

GEPHE SUMMARY

		Gephebase Gene		GepheID
SAP (Sterile Apetala) (https://www.gephebase.org/search-criteria?/and+Gene)			GP00001371	
Gephebase="SAP (Sterile Apetala)"#gephebase-summary-title)				Main curator
		Entry Status	Prigent	
Published				

PHENOTYPIC CHANGE

		Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait)				
Category="Morphology"#gephebase-summary-title)		Trait		
Petal size (https://www.gephebase.org/search-criteria?/and+Trait="Petal size"#gephebase-summary-title)				
		Trait State in Taxon A		
Capsella grandiflora ; large petals				
		Trait State in Taxon B		
Red Shepherd's Purse Capsella rubella ; small petals				
		Ancestral State		
Taxon A				
		Taxonomic Status		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)				
Status="Interspecific"#gephebase-summary-title)				
Taxon A		Taxon B		
	Latin Name		Latin Name	
Capsella grandiflora		Capsella rubella		
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Capsella grandiflora"#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Capsella rubella"#gephebase-summary-title)		
	Common Name		Common Name	
-		-		
	Synonyms		Synonyms	
Capsella grandiflora (Fauca & Chaub.) Boiss.		Capsella rubella Reut.		
	Rank		Rank	
species		species		
	Lineage		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Capsella		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Capsella		
	Parent		Parent	
Capsella () - (Rank: genus)		Capsella () - (Rank: genus)		
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3718)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 3718)		
264402	NCBI Taxonomy ID	81985	NCBI Taxonomy ID	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 264402)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 81985)		
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No		

GENOTYPIC CHANGE

		Generic Gene Name		UniProtKB Arabidopsis thaliana
SAP			Q9FKH1 (http://www.uniprot.org/uniprot/Q9FKH1)	
		Synonyms		GenebankID or UniProtKB
MXH1.20; MXH1_20; STERILE APETALA; At5g35770			()	
		String		
3702.AT5G35770.1				
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G35770.1)				
		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:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)				
GO:0009908 : flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009908)				
GO:0046622 : positive regulation of organ growth				
(https://www.ebi.ac.uk/QuickGO/term/GO:0046622)				

GO:0009554 : megasporogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0009554>)

GO:0030163 : protein catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030163>)

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](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

5 SNP in intron in particular

Experimental Evidence

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

Main Reference

Standing genetic variation in a tissue-specific enhancer underlies selfing-syndrome evolution in *Capsella*. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27849572>)

Authors

Sicard A; Kappel C; Lee YW; WoÅ°niak NJ; Marona C; Stinchcombe JR; Wright SI; Lenhard M

Abstract

Mating system shifts recurrently drive specific changes in organ dimensions. The shift in mating system from out-breeding to selfing is one of the most frequent evolutionary transitions in flowering plants and is often associated with an organ-specific reduction in flower size. However, the evolutionary paths along which polygenic traits, such as size, evolve are poorly understood. In particular, it is unclear how natural selection can specifically modulate the size of one organ despite the pleiotropic action of most known growth regulators. Here, we demonstrate that allelic variation in the intron of a general growth regulator contributed to the specific reduction of petal size after the transition to selfing in the genus *Capsella*. Variation within this intron affects an organ-specific enhancer that regulates the level of STERILE APETALA (SAP) protein in the developing petals. The resulting decrease in SAP activity leads to a shortening of the cell proliferation period and reduced number of petal cells. The absence of private polymorphisms at the causal region in the selfing species suggests that the small-petal allele was captured from standing genetic variation in the ancestral out-crossing population. Petal-size variation in the current out-crossing population indicates that several small-effect mutations have contributed to reduce petal-size. These data demonstrate how tissue-specific regulatory elements in pleiotropic genes contribute to organ-specific evolution. In addition, they provide a plausible evolutionary explanation for the rapid evolution of flower size after the out-breeding-to-selfing transition based on additive effects of segregating alleles.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

differ in frequency in both species ; small petal haplotype has combined several polymorphisms with individually small effects