

GEPHE SUMMARY

Gephebase Gene		GepheID
UDP-glycosyltransferase 89A2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^UDP-glycosyltransferase 89A2^#gephebase-summary-title)		GP00001278
Entry Status		Arnoult
Published		Main curator

PHENOTYPIC CHANGE

Trait Category			
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)			
Trait			
Plant secondary metabolites (xylosides vs. glucosides ratio) (https://www.gephebase.org/search-criteria?/and+Trait=^Plant secondary metabolites (xylosides vs. glucosides ratio)^#gephebase-summary-title)			
Trait State in Taxon A			
Arabidopsis thaliana- Col-0			
Trait State in Taxon B			
Arabidopsis thaliana- C24			
Ancestral State			
Unknown			
Taxonomic Status			
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Latin Name		Latin Name	
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Arabidopsis thaliana^#gephebase-summary-title)	
Common Name		Common Name	
thale cress		thale cress	
Synonyms		Synonyms	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Parent		Parent	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3701)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3702)	
is Taxon A an Infrappecies?		is Taxon B an Infrappecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Col-0		Arabidopsis thaliana- C24	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Arabidopsis thaliana
UGT89A2		Q9LZD8 (http://www.uniprot.org/uniprot/Q9LZD8)
Synonyms		GenebankID or UniProtKB
F12E4.260; F12E4_260; At5g03490		831823 (https://www.ncbi.nlm.nih.gov/nuccore/831823)
String		
3702.AT5G03490.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT5G03490.1)		
Sequence Similarities		
Belongs to the UDP-glycosyltransferase family.		
GO - Molecular Function		
GO:0080043 : quercetin 3-O-glucosyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0080043)		
GO:0080044 : quercetin 7-O-glucosyltransferase activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0080044>)
GO:0035251 : UDP-glucosyltransferase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035251>)
GO:0008194 : UDP-glycosyltransferase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008194>)

GO - Biological Process

-

GO - Cellular Component

GO:0043231 : intracellular membrane-bounded organelle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043231>)

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

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

Main Reference

Exploiting natural variation of secondary metabolism identifies a gene controlling the glycosylation diversity of dihydroxybenzoic acids in Arabidopsis thaliana. (2014)
(<https://pubmed.ncbi.nlm.nih.gov/25173843>)

Authors

Li X; Svedin E; Mo H; Atwell S; Dilkes BP; Chapple C

Abstract

Plant secondary metabolism is an active research area because of the unique and important roles the specialized metabolites have in the interaction of plants with their biotic and abiotic environment, the diversity and complexity of the compounds and their importance to human medicine. Thousands of natural accessions of Arabidopsis thaliana characterized with increasing genomic precision are available, providing new opportunities to explore the biochemical and genetic mechanisms affecting variation in secondary metabolism within this model species. In this study, we focused on four aromatic metabolites that were differentially accumulated among 96 Arabidopsis natural accessions as revealed by leaf metabolic profiling. Using UV, mass spectrometry, and NMR data, we identified these four compounds as different dihydroxybenzoic acid (DHBA) glycosides, namely 2,5-dihydroxybenzoic acid (gentisic acid) 5-O-Î²-D-glucoside, 2,3-dihydroxybenzoic acid 3-O-Î²-D-glucoside, 2,5-dihydroxybenzoic acid 5-O-Î²-D-xyloside, and 2,3-dihydroxybenzoic acid 3-O-Î²-D-xyloside. Quantitative trait locus (QTL) mapping using recombinant inbred lines generated from C24 and Col-0 revealed a major-effect QTL controlling the relative proportion of xylosides vs. glucosides. Association mapping identified markers linked to a gene encoding a UDP glycosyltransferase gene. Analysis of Transfer DNA (T-DNA) knockout lines verified that this gene is required for DHBA xylosylation in planta and recombinant protein was able to xylosylate DHBA in vitro. This study demonstrates that exploiting natural variation of secondary metabolism is a powerful approach for gene function discovery.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

putative null mutation