

GEPHE SUMMARY

	Gephebase Gene	GepheID
Root System Architecture 1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Root+System+Architecture+1^#gephebase-summary-title)	GP00001285	
	Entry Status	Main curator
Published	Arnoult	

PHENOTYPIC CHANGE

	Trait Category		Trait
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)			
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		Taxon B	
	Latin Name		Latin Name
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Arabidopsis+thaliana^#gephebase-summary-title)		Arabidopsis thaliana (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; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; 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 Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
Root System Architecture 1	F4JL94 (http://www.uniprot.org/uniprot/F4JL94)	
	Synonyms	GenebankID or UniProtKB
F2O09.90; F2O09_90; Root System Architecture 1; RSA1; At4g28410	828958 (https://www.ncbi.nlm.nih.gov/nuccore/828958)	
	String	
3702.AT4G28410.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G28410.1)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0030170 : pyridoxal phosphate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030170)		
GO:0008483 : transaminase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008483)		
	GO - Biological Process	
GO:0009058 : biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009058)		
GO:0006520 : cellular amino acid metabolic process		

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

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

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

348bp upstream of the 5'UTR

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

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

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

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

4 (AZI1, Brevis radix (BRX), ORGANIC CATION TRANSPORTER 1, Phosphate transporter PHO1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Root growth/and+groupHaplotypes=true#gephebase-summary-title>)

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