

## GEPHE SUMMARY

	Gephebase Gene	GephelD
GL3.1 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase="GL3.1">#gephebase-summary-title)	GP00000397	
	Entry Status	Main curator
Published	Martin	

## PHENOTYPIC CHANGE

	Trait Category		
Morphology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category="Morphology">#gephebase-summary-title)	Trait		
Grain size ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Grain%20size^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Grain size^#gephebase-summary-title</a> )	Trait State in Taxon A		
Oryza sativa - Indica FAZ1	Trait State in Taxon B		
Oryza sativa - Japonica WY3	Ancestral State		
Data not curated	Taxonomic Status		
Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status="Domesticated">#gephebase-summary-title)			
Taxon A		Taxon B	
Oryza sativa	Latin Name	Oryza sativa	Latin Name
( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Oryza</a> sativa">#gephebase-summary-title)		( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryza">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Oryza</a> sativa">#gephebase-summary-title)	
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; Oryzeae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	Lineage
Oryza () - (Rank: genus)	Parent	Oryza () - (Rank: genus)	Parent
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )	NCBI Taxonomy ID	( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )	NCBI Taxonomy ID
4530		4530	
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )		( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Oryza sativa - Indica FAZ1	Taxon A Description	Oryza sativa - Japonica WY3	Taxon B Description

## GENOTYPIC CHANGE

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

## GO - Biological Process

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

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

2 a.a. substitutions - both have a phenotypic effect

364D-E (1092C-A) and 499H-Y (1495C-T)

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Linkage+Mapping%22#gephebase-summary-title>)

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

## Main Reference

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

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

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 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

## Mutation #2

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%22No%22#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

2 a.a. substitutions - both have a phenotypic effect

364D-E (1092C-A) and 499H-Y (1495C-T)

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%22Linkage+Mapping%22#gephebase-summary-title>)

	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>)

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

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.

## RELATED GEPHE

### Related Genes

9 (GS3, GS5, GW2, OsPPKL1/qGL3, qSW5, OsSPL13, GL7, Os07g0603400, OsSPL16) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%5E4530%26Trait=Grain+size%26and+groupHaplotypes=true#gephebase-summary-title>)

### Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@SeveralMutationsWithEffect