

GEPHE SUMMARY

	Gephebase Gene		GepheID
Waxy /GBSS (#waxy-gbss)		GP00002069	
	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 - various glutinous paddy-rice and upland cultivars		
	Ancestral State	
Taxon A		
	Taxonomic Status	
Domesticated (#domesticated)		

Taxon A	Latin Name	Taxon B	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		No	

GENOTYPIC CHANGE

waxy	Generic Gene Name	UniProtKB Setaria italica
	Synonyms	Q8L699 (http://www.uniprot.org/uniprot/Q8L699)
GBSSI		GenebankID or UniProtKB
-	String	ABC17717 (https://www.ncbi.nlm.nih.gov/nucleotide/ABC17717)
	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

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 ([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

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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