

GEPHE SUMMARY

DEP1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^DEP1^#gephebase-summary-title)	Gephebase Gene	GP00000218	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	Trait Category		
Grain yield (https://www.gephebase.org/search-criteria?/and+Trait=^Grain+yield^#gephebase-summary-title)	Trait		
Oryza sativa L. ssp. Indica	Trait State in Taxon A		
Oryza sativa L. ssp. Japonica	Trait State in Taxon B		
Taxon A	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)	Latin Name	Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza+sativa^#gephebase-summary-title)	Latin Name
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza	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
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Oryza sativa L. ssp. Indica	Taxon A Description	Oryza sativa L. ssp. Japonica	Taxon B Description

GENOTYPIC CHANGE

P0046G12.12-1	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica
DN1; DEP1; pay1; Os09g0441900; OsJ_29530; OSNPB_090441900	Synonyms	Q67UU9 (http://www.uniprot.org/uniprot/Q67UU9)
39947.LOC_Os09g26999.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os09g26999.1)	String	0
-	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)	GO - Cellular Component	

GO:0005882 : intermediate filament (<https://www.ebi.ac.uk/QuickGO/term/GO:0005882>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes^#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Coding^#gephebase-summary-title))

Aberration Type

Indel ([https://www.gephebase.org/search-criteria?/and+Aberration Type=^Indel^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Indel^#gephebase-summary-title))

Indel Size

100-999 bp

Molecular Details of the Mutation

replacement of a 637bp stretch of the middle of exon5 by a 12-bp sequence creating a premature stop codon and consequently a loss of 230 residues from the C-terminus

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title))

Main Reference

Natural variation at the DEP1 locus enhances grain yield in rice. (2009) (<https://pubmed.ncbi.nlm.nih.gov/19305410>)

Authors

Huang X; Qian Q; Liu Z; Sun H; He S; Luo D; Xia G; Chu C; Li J; Fu X

Abstract

Grain yield is controlled by quantitative trait loci (QTLs) derived from natural variations in many crop plants. Here we report the molecular characterization of a major rice grain yield QTL that acts through the determination of panicle architecture. The dominant allele at the DEP1 locus is a gain-of-function mutation causing truncation of a phosphatidylethanolamine-binding protein-like domain protein. The effect of this allele is to enhance meristematic activity, resulting in a reduced length of the inflorescence internode, an increased number of grains per panicle and a consequent increase in grain yield. This allele is common to many Chinese high-yielding rice varieties and likely represents a relatively recent introduction into the cultivated rice gene pool. We also show that a functionally equivalent allele is present in the temperate cereals and seems to have arisen before the divergence of the wheat and barley lineages.

Additional References

RELATED GEPHE

Related Genes

4 (Chalk5, OsCKX2=Gn1a, OsSPL14 / WFP, THOUSAND-GRAIN WEIGHT 6 (TGW6)) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Grain yield/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4530^/and+Trait=Grain+yield/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS