

GEPHE SUMMARY

	Gephebase Gene	GepheID
EARLY FLOWERING 3(ELF3) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^EARLY FLOWERING 3(ELF3)^#gephebase-summary-title)	GP00000244	
	Entry Status	Martin
Published		Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait	
Flowering time (https://www.gephebase.org/search-criteria?/and+Trait=^Flowering time^#gephebase-summary-title)			
	Trait State in Taxon A		
Arabidopsis thaliana - Sha		Trait State in Taxon B	
Arabidopsis thaliana- Bay-0			
	Ancestral State		
Data not curated		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
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)	
	Common Name		Common Name
thale cress		thale cress	
	Synonyms		Synonyms
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	
	Rank		Rank
species		species	
	Lineage		Lineage
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	
	Parent		Parent
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)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
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)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Arabidopsis thaliana - Sha		Arabidopsis thaliana- Bay-0	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
ELF3		O82804 (http://www.uniprot.org/uniprot/O82804)
	Synonyms	GenebankID or UniProtKB
EARLY FLOWERING 3; F17H15.25; PYK20; At2g25930; T19L18.26		AY062963 (https://www.ncbi.nlm.nih.gov/nuccore/AY062963)
	String	
3702.AT2G25930.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 3702.AT2G25930.1)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		
	GO - Biological Process	
GO:0009733 : response to auxin (https://www.ebi.ac.uk/QuickGO/term/GO:0009733)		

GO:0009826 : unidimensional cell growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009826>)
GO:0009737 : response to abscisic acid
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009737>)
GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)
GO:0009409 : response to cold (<https://www.ebi.ac.uk/QuickGO/term/GO:0009409>)
GO:0009909 : regulation of flower development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009909>)
GO:2000028 : regulation of photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000028>)
GO:0010031 : circumnutation (<https://www.ebi.ac.uk/QuickGO/term/GO:0010031>)
GO:0048573 : photoperiodism, flowering
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048573>)
GO:0009585 : red, far-red light phototransduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009585>)
GO:0010119 : regulation of stomatal movement
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010119>)

GO - Cellular Component

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

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

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

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

100-999 bp

Background-dependent effects of extensive polyQ coding variation

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

Network analysis identifies ELF3 as a QTL for the shade avoidance response in Arabidopsis. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20838594>)

JimÃ©nez-GÃ³mez JM; Wallace AD; Maloof JN

Quantitative Trait Loci (QTL) analyses in immortal populations are a powerful method for exploring the genetic mechanisms that control interactions of organisms with their environment. However, QTL analyses frequently do not culminate in the identification of a causal gene due to the large chromosomal regions often underlying QTLs. A reasonable approach to inform the process of causal gene identification is to incorporate additional genome-wide information, which is becoming increasingly accessible. In this work, we perform QTL analysis of the shade avoidance response in the Bayreuth-0 (Bay-0, CS954) x Shahdara (Sha, CS929) recombinant inbred line population of Arabidopsis. We take advantage of the complex pleiotropic nature of this trait to perform network analysis using co-expression, eQTL and functional classification from publicly available datasets to help us find good candidate genes for our strongest QTL, SAR2. This novel network analysis detected EARLY FLOWERING 3 (ELF3; AT2G25930) as the most likely candidate gene affecting the shade avoidance response in our population. Further genetic and transgenic experiments confirmed ELF3 as the causative gene for SAR2. The Bay-0 and Sha alleles of ELF3 differentially regulate developmental time and circadian clock period length in Arabidopsis, and the extent of this regulation is dependent on the light environment. This is the first time that ELF3 has been implicated in the shade avoidance response and that different natural alleles of this gene are shown to have phenotypic effects. In summary, we show that development of networks to inform candidate gene identification for QTLs is a promising technique that can significantly accelerate the process of QTL cloning.

Combining genome-wide association mapping and transcriptional networks to identify novel genes controlling glucosinolates in Arabidopsis thaliana. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21857804>)

Genetic mapping of natural variation in a shade avoidance response: ELF3 is the candidate gene for a QTL in hypocotyl growth regulation. (2011) (<https://pubmed.ncbi.nlm.nih.gov/20713464>)

Background-dependent effects of polyglutamine variation in the Arabidopsis thaliana gene ELF3. (2012) (<https://pubmed.ncbi.nlm.nih.gov/23129635>)

RELATED GEPHE

12 (AGAMOUS-LIKE 50, Cryptochrome 2 (CRY2) EDI allele, FLC (Flowering Locus C), FLM (MAF1), Flowering locus T (FT), Frigida (FRI), Frigida like 1 (FRL1), Frigida like 2 (FRL2), MADS AFFECTING FLOWERING 2 (MAF2), SVP (SHORT VEGETATIVE PHASE), VIN3, HUA2) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Flowering time/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS

@Pleiotropy @GxE

