

GEPHE SUMMARY

Gephebase Gene
OsCKX2=Gn1a

Entry Status
Published

GepheID
GP00000807

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Grain yield

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

Taxon A

Latin Name
Oryza sativa

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; Oryzaceae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon A an Intraspecies?
Yes

Taxon A Description
Oryza sativa var. Koshihikari

Taxon B

Latin Name
Oryza sativa

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; Oryzaceae; Oryzinae; Oryza

Parent
Oryza () - (Rank: genus)

NCBI Taxonomy ID
4530

is Taxon B an Intraspecies?
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

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

GO - Molecular Function
GO:0071949 : FAD binding
GO:0019139 : cytokinin dehydrogenase activity

GO - Biological Process
GO:0009736 : cytokinin-activated signaling pathway
GO:0010229 : inflorescence development
GO:0009690 : cytokinin metabolic process

UniProtKB *Oryza sativa* subsp. japonica
Q4ADV8

GenebankID or UniProtKB
AB205193

GO - Cellular Component
GO:0005615 : extracellular space

Presumptive Null
Yes

Molecular Type
Coding

Aberration Type
Deletion

Deletion Size
10-99 bp

Molecular Details of the Mutation
11bp deletion causing premature stop codon

Experimental Evidence
Linkage Mapping

Main Reference
Cytokinin oxidase regulates rice grain production. (2005)

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 tailor-made crop improvement.

Additional References

RELATED GEPHE

Related Genes
4 (Chalk5, DEP1, OsSPL14 / WFP, THOUSAND-GRAIN WEIGHT 6 (TGW6))
Related Haplotypes
1

COMMENTS