

GEPHE SUMMARY

Gephebase Gene		GepheID
VvMybA1 VvMybA2 VvMybA3 and VvMybA4 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~VvMybA1+VvMybA2+VvMybA3+and+VvMybA4^#gephebase-summary-title)	GP00002098	
	Courtier	Main curator
Published	Entry Status	

PHENOTYPIC CHANGE

Trait Category		Trait	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)		Coloration (fruit) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+(fruit)^#gephebase-summary-title)	
Trait State in Taxon A		Trait State in Taxon B	
Vitis vinifera - Tempranillo Tinto with black berries		Vitis vinifera - Tempranillo Blanco (TB) with white berries	
Ancestral State		Taxonomic Status	
Taxon A		Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title)	
Taxon A		Taxon B	
Latin Name		Latin Name	
Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vitis+vinifera^#gephebase-summary-title)		Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Vitis+vinifera^#gephebase-summary-title)	
Common Name		Common Name	
wine grape		wine grape	
Synonyms		Synonyms	
Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.		Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis	
Parent		Parent	
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)	
NCBI Taxonomy ID		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)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Vitis vinifera - Tempranillo Tinto		Vitis vinifera - Tempranillo Blanco (TB)	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Vitis vinifera
VvmybA3	Q6L9M7 (http://www.uniprot.org/uniprot/Q6L9M7)	
Synonyms		GenebankID or UniProtKB
MybA3; MYBA3; VIT_02s0033g00450	0	
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

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

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

Molecular Type

Gene Loss ([https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Loss~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Gene+Loss~#gephebase-summary-title))

Aberration Type

Complex Change ([https://www.gephebase.org/search-criteria?/and+Aberration Type=~Complex Change~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Complex+Change~#gephebase-summary-title))

Molecular Details of the Mutation

catastrophic genome rearrangement: intrachromosomal and interchromosomal translocations and the deletion of 313 genes including the loss of the functional copy for the MYB transcription factors required for anthocyanin pigmentation in the berry skin

Experimental Evidence

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

Main Reference

Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. (2017) (<https://pubmed.ncbi.nlm.nih.gov/28811336>)

Authors

Carbonell-Bejerano P; Royo C; Torres-PÃ©rez R; Grimplet J; Fernandez L; Franco-Zorrilla JM; Lijavetzky D; Baroja E; MartÃ±ez J; GarcÃa-Escudero E; IbÃ±ez J; MartÃ±ez-Zapater JM

Abstract

Grape (*Vitis vinifera*) color somatic variants that can be used to develop new grapevine cultivars occasionally appear associated with deletion events of uncertain origin. To understand the mutational mechanisms generating somatic structural variation in grapevine, we compared the Tempranillo Blanco (TB) white berry somatic variant with its black berry ancestor, Tempranillo Tinto. Whole-genome sequencing uncovered a catastrophic genome rearrangement in TB that caused the hemizygous deletion of 313 genes, including the loss of the functional copy for the MYB transcription factors required for anthocyanin pigmentation in the berry skin. Loss of heterozygosity and decreased copy number delimited interspersed monosomic and disomic regions in the right arm of linkage groups 2 and 5. At least 11 validated clustered breakpoints involving intrachromosomal and interchromosomal translocations between three linkage groups flanked the deleted fragments, which, according to segregation analyses, are phased in a single copy of each of the affected chromosomes. These hallmarks, along with the lack of homology between breakpoint joins and the randomness of the order and orientation of the rearranged fragments, are all consistent with a chromothripsis-like pattern generated after chromosome breakage and illegitimate rejoining. This unbalanced genome reshuffling has additional consequences in reproductive development. In TB, lack of sexual transmission of rearranged chromosomes associates with low gamete viability, which compromises fruit set and decreases fruit production. Our findings show that catastrophic genome rearrangements arise spontaneously and stabilize during plant somatic growth. These dramatic rearrangements generate new interesting phenotypes that can be selected for the improvement of vegetatively propagated plant species.

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Additional References

RELATED GEPHE

Related Genes

3 (VvMYBA1, VvMYBA2, VvMYBA3) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~29760~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title](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