

MPK12 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MPK12^#gephebase-summary-title)	Gephebase Gene	GP00001283	GepheID
Published	Entry Status	Arnoult	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)		Trait Category	
Water absorption (water use efficiency) (https://www.gephebase.org/search-criteria?/and+Trait=~Water+absorption+(water+use+efficiency)~#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Ler0		Trait State in Taxon A	
Arabidopsis thaliana- Cvi		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
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)	
thale cress		thale cress	
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		species	
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	
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)	
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?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Cvi	

MPK12	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	Q8GYQ5 (http://www.uniprot.org/uniprot/Q8GYQ5)
ATMPK12; MAPK12; mitogen-activated protein kinase 12; T3F17.28; At2g46070	String	819215 (https://www.ncbi.nlm.nih.gov/nuccore/819215)
3702.AT2G46070.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT2G46070.1)	Sequence Similarities	
	GO - Molecular Function	

GO:0016301 : kinase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0016301>)
GO:0004707 : MAP kinase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0004707>)
GO - Biological Process

GO:0009734 : auxin-activated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009734>)
GO:0009733 : response to auxin (<https://www.ebi.ac.uk/QuickGO/term/GO:0009733>)
GO:0010468 : regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)
GO:0035556 : intracellular signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)
GO:0080026 : response to indolebutyric acid
(<https://www.ebi.ac.uk/QuickGO/term/GO:0080026>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
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](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

Nonsynonymous

Molecular Details of the Mutation

GGT to CGT @position 53

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

Variation in MPK12 affects water use efficiency in Arabidopsis and reveals a pleiotropic link between guard cell size and ABA response. (2014) (<https://pubmed.ncbi.nlm.nih.gov/24550314>)

Authors

Des Marais DL; Auchincloss LC; Sukamtoh E; McKay JK; Logan T; Richards JH; Juenger TE

Abstract

Plant water relations are critical for determining the distribution, persistence, and fitness of plant species. Studying the genetic basis of ecologically relevant traits, however, can be complicated by their complex genetic, physiological, and developmental basis and their interaction with the environment. Water use efficiency (WUE), the ratio of photosynthetic carbon assimilation to stomatal conductance to water, is a dynamic trait with tremendous ecological and agricultural importance whose genetic control is poorly understood. In the present study, we use a quantitative trait locus-mapping approach to locate, fine-map, clone, confirm, and characterize an allelic substitution that drives differences in WUE among natural accessions of *Arabidopsis thaliana*. We show that a single amino acid substitution in an abscisic acid-responsive kinase, AtMPK12, causes reduction in WUE, and we confirm its functional role using transgenics. We further demonstrate that natural alleles at AtMPK12 differ in their response to cellular and environmental cues, with the allele from the Cape Verde Islands (CVI) being less responsive to hormonal inhibition of stomatal opening and more responsive to short-term changes in vapor pressure deficit. We also show that the CVI allele results in constitutively larger stomata. Together, these differences cause higher stomatal conductance and lower WUE compared with the common allele. These physiological changes resulted in reduced whole-plant transpiration efficiency and reduced fitness under water-limited compared with well-watered conditions. Our work demonstrates how detailed analysis of naturally segregating functional variation can uncover the molecular and physiological basis of a key trait associated with plant performance in ecological and agricultural settings.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE - see also DOI:10.1111/j.1365-3040.2004.01313.x ; single point mutation in a conserved domain of the kinase ; lower WUE in the A. thaliana accession CVI compared with Ler is driven in part by variation in stomatal conductance ; CVI allele less sensitive to the effect of ABA on inhibition of stomatal opening and more responsive to short-term changes in VPD than the Ler allele ; 5 QTL for this trait detected by 10.1111/j.1365-3040.2004.01313.x

