GEPHE SUMMARY

Gephebase Gene
OsGA20ox1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^OsGA20ox1^#gephebase-summary-title)

GepheID
GP00000810

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Oryza sativa var. japonica Koshihikari

Trait State in Taxon B
Oryza sativa var. japonica Dunghan Shali

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 var. japonica 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. japonica Dunghan Shali

GENOTYPIC CHANGE

Generic Gene Name
GA20OX1

Synonyms
20ox1; GA20ox-1; Os03g0856700; LOC_Os03g63970; OSJNBa0059G06.22

String
39947.LOC_Os03g63970.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=39947.LOC_Os03g63970.1)

Sequence Similarities
Belongs to the iron/ascorbate-dependent oxidoreductase family. GA20OX subfamily.

GO - Molecular Function
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0051213 : dioxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051213)
GO:0045544 : gibberellin 20-oxidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0045544)

GO - Biological Process

UniProtKB Oryza sativa subsp. japonica
P93771 (http://www.uniprot.org/uniprot/P93771)

GenebankID or UniProtKB
U50333 (https://www.ncbi.nlm.nih.gov/nuccore/U50333)

GO:0009908 : flower development (https://www.ebi.ac.uk/QuickGO/term/GO:0009908)
GO:0009686 : gibberellin biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0009686)
GO:0009826 : unidimensional cell growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0009826)

GO - Cellular Component

-

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown ; no coding variation

Experimental Evidence

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

Main Reference

OsGA20ox1, a candidate gene for a major QTL controlling seedling vigor in rice. (2012) (https://pubmed.ncbi.nlm.nih.gov/22481119)

Authors

Abe A; Takagi H; Fujibe T; Aya K; Kojima M; Sakakibara H; Uemura A; Matsuoka M; Terauchi R

Abstract

Seedling vigor is among the major determinants of stable stand establishment in direct-seeded rice (Oryza sativa L.) in temperate regions. Quantitative trait loci (QTL) for seedling vigor were identified using 250 recombinant inbred lines (RILs) derived from a cross between two japonica rice cultivars Kakehashi and Dunghan Shali. Seedling heights measured at 14 days after sowing were 20.3 and 29.4 cm for Kakehashi and Dunghan Shali, respectively. For the RILs, the height ranged from 14.1 to 31.7 cm. Four putative QTLs associated with seedling height were detected. qPHS3-2, the major QTL that was located on the long arm of chromosome 3, accounted for 26.2 % of the phenotypic variance. Using progeny of the near isogenic lines (NILs) produced by the backcross introduction of a chromosome segment carrying this major QTL into an elite cultivar Iwatekko, we fine-mapped qPHS3-2 to a 81-kb interval between two markers, ID_CAPS_01 and RM16227. Within this mapped region, we identified the gene OsGA20ox1, which is related to gibberellin (GA) biosynthesis. The relative expression levels of GA20ox1 in seedlings of Dunghan Shali and NILs were higher than that of Iwatekko. Concomitantly, the amount of endogenous active GA was higher in Dunghan Shali and the NILs compared to the level detected in Iwatekko. These results indicate that OsGA20ox1 is a strong candidate gene for major QTL controlling seedling vigor in rice.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS