GEPHE SUMMARY

Gephebase Gene
MYB1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MYB1^#gephebase-summary-title)

GepheID
GP00002094

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Red flesh

Trait State in Taxon B
White flesh

Ancestral State
Taxon A

Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name
Raphanus sativus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Raphanus sativus^#gephebase-summary-title)

Common Name
radish

Synonyms
radish; Raphanus sativus L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Raphanus

Parent
Raphanus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3725)

NCBI Taxonomy ID
3726 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3726)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Raphanus sativus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Raphanus sativus^#gephebase-summary-title)

Common Name
radish

Synonyms
radish; Raphanus sativus L.

Rank
species

Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Raphanus

Parent
Raphanus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3725)

NCBI Taxonomy ID
3726 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3726)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
MYB1

Synonyms
Bv2g027795_jkkr; Bv_jkkr

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

GO - Biological Process
-

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

UniProtKB Beta vulgaris
M1ETA5 (http://www.uniprot.org/uniprot/M1ETA5)

GenebankID or UniProtKB
()

Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Epigenetic Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Epigenetic Change^#gephebase-summary-title)

Molecular Details of the Mutation

The taproot white-fleshed mutant is the result of altered DNA methylation in the RsMYB1 promoter. This heritable epigenetic change is due to a hypermethylated CACTA transposon (a 7372-bp TE) which induces the spreading of DNA methylation to the promoter region of RsMYB1. RsMYB1 expression is considerably downregulated and this inhibits anthocyanin biosynthesis in white-fleshed mutants.

Experimental Evidence

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

Main Reference

Transposon-induced methylation of the RsMYB1 promoter disturbs the anthocyanin accumulation in red-fleshed radish (Raphanus sativus L.). (2020) (https://pubmed.ncbi.nlm.nih.gov/31961436)

Authors

Wang Q; Wang Y; Sun H; Sun L; Zhang L

Abstract

Red-fleshed radish is a unique cultivar that is rich in anthocyanins beneficial to human health in taproot. However, the frequent occurrence of white-fleshed mutants affects the purity of commercially produced radish and mechanism has puzzled breeders for many years. In this study, we combined QTL-seq and transcriptome analyses to identify a candidate gene (RsMYB1) responsible for the anthocyanin accumulation in red-fleshed radish. However, no sequence variation was found in the coding and regulatory regions of the RsMYB1 genes of the red-fleshed (MTH01) and white-fleshed (JC01) lines, and a 7,372-bp CACTA transposon in the RsMYB1 promoter region occurred in both lines. A subsequent analysis suggested that the taproot white-fleshed mutant was the result of altered DNA methylation in the RsMYB1 promoter. This heritable epigenetic change was due to the hypermethylated CACTA transposon, which induced the spreading of DNA methylation to the promoter region of RsMYB1. Thus, RsMYB1 expression was considerably downregulated, which inhibited anthocyanin biosynthesis in white-fleshed mutants. An examination of transgenic radish calli and the results of a virus-induced gene silencing experiment confirmed the RsMYB1 is responsible for anthocyanins accumulation. Moreover, the mutant phenotype was partially eliminated by a treatment with a demethylating agent. This study explained the molecular regulation mechanism of appearance white-fleshed mutant in red-fleshed radish.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

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