

	Gephebase Gene	GepheID
PAP1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=PAP1#gephebase-summary-title)	GP00001232	
	Entry Status	Arnoult
Published		Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait Category	
Coloration (anthocyanin accumulation under high-light and low-temperature stress) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (anthocyanin accumulation under high-light and low-temperature stress)^#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Ler0		Trait State in Taxon A	
Arabidopsis thaliana- Eri-1		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^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)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Eri-1	

MYB75	Generic Gene Name	Q9FE25 (http://www.uniprot.org/uniprot/Q9FE25)	UniProtKB Arabidopsis thaliana
	Synonyms		GenebankID or UniProtKB
ATMYB75; F25P12.92; F25P12_92; MYB DOMAIN PROTEIN 75; MYB75; MYELOBLASTOSIS PROTEIN 75; phosphatidic acid phosphatase 1; production of anthocyanin pigment 1; SIAA1; SUC-INDUCED ANTHOCYANIN ACCUMULATION 1; PAPI1; At1g56650		842120 (https://www.ncbi.nlm.nih.gov/nucore/842120)	
	String		
3702.AT1G56650.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT1G56650.1)			
	Sequence Similarities		
-			
	GO - Molecular Function		

GO:0003700 : DNA-binding transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)
GO:0043565 : sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)
GO:0044212 : transcription regulatory region DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0044212>)

GO - Biological Process

GO:0009733 : response to auxin (<https://www.ebi.ac.uk/QuickGO/term/GO:0009733>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0009651 : response to salt stress (<https://www.ebi.ac.uk/QuickGO/term/GO:0009651>)
GO:0009718 : anthocyanin-containing compound biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009718>)
GO:0009867 : jasmonic acid mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009867>)
GO:0009723 : response to ethylene (<https://www.ebi.ac.uk/QuickGO/term/GO:0009723>)
GO:0009753 : response to jasmonic acid
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009753>)
GO:0031542 : positive regulation of anthocyanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031542>)
GO:0019430 : removal of superoxide radicals
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019430>)
GO:0002239 : response to oomycetes
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002239>)
GO:0031540 : regulation of anthocyanin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031540>)
GO:0009745 : sucrose mediated signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009745>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title>)

Molecular Type

Gene Loss (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Loss~#gephebase-summary-title>)

Aberration Type

Deletion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Deletion~#gephebase-summary-title>)

Deletion Size

-

Molecular Details of the Mutation

several deletions in the promoter; first intron; second exon and 3' UTR region (putative loss of function)

Experimental Evidence

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

Main Reference

Natural variation for anthocyanin accumulation under high-light and low-temperature stress is attributable to the ENHANCER OF AG-4 2 (HUA2) locus in combination with PRODUCTION OF ANTHOCYANIN PIGMENT1 (PAP1) and PAP2. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25425527>)

Authors

Ilk N; Ding J; Ihnatowicz A; Koornneef M; Reymond M

Abstract

Growing conditions combining high light intensities and low temperatures lead to anthocyanin accumulation in plants. This response was contrasted between two Arabidopsis thaliana accessions, which were used to decipher the genetic and molecular bases underlying the variation of this response. Quantitative trait loci (QTLs) for flowering time (FT) and anthocyanin accumulation under a high-light and low-temperature scenario versus a control environment were mapped. Major QTLs were confirmed using near-isogenic lines. Candidate genes were examined using mutants and gene expression studies as well as transgenic complementation. Several QTLs were found for FT and for anthocyanin content, of which one QTL co-located at the ENHANCER OF AG-4 2 (HUA2) locus. That HUA2 is a regulator of both pathways was confirmed by the analysis of loss-of-function mutants. For a strong expression of anthocyanin, additional allelic variation was detected for the PRODUCTION OF ANTHOCYANIN PIGMENT1 (PAP1) and PAP2 genes which control the anthocyanin pathway. The genetic control of variation for anthocyanin content was dissected in A. thaliana and shown to be affected by a common regulator of flowering and anthocyanin biosynthesis together with anthocyanin-specific regulators.

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Additional References

Sucrose-specific induction of anthocyanin biosynthesis in Arabidopsis requires the MYB75/PAP1 gene. (2005) (<https://pubmed.ncbi.nlm.nih.gov/16299184>)

RELATED GEPHE

Related Genes

3 (HUA2, PAP2, phytochrome D (PHYD)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

poor mutational resolution ; high-light and low-temperature stress