GEPHE SUMMARY

Gephebase Gene

Epithiospecifier Modifier1 (ESM1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Epithiospecifier Modifier1 (ESM1)^#gephebase-summary-title)

GepheID

GP00000277

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Arabidopsis thaliana- Col0

Trait State in Taxon B

Arabidopsis thaliana- Ler0

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- Ler0

GENOTYPIC CHANGE

Generic Gene Name

ESM1

Synonyms

epithiospecifier modifier 1; At3g14210; MAG2.6

String

3702.AT3G14210.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT3G14210.1)

Sequence Similarities

Belongs to the 'GDSL' lipolytic enzyme family.

GO - Molecular Function

GO:0016788 : hydrolase activity, acting on ester bonds (https://www.ebi.ac.uk/QuickGO/term/GO:0016788)

GO - Biological Process

GO:0042742 : defense response to bacterium

UniProtKB Arabidopsis thaliana

Q9LJG3 (http://www.uniprot.org/uniprot/Q9LJG3)

GenebankID or UniProtKB

AK221834 (https://www.ncbi.nlm.nih.gov/nuccore/AK221834)

(https://www.ebi.ac.uk/QuickGO/term/GO:0042742)
GO:0009409 : response to cold (https://www.ebi.ac.uk/QuickGO/term/GO:0009409)
GO:0019762 : glucosinolate catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0019762)
GO:0016042 : lipid catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0016042)
GO:0009625 : response to insect (https://www.ebi.ac.uk/QuickGO/term/GO:0009625)

GO - Cellular Component

GO:0009506 : plasmodesma (https://www.ebi.ac.uk/QuickGO/term/GO:0009506)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)
GO:0005777 : peroxisome (https://www.ebi.ac.uk/QuickGO/term/GO:0005777)
GO:0005773 : vacuole (https://www.ebi.ac.uk/QuickGO/term/GO:0005773)
GO:0022626 : cytosolic ribosome (https://www.ebi.ac.uk/QuickGO/term/GO:0022626)
GO:0048046 : apoplast (https://www.ebi.ac.uk/QuickGO/term/GO:0048046)
GO:0009941 : chloroplast envelope (https://www.ebi.ac.uk/QuickGO/term/GO:0009941)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Not identified

Experimental Evidence

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

Main Reference

The gene controlling the quantitative trait locus EPITHIOSPECIFIER MODIFIER1 alters glucosinolate hydrolysis and insect resistance in Arabidopsis. (2006)
(https://pubmed.ncbi.nlm.nih.gov/16679459)

Authors

Zhang Z; Ober JA; Kliebenstein DJ

Abstract

Glucosinolates are sulfur-rich plant secondary metabolites whose breakdown products have a wide range of biological activities in plant-herbivore and plant-pathogen interactions and anticarcinogenic properties. In Arabidopsis thaliana, hydrolysis by the enzyme, myrosinase, produces bioactive nitriles, epithionitriles, or isothiocyanates depending upon the plant's genotype and the glucosinolate's structure. A major determinant of this structural specificity is the epithiospecifier locus (ESP), whose protein causes the formation of epithionitriles and nitriles. A quantitative trait locus (QTL) on chromosome 3 epistatically affects nitrile formation in combination with ESP; this QTL has been termed EPITHIOSPECIFIER MODIFIER1 (ESM1). We identified a myrosinase-associated protein as the ESM1 QTL in Arabidopsis using map-based cloning with recombinant inbred lines, natural variation transcriptomic analysis, and metabolic profiling. In planta and in vitro analyses with natural ESM1 alleles, ESM1 knockouts, and overexpression lines show that ESM1 represses nitrile formation and favors isothiocyanate production. The glucosinolate hydrolysis profile change influenced by ESM1 is associated with the ability to deter herbivory by Trichoplusia ni. This gene could provide unique approaches toward improving human nutrition.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Epistasis