(05-1-75)

Identification of a rice basic helix-loop-helix homolog

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Objectives

The objective of this study is to elucidate the function of a rice basic helix-loop-helix (bHLH).

Materials and Methods

1. Material

Plant - All rice lines used in this study were derived from the japonica cultivar Dongjin.

2. Methods

Rice genomic DNA was prepared from young leaves using a urea extraction procedure. The copy number of *Ds* was confirmed by Southern hybridization. GUS activity was examined for screening of mutants.

Results and Discussion

An *AC/DS* transposable element-mediated gene trapping system was used to isolate genes in higher plant. In this study, we report the characteristics of a rice *bHLH* homolog. The bHLH proteins are a superfamily of transcription factors and play important roles in anthocyanin biosynthesis, phytochrome signaling, globulin expression, fruit dehiscence, carpel and epidermal development in plant. In the *bhlh* mutant, T-DNA was inserted at the fourth intron of *OsbHLH*. GUS activity of *OsbHLH* was detected mainly in root. To clone the Ds flanking DNA of *OsbHLH,* we used iPCR method. The *OsbHLH* has an insert of 1,065bp and coding for a polypeptide of 381 amino acid residues, which calculates to a molecular mass of 41.03 kDa. The calculated pI of this protein is 5.14. Sequence alignment analysis revealed that the OsbHLH has high homology with AtbHLH, AtICE, and OsATP in bHLH domain region.

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