

MdMYB110a (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^MdMYB110a^#gephebase-summary-title)	Gephebase Gene	GP00000640	GepheID
Published	Entry Status	Martin	Main curator

	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)	
	Trait
Coloration (fruit flesh) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (fruit flesh)^#gephebase-summary-title)	
	Trait State in Taxon A
Malus x domestica - Sciros	
	Trait State in Taxon B
Malus x domestica - red-fleshed cv Sangrado	
	Ancestral State
Data not curated	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)	

	Generic Gene Name	UniProtKB <i>Malus domestica</i>
-		
	Synonyms	GenebankID or UniProtKB
-		
	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)	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Molecular Details of the Mutation
unknown	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	Main Reference
An ancient duplication of apple MYB transcription factors is responsible for novel red fruit-flesh phenotypes. (2013) (https://pubmed.ncbi.nlm.nih.gov/23096157)	Authors
Chagnon D; Lin-Wang K; Espley RV; Volz RK; How NM; Rouse S; Brendolise C; Carlisle CM; Kumar S; De Silva N; Micheletti D; McGhie T; Crowhurst RN; Storey RD; Velasco R; Hellens RP; Gardiner SE; Allan AC	Abstract
Anthocyanin accumulation is coordinated in plants by a number of conserved transcription factors. In apple (<i>Malus domestica</i>), an R2R3 MYB transcription factor has been shown to control fruit flesh and foliage anthocyanin pigmentation (MYB10) and fruit skin color (MYB1). However, the pattern of expression and allelic variation at these loci does not explain all anthocyanin-related apple phenotypes. One such example is an open-pollinated seedling of cv Sangrado that has green foliage and develops red flesh in the fruit cortex late in maturity. We used methods that combine plant breeding, molecular biology, and genomics to identify duplicated MYB transcription factors that could control this phenotype. We then demonstrated that the red-flesh cortex phenotype is associated with enhanced expression of MYB110a, a paralog of MYB10. Functional characterization of MYB110a showed that it was able to up-regulate anthocyanin biosynthesis in tobacco (<i>Nicotiana tabacum</i>). The chromosomal location of MYB110a is consistent with a whole-genome duplication event that occurred during the evolution of apple within the Maloideae family. Both MYB10 and MYB110a have conserved function in some cultivars, but they differ in their expression pattern and response to fruit maturity.	
	Additional References

RELATED GEPHE

1 (MdMYB10) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^3750^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS