

GEPHE SUMMARY

ETC2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~ETC2~#gephebase-summary-title)	Gephebase Gene	GP00001237	GepheID
	Entry Status	Arnoult	Main curator
	Published		

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)		Trait Category	
Trichome density (leaf) (https://www.gephebase.org/search-criteria?/and+Trait=~Trichome density (leaf)~#gephebase-summary-title)		Trait	
Arabidopsis thaliana- Gr-1		Trait State in Taxon A	
Arabidopsis thaliana Can-0		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana~#gephebase-summary-title)		Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Arabidopsis thaliana~#gephebase-summary-title)	
thale cress		thale cress	
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress		thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	
species		species	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)		Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)		3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	
Yes		Yes	
Arabidopsis thaliana- Gr-1		Arabidopsis thaliana Can-0	

GENOTYPIC CHANGE

ETC2		Generic Gene Name	UniProtKB Arabidopsis thaliana
ENHANCER OF TRY AND CPC 2; T9D9.23; T9D9_23; At2g30420; T6B20; T9D9		Synonyms	GenebankID or UniProtKB
3702.AT2G30420.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT2G30420.1)		String	NM_179814.3 (https://www.ncbi.nlm.nih.gov/nucleotide/NM_179814.3)
-		Sequence Similarities	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		GO - Molecular Function	
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:0006355 : regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0048629 : trichome patterning (<https://www.ebi.ac.uk/QuickGO/term/GO:0048629>)
GO:1900033 : negative regulation of trichome patterning
(<https://www.ebi.ac.uk/QuickGO/term/GO:1900033>)
GO:0080147 : root hair cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0080147>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

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

Molecular Type

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

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

K19E

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

A single amino acid replacement in ETC2 shapes trichome patterning in natural Arabidopsis populations. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19818620>)

Authors

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Abstract

Our understanding of the evolution of organismal diversity is restricted by the current resolution of the genotype-phenotype map. In particular, the genetic basis of environmentally relevant phenotypic variation among natural populations remains poorly understood. Trichomes are single-cell outgrowths on the surface of plant leaves and other above-ground organs. Consistent with trichomes’ suggested function to protect plants from predators and abiotic stressors [1-3], trichome density is strikingly variable among natural populations (e.g., [2, 4]). Despite substantial progress in the genetic dissection of trichome development [5], how trichome number is modulated in natural populations remains enigmatic. Here, we show that the ENHANCER OF TRY AND CPC 2 (ETC2) from the single-repeat R3 MYB family is the major locus determining trichome patterning in natural Arabidopsis populations. Our study identifies a single amino acid substitution in ETC2 (K19E) as the causal quantitative trait nucleotide (QTN). We suggest that this amino acid replacement might affect the stability of the ETC2 repressor, which results in a reduced trichome number. This is consistent with the view that morphology can evolve by coding changes that can subtly modulate protein activity as well as cis-regulatory changes that alter expression patterns.

Additional References

RELATED GEPHE

Related Genes

2 (AtMYC1, GLABROUS1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702^/and+Trait=Trichome density/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

functional test of QTN + mutant complementation

