

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

	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)			
Taxon A		Taxon B	
Malus domestica (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Malus+domestica^#gephebase-summary-title)	Latin Name	Malus domestica (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Malus+domestica^#gephebase-summary-title)	Latin Name
apple	Common Name	apple	Common Name
	Synonyms		Synonyms
Malus communis; Malus pumila auct.; Malus pumila var. domestica; Malus sylvestris var. domestica; Malus x domestica; Pyrus malus; apple; apple tree; cultivated apple; Malus communis Desf.; Malus domestica Borkh., nom. cons. prop.; Malus pumila var. domestica (Borkh.) C.K.Schneid.; Malus sylvestris var. domestica (Borkh.) Mansf.; Pyrus malus L.		Malus communis; Malus pumila auct.; Malus pumila var. domestica; Malus sylvestris var. domestica; Malus x domestica; Pyrus malus; apple; apple tree; cultivated apple; Malus communis Desf.; Malus domestica Borkh., nom. cons. prop.; Malus pumila var. domestica (Borkh.) C.K.Schneid.; Malus sylvestris var. domestica (Borkh.) Mansf.; Pyrus malus L.	
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophytina; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Amygdaloideae; Maleae; Malus		cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophytina; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Amygdaloideae; Maleae; Malus	
Malus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3749)	Parent	Malus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3749)	Parent
3750 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3750)	NCBI Taxonomy ID	3750 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3750)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Malus x domestica - Sciros	Taxon A Description	Malus x domestica - red-fleshed cv Sangrado	Taxon B Description

GENOTYPIC CHANGE

-	Generic Gene Name	UniProtKB Malus domestica
-	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	

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

unknown

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title>)An ancient duplication of apple MYB transcription factors is responsible for novel red fruit-flesh phenotypes. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23096157/>)

Chagné 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

Anthocyanin accumulation is coordinated in plants by a number of conserved transcription factors. In apple (*Malus* Å— *domestica*), 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 (*Nicotiana tabacum*). 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.

RELATED GEPHE

1 (MdMYB10) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^3750^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS