” Genome-wide association mapping identified the known gene PHOSPHATE 1 (PHO1) and other genes such as Root System Architecture 1 (RSA1) associated with differences in root allometry, a highly plastic trait capturing the distribution of lateral roots along the primary axis. The response of mutants in the Columbia-0 background suggests their involvement in signaling key modulators of root development including auxin, abscisic acid, and nitrate. Moreover, genotype-by-environment interactions for the PHO1 and RSA1 genes in Columbia-0 phenocopy the root allometry of other natural variants. This finding supports a role for plasticity responses in phenotypic evolution in natural environments.

Additional References

RELATED GEPHE

Related Genes

4 (AZI1, Brevis radix (BRX), ORGANIC CATION TRANSPORTER 1, Root System Architecture 1) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^3702/and+Trait=Root+growth/and+groupHaplotypes=true))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE - no strong demonstration of the putative causal SNP; natural variation between accessions recapitulates phenotypic plasticity in Col-0

