

## GEPHE SUMMARY

	Gephebase Gene	GephelD
Waxy /GBSS ( <a href="https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%Waxy%2FGBSS%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Gene Gephebase=%Waxy%2FGBSS%#gephebase-summary-title</a> )	GP00002069	Main curator
Published	Entry Status	Courtier

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title</a> )	Trait	
Amylose content (glutinous rice) ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=%Amylose+content+(glutinous+rice)%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=%Amylose+content+(glutinous+rice)%#gephebase-summary-title</a> )	Trait State in Taxon A	
Oryza sativa	Trait State in Taxon B	
Oryza sativa - various glutinous paddy-rice and upland cultivars	Ancestral State	
Taxon A	Taxonomic Status	
Domesticated ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=%Domesticated%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=%Domesticated%#gephebase-summary-title</a> )		

Taxon A	Latin Name	Taxon B	Latin Name
Oryza sativa ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Oryza+sativa%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Oryza+sativa%#gephebase-summary-title</a> )		Oryza sativa ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Oryza+sativa%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Oryza+sativa%#gephebase-summary-title</a> )	
rice	Common Name	rice	Common Name
rice; red rice; Oryza sativa L.	Synonyms	rice; red rice; Oryza sativa L.	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza	
Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )	Parent	Oryza () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4527</a> )	Parent
4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )	NCBI Taxonomy ID	4530 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4530</a> )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

waxy	Generic Gene Name	UniProtKB Setaria italica
GBSSI	Synonyms	GenebankID or UniProtKB
-	String	
	Sequence Similarities	
Belongs to the glycosyltransferase 1 family. Bacterial/plant glycogen synthase subfamily.		
GO:0004373 : glycogen (starch) synthase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004373">https://www.ebi.ac.uk/QuickGO/term/GO:0004373</a> )	GO - Molecular Function	
GO:0019252 : starch biosynthetic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0019252">https://www.ebi.ac.uk/QuickGO/term/GO:0019252</a> )	GO - Biological Process	
	GO - Cellular Component	
GO:0009501 : amyloplast ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0009501">https://www.ebi.ac.uk/QuickGO/term/GO:0009501</a> )		
GO:0009507 : chloroplast ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0009507">https://www.ebi.ac.uk/QuickGO/term/GO:0009507</a> )		Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

10-99 bp

Molecular Details of the Mutation

23-bp duplication in the second exon which causes loss of the function of granule-bound starch synthase (GBSS) encoded by the Wx gene

Experimental Evidence

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

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

Related Haplotypes

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

## EXTERNAL LINKS

## COMMENTS