

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Trait #1	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- Ler0	Trait State in Taxon B
Arabidopsis thaliana- Sy-0	

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

Ancestral State	Taxonomic Status		
Taxon A	Latin Name	Taxon B	Latin Name
Data not curated			
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Arabidopsis+thaliana^#gephebase-summary-title)	Common Name	Arabidopsis thaliana (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Arabidopsis+thaliana^#gephebase-summary-title)	Common Name
thale cress	Synonyms	thale cress	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	
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; Arabidopsis	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelinae; 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 Infraspecies?		is Taxon B an Infraspecies?	
Yes	Taxon A Description	Yes	Taxon B Description
Arabidopsis thaliana- Ler0		Arabidopsis thaliana- Sy-0	

GENOTYPIC CHANGE

HUA2	Generic Gene Name	UniProtKB Arabidopsis thaliana		
ENHANCER OF AG-4 2; MYJ24.14; MYJ24_14; ART1; At5g23150; MKD15	Synonyms	GenebankID or UniProtKB		
3702.AT5G23150.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G23150.1)	String			
	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:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Cellular Component	Presumptive Null		
Yes (https://www.gephbase.org/search-criteria/?and+Presumptive+Null=%Yes%#gephbase-summary-title)		Molecular Type		
Coding (https://www.gephbase.org/search-criteria/?and+Molecular+Type=%Coding%#gephbase-summary-title)		Aberration Type		
SNP (https://www.gephbase.org/search-criteria/?and+Aberration+Type=%SNP%#gephbase-summary-title)		SNP Coding Change		
Nonsynonymous		Molecular Details of the Mutation		
K525E		Experimental Evidence		
Linkage Mapping (https://www.gephbase.org/search-criteria/?and+Experimental+Evidence=%Linkage+Mapping%#gephbase-summary-title)		Main Reference		
	Taxon A	Taxon B	Position	
Codon	-	-	-	
Amino-acid	-	-	-	
			Authors	
HUA2 caused natural variation in shoot morphology of <i>A. thaliana</i> . (2007) (https://pubmed.ncbi.nlm.nih.gov/17764945)			Abstract	
Wang Q; Sajja U; Rosloski S; Humphrey T; Kim MC; Bomblies K; Weigel D; Grbic V			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 <i>Arabidopsis</i> . 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

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.gephbase.org/search-criteria/?or+Taxon+ID=%3702%and+Trait=Flowering+time/or+Taxon+ID=%3702%and+Trait=Shoot+morphology/and+groupHaplotypes=true#gephbase-summary-title)	Related Genes
1 (https://www.gephbase.org/search-criteria/?or+Gene+Gephebase=%HUA2%and+Taxon+ID=%3702%or+Gene+Gephebase=%HUA2%and+Taxon+ID=%3702%#gephbase-summary-title)	Related Haplotypes

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