GEPHE SUMMARY

Gephebase Gene

VTE3(1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^VTE3(1)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001684

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

Vitamin-E synthesis (https://www.gephebase.org/search-criteria?/and+Trait=^Vitamin-E synthesis^#gephebase-summary-title)

Trait State in Taxon A

Solanum lycopersicum domesticated - low total- and alpha-tocopherol content

Trait State in Taxon B

Solanum lycopersicum domesticated - high total- and alpha-tocopherol content

Ancestral State

Unknown

Taxonomic Status

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

	Taxon A	Taxon B
Latin Name	Solanum lycopersicum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Solanum lycopersicum^#gephebase-summary-title)	Solanum lycopersicum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Solanum lycopersicum^#gephebase-summary-title)
Common Name	tomato	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	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	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	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)	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)	4081 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4081)
is Taxon A an Infraspecies? / is Taxon B an Infraspecies?	No	No

GENOTYPIC CHANGE

Generic Gene Name

VTE3

Synonyms

ALBINO OR PALE GREEN MUTANT 1; E37; IEP37; INNER ENVELOPE PROTEIN 37; VITAMIN E DEFECTIVE 3; VTE3; APG1; IE37; At3g63410; MAA21.40

String

3702.AT3G63410.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT3G63410.1)

Sequence Similarities

Belongs to the class I-like SAM-binding methyltransferase superfamily. MPBQ/MBSQ MT family.

GO - Molecular Function

GO:0102550 : 2-methyl-6-geranylgeranyl-1,4-benzoquinol methyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102550)

UniProtKB Arabidopsis thaliana

Q9LY74 (http://www.uniprot.org/uniprot/Q9LY74)

GenebankID or UniProtKB

()

GO:0051741 : 2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051741)
GO:0008757 : S-adenosylmethionine-dependent methyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008757)

GO - Biological Process

GO:0010236 : plastoquinone biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0010236)
GO:0010189 : vitamin E biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0010189)

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0009507 : chloroplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009507)
GO:0009941 : chloroplast envelope (https://www.ebi.ac.uk/QuickGO/term/GO:0009941)
GO:0009536 : plastid (https://www.ebi.ac.uk/QuickGO/term/GO:0009536)
GO:0009706 : chloroplast inner membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0009706)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

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Experimental Evidence

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

Main Reference

Natural occurring epialleles determine vitamin E accumulation in tomato fruits. (2014) (https://pubmed.ncbi.nlm.nih.gov/24967512)

Authors

Quadrana L; Almeida J; AsÃs R; Duffy T; Dominguez PG; BermÃºdez L; Conti G; CorrÃªa da Silva JV; Peralta IE; Colot V; Asurmendi S; Fernie AR; Rossi M; Carrari F

Abstract

Vitamin E (VTE) content is a low heritability nutritional trait for which the genetic determinants are poorly understood. Here, we focus on a previously detected major tomato VTE quantitative trait loci (QTL; mQTL(9-2-6)) and identify the causal gene as one encoding a 2-methyl-6-phytylquinol methyltransferase (namely VTE3(1)) that catalyses one of the final steps in the biosynthesis of Î³- and Î±-tocopherols, which are the main forms of VTE. By reverse genetic approaches, expression analyses, siRNA profiling and DNA methylation assays, we demonstrate that mQTL(9-2-6) is an expression QTL associated with differential methylation of a SINE retrotransposon located in the promoter region of VTE3(1). Promoter DNA methylation can be spontaneously reverted leading to different epialleles affecting VTE3(1) expression and VTE content in fruits. These findings indicate therefore that naturally occurring epialleles are responsible for regulation of a nutritionally important metabolic QTL and provide direct evidence of a role for epigenetics in the determination of agronomic traits.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS