



(<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

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="Yes" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

premature stop codon in exon 4; TGG>TGA; truncated protein missing approximately two-thirds of the C terminus

Experimental Evidence

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

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

Main Reference

Natural genetic variation in Arabidopsis identifies BREVIS RADIX, a novel regulator of cell proliferation and elongation in the root. (2004) (<https://pubmed.ncbi.nlm.nih.gov/15031265>)

Authors

Mouchel CF; Briggs GC; Hardtke CS

Abstract

Mutant analysis has been tremendously successful in deciphering the genetics of plant development. However, less is known about the molecular basis of morphological variation within species, which is caused by naturally occurring alleles. In this study, we succeeded in isolating a novel regulator of root growth by exploiting natural genetic variation in the model plant Arabidopsis. Quantitative trait locus analysis of a cross between isogenized accessions revealed that a single locus is responsible for approximately 80% of the variance of the observed difference in root length. This gene, named BREVIS RADIX (BRX), controls the extent of cell proliferation and elongation in the growth zone of the root tip. We isolated BRX by positional cloning. BRX is a member of a small group of highly conserved genes, the BRX gene family, which is only found in multicellular plants. Analyses of Arabidopsis single and double mutants suggest that BRX is the only gene of this family with a role in root development. The BRX protein is nuclear localized and activates transcription in a heterologous yeast system, indicating that BRX family proteins represent a novel class of transcription factors. Thus, we have identified a novel regulatory factor controlling quantitative aspects of root growth.

Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

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=))

## EXTERNAL LINKS

## COMMENTS

