

GEPHE SUMMARY

Brevis radix (BRX) (https://www.gephebase.org/search-criteria/?and+Gene	Gephebase Gene	GP00001262	GephelD
Gephebase=^Brevis radix (BRX)^#gephebase-summary-title)			Main curator
Published	Entry Status	Arnoult	

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria/?and+Trait	Trait Category		
Category="Morphology">#gephebase-summary-title)			
Root growth (https://www.gephebase.org/search-criteria/?and+Trait=^Root	Trait		
growth#gephebase-summary-title)			
Arabidopsis thaliana- Eil0	Trait State in Taxon A		
Arabidopsis thaliana- Lov5; Lc-0; Kz-1; Pu2-; Ws-0	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic	Taxonomic Status		
Status="Intraspecific">#gephebase-summary-title)			
Arabidopsis thaliana	Taxon A	Taxon B	
(https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Arabidopsis	Latin Name		Latin Name
thaliana">#gephebase-summary-title)			
thale cress	Common Name		Common Name
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	Synonyms		Synonyms
species	Rank		Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	Lineage		Lineage
Arabidopsis () - (Rank: genus)	Parent		Parent
(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)			
Yes	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
Arabidopsis thaliana- Eil0	Taxon A Description		Taxon B Description

GENOTYPIC CHANGE

BRX	Generic Gene Name	UniProtKB Arabidopsis thaliana
BREVIS RADIX; F5M6_11; F5M6_11; NIP3;1; NLM9; NOD26-like intrinsic protein 3;1; At1g31880	Synonyms	Q17T15 (http://www.uniprot.org/uniprot/Q17T15)
3702.AT1G31880.1	String	GenebankID or UniProtKB
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT1G31880.1)		NM_102925 (https://www.ncbi.nlm.nih.gov/nuccore/NM_102925)
Belongs to the BRX family.	Sequence Similarities	
-	GO - Molecular Function	
GO:0009734 : auxin-activated signaling pathway	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009734>)
 GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
 GO:0048364 : root development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048364>)
 GO:0009736 : cytokinin-activated signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009736>)
 GO:0048527 : lateral root development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0048527>)
 GO:0010088 : phloem development (<https://www.ebi.ac.uk/QuickGO/term/GO:0010088>)
 GO:2000280 : regulation of root development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2000280>)
 GO:0009737 : response to abscisic acid
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009737>)

GO - Cellular Component

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

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

Deletion Size

10-99 bp Molecular Details of the Mutation

21bp deletion at position in spacer 3 (position not given)

Experimental Evidence

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

Main Reference

A hyperactive quantitative trait locus allele of *Arabidopsis* BRX contributes to natural variation in root growth vigor. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20404146>)

Authors

Beuchat J; Li S; Ragni L; Shindo C; Kohn MH; Hardtke CS

Abstract

Quantitative trait loci analysis of natural *Arabidopsis thaliana* accessions is increasingly exploited for gene isolation. However, to date this has mostly revealed deleterious mutations. Among them, a loss-of-function allele identified the root growth regulator BREVIS RADIX (BRX). Here we present evidence that BRX and the paralogous BRX-LIKE (BRXL) genes are under selective constraint in monocotyledons as well as dicotyledons. Unexpectedly, however, whereas none of the *Arabidopsis* orthologs except AtBRXL1 could complement brx null mutants when expressed constitutively, nearly all monocotyledon BRXLs tested could. Thus, BRXL proteins seem to be more diversified in dicotyledons than in monocotyledons. This functional diversification was correlated with accelerated rates of sequence divergence in the N-terminal regions. Population genetic analyses of 30 haplotypes are suggestive of an adaptive role of AtBRX and AtBRXL1. In two accessions, Lc-0 and Lov-5, seven amino acids are deleted in the variable region between the highly conserved C-terminal, so-called BRX domains. Genotyping of 42 additional accessions also found this deletion in Kz-1, Pu2-7, and Ws-0. In segregating recombinant inbred lines, the Lc-0 allele (AtBRX(Lc-0)) conferred significantly enhanced root growth. Moreover, when constitutively expressed in the same regulatory context, AtBRX(Lc-0) complemented brx mutants more efficiently than an allele without deletion. The same was observed for AtBRXL1, which compared with AtBRX carries a 13 amino acid deletion that encompasses the deletion found in AtBRX(Lc-0). Thus, the AtBRX(Lc-0) allele seems to contribute to natural variation in root growth vigor and provides a rare example of an experimentally confirmed, hyperactive allelic variant.

Additional References

RELATED GEPHE

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

Related Genes

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Brevis radix \(BRX\)^/and+Taxon ID=^3702^/or+Gene Gephebase=^Brevis radix \(BRX\)^/and+Taxon ID=^3702^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Brevis radix (BRX)^/and+Taxon ID=^3702^/or+Gene Gephebase=^Brevis radix (BRX)^/and+Taxon ID=^3702^#gephebase-summary-title))

Related Haplotypes

EXTERNAL LINKS

COMMENTS

gene previously detected by QTL