GEPHE SUMMARY

Gephebase Gene

HAC1 (=ATQ1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^HAC1 (=ATQ1)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000435

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Xenobiotic resistance (soil contamination; arsenate) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (soil contamination; arsenate)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana- Col0

Trait State in Taxon B

Arabidopsis thaliana - Kashmir

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- 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 - Kashmir

GENOTYPIC CHANGE

Generic Gene Name

HAC1

Synonyms

ARABIDOPSIS HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 1; ARABIDOPSIS THALIANA P300/CBP ACETYLTRANSFERASE-RELATED PROTEIN 2; ATHAC1; ATHPCAT2; histone acetyltransferase of the CBP family 1; P300/CBP ACETYLTRANSFERASE-RELATED PROTEIN 2; PCAT2; YUP8H12R.38; YUP8H12R_38; At1g79000; YUP8H12R_22

String

3702.AT1G79000.2 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G79000.2)

Sequence Similarities

-

UniProtKB Arabidopsis thaliana

Q9C5X9 (http://www.uniprot.org/uniprot/Q9C5X9)

GenebankID or UniProtKB

()

GO - Molecular Function

GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)
GO:0003712 : transcription coregulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003712)
GO:0004402 : histone acetyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004402)

GO - Biological Process

GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

1bp deletion resulting in frameshift

Experimental Evidence

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

Main Reference

Genome-wide association mapping identifies a new arsenate reductase enzyme critical for limiting arsenic accumulation in plants. (2014) (https://pubmed.ncbi.nlm.nih.gov/25464340)

Authors

Chao DY; Chen Y; Chen J; Shi S; Chen Z; Wang C; Danku JM; Zhao FJ; Salt DE

Abstract

Inorganic arsenic is a carcinogen, and its ingestion through foods such as rice presents a significant risk to human health. Plants chemically reduce arsenate to arsenite. Using genome-wide association (GWA) mapping of loci controlling natural variation in arsenic accumulation in Arabidopsis thaliana allowed us to identify the arsenate reductase required for this reduction, which we named High Arsenic Content 1 (HAC1). Complementation verified the identity of HAC1, and expression in Escherichia coli lacking a functional arsenate reductase confirmed the arsenate reductase activity of HAC1. The HAC1 protein accumulates in the epidermis, the outer cell layer of the root, and also in the pericycle cells surrounding the central vascular tissue. Plants lacking HAC1 lose their ability to efflux arsenite from roots, leading to both increased transport of arsenic into the central vascular tissue and on into the shoot. HAC1 therefore functions to reduce arsenate to arsenite in the outer cell layer of the root, facilitating efflux of arsenic as arsenite back into the soil to limit both its accumulation in the root and transport to the shoot. Arsenate reduction by HAC1 in the pericycle may play a role in limiting arsenic loading into the xylem. Loss of HAC1-encoded arsenic reduction leads to a significant increase in arsenic accumulation in shoots, causing an increased sensitivity to arsenate toxicity. We also confirmed the previous observation that the ACR2 arsenate reductase in A. thaliana plays no detectable role in arsenic metabolism. Furthermore, ACR2 does not interact epistatically with HAC1, since arsenic metabolism in the acr2 hac1 double mutant is disrupted in an identical manner to that described for the hac1 single mutant. Our identification of HAC1 and its associated natural variation provides an important new resource for the development of low arsenic-containing food such as rice.

Additional References

RELATED GEPHE

Related Genes

1 (CLH1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^HAC1 (=ATQ1)^/and+Taxon ID=^3702^/or+Gene Gephebase=^HAC1 (=ATQ1)^/and+Taxon ID=^3702^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Mapped independentyl in two studies