GEPHE SUMMARY

Gephebase Gene
VvMYBA3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^VvMYBA3^#gephebase-summary-title)

GepheID
GP00001196

Entry Status
Published

Main curator
Martin

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 - Syrah

Trait State in Taxon B
Vitis vinifera - Grenache with white berries

Ancestral State
Data not curated

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?
Yes

Taxon A Description
Vitis vinifera - Syrah

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?
Yes

Taxon B Description
Vitis vinifera - Grenache

GENOTYPIC CHANGE

Generic Gene Name
VvmybA3

Synonyms
MybA3; MYBA3; VIT_02s0033g00450

String
29760.VIT_02s0033g00450.t01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=29760.VIT_02s0033g00450.t01)

Sequence Similarities
-

GO - Molecular Function
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0044212 : transcription regulatory region DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0044212)

GO - Biological Process

UniProtKB Vitis vinifera
Q6L9M7 (http://www.uniprot.org/uniprot/Q6L9M7)

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

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 (Vitis vinifera L. ssp. sativa) 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

RELATED GEPHE

Related Genes

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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS