

GEPHE SUMMARY

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

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=~Morphology^#gephebase-summary-title)</p> <p>Coloration (fruit) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration (fruit)^#gephebase-summary-title)</p> <p>Vitis vinifera - Tempranillo Tinto with black berries</p> <p>Vitis vinifera - Tempranillo Blanco (TB) with white berries</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Domesticated^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Vitis vinifera^#gephebase-summary-title)</p> <p>Common Name</p> <p>wine grape</p> <p>Synonyms</p> <p>Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis</p> <p>Parent</p> <p>Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)</p> <p>NCBI Taxonomy ID</p> <p>29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29760)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Vitis vinifera - Tempranillo Tinto</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Vitis vinifera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Vitis vinifera^#gephebase-summary-title)</p> <p>Common Name</p> <p>wine grape</p> <p>Synonyms</p> <p>Vitis vinifera subsp. vinifera; wine grape; Vitis vinifera L.</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; rosids incertae sedis; Vitales; Vitaceae; Viteae; Vitis</p> <p>Parent</p> <p>Vitis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3603)</p> <p>NCBI Taxonomy ID</p> <p>29760 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29760)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Vitis vinifera - Tempranillo Blanco (TB)</p>
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GENOTYPIC CHANGE

<p>VvmybA3</p> <p>MybA3; MYBA3; VIT_02s0033g00450</p> <p>29760.VIT_02s0033g00450.t01 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=29760.VIT_02s0033g00450.t01)</p> <p>-</p> <p>GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)</p> <p>GO:0044212 : transcription regulatory region DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0044212)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Vitis vinifera</p> <p>Q6L9M7 (http://www.uniprot.org/uniprot/Q6L9M7)</p> <p>GenebankID or UniProtKB</p> <p>0</p>
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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>)

Molecular Type

Gene Loss (<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>)

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>)

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¡Ã±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>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS