

GEPHE SUMMARY

GL3.1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^GL3.1^#gephebase-summary-title)	Gephebase Gene	GP00000397	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 size (https://www.gephebase.org/search-criteria?/and+Trait=^Grain+size^#gephebase-summary-title)	Trait		
Oryza sativa - Indica FAZ1	Trait State in Taxon A		
Oryza sativa - Japonica WY3	Trait State in Taxon B		
Data not curated	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 - Indica FAZ1	Taxon A Description	Oryza sativa - Japonica WY3	Taxon B Description

GENOTYPIC CHANGE

GL3	Generic Gene Name	Q9FN69 (http://www.uniprot.org/uniprot/Q9FN69)	UniProtKB Arabidopsis thaliana
GLABRA 3; GLABROUS 3; MYC6.2; BHLH1; EN31; MYC6; SST; At5g41315	Synonyms	0	GenebankID or UniProtKB
3702.AT5G41315.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=3702.AT5G41315.1)	String		
-	Sequence Similarities		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			

GO:0007275 : multicellular organism development
<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)
 GO:0001708 : cell fate specification (<https://www.ebi.ac.uk/QuickGO/term/GO:0001708>)
 GO:0009867 : jasmonic acid mediated signaling pathway
<https://www.ebi.ac.uk/QuickGO/term/GO:0009867>)
 GO:0009957 : epidermal cell fate specification
<https://www.ebi.ac.uk/QuickGO/term/GO:0009957>)
 GO:0031542 : positive regulation of anthocyanin biosynthetic process
<https://www.ebi.ac.uk/QuickGO/term/GO:0031542>)
 GO:0010091 : trichome branching (<https://www.ebi.ac.uk/QuickGO/term/GO:0010091>)
 GO:0010026 : trichome differentiation
<https://www.ebi.ac.uk/QuickGO/term/GO:0010026>)

GO - Cellular Component

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

Mutation #1

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title>) Presumptive Null

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

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title>) Aberration Type

Nonsynonymous SNP Coding Change

2 a.a. substitutions - both have a phenotypic effect
 364D-E (1092C-A) and 499H-Y (1495C-T) Molecular Details of the Mutation

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asp	Glu	364

The novel quantitative trait locus GL3.1 controls rice grain size and yield by regulating Cyclin-T1;3. (2012) (<https://pubmed.ncbi.nlm.nih.gov/23147796>) Main Reference

Qi P; Lin YS; Song XJ; Shen JB; Huang W; Shan JX; Zhu MZ; Jiang L; Gao JP; Lin HX Authors

Abstract

Increased crop yields are required to support rapid population growth worldwide. Grain weight is a key component of rice yield, but the underlying molecular mechanisms that control it remain elusive. Here, we report the cloning and characterization of a new quantitative trait locus (QTL) for the control of rice grain length, weight and yield. This locus, GL3.1, encodes a protein phosphatase kelch (PPKL) family - Ser/Thr phosphatase. GL3.1 is a member of the large grain WY3 variety, which is associated with weaker dephosphorylation activity than the small grain FAZ1 variety. GL3.1-WY3 influences protein phosphorylation in the spikelet to accelerate cell division, thereby resulting in longer grains and higher yields. Further studies have shown that GL3.1 directly dephosphorylates its substrate, Cyclin-T1;3, which has only been rarely studied in plants. The downregulation of Cyclin-T1;3 resulted in a shorter grain, which indicates a novel function for Cyclin-T in cell cycle regulation. Our findings suggest a new mechanism for the regulation of grain size and yield that is driven through a novel phosphatase-mediated process that affects the phosphorylation of Cyclin-T1;3 during cell cycle progression, and thus provide new insight into the mechanisms underlying crop seed development. We bred a new variety containing the natural GL3.1 allele that demonstrated increased grain yield, which indicates that GL3.1 is a powerful tool for breeding high-yield crops.

Additional References

Mutation #2

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title>) Presumptive Null

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

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title>) Aberration Type

Nonsynonymous SNP Coding Change

2 a.a. substitutions - both have a phenotypic effect
 364D-E (1092C-A) and 499H-Y (1495C-T) Molecular Details of the Mutation

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	His	Tyr	499

The novel quantitative trait locus GL3.1 controls rice grain size and yield by regulating Cyclin-T1;3. (2012) (<https://pubmed.ncbi.nlm.nih.gov/23147796>)

Authors

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Increased crop yields are required to support rapid population growth worldwide. Grain weight is a key component of rice yield, but the underlying molecular mechanisms that control it remain elusive. Here, we report the cloning and characterization of a new quantitative trait locus (QTL) for the control of rice grain length, weight and yield. This locus, GL3.1, encodes a protein phosphatase kelch (PPKL) family - Ser/Thr phosphatase. GL3.1 is a member of the large grain WY3 variety, which is associated with weaker dephosphorylation activity than the small grain FAZ1 variety. GL3.1-WY3 influences protein phosphorylation in the spikelet to accelerate cell division, thereby resulting in longer grains and higher yields. Further studies have shown that GL3.1 directly dephosphorylates its substrate, Cyclin-T1;3, which has only been rarely studied in plants. The downregulation of Cyclin-T1;3 in rice resulted in a shorter grain, which indicates a novel function for Cyclin-T in cell cycle regulation. Our findings suggest a new mechanism for the regulation of grain size and yield that is driven through a novel phosphatase-mediated process that affects the phosphorylation of Cyclin-T1;3 during cell cycle progression, and thus provide new insight into the mechanisms underlying crop seed development. We bred a new variety containing the natural GL3.1 allele that demonstrated increased grain yield, which indicates that GL3.1 is a powerful tool for breeding high-yield crops.

Additional References

RELATED GEPHE

Related Genes

9 (GS3, GS5, GW2, OsPPKL1/qGL3, qSW5, OsSPL13, GL7, Os07g0603400, OsSPL16) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Grain size/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect