

GEPHE SUMMARY

		Gephebase Gene		GepheID
Shattering1 - OsSh1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Shattering1+OsSh1#gephebase-summary-title)			GP00001039	
Published		Entry Status	Martin	Main curator

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	
Oryza sativa - wild-type			
		Trait State in Taxon B	
Oryza sativa- mutant and domesticated non-shattering strains			
		Ancestral State	
Taxon A			
		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated#gephebase-summary-title)			
Taxon A		Taxon B	
		Latin Name	
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+Synonyms+Oryza+sativa#gephebase-summary-title)		Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+Synonyms+Oryza+sativa#gephebase-summary-title)	
		Common Name	
rice		rice	
		Synonyms	
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
		Rank	
species		species	
		Lineage	
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	
		Parent	
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)		Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527)	
		NCBI Taxonomy ID	
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)		4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	
		is Taxon A an Intraspecies?	
No		No	
		is Taxon B an Intraspecies?	

GENOTYPIC CHANGE

		Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
YAB2			Q10FZ7 (http://www.uniprot.org/uniprot/Q10FZ7)
		Synonyms	GenebankID or UniProtKB
FIL2; Os03g0650000; LOC_Os03g44710			0
		String	
39947.LOC_Os03g44710.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os03g44710.1)			
		Sequence Similarities	
Belongs to the YABBY family.			
		GO - Molecular Function	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)			
		GO - Biological Process	
GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)			
GO:0045165 : cell fate commitment (https://www.ebi.ac.uk/QuickGO/term/GO:0045165)			
GO:0010158 : abaxial cell fate specification (https://www.ebi.ac.uk/QuickGO/term/GO:0010158)			

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

	Presumptive Null
No (<a +no^"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=">#gephebase-summary-title)	
	Molecular Type
Unknown (<a +unknown^"="" href="https://www.gephebase.org/search-criteria?/and+Molecular+Type=">#gephebase-summary-title)	
	Aberration Type
Insertion (<a +insertion^"="" href="https://www.gephebase.org/search-criteria?/and+Aberration+Type=">#gephebase-summary-title)	
	Insertion Size
1-10 kb	
	Molecular Details of the Mutation
>4kb insertion in intron (unclear)	
	Experimental Evidence
Association Mapping (<a +association+mapping^"="" href="https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=">#gephebase-summary-title)	
	Main Reference
Parallel domestication of the Shattering1 genes in cereals. (2012) (https://pubmed.ncbi.nlm.nih.gov/22581231)	
	Authors
Lin Z; Li X; Shannon LM; Yeh CT; Wang ML; Bai G; Peng Z; Li J; Trick HN; Clemente TE; Doebley J; Schnable PS; Tuinstra MR; Tesso TT; White F; Yu J	
	Abstract
A key step during crop domestication is the loss of seed shattering. Here, we show that seed shattering in sorghum is controlled by a single gene, Shattering1 (Sh1), which encodes a YABBY transcription factor. Domesticated sorghums harbor three different mutations at the Sh1 locus. Variants at regulatory sites in the promoter and intronic regions lead to a low level of expression, a 2.2-kb deletion causes a truncated transcript that lacks exons 2 and 3, and a GT-to-GG splice-site variant in the intron 4 results in removal of the exon 4. The distributions of these non-shattering haplotypes among sorghum landraces suggest three independent origins. The function of the rice ortholog (OsSh1) was subsequently validated with a shattering-resistant mutant, and two maize orthologs (ZmSh1-1 and ZmSh1-5.1+ZmSh1-5.2) were verified with a large mapping population. Our results indicate that Sh1 genes for seed shattering were under parallel selection during sorghum, rice and maize domestication.	
	Additional References
Two evolutionary histories in the genome of rice: the roles of domestication genes. (2011) (https://pubmed.ncbi.nlm.nih.gov/21695282)	
Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. (2011) (https://pubmed.ncbi.nlm.nih.gov/22158310)	

RELATED GEPHE

	Related Genes
3 (OsLG1, shattering4 - sh4, qSH1) (<a +4530^="" and+trait='Seed+shattering/and+groupHaplotypes=true#gephebase-summary-title"' href="https://www.gephebase.org/search-criteria?/or+Taxon+ID=">https://www.gephebase.org/search-criteria?/or+Taxon+ID="+4530^/and+Trait=Seed+shattering/and+groupHaplotypes=true#gephebase-summary-title)	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

Verify Orthology