GEPHE SUMMARY

Gephebase Gene

Molybdenum transporter1 (MOT1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Molybdenum transporter1 (MOT1)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000676

Main curator

Martin

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

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

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)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Arabidopsis thaliana- Col0

Taxon B

Latin Name

Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)

Common Name

thale cress

Synonyms

thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis

Parent

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)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Arabidopsis thaliana- Ler0

GENOTYPIC CHANGE

Generic Gene Name

MOT1

Synonyms

F3N11.13; F3N11_13; molybdate transporter 1; ST5.2; SULTR5.2; At2g25680

String

3702.AT2G25680.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G25680.1)

Sequence Similarities

Belongs to the SLC26A/SulP 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

UniProtKB Arabidopsis thaliana

Q9SL95 (http://www.uniprot.org/uniprot/Q9SL95)

GenebankID or UniProtKB

AK221594 (https://www.ncbi.nlm.nih.gov/nuccore/AK221594)

(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

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

Aberration Type

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

53bp deletion in promoter

Experimental Evidence

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

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)

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)

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)