GEPHE SUMMARY

Gephebase Gene

PAP1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PAP1^#gephebase-summary-title)

GepheID

GP00001232

Entry Status

Published

Main curator

Arnoult

PHENOTYPIC CHANGE

Trait Category

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

Trait

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 State in Taxon A

Arabidopsis thaliana- Ler0

Trait State in Taxon B

Arabidopsis thaliana- Eri-1

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- Ler0

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- Eri-1

GENOTYPIC CHANGE

Generic Gene Name

MYB75

Synonyms

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; PAP1; At1g56650

String

3702.AT1G56650.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G56650.1)

Sequence Similarities

-

GO - Molecular Function

UniProtKB Arabidopsis thaliana

Q9FE25 (http://www.uniprot.org/uniprot/Q9FE25)

GenebankID or UniProtKB

842120 (https://www.ncbi.nlm.nih.gov/nuccore/842120)

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.

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