GEPHE SUMMARY

Gephebase Gene
PAP2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^PAP2^#gephebase-summary-title)

GepheID
GP00001231

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
MYB90

Synonyms
ATMYB90; myb domain protein 90; PAP2; PRODUCTION OF ANTHOCYANIN PIGMENT 2; T27F4.14; T27F4_14; At1g66390

String
3702.AT1G66390.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT1G66390.1)

Sequence Similarities
-

GO - Molecular Function
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)

UniProtKB Arabidopsis thaliana
Q9ZTC3 (http://www.uniprot.org/uniprot/Q9ZTC3)

GenebankID or UniProtKB
842957 (https://www.ncbi.nlm.nih.gov/nuccore/842957)

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:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0080167 : response to karrikin (https://www.ebi.ac.uk/QuickGO/term/GO:0080167)

GO - Cellular Component

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

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

one SNP in the coding region and several in the putative promoter region

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

RELATED GEPHE

Related Genes

3 (HUA2, PAP1, 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