

GEPHE SUMMARY

	Gephebase Gene	GephelD
MYB1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=%MYB1%#gephebase-summary-title)	GP00002094	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

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

Taxon A	Latin Name	Taxon B	Latin Name
Raphanus sativus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Raphanus+sativus%#gephebase-summary-title)		Raphanus sativus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Raphanus+sativus%#gephebase-summary-title)	
radish	Common Name	radish	Common Name
radish; Raphanus sativus L.	Synonyms	radish; Raphanus sativus L.	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Raphanus	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliopsida; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Raphanus	Lineage
Raphanus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3725)	Parent	Raphanus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3725)	Parent
3726 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3726)	NCBI Taxonomy ID	3726 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3726)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

MYB1	Generic Gene Name	UniProtKB Beta vulgaris
Bv2g027795_jkkr; Bv_jkkr	Synonyms	GenebankID or UniProtKB
-	String	0
-	Sequence Similarities	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Biological Process	
-	GO - Cellular Component	
No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%No%#gephebase-summary-title)		Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular+Type=%Cis-regulatory%#gephebase-summary-title)		Molecular Type

Epigenetic Change ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Epigenetic Change%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27Epigenetic%20Change%27#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=%27Candidate Gene%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Candidate%20Gene%27#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.

© The Author(s) 2020. Published by Oxford University Press on behalf of the Society for Experimental Biology. All rights reserved. For permissions, please email: journals.permissions@oup.com.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@TE