

GEPHE SUMMARY

| | | | |
|---|----------------|------------|--------------|
| VTE3(1) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^VTE3(1)^#gephebase-summary-title) | Gephebase Gene | GP00001684 | GepheID |
| Published | Entry Status | Courtier | Main curator |
| | | | |

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 | Latin Name | 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) | |
| tomato | Common Name | tomato | Common Name |
| 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 | 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 | Synonyms |
| species | Rank | species | Rank |
| cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Iamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum; Lycopersicon | Lineage | cellular organisms; Eukaryota; Viriplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphylophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; asterids; Iamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum; Lycopersicon | Lineage |
| Lycopersicon () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274) | Parent | Lycopersicon () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=49274) | Parent |
| 4081 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4081) | NCBI Taxonomy ID | 4081 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4081) | NCBI Taxonomy ID |
| | is Taxon A an Infraspecies? | | is Taxon B an Infraspecies? |
| No | | No | |

GENOTYPIC CHANGE

| Generic Gene Name | | UniProtKB Arabidopsis thaliana |
|---|-------------------------|--|
| VTE3 | Synonyms | Q9LY74 (http://www.uniprot.org/uniprot/Q9LY74) |
| ALBINO OR PALE GREEN MUTANT 1; E37; IEP37; INNER ENVELOPE PROTEIN 37; VITAMIN E DEFECTIVE 3; VTE3; APG1; IE37; At3g63410; MAA21.40 | | GenebankID or UniProtKB |
| 3702.AT3G63410.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT3G63410.1) | String | 0 |
| | 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) | | |

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

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Experimental Evidence

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

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; AsÁs R; Duffy T; Dominguez PG; BermÁdez L; Conti G; CorrÁa 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(l)) that catalyses one of the final steps in the biosynthesis of γ - and α -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(l). Promoter DNA methylation can be spontaneously reverted leading to different epialleles affecting VTE3(l) 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