

## GEPHE SUMMARY

<p>SIMYBATV (<a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^SIMYBATV^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^SIMYBATV^#gephebase-summary-title</a>)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001906</p> <p>Courtier</p>	<p>GepheID</p> <p>Main curator</p>
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## PHENOTYPIC CHANGE

<p>Morphology, Physiology (<a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^/and+Trait+Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^/and+Trait+Category=^Physiology^#gephebase-summary-title</a>)</p> <p>Coloration (anthocyanin accumulation in fruits) (<a href="https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+(anthocyanin+accumulation+in+fruits)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+(anthocyanin+accumulation+in+fruits)^#gephebase-summary-title</a>)</p> <p>domesticated tomato</p> <p>atroviolacium locus - enhances anthocyanin accumulation when introgressed into domesticated tomato</p> <p>Taxon A</p> <p>Intraspecific (<a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title</a>)</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>Solanum lycopersicum (<a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+lycopersicum^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+lycopersicum^#gephebase-summary-title</a>)</p> <p>tomato</p> <p>Lycopersicon esculentum var. esculentum; Solanum esculentum; Solanum lycopersicum var. humboldtii; tomato; Lycopersicon esculentum Mill.; Solanum esculentum Dunal; Solanum lycopersicum L.; Lycopersicon lycopersicum; Lycopersicum esculentum; Solanum lycopersicon</p> <p>species</p> <p>cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum; Lycopersicon</p> <p>Lycopersicon () - (Rank: subgenus) (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274</a>)</p> <p>4081 (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4081">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4081</a>)</p> <p>No</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p>
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## GENOTYPIC CHANGE

<p>CPC</p> <p>CAPRICE; F11C10.10; MYB FAMILY TRANSCRIPTION FACTOR CPC; At2g46410</p> <p>3702.AT2G46410.1 (<a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G46410.1">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=3702.AT2G46410.1</a>)</p> <p>-</p> <p>GO:0003700 : DNA-binding transcription factor activity (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003700">https://www.ebi.ac.uk/QuickGO/term/GO:0003700</a>)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>O22059 (<a href="http://www.uniprot.org/uniprot/O22059">http://www.uniprot.org/uniprot/O22059</a>)</p> <p>()</p> <p>-</p>	<p>UniProtKB Arabidopsis thaliana</p> <p>GenebankID or UniProtKB</p>
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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:0009751 : response to salicylic acid  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009751>)  
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)  
GO:0009753 : response to jasmonic acid  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009753>)  
GO:0009913 : epidermal cell differentiation  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009913>)  
GO:0010063 : positive regulation of trichoblast fate specification  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010063>)  
GO:0010376 : stomatal complex formation  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010376>)

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

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

Aberration Type

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

Insertion Size

1-9 bp

Molecular Details of the Mutation

SIMYBATV encodes a R3 MYB transcription factor. 4-bp insertion predicted to result in a frame-shift that would alter the protein sequence from amino-acid position 20 onwards by inducing premature termination of translation including the R3/bHLH-binding domain

Experimental Evidence

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

Main Reference

A putative R3 MYB repressor is the candidate gene underlying atroviolacium, a locus for anthocyanin pigmentation in tomato fruit. (2017) (<https://pubmed.ncbi.nlm.nih.gov/29186488>)

Authors

Cao X; Qiu Z; Wang X; Van Giang T; Liu X; Wang J; Wang X; Gao J; Guo Y; Du Y; Wang G; Huang Z

Abstract

Anthocyanins are potential health-promoting compounds in the human diet. The atv (atroviolacium) locus, derived from the wild tomato species *Solanum cheesmaniae*, has been shown to enhance anthocyanin pigmentation in tomato fruit when it co-exists with either the Aft (Anthocyanin fruit) or the Abg (Aubergine) locus. In the present study, the atv locus was fine-mapped to an approximately 5.0-kb interval on chromosome 7. A putative R3 MYB repressor was identified in this interval and is hereby designated as SIMYBATV. The allele of SIMYBATV underlying the atv locus harbored a 4-bp insertion in its coding region, which is predicted to result in a frame-shift and premature protein truncation. The other candidate R3 MYB and R2R3 MYB repressors of anthocyanin biosynthesis were also identified in tomato via a genome-wide search. Transcriptional analysis showed that most of the structural genes and several regulatory genes of anthocyanin biosynthesis were up-regulated in the tomato SIMYBATV mutant lines. These findings may facilitate the elucidation of the molecular mechanisms underlying anthocyanin pigmentation in tomato fruit and help in the marker-assisted selection of anthocyanin-enriched tomato cultivars.

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Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

This mutation comes from the wild relative of tomato: *S. cheesmaniae*. The locus was introduced into varieties of domesticated tomatoes such as the variety Indigo Rose. QTL mapping between Indigo Rose and Heinz1706 (considered as wild-type).

