

GEPHE SUMMARY

	Gephebase Gene	GephelD
Waxy /GBSS (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^Waxy /GBSS^#gephebase-summary-title)	GP00001197	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category=^Physiology^#gephebase-summary-title)		Trait	
Amylose content (https://www.gephebase.org/search-criteria/?and+Trait=Amylose content^#gephebase-summary-title)		Trait State in Taxon A	
Hordeum vulgare		Trait State in Taxon B	
Hordeum vulgare - waxy accessions from Korea and Japan		Ancestral State	
Taxon A		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Domesticated^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Hordeum vulgare (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Hordeum vulgare^#gephebase-summary-title)		Hordeum vulgare (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Hordeum vulgare^#gephebase-summary-title)	
-	Common Name	-	Common Name
barley; Hordeum vulgare L.; Horedum vulgare	Synonyms	barley; Hordeum vulgare L.; Horedum vulgare	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; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum		cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum	
Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)	Parent	Hordeum () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4512)	Parent
4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4513)	NCBI Taxonomy ID	4513 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4513)	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 (https://www.ebi.ac.uk/QuickGO/term/GO:0004373)	GO - Molecular Function	
GO:0019252 : starch biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019252)	GO - Biological Process	
	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

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

Molecular Type

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

Aberration Type

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

Deletion Size

100-999 bp

Molecular Details of the Mutation

403-bp deletion spanning from position -129 bp to position +274 relative to the deduced starting point of transcription in the barley waxy gene and

Experimental Evidence

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

Main Reference

The insertion/deletion polymorphisms in the waxy gene of barley genetic resources from East Asia. (2002) (<https://pubmed.ncbi.nlm.nih.gov/12579438>)

Authors

Domon E; Fujita M; Ishikawa N

Abstract

The length polymorphism in the waxy gene, which encodes a granule-bound ADP-glucose-glucosyl transferase [granule-bound starch synthase I (GBSS I), E.C. 2.4.1.11] in barley (*Hordeum vulgare*), was found. The 5' leader sequence of the waxy gene of barley germplasm from Japan and Korea was analyzed by the polymerase chain reaction (PCR). The waxy gene of these genetic stocks had three types of length polymorphisms, suggesting that there are insertion/deletion mutations at the 5' leader sequence of the waxy gene. DNA sequence analysis of the polymorphic PCR products showed that: (1) a 403-bp deletion mutation, which included a complete exon I, was found in the wax allele and a 193-bp insertion sequence was located in the intron I, and (2) the insertion sequence was also located in intron I of the Wax allele. The identity of the insertion sequence was completely conserved between the wax allele and the novel Wax allele. These findings implying that the wax allele, which was found in indigenous waxy barley, originated in non-waxy barley with the novel Wax allele.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS