

	Gephebase Gene	GepheID
OsCKX2=Gn1a (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^OsCKX2=Gn1a^#gephebase-summary-title)	GP00000808	Main curator
Published	Entry Status: Martin	

	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. Habataki	
	Ancestral State
Data not curated	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)	

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; 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) (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
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Oryza sativa var. Koshihikari	Taxon A Description	Oryza sativa var. Habataki	Taxon B Description

CKX2	Generic Gene Name	UniProtKB Oryza sativa subsp. japonica Q4ADV8 (http://www.uniprot.org/uniprot/Q4ADV8)
CKX2; Gn1a; OsCKX2; OsJ_00744; B1046G12.8; Os01g0197700; LOC_Os01g10110; P0419B01.20	Synonyms	GenebankID or UniProtKB AB205193 (https://www.ncbi.nlm.nih.gov/nucore/AB205193)
39947.LOC_Os01g10110.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=39947.LOC_Os01g10110.1)	String	
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)	Sequence Similarities	
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 - Molecular Function	
	GO - Biological Process	

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>)

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title>)

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

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

Not identified

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

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

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

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, G_n1a, 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.

RELATED GEPHE

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>)

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