

Gephebase Gene		GepheID
Molybdenum transporter1 (MOT1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Molybdenum+transporter1+(MOT1)+#gephebase-summary-title)	GP00000677	Main curator
Entry Status	Martin	
Published		

Physiology (#gephebase-summary-title)		Trait Category	
Metal tolerance (#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Col0		Trait State in Taxon A	
Arabidopsis thaliana- Ler0		Trait State in Taxon B	
Taxon A		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- Col0		Arabidopsis thaliana- Ler0	
Taxon A Description		Taxon B Description	

MOT1	Generic Gene Name	Q9SL95 (http://www.uniprot.org/uniprot/Q9SL95)	UniProtKB Arabidopsis thaliana
F3N11.13; F3N11_13; molybdate transporter 1; ST5.2; SULTR5.2; At2g25680	Synonyms	AK221594 (https://www.ncbi.nlm.nih.gov/nuccore/AK221594)	GenebankID or UniProtKB
3702.AT2G25680.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT2G25680.1)	String		
Belongs to the SLC26A/SulP transporter (TC 2.A.53) family.	Sequence Similarities		
GO:0015098 : molybdate ion transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015098)	GO - Molecular Function		
GO:0015689 : molybdate ion transport	GO - Biological Process		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015689>)

GO - Cellular Component

GO:0016021 : integral component of membrane

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

GO:0031966 : mitochondrial membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031966>)

GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)

GO:0005773 : vacuole (<https://www.ebi.ac.uk/QuickGO/term/GO:0005773>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Insertion Size

100-999 bp

Molecular Details of the Mutation

330bp duplication followed by minor indels

Experimental Evidence

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

Main Reference

The Multi-allelic Genetic Architecture of a Variance-Heterogeneity Locus for Molybdenum Concentration in Leaves Acts as a Source of Unexplained Additive Genetic Variance. (2015)

(<https://pubmed.ncbi.nlm.nih.gov/26599497>)

Authors

Forsberg SK; Andreatta ME; Huang XY; Danku J; Salt DE; Carlborg Å-

Abstract

Genome-wide association (GWA) analyses have generally been used to detect individual loci contributing to the phenotypic diversity in a population by the effects of these loci on the trait mean. More rarely, loci have also been detected based on variance differences between genotypes. Several hypotheses have been proposed to explain the possible genetic mechanisms leading to such variance signals. However, little is known about what causes these signals, or whether this genetic variance-heterogeneity reflects mechanisms of importance in natural populations. Previously, we identified a variance-heterogeneity GWA (vGWA) signal for leaf molybdenum concentrations in *Arabidopsis thaliana*. Here, fine-mapping of this association reveals that the vGWA emerges from the effects of three independent genetic polymorphisms that all are in strong LD with the markers displaying the genetic variance-heterogeneity. By revealing the genetic architecture underlying this vGWA signal, we uncovered the molecular source of a significant amount of hidden additive genetic variation or “missing heritability”. Two of the three polymorphisms underlying the genetic variance-heterogeneity are promoter variants for Molybdate transporter 1 (MOT1), and the third a variant located ~25 kb downstream of this gene. A fourth independent association was also detected ~600 kb upstream of MOT1. Use of a T-DNA knockout allele highlights Copper Transporter 6; COPT6 (AT2G26975) as a strong candidate gene for this association. Our results show that an extended LD across a complex locus including multiple functional alleles can lead to a variance-heterogeneity between genotypes in natural populations. Further, they provide novel insights into the genetic regulation of ion homeostasis in *A. thaliana*, and empirically confirm that variance-heterogeneity based GWA methods are a valuable tool to detect novel associations of biological importance in natural populations.

Additional References

RELATED GEPHE

Related Genes

5 (FPN2, FRD3 (FERRIC REDUCTASE DEFECTIVE3), heavy metal atpase3 (HMA3), heavy metal atpase5 (HMA5), 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

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Molybdenum transporter1 \(MOT1\)^/and+Taxon ID=^3702^/or+Gene Gephebase=^Molybdenum transporter1 \(MOT1\)^/and+Taxon ID=^3702^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Molybdenum transporter1 (MOT1)^/and+Taxon ID=^3702^/or+Gene Gephebase=^Molybdenum transporter1 (MOT1)^/and+Taxon ID=^3702^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

Genetic heterogeneity; Complex locus with additional loci with multiple alleles; two promoter variants + 1 25kb downstream + LD with other site 600kb away with putative role of Copper Transporter 6 (COPT6)