

heavy metal atpase5 (HMA5) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~heavy+metal+atpase5 (HMA5)^#gephebase-summary-title)	Gephebase Gene	GP00000451	GepheID
Published	Entry Status	Martin	Main curator

Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)	
Trait	
Metal tolerance (https://www.gephebase.org/search-criteria?/and+Trait=~Metal tolerance^#gephebase-summary-title)	
Trait State in Taxon A	
Arabidopsis thaliana- Ler0	
Trait State in Taxon B	
Arabidopsis thaliana- Cvi	
Ancestral State	
Data not curated	
Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Intraspecific^#gephebase-summary-title)	
Taxon A	Taxon B
Arabidopsis thaliana	Arabidopsis thaliana
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana^#gephebase-summary-title)	(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana^#gephebase-summary-title)
Common Name	Common Name
thale cress	thale cress
Synonyms	Synonyms
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
Rank	Rank
species	species
Lineage	Lineage
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
Parent	Parent
Arabidopsis () - (Rank: genus)	Arabidopsis () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)
NCBI Taxonomy ID	NCBI Taxonomy ID
3702	3702
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?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
Taxon A Description	Taxon B Description
Arabidopsis thaliana- Ler0	Arabidopsis thaliana- Cvi

HMA5	Generic Gene Name	Q9SH30 (http://www.uniprot.org/uniprot/Q9SH30)	UniProtKB Arabidopsis thaliana
F2K11.18; F2K11_18; heavy metal atpase 5; At1g63440	Synonyms	AC008047 (https://www.ncbi.nlm.nih.gov/nucore/AC008047)	GenebankID or UniProtKB
3702.AT1G63440.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT1G63440.1)	String		
	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

N923T

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

