

GEPHE SUMMARY

	Gephebase Gene	GephelD
Shattering1 - OsSh1 (#gephebase-summary-title)	GP00001039	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category		
	Trait		
Physiology (#gephebase-summary-title)			
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 (#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Oryza sativa (#gephebase-summary-title))	Oryza sativa (#gephebase-summary-title))		
rice	Common Name		Common Name
rice; red rice; Oryza sativa L.	Synonyms		Synonyms
species	Rank		Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Lineage		Lineage
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	Parent	Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	Parent
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	NCBI Taxonomy ID	4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name		
YAB2		UniProtKB Oryza sativa subsp. japonica	
FIL2; Os03g065000; LOC_Os03g44710	Synonyms		GenebankID or UniProtKB
39947.LOC_Os03g44710.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os03g44710.1)	String	Q10FZ7 (http://www.uniprot.org/uniprot/Q10FZ7)	
Belongs to the YABBY family.	Sequence Similarities		
	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 - 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=%22No%22#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=%22Unknown%22#gephebase-summary-title>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=%22Insertion%22#gephebase-summary-title>)

Insertion Size

1-10 kb

Molecular Details of the Mutation

>4kb insertion in intron (unclear)

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Association+Mapping%22#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) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%224530%22/and+Trait=Seed+shattering/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Verify Orthology