

GEPHE SUMMARY

	Gephebase Gene		GepheID
qSH1 (REPLUMLESS) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] qSH1 (REPLUMLESS) [^] #gephebase-summary-title)		GP00000943	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category= [^] Physiology [^] #gephebase-summary-title)			
	Trait		
Seed shattering (<a href="https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Seed">https://www.gephebase.org/search-criteria?/and+Trait=[^]Seed shattering [^] #gephebase-summary-title)			
	Trait State in Taxon A		
Brassicaceae			
	Trait State in Taxon B		
Brassicaceae			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Interspecific [^] #gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Brassicaceae (https://www.gephebase.org/search-criteria?/and+Taxon Synonyms= [^] Brassicaceae [^] #gephebase-summary-title)		Brassicaceae (https://www.gephebase.org/search-criteria?/and+Taxon Synonyms= [^] Brassicaceae [^] #gephebase-summary-title)	
	Common Name		Common Name
mustard family		mustard family	
	Synonyms		Synonyms
Cruciferae; mustard family; Brassicaceae Burnett, 1835		Cruciferae; mustard family; Brassicaceae Burnett, 1835	
	Rank		Rank
family		family	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales	
	Parent		Parent
Brassicales () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3699)		Brassicales () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3699)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
3700 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3700)		3700 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3700)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Oryza sativa subsp. japonica
qSH1		Q941S9 (http://www.uniprot.org/uniprot/Q941S9)	
	Synonyms		GenebankID or UniProtKB
qSH1; qSH-1; Os01g0848400; OsJ_04077; OSNPB_010848400; P0005H10.27		()	
	String		
39947.LOC_Os01g62920.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os01g62920.1)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			
	GO - Biological Process		
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)			
	GO - Cellular Component		
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)			
			Presumptive Null
No (<a href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=<sup>^</sup>No<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive+Null=[^]No[^]#gephebase-summary-title)			

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

Molecular Type

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

Aberration Type

1bp change

Molecular Details of the Mutation

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

Experimental Evidence

The same regulatory point mutation changed seed-dispersal structures in evolution and domestication. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21737279>)

Main Reference

Arnaud N; Lawrenson T; Åstergaard L; Sablowski R

Authors

Abstract
It is unclear whether gene regulatory changes that drive evolution at the population and species levels [1-3] can be extrapolated to higher taxonomic levels. Here, we investigated the role of cis-regulatory changes in fruit evolution within the Brassicaceae family. REPLUMLESS (RPL, At5g02030) controls development of the replum, a structure with an important role in fruit opening and seed dispersal [6]. We show that reduced replum resembling the Arabidopsis rpl mutant correlated across the Brassicaceae with a point mutation in a conserved cis-element of RPL. When introduced in Arabidopsis, this nucleotide change specifically reduced RPL expression and function in the fruit. Conversely, Brassica RPL containing the Arabidopsis version of the cis-element was sufficient to convert the Brassica replum to an Arabidopsis-like morphology. A mutation in the same nucleotide position of the same cis-element in a RPL ortholog has been independently selected to reduce seed dispersal during domestication of rice, in spite of its very different fruit anatomy. Thus, single-nucleotide regulatory mutations at the same position explain developmental variation in seed-dispersal structures at the population and family levels and suggest that the same genetic toolkit is relevant to domestication and natural evolution in widely diverged species.

Abstract

Copyright © 2011 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Parallel Domestication of Shattering with Asian rice