

GEPHE SUMMARY

<p>GS3 (<a +gs3+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+GS3+"#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000417</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)</p> <p>Grain size (<a +grain+size+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Grain+size+"#gephebase-summary-title)</p> <p>Oryza sativa - Chuan 7</p> <p>Oryza sativa - Minghui 63</p> <p>Data not curated</p> <p>Domesticated (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Oryza sativa - Chuan 7</p> <p>Oryza sativa - Minghui 63</p> <p>Data not curated</p> <p>Domesticated</p>
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Taxon A	Latin Name	Taxon B	Latin Name
Oryza sativa (<a +oryza+sativa+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Oryza+sativa+"#gephebase-summary-title)	Oryza sativa	Oryza sativa (<a +oryza+sativa+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Oryza+sativa+"#gephebase-summary-title)	Oryza sativa
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; Oryzaceae; Oryzinae; Oryza	Lineage	cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; 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
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Oryza sativa - Chuan 7	Taxon A Description	Oryza sativa - Minghui 63	Taxon B Description

GENOTYPIC CHANGE

<p>GS3</p> <p>GS3; Os03g0407400; OSNPB_030407400</p> <p>-</p> <p>-</p> <p>-</p> <p>GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)</p> <p>-</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p> <p>GO - Cellular Component</p>	<p>UniProtKB Oryza sativa subsp. japonica</p> <p>C6L686 (http://www.uniprot.org/uniprot/C6L686)</p> <p>0</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p> <p>-</p>	<p>GenebankID or UniProtKB</p>
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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

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

C55*;TGC>TGA causing a 178-aa truncation in the C-terminus of the predicted protein

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	-	-	-

Main Reference

GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16453132>)

Authors

Fan C; Xing Y; Mao H; Lu T; Han B; Xu C; Li X; Zhang Q

Abstract

The GS3 locus located in the pericentromeric region of rice chromosome 3 has been frequently identified as a major QTL for both grain weight (a yield trait) and grain length (a quality trait) in the literature. Near isogenic lines of GS3 were developed by successive crossing and backcrossing Minghui 63 (large grain) with Chuan 7 (small grain), using Minghui 63 as the recurrent parent. Analysis of a random subpopulation of 201 individuals from the BC3F2 progeny confirmed that the GS3 locus explained 80-90% of the variation for grain weight and length in this population. In addition, this locus was resolved as a minor QTL for grain width and thickness. Using 1,384 individuals with recessive phenotype (large grain) from a total of 5,740 BC3F2 plants and 11 molecular markers based on sequence information, GS3 was mapped to a DNA fragment approximately 7.9 kb in length. A full-length cDNA corresponding to the target region was identified, which provided complete sequence information for the GS3 candidate. This gene consists of five exons and encodes 232 amino acids with a putative PEBP-like domain, a transmembrane region, a putative TNFR/NGFR family cysteine-rich domain and a VWFC module. Comparative sequencing analysis identified a nonsense mutation, shared among all the large-grain varieties tested in comparison with the small grain varieties, in the second exon of the putative GS3 gene. This mutation causes a 178-aa truncation in the C-terminus of the predicted protein, suggesting that GS3 may function as a negative regulator for grain size. Cloning of such a gene provided the opportunity for fully characterizing the regulatory mechanism and related processes during grain development.

Additional References

Genome-wide association studies of 14 agronomic traits in rice landraces. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20972439>)

RELATED GEPHE

Related Genes

9 (GL3.1, 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