

GEPHE SUMMARY

	Gephebase Gene		GepheID
Waxy /GBSS (#waxy-gbss)		GP00002070	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (#physiology)			
	Trait		
Amylose content (glutinous rice) (amylose-content)			
	Trait State in Taxon A		
Oryza sativa			
	Trait State in Taxon B		
Oryza sativa - glutinous - Oragamochi and Hidekomochi cultivars			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Domesticated (#domesticated)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Oryza sativa (#oryza-sativa)		Oryza sativa (#oryza-sativa)	
	Common Name		Common Name
rice		rice	
	Synonyms		Synonyms
rice; red rice; Oryza sativa L.		rice; red rice; Oryza sativa L.	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzaceae; 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)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)		4530 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		Oragamochi and Hidekomochi cultivars	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Setaria italica
waxy		Q8L699 (http://www.uniprot.org/uniprot/Q8L699)	
	Synonyms		GenebankID or UniProtKB
GBSSI		ABC17717 (https://www.ncbi.nlm.nih.gov/nuccore/ABC17717)	
-	String		
	Sequence Similarities		
Belongs to the glycosyltransferase 1 family. Bacterial/plant glycogen synthase subfamily.			
	GO - Molecular Function		
GO:0004373 : glycogen (starch) synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004373)			
	GO - Biological Process		
GO:0019252 : starch biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019252)			
	GO - Cellular Component		
GO:0009501 : amyloplast (https://www.ebi.ac.uk/QuickGO/term/GO:0009501)			

GO:0009507 : chloroplast (<https://www.ebi.ac.uk/QuickGO/term/GO:0009507>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title](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](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Coding^#gephebase-summary-title))

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

insertion of 7764 bp in the ninth exon of the wx gene. Transcripts of the 'Oragamochi' wx allele are about 1-kb shorter and the deduced amino acid sequence of the transcript lacks a motif important for GBSS. The 7,764-bp insertion is a retrotransposon-like sequence with long terminal repeats; a primer binding site and a polypurine tract

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Candidate+Gene^#gephebase-summary-title))

Main Reference

A novel wx mutation caused by insertion of a retrotransposon-like sequence in a glutinous cultivar of rice (*Oryza sativa*). (2007) (<https://pubmed.ncbi.nlm.nih.gov/17492423>)

Authors

Hori Y; Fujimoto R; Sato Y; Nishio T

Abstract

DNA polymorphism of the Wx gene in glutinous rice cultivars was investigated by PCR-RF-SSCP and heteroduplex cleavage analysis using Brassica petiole extract, and the nucleotide sequence variations were identified. Most japonica-type glutinous rice was found to have a 23-bp duplication in the second exon, which causes loss of the function of granule-bound starch synthase (GBSS) encoded by the Wx gene. Without the 23-bp duplication, there was an insertion of 7,764 bp in the ninth exon of the wx allele of 'Oragamochi'. Expression analysis of the wx allele using RT-PCR and Northern blot analysis revealed that transcripts of the 'Oragamochi' wx allele are about 1-kb shorter and that the deduced amino acid sequence of the transcript lacks a motif important for GBSS. Therefore, this insertion was considered to be the cause of the glutinous trait of 'Oragamochi'. This 7,764-bp insertion had long terminal repeats, a primer binding site, and a polypurine tract, but no sequence homologous with gag and pol, suggesting that it is a non-autonomous element. Furthermore, it had a structure similar to Dasheng and may be a member of Dasheng.

Additional References

RELATED GEPHE

Related Genes

1 (Chalk5) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=^4530^/and+Trait=Amylose content/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^4530^/and+Trait=Amylose+content/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Waxy /GBSS^/and+Taxon ID=^4530^/or+Gene Gephebase=^Waxy /GBSS^/and+Taxon ID=^4530^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^Waxy+GBSS^/and+Taxon+ID=^4530^/or+Gene+Gephebase=^Waxy+GBSS^/and+Taxon+ID=^4530^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@TE