GEPHE SUMMARY

Gephebase Gene

GL3.1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^GL3.1^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00000397

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Grain size (https://www.gephebase.org/search-criteria?/and+Trait=^Grain size^#gephebase-summary-title)

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 (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza sativa^#gephebase-summary-title)

Common Name

rice

Synonyms

rice; red rice; Oryza sativa L.

Rank

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

Parent

Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Oryza sativa - Indica FAZ1

Taxon B

Latin Name

Oryza sativa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Oryza sativa^#gephebase-summary-title)

Common Name

rice

Synonyms

rice; red rice; Oryza sativa L.

Rank

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

Parent

Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)

NCBI Taxonomy ID

4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4530)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Oryza sativa - Japonica WY3

GENOTYPIC CHANGE

Generic Gene Name

GL3

Synonyms

GLABRA 3; GLABROUS 3; MYC6.2; BHLH1; EN31; MYC6; SST; At5g41315

String

3702.AT5G41315.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 3702.AT5G41315.1)

Sequence Similarities

-

GO - Molecular Function

GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
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)

UniProtKB Arabidopsis thaliana

Q9FN69 (http://www.uniprot.org/uniprot/Q9FN69)

GenebankID or UniProtKB

()

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=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#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=^Linkage Mapping^#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=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

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

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

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