

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

	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	
	Trait
Root growth (https://www.gephebase.org/search-criteria?/and+Trait=~Root+growth^#gephebase-summary-title)	
	Trait State in Taxon A
Arabidopsis thaliana- Eil0	
	Trait State in Taxon B
Arabidopsis thaliana- Lov5; Lc-0; Kz-1; Pu2-; Ws-0	
	Ancestral State
Taxon A	
	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)	

GENOTYPIC CHANGE		
	Generic Gene Name	UniProtKB Arabidopsis thaliana
BRX		Q17TI5 (http://www.uniprot.org/uniprot/Q17TI5)
	Synonyms	GenebankID or UniProtKB
BREVIS RADIX; F5M6.11; F5M6_11; NIP3;1; NLM9; NOD26-like intrinsic protein 3;1; At1g31880		NM_102925 (https://www.ncbi.nlm.nih.gov/nuccore/NM_102925)
	String	
3702.AT1G31880.1 (http://string-db.org/newstring_cgj/show_network_section.pl?identifier=3702.AT1G31880.1)		
	Sequence Similarities	
Belongs to the BRX family.		
	GO - Molecular Function	
-		
	GO - Biological Process	
GO:0009734 : auxin-activated signaling pathway		

(<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>)

No (<a #gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=" no"="">https://www.gephebase.org/search-criteria?/and+Presumptive Null="No" #gephebase-summary-title)	Presumptive Null
Coding (<a #gephebase-summary-title"="" coding"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type="Coding" #gephebase-summary-title)	Molecular Type
Deletion (<a #gephebase-summary-title"="" deletion"="" href="https://www.gephebase.org/search-criteria?/and+Aberration Type=">https://www.gephebase.org/search-criteria?/and+Aberration Type="Deletion" #gephebase-summary-title)	Aberration Type
10-99 bp	Deletion Size
21bp deletion at position in spacer 3 (position not given)	Molecular Details of the Mutation
Linkage Mapping (<a #gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=" linkage="" mapping"="">https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Linkage Mapping" #gephebase-summary-title)	Experimental Evidence
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)	Main Reference
Beuchat J; Li S; Ragni L; Shindo C; Kohn MH; Hardtke CS	Authors

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) (<a 3702"="" and+grouphaplotypes='true#gephebase-summary-title"' and+trait="Root" growth="" href="https://www.gephebase.org/search-criteria?/or+Taxon ID=">https://www.gephebase.org/search-criteria?/or+Taxon ID="3702" /and+Trait=Root growth/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
2 (<a #gephebase-summary-title"="" (brx)"="" and+taxon="" brevis="" gephebase="Brevis radix (BRX)" href="https://www.gephebase.org/search-criteria?/or+Gene Gephebase=" id="3702" or+gene="" radix="">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