# GEPHE SUMMARY

Gephebase Gene

VvMYBA1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^VvMYBA1^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002097

Main curator

Courtier

# PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Coloration (fruit) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (fruit)^#gephebase-summary-title)

Trait State in Taxon A

Vitis vinifera - red-skinned cultivar

Trait State in Taxon B

Vitis vinifera - pink-skinned cultivar

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

## Taxon A

Latin Name

Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Vitis vinifera^#gephebase-summary-title)

Common Name

wine grape

Synonyms

Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; 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

29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 29760 )

is Taxon A an Infraspecies?

No

## Taxon B

Latin Name

Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Vitis vinifera^#gephebase-summary-title)

Common Name

wine grape

Synonyms

Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; 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

29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 29760 )

is Taxon B an Infraspecies?

No

# GENOTYPIC CHANGE

Generic Gene Name

VvmybA1

Synonyms

mybA; MybA3; mybA1; VVMYBA1; VvmybA3; MYBA1; VIT_02s0033g00410

String

29760.VIT_02s0033g00410.t01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 29760.VIT_02s0033g00410.t01 )

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)

UniProtKB Vitis vinifera

Q6L973 (http://www.uniprot.org/uniprot/Q6L973)

GenebankID or UniProtKB

FN596505 (https://www.ncbi.nlm.nih.gov/nuccore/FN596505)

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

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)

Insertion Size

10-99 bp

Molecular Details of the Mutation

33â€‰bp insertion in the second intron of the MYBA1 red allele which affects messenger RNA (mRNA) stability - 16 bp of the 3′ end in the insertion is a key structure for a defect in splicing of MybA1 transcripts

Experimental Evidence

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

Main Reference

Pink-colored grape berry is the result of short insertion in intron of color regulatory gene. (2011) (https://pubmed.ncbi.nlm.nih.gov/21695059)

Authors

Shimazaki M; Fujita K; Kobayashi H; Suzuki S

Abstract

We report here that pink grape berries were obtained by a short insertion in the intron of the MybA1 gene, a gene that regulates grape berry color. Genetic variation was detected among the MybA1 genes from grapes cultivated worldwide. PCR analysis of the MybA1 gene demonstrated that the size of the MybA1 gene in the red allele differs among grapes. Oriental V. vinifera bearing pink berries has the longest MybA1 gene among grapes, whereas the shortest MybA1 gene was detected in occidental V. vinifera grapes. The nucleotide sequences of the MybA1 genes demonstrated that oriental V. vinifera has two additional gene fragments (44 bp and 111 bp) in the promoter region of the MybA1 gene in the red allele and another 33 bp fragment in the second intron of the MybA1 gene in the red allele. The short insertion in the intron decreased the transcription activity in the model system and retained MybA1 transcripts with unspliced intron in the total RNA. From the experiments using deletion mutants of the 33 bp short insertion, 16 bp of the 3′ end in the insertion is a key structure for a defect in splicing of MybA1 transcripts. Thus, a weakly colored grape berry might be a result of the short insertion in the intron of a color regulatory gene. This is new evidence concerning the molecular mechanism of the fate of grape berry color. These findings are expected to contribute to the further understanding of the color variation in grape berries, which is correlated with the evolutional events occurring in the MybA1 gene of grapes.

Additional References

## RELATED GEPHE

Related Genes

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

Related Haplotypes

5 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^VvMYBA1^/and+Taxon ID=^29760^/or+Gene Gephebase=^VvMYBA1^/and+Taxon ID=^29760^#gephebase-summary-title)

## EXTERNAL LINKS

## COMMENTS