

MdMYB10 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MdMYB10^#gephebase-summary-title)	Gephebase Gene	GP00000639	GepheID
Published	Entry Status	Martin	Main curator

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)		Trait Category	
Coloration (fruit flesh; foliage) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (fruit flesh; foliage)^#gephebase-summary-title)		Trait	
Malus x domestica - Sciros		Trait State in Taxon A	
Malus x domestica - red-fleshed 91.136 B6-77		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Latin Name		Latin Name	
Malus domestica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Malus+domestica^#gephebase-summary-title)		Malus domestica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Malus+domestica^#gephebase-summary-title)	
Common Name		Common Name	
apple		apple	
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.	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Amygdaloideae; Maleae; Malus		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Rosales; Rosaceae; Amygdaloideae; Maleae; Malus	
Parent		Parent	
Malus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3749)		Malus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3749)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
3750 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3750)		3750 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3750)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Malus x domestica - Sciros		Malus x domestica - red-fleshed 91.136 B6-77	

MYB1	Generic Gene Name	UniProtKB Malus domestica
	Synonyms	A0SQ35 (http://www.uniprot.org/uniprot/A0SQ35)
MdMYBA; MYB10	String	GenebankID or UniProtKB
-		DQ886414 (https://www.ncbi.nlm.nih.gov/nuccore/DQ886414)
-	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
Mapping a candidate gene (MdMYB10) for red flesh and foliage colour in apple. (2007) (https://pubmed.ncbi.nlm.nih.gov/17608951)	Authors
Chagn�� D; Carlisle CM; Blond C; Volz RK; Whitworth CJ; Oraguzie NC; Crowhurst RN; Allan AC; Espley RV; Hellens RP; Gardiner SE	Abstract

Integrating plant genomics and classical breeding is a challenge for both plant breeders and molecular biologists. Marker-assisted selection (MAS) is a tool that can be used to accelerate the development of novel apple varieties such as cultivars that have fruit with anthocyanin through to the core. In addition, determining the inheritance of novel alleles, such as the one responsible for red flesh, adds to our understanding of allelic variation. Our goal was to map candidate anthocyanin biosynthetic and regulatory genes in a population segregating for the red flesh phenotypes.

We have identified the Rni locus, a major genetic determinant of the red foliage and red colour in the core of apple fruit. In a population segregating for the red flesh and foliage phenotype we have determined the inheritance of the Rni locus and DNA polymorphisms of candidate anthocyanin biosynthetic and regulatory genes. Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs) in the candidate genes were also located on an apple genetic map. We have shown that the MdMYB10 gene co-segregates with the Rni locus and is on Linkage Group (LG) 09 of the apple genome.

We have performed candidate gene mapping in a fruit tree crop and have provided genetic evidence that red colouration in the fruit core as well as red foliage are both controlled by a single locus named Rni. We have shown that the transcription factor MdMYB10 may be the gene underlying Rni as there were no recombinants between the marker for this gene and the red phenotype in a population of 516 individuals. Associating markers derived from candidate genes with a desirable phenotypic trait has demonstrated the application of genomic tools in a breeding programme of a horticultural crop species.

	Additional References
An ancient duplication of apple MYB transcription factors is responsible for novel red fruit-flesh phenotypes. (2013) (https://pubmed.ncbi.nlm.nih.gov/23096157)	

RELATED GEPHE

	Related Genes
1 (MdMYB110a) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~3750^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS