

GEPHE SUMMARY

	Gephebase Gene		GepheID
Molybdenum transporter1 (MOT1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=Molybdenum+transporter1+(MOT1)^#gephebase-summary-title)		GP00000676	
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

	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- Col0			
	Trait State in Taxon B		
Arabidopsis thaliana- Ler0			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
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)	
	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; 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	
	Parent		Parent
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		NCBI Taxonomy ID
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- Col0		Arabidopsis thaliana- Ler0	

GENOTYPIC CHANGE

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

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

Molecular Type

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

Aberration Type

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

53bp deletion in promoter

Experimental Evidence

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

Main Reference

Variation in molybdenum content across broadly distributed populations of *Arabidopsis thaliana* is controlled by a mitochondrial molybdenum transporter (MOT1). (2008)

(<https://pubmed.ncbi.nlm.nih.gov/18454190>)

Authors

Baxter I; Muthukumar B; Park HC; Buchner P; Lahner B; Danku J; Zhao K; Lee J; Hawkesford MJ; Guerinot ML; Salt DE

Abstract

Molybdenum (Mo) is an essential micronutrient for plants, serving as a cofactor for enzymes involved in nitrate assimilation, sulfite detoxification, abscisic acid biosynthesis, and purine degradation. Here we show that natural variation in shoot Mo content across 92 *Arabidopsis thaliana* accessions is controlled by variation in a mitochondrially localized transporter (Molybdenum Transporter 1 - MOT1) that belongs to the sulfate transporter superfamily. A deletion in the MOT1 promoter is strongly associated with low shoot Mo, occurring in seven of the accessions with the lowest shoot content of Mo. Consistent with the low Mo phenotype, MOT1 expression in low Mo accessions is reduced. Reciprocal grafting experiments demonstrate that the roots of Ler-0 are responsible for the low Mo accumulation in shoot, and GUS localization demonstrates that MOT1 is expressed strongly in the roots. MOT1 contains an N-terminal mitochondrial targeting sequence and expression of MOT1 tagged with GFP in protoplasts and transgenic plants, establishing the mitochondrial localization of this protein. Furthermore, expression of MOT1 specifically enhances Mo accumulation in yeast by 5-fold, consistent with MOT1 functioning as a molybdate transporter. This work provides the first molecular insight into the processes that regulate Mo accumulation in plants and shows that novel loci can be detected by association mapping.

Additional References

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>)

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](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

2 ([#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](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

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)