

GEPHE SUMMARY

AOP3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=AOP3#gephebase-summary-title)	Gephebase Gene	GP00000096	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=Physiology#gephebase-summary-title)		Trait Category	
Glucosinolate content (https://www.gephebase.org/search-criteria?/and+Trait=Glucosinolate content#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Colo		Trait State in Taxon A	
Arabidopsis thaliana- Ler0		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=Intraspecific#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
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)	
thale cress		thale cress	
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	
species		species	
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	
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)	
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)	
Yes		Yes	
Arabidopsis thaliana- Colo		Arabidopsis thaliana- Ler0	

GENOTYPIC CHANGE

AOP3		Generic Gene Name		UniProtKB Arabidopsis thaliana	
T4l9.7; T4l9_7; At4g03050		Synonyms		GenebankID or UniProtKB	
3702.AT4G03050.2 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT4G03050.2)		String		AF069442 (https://www.ncbi.nlm.nih.gov/nucleotide/AF069442)	
Belongs to the iron/ascorbate-dependent oxidoreductase family.		Sequence Similarities			
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		GO - Molecular Function			
GO:0016706 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors (https://www.ebi.ac.uk/QuickGO/term/GO:0016706)					

GO:0051213 : dioxigenase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0051213>)
GO - Biological Process

GO:0019761 : glucosinolate biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019761>)
GO - Cellular Component

-	Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#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
Gene duplication in the diversification of secondary metabolism: tandem 2-oxoglutarate-dependent dioxigenases control glucosinolate biosynthesis in Arabidopsis. (2001) (https://pubmed.ncbi.nlm.nih.gov/11251105)	Authors
Kliebenstein DJ; Lambrix VM; Reichelt M; Gershenzon J; Mitchell-Olds T	Abstract

Secondary metabolites are a diverse set of plant compounds believed to have numerous functions in plant-environment interactions. The large chemical diversity of secondary metabolites undoubtedly arises from an equally diverse set of enzymes responsible for their biosynthesis. However, little is known about the evolution of enzymes involved in secondary metabolism. We are studying the biosynthesis of glucosinolates, a large group of secondary metabolites, in Arabidopsis to investigate the evolution of enzymes involved in secondary metabolism. Arabidopsis contains natural variations in the presence of methylsulfinylalkyl, alkenyl, and hydroxyalkyl glucosinolates. In this article, we report the identification of genes encoding two 2-oxoglutarate--dependent dioxigenases that are responsible for this variation. These genes, AOP2 and AOP3, which map to the same position on chromosome IV, result from an apparent gene duplication and control the conversion of methylsulfinylalkyl glucosinolate to either the alkenyl or the hydroxyalkyl form. By heterologous expression in Escherichia and the correlation of gene expression patterns to the glucosinolate phenotype, we show that AOP2 catalyzes the conversion of methylsulfinylalkyl glucosinolates to alkenyl glucosinolates. Conversely, AOP3 directs the formation of hydroxyalkyl glucosinolates from methylsulfinylalkyl glucosinolates. No ecotype coexpressed both genes. Furthermore, the absence of functional AOP2 and AOP3 leads to the accumulation of the precursor methylsulfinylalkyl glucosinolates. A third member of this gene family, AOP1, is present in at least two forms and found in all ecotypes examined. However, its catalytic role is still uncertain.

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)	Additional References
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RELATED GEPHE

3 (AOP2, MAM1, CYP81F2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702^/and+Trait=Glucosinolate content/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS