GEPHE SUMMARY

Gephebase Gene

VvMYBA2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^VvMYBA2^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001195

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

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?

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

VvmybA2

Synonyms

VIT_02s0033g00390

String

29760.VIT_02s0033g00390.t01 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 29760.VIT_02s0033g00390.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

Q6L9M8 (http://www.uniprot.org/uniprot/Q6L9M8)

GenebankID or UniProtKB

AB097924 (https://www.ncbi.nlm.nih.gov/nuccore/AB097924)

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)

Mutation #1

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

deletion of a dinucleotide (CA) in the white allele altering the reading frame at amino acid 258; terminating the protein after the addition of another seven amino acids - Frameshift leading to a truncated 265-amino-acid protein instead of 344

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

Mutation #2

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

SNP

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	CGN	CTN	-
Amino-acid	Arg	Leu	44

Main Reference

White grapes arose through the mutation of two similar and adjacent regulatory genes. (2007) (https://pubmed.ncbi.nlm.nih.gov/17316172)

Authors

Walker AR; Lee E; Bogs J; McDavid DA; Thomas MR; Robinson SP

Abstract

Most of the thousands of grapevine cultivars (Vitis vinifera L.) can be divided into two groups, red and white, based on the presence or absence of anthocyanin in the berry skin, which has been found from genetic experiments to be controlled by a single locus. A regulatory gene, VvMYBA1, which could activate anthocyanin biosynthesis in a transient assay, was recently shown not to be transcribed in white berries due to the presence of a retrotransposon in the promoter. We have found that the berry colour locus comprises two very similar genes, VvMYBA1 and VvMYBA2, located on a single bacterial artificial chromosome. Either gene can regulate colour in the grape berry. The white berry allele of VvMYBA2 is inactivated by two non-conservative mutations, one leads to an amino acid substitution and the other to a frame shift resulting in a smaller protein. Transient assays showed that either mutation removed the ability of the regulator to switch on anthocyanin biosynthesis. VvMYBA2 sequence analyses, together with marker information, confirmed that 55 white cultivars all contain the white berry allele, but not red berry alleles. These results suggest that all extant white cultivars of grape vines have a common origin. We conclude that rare mutational events occurring in two adjacent genes were essential for the genesis of the white grapes used to produce the white wines and white table grapes we enjoy today.

Additional References

RELATED GEPHE

Related Genes

3 (VvMYBA1, VvMybA1 VvMybA2 VvMybA3 and VvMybA4, VvMYBA3) (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

@SeveralMutationsWithEffect