

GEPHE SUMMARY

	Gephebase Gene	GephelD
GW7 (https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%22GW7%22#gephebase-summary-title)	GP00001540	
Published	Entry Status	Main curator

PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria/?and+Trait+Category=%22Morphology%22#gephebase-summary-title)	Trait
Grain shape (https://www.gephebase.org/search-criteria/?and+Trait=%22Grain+shape%22#gephebase-summary-title)	Trait State in Taxon A
Indica variety HJX74 with shorter and wider grains of lower quality (?)	Trait State in Taxon B
line TaifengA (TFA) derived from japonica variety Mi31 with slender grains and better grain quality	

Trait #2	Trait Category
Physiology (https://www.gephebase.org/search-criteria/?and+Trait+Category=%22Physiology%22#gephebase-summary-title)	Trait
Grain quality (https://www.gephebase.org/search-criteria/?and+Trait=%22Grain+quality%22#gephebase-summary-title)	Trait State in Taxon A
-	Trait State in Taxon B
-	

Unknown	Ancestral State	
Taxonomic Status		
Taxon A	Latin Name	Taxon B
Oryza sativa (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%22Oryza+sativa%22#gephebase-summary-title)	Common Name	Latin Name
rice	Synonyms	Common Name
rice; red rice; Oryza sativa L.	Rank	Synonyms
species	Lineage	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Parent	Lineage
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	NCBI Taxonomy ID	Parent
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)	is Taxon A an Infraspecies?	NCBI Taxonomy ID
Yes	Taxon A Description	is Taxon B an Infraspecies?
Indica variety HJX74 with shorter and wider grains of lower quality (?)	Rice line TaifengA (TFA) derived from japonica variety Mi31 with slender grains and better grain quality	Taxon B Description

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Arabidopsis thaliana
TON1A	Q9FQ25 (http://www.uniprot.org/uniprot/Q9FQ25)	
T15C9.7; TON1; TONNEAU 1; TONNEAU 1A; At3g55000; F28P10	0	GenebankID or UniProtKB
3702.AT3G55000.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT3G55000.1)	String	
	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
GO:0030865 : cortical cytoskeleton organization (https://www.ebi.ac.uk/QuickGO/term/GO:0030865)		
GO:0000226 : microtubule cytoskeleton organization (https://www.ebi.ac.uk/QuickGO/term/GO:0000226)		
GO:0000913 : preprophase band assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0000913)		
	GO - Cellular Component	
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)		
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)		
GO:0005938 : cell cortex (https://www.ebi.ac.uk/QuickGO/term/GO:0005938)		
GO:0030863 : cortical cytoskeleton (https://www.ebi.ac.uk/QuickGO/term/GO:0030863)		
GO:0030981 : cortical microtubule cytoskeleton (https://www.ebi.ac.uk/QuickGO/term/GO:0030981)		
GO:0009574 : preprophase band (https://www.ebi.ac.uk/QuickGO/term/GO:0009574)		
No (https://www.gephbase.org/search-criteria/?and+Presumptive Null^No^#gephbase-summary-title)		Presumptive Null
Cis-regulatory (https://www.gephbase.org/search-criteria/?and+Molecular Type^Cis-regulatory^#gephbase-summary-title)		Molecular Type
Unknown (https://www.gephbase.org/search-criteria/?and+Aberration Type^Unknown^#gephbase-summary-title)		Aberration Type
18 SNPs and 9 indels observed in the promoter region and exon 1 and in particular an 11-bp deletion and 18-bp insertion near GTAC motifs which are normally binded by OsSPL16 repressor (reduced binding increasing transcription)		Molecular Details of the Mutation
Linkage Mapping (https://www.gephbase.org/search-criteria/?and+Experimental Evidence^Linkage Mapping^#gephbase-summary-title)		Experimental Evidence
The OsSPL16-GW7 regulatory module determines grain shape and simultaneously improves rice yield and grain quality. (2015) (https://pubmed.ncbi.nlm.nih.gov/26147620)		Main Reference
Wang S; Li S; Liu Q; Wu K; Zhang J; Wang S; Wang Y; Chen X; Zhang Y; Gao C; Wang F; Huang H; Fu X		Authors
The deployment of heterosis in the form of hybrid rice varieties has boosted grain yield, but grain quality improvement still remains a challenge. Here we show that a quantitative trait locus for rice grain quality, qGW7, reflects allelic variation of GW7, a gene encoding a TONNEAU1-recruiting motif protein with similarity to C-terminal motifs of the human centrosomal protein CAP350. Upregulation of GW7 expression was correlated with the production of more slender grains, as a result of increased cell division in the longitudinal direction and decreased cell division in the transverse direction. OsSPL16 (GW8), an SBP-domain transcription factor that regulates grain width, bound directly to the GW7 promoter and repressed its expression. The presence of a semidominant GW7(TFA) allele from tropical japonica rice was associated with higher grain quality without the yield penalty imposed by the Basmati gw8 allele. Manipulation of the OsSPL16-GW7 module thus represents a new strategy to simultaneously improve rice yield and grain quality.		Abstract
		Additional References

RELATED GEPHE

	Related Genes
3 (GL7, Os07g0603400, OsSPL16) (https://www.gephbase.org/search-criteria/?or+Taxon ID^4530^and+Trait=Grain shape/or+Taxon ID^4530^and+Trait=Grain quality/and+groupHaplotypes=true#gephbase-summary-title)	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

