GEPHE SUMMARY

Gephebase Gene

CLH1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CLH1^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001234

Main curator

Arnoult

PHENOTYPIC CHANGE

Trait Category

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

Trait

Xenobiotic resistance (fungicide: guazatine) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (fungicide: guazatine)^#gephebase-summary-title)

Trait State in Taxon A

Arabidopsis thaliana

Trait State in Taxon B

Arabidopsis thaliana

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?

No

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?

No

GENOTYPIC CHANGE

Generic Gene Name

CLH1

Synonyms

ATCLH1; ATHCOR1; CHLOROPHYLLASE; chlorophyllase 1; CORI1; CORONATINE-INDUCED PROTEIN 1; F6F9.28; F6F9_28; COR1; At1g19670

String

3702.AT1G19670.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G19670.1)

Sequence Similarities

Belongs to the AB hydrolase superfamily. Lipase family.

GO - Molecular Function

GO:0047746 : chlorophyllase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0047746)
GO:0102293 : pheophytinase b activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102293)

GO - Biological Process

UniProtKB Arabidopsis thaliana

O22527 (http://www.uniprot.org/uniprot/O22527)

GenebankID or UniProtKB

()

GO:0042742 : defense response to bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0042742)
GO:0050832 : defense response to fungus (https://www.ebi.ac.uk/QuickGO/term/GO:0050832)
GO:0015996 : chlorophyll catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0015996)

GO - Cellular Component

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

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Genome Wide Association Mapping for the Tolerance to the Polyamine Oxidase Inhibitor Guazatine in Arabidopsis thaliana. (2016) (https://pubmed.ncbi.nlm.nih.gov/27092150)

Authors

Atanasov KE; Barboza-Barquero L; Tiburcio AF; AlcÃizar R

Abstract

Guazatine is a potent inhibitor of polyamine oxidase (PAO) activity. In agriculture, guazatine is used as non-systemic contact fungicide efficient in the protection of cereals and citrus fruits against disease. The composition of guazatine is complex, mainly constituted by a mixture of synthetic guanidated polyamines (polyaminoguanidines). Here, we have studied the effects from exposure to guazatine in the weed Arabidopsis thaliana. We report that micromolar concentrations of guazatine are sufficient to inhibit growth of Arabidopsis seedlings and induce chlorosis, whereas germination is barely affected. We observed the occurrence of quantitative variation in the response to guazatine between 107 randomly chosen Arabidopsis accessions. This enabled us to undertake genome-wide association (GWA) mapping that identified a locus on chromosome one associated with guazatine tolerance. CHLOROPHYLLASE 1 (CLH1) within this locus was studied as candidate gene, together with its paralog (CLH2). The analysis of independent clh1-2, clh1-3, clh2-3, clh2-2, and double clh1-2 clh2-3 mutant alleles indicated that CLH1 and/or CLH2 loss-of-function or expression down-regulation promote guazatine tolerance in Arabidopsis. We report a natural mechanism by which Arabidopsis populations can overcome toxicity by the fungicide guazatine.

Additional References

RELATED GEPHE

Related Genes

1 (HAC1 (=ATQ1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

CLH2 paralog also involved in the trait variation