

GEPHE SUMMARY

Gephebase Gene		GepheID
GRAIN INCOMPLETE FILLING 1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~GRAIN INCOMPLETE FILLING 1~#gephebase-summary-title)	GP00000413	
Entry Status	Martin	Main curator
Published		

PHENOTYPIC CHANGE

		Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)			
		Trait	
Grain weight (https://www.gephebase.org/search-criteria?/and+Trait=~Grainweight~#gephebase-summary-title)			
		Trait State in Taxon A	
Oryza rufipogon - wild rice			
		Trait State in Taxon B	
Oryza sativa - Teqing			
		Ancestral State	
Data not curated			
		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)			
Taxon A		Taxon B	
		Latin Name	
Oryza rufipogon (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Oryza rufipogon~#gephebase-summary-title)		Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Oryza sativa~#gephebase-summary-title)	
		Common Name	
-		rice	
		Synonyms	
red rice; common wild rice; Oryza rufipogon Griff.		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; Oryzeae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; 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	
4529 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4529)		4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		Yes	
		Taxon B Description	
		Oryza sativa - Teqing	

GENOTYPIC CHANGE

		Generic Gene Name	
CIN2		UniProtKB Oryza sativa subsp. japonica Q0JDC5 (http://www.uniprot.org/uniprot/Q0JDC5)	
		Synonyms	
WB1; CIN2; GIF1; OsCIN2; OsJ_014165; OJ000126_13.8; Os04g0413500; LOC_Os04g33740		GenebankID or UniProtKB ABW80997 (https://www.ncbi.nlm.nih.gov/nuccore/ABW80997)	
		String	
39947.LOC_Os04g33740.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os04g33740.1)			
		Sequence Similarities	
Belongs to the glycosyl hydrolase 32 family.			
		GO - Molecular Function	
GO:0004564 : beta-fructofuranosidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004564)			
		GO - Biological Process	
GO:0005975 : carbohydrate metabolic process			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005975>)
GO:0042742 : defense response to bacterium
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042742>)
GO:0050832 : defense response to fungus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050832>)
GO:0052576 : carbohydrate storage (<https://www.ebi.ac.uk/QuickGO/term/GO:0052576>)
GO - Cellular Component
GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0005618 : cell wall (<https://www.ebi.ac.uk/QuickGO/term/GO:0005618>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	
	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	
	Molecular Details of the Mutation
unknown	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)	
	Main Reference
Control of rice grain-filling and yield by a gene with a potential signature of domestication. (2008) (https://pubmed.ncbi.nlm.nih.gov/18820698)	
	Authors
Wang E; Wang J; Zhu X; Hao W; Wang L; Li Q; Zhang L; He W; Lu B; Lin H; Ma H; Zhang G; He Z	

	Abstract
Grain-filling, an important trait that contributes greatly to grain weight, is regulated by quantitative trait loci and is associated with crop domestication syndrome. However, the genes and underlying molecular mechanisms controlling crop grain-filling remain elusive. Here we report the isolation and functional analysis of the rice GIF1 (GRAIN INCOMPLETE FILLING 1) gene that encodes a cell-wall invertase required for carbon partitioning during early grain-filling. The cultivated GIF1 gene shows a restricted expression pattern during grain-filling compared to the wild rice allele, probably a result of accumulated mutations in the gene’s regulatory sequence through domestication. Fine mapping with introgression lines revealed that the wild rice GIF1 is responsible for grain weight reduction. Ectopic expression of the cultivated GIF1 gene with the 35S or rice Waxy promoter resulted in smaller grains, whereas overexpression of GIF1 driven by its native promoter increased grain production. These findings, together with the domestication signature that we identified by comparing nucleotide diversity of the GIF1 loci between cultivated and wild rice, strongly suggest that GIF1 is a potential domestication gene and that such a domestication-selected gene can be used for further crop improvement.	
	Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS