GEPHE SUMMARY

Gephebase Gene
MAM1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MAM1^#gephebase-summary-title)

GepheID
GP00000562

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
Glucosinolate content (https://www.gephebase.org/search-criteria?/and+Trait=^Glucosinolate 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
MAM1

Synonyms
2-ISOPROPYLMALATE SYNTHASE; 2-ISOPROPYLMALATE SYNTHASE 3; IMS3; METHYLTHIOALKYLMALATE SYNTHASE; methylthioalkylmalate synthase 1; T20O7.3; T20O7_3; IPMS_AT2; MAM-L; MAML; At5g23010

String
3702.AT5G23010.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G23010.1)

Sequence Similarities
Belongs to the alpha-IPM synthase/homocitrate synthase family.

GO - Molecular Function
GO:0010177 : 2-(2'-methylthio)ethylmalate synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0010177)

UniProtKB Arabidopsis thaliana
Q9FG67 (http://www.uniprot.org/uniprot/Q9FG67)

GenebankID or UniProtKB
AJ486888 (https://www.ncbi.nlm.nih.gov/nuccore/AJ486888)

GO:0003852 : 2-isopropylmalate synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003852)

GO - Biological Process

GO:0019761 : glucosinolate biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019761)
GO:0009414 : response to water deprivation (https://www.ebi.ac.uk/QuickGO/term/GO:0009414)
GO:0009625 : response to insect (https://www.ebi.ac.uk/QuickGO/term/GO:0009625)
GO:0009098 : leucine biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009098)

GO - Cellular Component

GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)

Presumptive Null

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

Molecular Type

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

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

Main Reference

A gene controlling variation in Arabidopsis glucosinolate composition is part of the methionine chain elongation pathway. (2001) (https://pubmed.ncbi.nlm.nih.gov/11706188)

Authors

Kroymann J; Textor S; Tokuhisa JG; Falk KL; Bartram S; Gershenzon J; Mitchell-Olds T

Abstract

Arabidopsis and other Brassicaceae produce an enormous diversity of aliphatic glucosinolates, a group of methionine (Met)-derived plant secondary compounds containing a beta-thio-glucose moiety, a sulfonated oxime, and a variable side chain. We fine-scale mapped GSL-ELONG, a locus controlling variation in the side-chain length of aliphatic glucosinolates. Within this locus, a polymorphic gene was identified that determines whether Met is extended predominantly by either one or by two methylene groups to produce aliphatic glucosinolates with either three- or four-carbon side chains. Two allelic mutants deficient in four-carbon side-chain glucosinolates were shown to contain independent missense mutations within this gene. In cell-free enzyme assays, a heterologously expressed cDNA from this locus was capable of condensing 2-oxo-4-methylthiobutanoic acid with acetyl-coenzyme A, the initial reaction in Met chain elongation. The gene methylthioalkylmalate synthase1 (MAM1) is a member of a gene family sharing approximately 60% amino acid sequence similarity with 2-isopropylmalate synthase, an enzyme of leucine biosynthesis that condenses 2-oxo-3-methylbutanoate with acetyl-coenzyme A.

Additional References

Understanding the evolution of defense metabolites in Arabidopsis thaliana using genome-wide association mapping. (2010) (https://pubmed.ncbi.nlm.nih.gov/19737743)
Combining genome-wide association mapping and transcriptional networks to identify novel genes controlling glucosinolates in Arabidopsis thaliana. (2011) (https://pubmed.ncbi.nlm.nih.gov/21857804)
Natural enemies drive geographic variation in plant defenses. (2012) (https://pubmed.ncbi.nlm.nih.gov/23042895)

RELATED GEPHE

Related Genes

3 (AOP2, AOP3, CYP81F2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3702^/and+Trait=Glucosinolate content/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS