GEPHE SUMMARY

Gephebase Gene

FRD3 (FERRIC REDUCTASE DEFECTIVE3) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FRD3 (FERRIC REDUCTASE DEFECTIVE3)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000355

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 - Sha

Trait State in Taxon B

Arabidopsis thaliana- Bay-0 (Zn tolerant)

Ancestral State

Data not curated

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 - Sha

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- Bay-0 (Zn tolerant)

GENOTYPIC CHANGE

Generic Gene Name

DTX43

Synonyms

ATFRD3; FERRIC REDUCTASE DEFECTIVE 3; MAN1; MANGANESE ACCUMULATOR 1; FRD3; At3g08040; F17A17.38; T8G24.8

String

3702.AT3G08040.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT3G08040.1)

Sequence Similarities

Belongs to the multi antimicrobial extrusion (MATE) (TC 2.A.66.1) family.

GO - Molecular Function

GO:0015297 : antiporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015297)
GO:0015137 : citrate transmembrane transporter activity

UniProtKB Arabidopsis thaliana

Q9SFB0 (http://www.uniprot.org/uniprot/Q9SFB0)

GenebankID or UniProtKB

AC074395 (https://www.ncbi.nlm.nih.gov/nuccore/AC074395)

(https://www.ebi.ac.uk/QuickGO/term/GO:0015137)
GO:0046873 : metal ion transmembrane transporter activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0046873)
GO:0005215 : transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005215)

GO - Biological Process

GO:0006879 : cellular iron ion homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0006879)
GO:0071281 : cellular response to iron ion
(https://www.ebi.ac.uk/QuickGO/term/GO:0071281)
GO:0009737 : response to abscisic acid
(https://www.ebi.ac.uk/QuickGO/term/GO:0009737)
GO:0016036 : cellular response to phosphate starvation
(https://www.ebi.ac.uk/QuickGO/term/GO:0016036)
GO:0055072 : iron ion homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0055072)
GO:0071369 : cellular response to ethylene stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0071369)
GO:0071732 : cellular response to nitric oxide
(https://www.ebi.ac.uk/QuickGO/term/GO:0071732)
GO:0030001 : metal ion transport (https://www.ebi.ac.uk/QuickGO/term/GO:0030001)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)

Mutation #1

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

the Sha allele (Zn-sensitive) shows non-functional protein due to N116S and L117P

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	Asn	Ser	116

Main Reference

Natural variation at the FRD3 MATE transporter locus reveals cross-talk between Fe homeostasis and Zn tolerance in Arabidopsis thaliana. (2012)
(https://pubmed.ncbi.nlm.nih.gov/23236296)

Authors

Pineau C; Loubet S; Lefoulon C; Chalies C; Fizames C; Lacombe B; Ferrand M; Loudet O; Berthomieu P; Richard O

Abstract

Zinc (Zn) is essential for the optimal growth of plants but is toxic if present in excess, so Zn homeostasis needs to be finely tuned. Understanding Zn homeostasis mechanisms in plants will help in the development of innovative approaches for the phytoremediation of Zn-contaminated sites. In this study, Zn tolerance quantitative trait loci (QTL) were identified by analyzing differences in the Bay-0 and Shahdara accessions of Arabidopsis thaliana. Fine-scale mapping showed that a variant of the Fe homeostasis-related FERRIC REDUCTASE DEFECTIVE3 (FRD3) gene, which encodes a multidrug and toxin efflux (MATE) transporter, is responsible for reduced Zn tolerance in A. thaliana. Allelic variation in FRD3 revealed which amino acids are necessary for FRD3 function. In addition, the results of allele-specific expression assays in F1 individuals provide evidence for the existence of at least one putative metal-responsive cis-regulatory element. Our results suggest that FRD3 works as a multimer and is involved in loading Zn into xylem. Cross-homeostasis between Fe and Zn therefore appears to be important for Zn tolerance in A. thaliana with FRD3 acting as an essential regulator.

Additional References

Mutation #2

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

the Sha allele (Zn-sensitive) shows non-functional protein due to N116S and L117P

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	Leu	Phe	117

Main Reference

Natural variation at the FRD3 MATE transporter locus reveals cross-talk between Fe homeostasis and Zn tolerance in Arabidopsis thaliana. (2012) (https://pubmed.ncbi.nlm.nih.gov/23236296)

Authors

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Additional References

RELATED GEPHE

Related Genes

5 (FPN2, heavy metal atpase3 (HMA3), heavy metal atpase5 (HMA5), 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

No matches found.

EXTERNAL LINKS

COMMENTS

The weaker expression of the gene is possibly due to 27-bp and 28bp deletions in promoter @SeveralMutationsWithEffect