

Gephebase Gene		GepheID
heavy metal atpase5 (HMA5) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~heavy+metal+atpase5+(HMA5)*#gephebase-summary-title)	GP00000450	Main curator
Entry Status	Martin	
Published		

Physiology (#gephebase-summary-title)		Trait Category	
Metal tolerance (#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Ler0		Trait State in Taxon A	
Arabidopsis thaliana- Chisdra-2		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Arabidopsis thaliana (#gephebase-summary-title)		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; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; 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)	
NCBI Taxonomy ID 3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		NCBI Taxonomy ID 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	
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Chisdra-2	
Taxon A Description		Taxon B Description	

HMA5	Generic Gene Name	UniProtKB Arabidopsis thaliana
	Synonyms	Q9SH30 (http://www.uniprot.org/uniprot/Q9SH30) GenebankID or UniProtKB
F2K11.18; F2K11_18; heavy metal atpase 5; At1g63440	String	AC008047 (https://www.ncbi.nlm.nih.gov/nucore/AC008047)
3702.AT1G63440.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT1G63440.1)	Sequence Similarities	
	Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type 1B subfamily.	
	GO - Molecular Function	
	GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	
	GO:0019829 : cation-transporting ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0019829)	
	GO:0005507 : copper ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005507)	

GO - Biological Process

GO:0006825 : copper ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006825>)
GO:0010273 : detoxification of copper ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010273>)
GO:0046688 : response to copper ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046688>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

P626L

Experimental Evidence

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

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

Main Reference

Amino acid polymorphisms in strictly conserved domains of a P-type ATPase HMA5 are involved in the mechanism of copper tolerance variation in Arabidopsis. (2008)
(<https://pubmed.ncbi.nlm.nih.gov/18701674>)

Authors

Kobayashi Y; Kuroda K; Kimura K; Southron-Francis JL; Furuzawa A; Kimura K; Iuchi S; Kobayashi M; Taylor GJ; Koyama H

Abstract

Copper (Cu) is an essential element in plant nutrition, but it inhibits the growth of roots at low concentrations. Accessions of Arabidopsis (*Arabidopsis thaliana*) vary in their tolerance to Cu. To understand the molecular mechanism of Cu tolerance in Arabidopsis, we performed quantitative trait locus (QTL) analysis and accession studies. One major QTL on chromosome 1 (QTL1) explained 52% of the phenotypic variation in Cu tolerance in roots in a Landsberg erecta/Cape Verde Islands (Ler/Cvi) recombinant inbred population. This QTL regulates Cu translocation capacity and involves a Cu-transporting P(1B-1)-type ATPase, HMA5. The Cvi allele carries two amino acid substitutions in comparison with the Ler allele and is less functional than the Ler allele in Cu tolerance when judged by complementation assays using a T-DNA insertion mutant. Complementation assays of the ccc2 mutant of yeast using chimeric HMA5 proteins revealed that N923T of the Cvi allele, which was identified in the tightly conserved domain N(x)(6)YN(x)(4)P (where the former asparagine was substituted by threonine), is a cause of dysfunction of the Cvi HMA5 allele. Another dysfunctional HMA5 allele was identified in Chisdra-2, which showed Cu sensitivity and low capacity of Cu translocation from roots to shoots. A unique amino acid substitution of Chisdra-2 was identified in another strictly conserved domain, CPC(x)(6)P, where the latter proline was replaced with leucine. These results indicate that a portion of the variation in Cu tolerance of Arabidopsis is regulated by the functional integrity of the Cu-translocating ATPase, HMA5, and in particular the amino acid sequence in several strictly conserved motifs.

Additional References

RELATED GEPHE

Related Genes

5 (FPN2, FRD3 (FERRIC REDUCTASE DEFECTIVE3), heavy metal atpase3 (HMA3), Molybdenum transporter1 (MOT1), heavy metal atpase4 (HMA4))
(<https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Metal tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^heavy metal atpase5 \(HMA5\)^/and+Taxon ID=^3702^/or+Gene Gephebase=^heavy metal atpase5 \(HMA5\)^/and+Taxon ID=^3702^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^heavy metal atpase5 (HMA5)^/and+Taxon ID=^3702^/or+Gene Gephebase=^heavy metal atpase5 (HMA5)^/and+Taxon ID=^3702^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

