

GEPHE SUMMARY

	Gephebase Gene	GepheID
SIMYBATV (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SIMYBATV^#gephebase-summary-title)	GP00001906	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

Morphology, Physiology (<https://www.gephebase.org/search-criteria?/and+Trait>
Category=^Morphology^/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Coloration (anthocyanin accumulation in fruits) (<https://www.gephebase.org/search-criteria?/and+Trait=^Coloration%20%28anthocyanin%20accumulation%20in%20fruits%29^#gephebase-summary-title>)

Trait State in Taxon A

domesticated tomato

Trait State in Taxon B

atrovilacum locus - enhances anthocyanin accumulation when introgressed into
domesticated tomato

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (<https://www.gephebase.org/search-criteria?/and+Taxonomic>
Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Solanum lycopersicum
(<https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+lycopersicum^#gephebase-summary-title>)

Common Name

tomato

Synonyms

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*

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta;
Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae;
eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
Solanoideae; Solaneae; Solanum; *Lycopersicon*

Parent

Lycopersicon () - (Rank: subgenus)

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274>)

NCBI Taxonomy ID

4081

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4081>)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Solanum cheesmaniae

(<https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Solanum+cheesmaniae^#gephebase-summary-title>)

Common Name

-

Synonyms

Lycopersicon cheesmaniae; *Lycopersicon cheesmanii*; non *Solanum cheesmanii* Geras.;
Lycopersicon cheesmaniae L.Riley; *Solanum cheesmaniae* (L.Riley) Fosberg

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta;
Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae;
eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
Solanoideae; Solaneae; Solanum; *Lycopersicon*

Parent

Lycopersicon () - (Rank: subgenus)

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274>)

NCBI Taxonomy ID

142759

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=142759>)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
CPC	O22059 (http://www.uniprot.org/uniprot/O22059)	
	Synonyms	GenebankID or UniProtKB
CAPRICE; F11C10.10; MYB FAMILY TRANSCRIPTION FACTOR CPC; At2g46410	0	
3702.AT2G46410.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT2G46410.1)	String	
	Sequence Similarities	
-	GO - Molecular Function	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		

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=%27Yes%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%27Yes%27#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Coding%27#gephebase-summary-title))

Aberration Type

Insertion ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Insertion%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27Insertion%27#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=%27Linkage Mapping%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Linkage%20Mapping%27#gephebase-summary-title))

Main Reference

A putative R3 MYB repressor is the candidate gene underlying atroviolacum, 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* (*atroviolacum*) 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

No matches found.

Related Genes

No matches found.

Related Haplotypes

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).

