

GEPHE SUMMARY

VvMYBA3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~VvMYBA3~#gephebase-summary-title)	Gephebase Gene	GP00001196	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)		Trait Category	
Coloration (fruit) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration(fruit)~#gephebase-summary-title)		Trait	
Vitis vinifera - Syrah		Trait State in Taxon A	
Vitis vinifera - Grenache with white berries		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vitisvinifera~#gephebase-summary-title)		Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vitisvinifera~#gephebase-summary-title)	
wine grape		wine grape	
Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.		Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis	
Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)		Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)	
29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29760)		29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29760)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Vitis vinifera - Syrah		Vitis vinifera - Grenache	

GENOTYPIC CHANGE

VvmybA3	Generic Gene Name	Q6L9M7 (http://www.uniprot.org/uniprot/Q6L9M7)	UniProtKB Vitis vinifera
MybA3; MYBA3; VIT_02s0033g00450	Synonyms	FN596505 (https://www.ncbi.nlm.nih.gov/nuccore/FN596505)	GenebankID or UniProtKB
29760.VIT_02s0033g00450.t01 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=29760.VIT_02s0033g00450.t01)	String		
-	Sequence Similarities		
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)	GO - Molecular Function		
GO:0044212 : transcription regulatory region DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0044212)	GO - Biological Process		

GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)	
GO - Cellular Component	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	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
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title)	Molecular Details of the Mutation
Substitution in promoter	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Main Reference
Quantitative genetic bases of anthocyanin variation in grape (<i>Vitis vinifera</i> L. ssp. <i>sativa</i>) berry: a quantitative trait locus to quantitative trait nucleotide integrated study. (2009) (https://pubmed.ncbi.nlm.nih.gov/19720862)	Authors
Fournier-Level A; Le Cunff L; Gomez C; Doligez A; Ageorges A; Roux C; Bertrand Y; Souquet JM; Cheynier V; This P	Abstract

The combination of QTL mapping studies of synthetic lines and association mapping studies of natural diversity represents an opportunity to throw light on the genetically based variation of quantitative traits. With the positional information provided through quantitative trait locus (QTL) mapping, which often leads to wide intervals encompassing numerous genes, it is now feasible to directly target candidate genes that are likely to be responsible for the observed variation in completely sequenced genomes and to test their effects through association genetics. This approach was performed in grape, a newly sequenced genome, to decipher the genetic architecture of anthocyanin content. Grapes may be either white or colored, ranging from the lightest pink to the darkest purple tones according to the amount of anthocyanin accumulated in the berry skin, which is a crucial trait for both wine quality and human nutrition. Although the determinism of the white phenotype has been fully identified, the genetic bases of the quantitative variation of anthocyanin content in berry skin remain unclear. A single QTL responsible for up to 62% of the variation in the anthocyanin content was mapped on a Syrah x Grenache F(1) pseudo-testcross. Among the 68 unigenes identified in the grape genome within the QTL interval, a cluster of four Myb-type genes was selected on the basis of physiological evidence (VvMybA1, VvMybA2, VvMybA3, and VvMybA4). From a core collection of natural resources (141 individuals), 32 polymorphisms revealed significant association, and extended linkage disequilibrium was observed. Using a multivariate regression method, we demonstrated that five polymorphisms in VvMybA genes except VvMybA4 (one retrotransposon, three single nucleotide polymorphisms and one 2-bp insertion/deletion) accounted for 84% of the observed variation. All these polymorphisms led to either structural changes in the MYB proteins or differences in the VvMybAs promoters. We concluded that the continuous variation in anthocyanin content in grape was explained mainly by a single gene cluster of three VvMybA genes. The use of natural diversity helped to reduce one QTL to a set of five quantitative trait nucleotides and gave a clear picture of how isogenes combined their effects to shape grape color. Such analysis also illustrates how isogenes combine their effect to shape a complex quantitative trait and enables the definition of markers directly targeted for upcoming breeding programs.	Additional References
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RELATED GEPHE

3 (VvMYBA1, VvMybA1 VvMybA2 VvMybA3 and VvMybA4, VvMYBA2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~29760~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS