

GEPHE SUMMARY

VvMYBA1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^VvMYBA1^#gephebase-summary-title)	Gephebase Gene	GP00002099	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=Morphology^#gephebase-summary-title)	Trait Category
Coloration (fruit) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (fruit)^#gephebase-summary-title)	Trait
Vitis vinifera - white-skinned cultivar Italia	Trait State in Taxon A
Vitis vinifera - pink-skinned cultivar Benitaka	Trait State in Taxon B
Taxon A	Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=Domesticated^#gephebase-summary-title)	Taxonomic Status

Taxon A	Latin Name	Taxon B	Latin Name
Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Vitis+vinifera^#gephebase-summary-title)	Common Name	Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Vitis+vinifera^#gephebase-summary-title)	Common Name
wine grape	Synonyms	wine grape	Synonyms
Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.	Rank	Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis	Parent	cellular organisms; Eukaryota; Viriplantae; Streptophytina; Embryophytina; Tracheophytina; Euphyllophyta; Spermatophytina; Magnoliophytina; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis	Parent
Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)	NCBI Taxonomy ID	Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)	NCBI Taxonomy ID
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)	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
cv Italia™	Taxon A Description	cv. Benitaka™	Taxon B Description

GENOTYPIC CHANGE

VvmybA1	Generic Gene Name	UniProtKB Vitis vinifera
mybA; MybA3; mybA1; VVMYBA1; VvmybA3; MYBA1; VIT_02s0033g00410	Synonyms	GenebankID or UniProtKB
29760.VIT_02s0033g00410.t01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=29760.VIT_02s0033g00410.t01)	String	FN596505 (https://www.ncbi.nlm.nih.gov/nucore/FN596505)
-	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

Other (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Other%#gephebase-summary-title>) Molecular Type

Deletion (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Deletion%#gephebase-summary-title>) Aberration Type

10-100 kb Deletion Size

homologous recombination between the non-functional allele of MybA1 and the truncated MybA3 gene at their promoter region, resulting in the recovery of MybA1 genomic integrity (and therefore its transcription) on cv. 'Benitaka'. The VvmybA1 locus of 'Benitaka' is heterozygous for the VvmybA1a allele (non-functional) and a novel VvmybA1(BEN) allele. VvmybA1(BEN) restores VvmybA1 transcripts. Molecular Details of the Mutation

Candidate Gene (<https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gephebase-summary-title>) Experimental Evidence

Color recovery in berries of grape (*Vitis vinifera* L.) 'Benitaka', a bud sport of 'Italia', is caused by a novel allele at the VvmybA1 locus. (2009) (<https://pubmed.ncbi.nlm.nih.gov/26493136>) Main Reference

Azuma A; Kobayashi S; Goto-Yamamoto N; Shiraishi M; Mitani N; Yakushiji H; Koshita Y Authors

Color mutations in grape berry skin are relatively frequent events, and can be easily seen in the vineyard. Both light-red-skinned 'Ruby Okuyama' and more intense and uniform rosy-skinned 'Benitaka' (*Vitis vinifera* L.) are bud sports of white-skinned 'Italia'. Previously, we reported that 'Ruby Okuyama' was caused by the recovery of VvmybA1 expression, which may have occurred as a result of intra-LTR (long terminal repeat) recombination within a retrotransposon, Gret1. However, the molecular basis of the color recovery in 'Benitaka' has not been elucidated so far. Here, we found that the VvmybA1 locus of 'Benitaka' is heterozygous for the VvmybA1a allele (non-functional) and a novel VvmybA1(BEN) allele, and that VvmybA1(BEN) restored VvmybA1 transcripts. We hypothesized that VvmybA1(BEN) allele was caused by homologous recombination between VvmybA1a and VvmybA3. In addition, the content and composition of anthocyanins in berry skins differed greatly between 'Ruby Okuyama' and 'Benitaka'. The levels of expression of the genes for flavonoid 3',5'-hydroxylase (F3'5'H), O-methyltransferase (OMT), and glutathione-S-transferase (GST) were associated with differences in the anthocyanin content and composition between the two cultivars. Abstract

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Additional References

RELATED GEPHE

Related Genes

3 (VvMybA1 VvMybA2 VvMybA3 and VvMybA4, VvMYBA2, VvMYBA3) (<https://www.gephebase.org/search-criteria/?or+TaxonID=%29760%and+Trait=Coloration%and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

5 (<https://www.gephebase.org/search-criteria/?or+Gene=Gephebase=%VvMYBA1%and+TaxonID=%29760%or+Gene=Gephebase=%VvMYBA1%and+TaxonID=%29760%#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS