GEPHE SUMMARY

Gephebase Gene
OsCKX2=Gn1a (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^OsCKX2=Gn1a^#gephebase-summary-title)

GepheID
GP00000807

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Oryza sativa var. Koshihikari

Trait State in Taxon B
Oryza sativa var. 5150 from China

Ancestral State
Taxon A

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 var. Koshihikari

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 var. 5150 from China

GENOTYPIC CHANGE

Generic Gene Name
CKX2

Synonyms
CKX2; Gn1a; OsCKX2; OsJ_00744; B1046G12.8; Os01g0197700; LOC_Os01g10110; P0419B01.20

String
39947.LOC_Os01g10110.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os01g10110.1)

Sequence Similarities
Belongs to the oxygen-dependent FAD-linked oxidoreductase family.

GO - Molecular Function
GO:0071949 : FAD binding (https://www.ebi.ac.uk/QuickGO/term/GO:0071949)
GO:0019139 : cytokinin dehydrogenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0019139)

GO - Biological Process

UniProtKB Oryza sativa subsp. japonica
Q4ADV8 (http://www.uniprot.org/uniprot/Q4ADV8)

GenebankID or UniProtKB
AB205193 (https://www.ncbi.nlm.nih.gov/nuccore/AB205193)

GO:0009736 : cytokinin-activated signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0009736)
GO:0010229 : inflorescence development (https://www.ebi.ac.uk/QuickGO/term/GO:0010229)
GO:0009690 : cytokinin metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009690)

GO - Cellular Component

GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)

Presumptive Null

Yes (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)

Aberration Type

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

Deletion Size

10-99 bp

Molecular Details of the Mutation

11bp deletion causing premature stop codon

Experimental Evidence

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

Main Reference

Cytokinin oxidase regulates rice grain production. (2005) (https://pubmed.ncbi.nlm.nih.gov/15976269)

Authors

Ashikari M; Sakakibara H; Lin S; Yamamoto T; Takashi T; Nishimura A; Angeles ER; Qian Q; Kitano H; Matsuoka M

Abstract

Most agriculturally important traits are regulated by genes known as quantitative trait loci (QTLs) derived from natural allelic variations. We here show that a QTL that increases grain productivity in rice, Gn1a, is a gene for cytokinin oxidase/dehydrogenase (OsCKX2), an enzyme that degrades the phytohormone cytokinin. Reduced expression of OsCKX2 causes cytokinin accumulation in inflorescence meristems and increases the number of reproductive organs, resulting in enhanced grain yield. QTL pyramiding to combine loci for grain number and plant height in the same genetic background generated lines exhibiting both beneficial traits. These results provide a strategy for tailormade crop improvement.

Additional References

RELATED GEPHE

Related Genes

4 (Chalk5, DEP1, 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)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^OsCKX2=Gn1a^/and+Taxon ID=^4530^/or+Gene Gephebase=^OsCKX2=Gn1a^/and+Taxon ID=^4530^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS