

GEPHE SUMMARY

HUA2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~HUA2^#gephebase-summary-title)	Gephebase Gene	GP00000491	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)	
Flowering time (https://www.gephebase.org/search-criteria?/and+Trait=~Floweringtime^#gephebase-summary-title)	Trait
Arabidopsis thaliana- Ler0	Trait State in Taxon A
Arabidopsis thaliana- Sy-0	Trait State in Taxon B

Trait #2	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology^#gephebase-summary-title)	
Shoot morphology (https://www.gephebase.org/search-criteria?/and+Trait=~Shootmorphology^#gephebase-summary-title)	Trait
-	Trait State in Taxon A
-	Trait State in Taxon B

Ancestral State			
Data not curated			
Taxonomic Status			
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	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)	
thale cress	Common Name	thale cress	Common Name
thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	Synonyms	thale cress; mouse-ear cress; thale-cress; Arabidopsis thaliana (L.) Heynh.; Arabidopsis thaliana (thale cress); Arabidopsis_thaliana; Arbisopsis thaliana; thale kress	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis	Lineage
Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent	Arabidopsis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3701)	Parent
3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	NCBI Taxonomy ID	3702 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3702)	NCBI Taxonomy ID
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Sy-0	

GENOTYPIC CHANGE

Generic Gene Name

HUA2

Synonyms

ENHANCER OF AG-4 2; MYJ24.14; MYJ24_14; ART1; At5g23150; MKD15

String

3702.AT5G23150.1
([http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G23150.1](http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G23150.1))

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:0043481 : anthocyanin accumulation in tissues in response to UV light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043481>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0009910 : negative regulation of flower development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009910>)
GO:0048497 : maintenance of floral organ identity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048497>)
GO:0006397 : mRNA processing (<https://www.ebi.ac.uk/QuickGO/term/GO:0006397>)
GO:0048510 : regulation of timing of transition from vegetative to reproductive phase
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048510>)

GO - Cellular Component

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

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

K525E

Experimental Evidence

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

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

Main Reference

HUA2 caused natural variation in shoot morphology of *A. thaliana*. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17764945>)

Authors

Wang Q; Sajja U; Rosloski S; Humphrey T; Kim MC; Bomblies K; Weigel D; Grbic V

Abstract

Differences in life-history strategy are thought to contribute to adaptation to specific environmental conditions. Among life-history traits in plants, flowering time and shoot morphology are particularly important for reproductive success. Even though flowering time and shoot morphology are linked, the evolutionary changes in the genetic circuitry that simultaneously affects both traits remain obscure. Here, we have identified changes in a putative pre-mRNA processing factor, HUA2, as being responsible for the distinct shoot morphology and flowering behavior in Sy-0, a natural strain of *Arabidopsis*. HUA2 has previously been shown to positively regulate two MADS box genes affecting flowering time (FLOWERING LOCUS C [FLC]) and floral patterning (AGAMOUS [AG]) [1, 2]. We demonstrate that natural changes in HUA2 activity have opposite effects on its known functions, thus having implications for the coordinate control of induction and maintenance of floral fate. The changes in Sy-0 lead to enhanced FLC expression, resulting in an enlarged basal rosette and aerial rosettes, whereas suppression of AG function favors a reversion of floral meristems from determinate to indeterminate development. Natural variation in HUA2 activity thus coordinates changes in two important life-history traits, flowering time and shoot morphology.

Additional References

RELATED GEPHE

Related Genes

12 (AGAMOUS-LIKE 50, Cryptochrome 2 (CRY2) EDI allele, EARLY FLOWERING 3(ELF3), 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) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~3702~/and+Trait=Flowering time/or+Taxon ID=~3702~/and+Trait=Shoot morphology/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~3702~/and+Trait=Flowering+time/or+Taxon+ID=~3702~/and+Trait=Shoot+morphology/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

1 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~HUA2~/and+Taxon+ID=~3702~/or+Gene+Gephebase=~HUA2~/and+Taxon+ID=~3702))

EXTERNAL LINKS

COMMENTS

@GxE