

GEPHE SUMMARY

	Gephebase Gene	GephelD
Os07g0603400 (https://www.gephebase.org/search-criteria/?and+Gene	GP00001542	
Gephebase=^Os07g0603400^#gephebase-summary-title)		Main curator
	Entry Status	Prigent
Published		

PHENOTYPIC CHANGE

Trait #1	Trait Category	
Morphology (https://www.gephebase.org/search-criteria/?and+Trait		
Category="Morphology">#gephebase-summary-title)		
	Trait	
Grain size (https://www.gephebase.org/search-criteria/?and+Trait=^Grain		
size^#gephebase-summary-title)		
	Trait State in Taxon A	
Nipponbare japonica (NPB) cultivar		
	Trait State in Taxon B	
Ping13 (P13) indica variety with superior grain length and appearance quality (decreased chalkiness & larger starch granules)		

Trait #2	Trait Category	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait		
Category="Physiology">#gephebase-summary-title)		
	Trait	
Grain quality (https://www.gephebase.org/search-criteria/?and+Trait=^Grain		
quality^#gephebase-summary-title)		
	Trait State in Taxon A	
-		
	Trait State in Taxon B	
-		

Taxon A	Ancestral State	
	Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria/?and+Taxonomic		
Status="Domesticated">#gephebase-summary-title)		

Taxon A	Latin Name	Taxon B	Latin Name
	Common Name		Common Name
	Synonyms		Synonyms
Oryza sativa (#gephebase-summary-title)		Oryza sativa (#gephebase-summary-title)	
rice		rice	
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	
	Parent		Parent
Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)		Oryza () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4527)	
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 Infraspecies?		is Taxon B an Infraspecies?	
Yes	Taxon A Description	Yes	Taxon B Description
Nipponbare japonica (NPB) cultivar		Ping13 (P13) indica variety with superior grain length and appearance quality (decreased chalkiness & larger starch granules)	

GENOTYPIC CHANGE

Os07g0603400	Generic Gene Name	A3BLY4 (http://www.uniprot.org/uniprot/A3BLY4)	UniProtKB Oryza sativa subsp. japonica
OsJ_25030; OSNPB_070603400	Synonyms	0	GenebankID or UniProtKB
-	String	-	-
-	Sequence Similarities	-	-
-	GO - Molecular Function	-	-
-	GO - Biological Process	-	-
-	GO - Cellular Component	-	-

Mutation #1

Yes (https://www.gephbase.org/search-criteria/?and+Presumptive Null=%27Yes%27#gephbase-summary-title)	Presumptive Null
Coding (https://www.gephbase.org/search-criteria/?and+Molecular Type=%27Coding%27#gephbase-summary-title)	Molecular Type
SNP (https://www.gephbase.org/search-criteria/?and+Aberration Type=%27SNP%27#gephbase-summary-title)	Aberration Type
Nonsense	SNP Coding Change
first null mutation resulting in a truncated protein of a negative regulator of GL7 in long-grain varieties - GAA>TAA (Fig S15 - the stop codon has not been highlighted)	Molecular Details of the Mutation
Linkage Mapping (https://www.gephbase.org/search-criteria/?and+Experimental Evidence=%27Linkage Mapping%27#gephbase-summary-title)	Experimental Evidence

Taxon A	Taxon B	Position
Codon		
Amino-acid		
GAA	TAA	-
Glu	STP	-

Copy number variation at the GL7 locus contributes to grain size diversity in rice. (2015) (https://pubmed.ncbi.nlm.nih.gov/26147619)	Main Reference
Wang Y; Xiong G; Hu J; Jiang L; Yu H; Xu J; Fang Y; Zeng L; Xu E; Xu J; Ye W; Meng X; Liu R; Chen H; Jing Y; Wang Y; Zhu X; Li J; Qian Q	Authors
Copy number variants (CNVs) are associated with changes in gene expression levels and contribute to various adaptive traits. Here we show that a CNV at the Grain Length on Chromosome 7 (GL7) locus contributes to grain size diversity in rice (<i>Oryza sativa</i> L.). GL7 encodes a protein homologous to <i>Arabidopsis thaliana</i> LONGIFOLIA proteins, which regulate longitudinal cell elongation. Tandem duplication of a 17.1-kb segment at the GL7 locus leads to upregulation of GL7 and downregulation of its nearby negative regulator, resulting in an increase in grain length and improvement of grain appearance quality. Sequence analysis indicates that allelic variants of GL7 and its negative regulator are associated with grain size diversity and that the CNV at the GL7 locus was selected for and used in breeding. Our work suggests that pyramiding beneficial alleles of GL7 and other yield- and quality-related genes may improve the breeding of elite rice varieties.	Abstract
	Additional References

Mutation #2

Yes (https://www.gephbase.org/search-criteria/?and+Presumptive Null=%27Yes%27#gephbase-summary-title)	Presumptive Null
Coding (https://www.gephbase.org/search-criteria/?and+Molecular Type=%27Coding%27#gephbase-summary-title)	Molecular Type
SNP (https://www.gephbase.org/search-criteria/?and+Aberration Type=%27SNP%27#gephbase-summary-title)	Aberration Type
Nonsense	SNP Coding Change
second null mutation resulting in a truncated protein of a negative regulator of GL7 in long-grain varieties - TGG>TAG (Fig S15 - this second stop codon has been highlighted)	Molecular Details of the Mutation
Linkage Mapping (https://www.gephbase.org/search-criteria/?and+Experimental Evidence=%27Linkage Mapping%27#gephbase-summary-title)	Experimental Evidence

Taxon A	Taxon B	Position
Codon		
Amino-acid		
TGG	TAG	-
Trp	STP	-

Copy number variation at the GL7 locus contributes to grain size diversity in rice. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26147619>)

Main Reference

Copy number variants (CNVs) are associated with changes in gene expression levels and contribute to various adaptive traits. Here we show that a CNV at the Grain Length on Chromosome 7 (GL7) locus contributes to grain size diversity in rice (*Oryza sativa* L.). GL7 encodes a protein homologous to *Arabidopsis thaliana* LONGIFOLIA proteins, which regulate longitudinal cell elongation. Tandem duplication of a 17.1-kb segment at the GL7 locus leads to upregulation of GL7 and downregulation of its nearby negative regulator, resulting in an increase in grain length and improvement of grain appearance quality. Sequence analysis indicates that allelic variants of GL7 and its negative regulator are associated with grain size diversity and that the CNV at the GL7 locus was selected for and used in breeding. Our work suggests that pyramiding beneficial alleles of GL7 and other yield- and quality-related genes may improve the breeding of elite rice varieties.

RELATED GEPHE

Related Genes

10 (GL3.1, GS3, GS5, GW2, OsPPKL1/qGL3, qSW5, OsSPL13, GL7, GW7, OsSPL16) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%274530%27&Trait=Grain size/or+Taxon ID=%274530%27&Trait=Grain quality/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%274530%27&Trait=Grain%20size/or+Taxon%20ID=%274530%27&Trait=Grain%20quality/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

same allele found in *Oryza rufipogon* indicating that this natural variation could be an ancient event