

GEPHE SUMMARY

Gephebase Gene

Waxy /GBSS

Entry Status

Published

GepheID

GP00001197

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Physiology

Trait

Amylose content

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

Taxon A

Latin Name

Hordeum vulgare

Common Name

-

Synonyms

barley; Hordeum vulgare L.; Horedum vulgare

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoideae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus)

NCBI Taxonomy ID

4513

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Hordeum vulgare

Common Name

-

Synonyms

barley; Hordeum vulgare L.; Horedum vulgare

Rank

species

Lineage

cellular organisms; Eukaryota; Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; Liliopsida; Petrosaviidae; commelinids; Poales; Poaceae; BOP clade; Pooideae; Triticoideae; Triticeae; Hordeinae; Hordeum

Parent

Hordeum () - (Rank: genus)

NCBI Taxonomy ID

4513

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

waxy

Synonyms

GBSSI

String

-

Sequence Similarities

Belongs to the glycosyltransferase 1 family. Bacterial/plant glycogen synthase subfamily.

GO - Molecular Function

GO:0004373 : glycogen (starch) synthase activity

GO - Biological Process

GO:0019252 : starch biosynthetic process

GO - Cellular Component

GO:0009501 : amyloplast

GO:0009507 : chloroplast

Presumptive Null

Unknown

UniProtKB Setaria italica

Q8L699

GenebankID or UniProtKB

AAQ55449

Molecular Type

Cis-regulatory

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

Main Reference

The insertion/deletion polymorphisms in the waxy gene of barley genetic resources from East Asia. (2002)

Authors

Domon E; Fujijita 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 imply 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