

GEPHE SUMMARY

Gephebase Gene

teosinte branched 1 (tb1) = IntC

Entry Status

Published

GepheID

GP00001117

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

Morphology

Trait

Plant architecture

Trait State in Taxon A

Hordeum vulgare

Trait State in Taxon B

Hordeum vulgare

Trait #2

Trait Category

Morphology

Trait

Inflorescence architecture

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Data not curated

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

TB1

Synonyms

UniProtKB

Zea mays
Q93W12

GenebankID or UniProtKB

String

4577.AC233950.1_FGP002

Sequence Similarities

-

GO - Molecular Function

GO:0003700 : DNA-binding transcription factor activity

GO:0043565 : sequence-specific DNA binding

GO - Biological Process

GO:0007275 : multicellular organism development

GO:2000032 : regulation of secondary shoot formation

GO:0048831 : regulation of shoot system development

GO - Cellular Component

GO:0005634 : nucleus

Presumptive Null

Unknown

Molecular Type

Coding

Aberration Type

Unknown

Molecular Details of the Mutation

Large haplotypes; unknown

Experimental Evidence**Association Mapping****Main Reference**

INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. (2011)

Authors

Ramsay L; Comadran J; Druka A; Marshall DF; Thomas WT; Macaulay M; MacKenzie K; Simpson C; Fuller J; Bonar N; Hayes PM; Lundqvist U; Franckowiak JD; Close TJ; Muehlbauer GJ; Waugh R

Abstract

The domestication of cereals has involved common changes in morphological features, such as seed size, seed retention and modification of vegetative and inflorescence architecture that ultimately contributed to an increase in harvested yield. In barley, this process has resulted in two different cultivated types, two-rowed and six-rowed forms, both derived from the wild two-rowed ancestor, with archaeo-botanical evidence indicating the origin of six-rowed barley early in the domestication of the species, some 8,600-8,000 years ago. Variation at SIX-ROWED SPIKE 1 (VRS1) is sufficient to control this phenotype. However, phenotypes imposed by VRS1 alleles are modified by alleles at the INTERMEDIUM-C (INT-C) locus. Here we show that INT-C is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1 (TB1) and identify 17 coding mutations in barley TB1 correlated with lateral spikelet fertility phenotypes.

Additional References**RELATED GEPHE****Related Genes**

1 (VRS1 = SIX-ROWED SPIKE 1)

Related Haplotypes

No matches found.

EXTERNAL LINKS**COMMENTS**