

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=Physiology #gephebase-summary-title)	Trait		
Seed shattering (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	
Brassicaceae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Brassicaceae #gephebase-summary-title)	Latin Name	Brassicaceae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Brassicaceae #gephebase-summary-title)	Latin Name
mustard family	Common Name	mustard family	Common Name
Cruciferae; mustard family; Brassicaceae Burnett, 1835	Synonyms	Cruciferae; mustard family; Brassicaceae Burnett, 1835	Synonyms
family	Rank	family	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales	Lineage
Brassicales () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3699)	Parent	Brassicales () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3699)	Parent
3700 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3700)	NCBI Taxonomy ID	3700 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3700)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

qSH1	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
qSH1; qSH-1; Os01g0848400; OsJ_04077; OSNPB_010848400; P0005H10.27	Synonyms	GenebankID or UniProtKB
39947.LOC_Os01g62920.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os01g62920.1)	String	0
-	Sequence Similarities	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)	GO - Molecular Function	
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)	GO - Biological Process	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)	GO - Cellular Component	
No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No #gephebase-summary-title)		Presumptive Null

Cis-regulatory (#gephebase-summary-title)	Molecular Type
SNP (#gephebase-summary-title)	Aberration Type
1bp change	Molecular Details of the Mutation
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
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 repla resembling the <i>Arabidopsis rpl</i> mutant correlated across the Brassicaceae with a point mutation in a conserved cis-element of RPL. When introduced in <i>Arabidopsis</i> , this nucleotide change specifically reduced RPL expression and function in the fruit. Conversely, <i>Brassica</i> RPL containing the <i>Arabidopsis</i> version of the cis-element was sufficient to convert the <i>Brassica</i> replum to an <i>Arabidopsis</i> -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.	

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