(05-1-101)

Sequence comparisons among 5′ flanking regions with cloning of *SP11/SCR* genes in *Brassica rapa* L.

Hyo-Jin Jung[1], Da-Yeung Seo[1], Jong-In Park[2], Kwon-Kyu Kang[3], and Ill-Sup Nou[1*]

[1]Faculty of plant Science, Sunchon National University, 315, Maegok-Dong, Sunchon 540-742, Korea

[2]Laboratory of Plant Breeding, Faculty of Agriculture, Iwate University, 3-18-8, Ueda, Morioka 020-8550, Japan

[3]Department of Horticulture, Hankyong National University, Anseong 456-749, Korea

Objectives

Here we tried to the cloning of 12 alleles of SP11 from Brassica rapa by using the PCR method, and comparison of the deduced nucleotide sequences.

Materials and Methods

1. Material

Plant nine(Class I) and three(Class II) inbred lines of *Brassca rapa* were used as PCR cloning.

2. Methods

PCR cloning, Sequencing

Results and Discussion

SP11/SCR have been identified in and have definitively established that *SP11/SCR* is the sole male determinant of SI in the genus *Brassica*. It was revealed by deletion analyses of the S^9-*SP11* promoter-gus fusions that the region around -192 bp contains the element(s) required for GUS expression in the tapetum, and that the region between -124 and -143 represents the minimal promoter region for pollen expression. In this paper, we extend the analysis of the 5′-flanking regions of *SP11/SCR* genes by comparing the genomic sequences of the genera *Brassica* and *Raphanus*. Twenty-two inbred were used as plant materials. The 5′-flanking regions of *SP11/SCR* genes amplified with a set of primers, *SP11*-PF designed based on the 5′-flanking region of S^9 and *SP11*-PR2 and *SP11*-PR3 designed based on the conserved signal peptide coding region of four alleles of *SP11* and sequenced.

Alignment of these sequences are highly conserved (53-96% identity) in the 5′-flanking region of *SP11/SCR* genes. Similarities between the nucleotide sequences from the *B. rapa* and *B. oleracea* lines ranged from 76% to 96%, not significantly higher than the similarities of *R. sativus* lines (from 60% to 91%). In addition, the position and sequence of the putative TATA box were conserved in *B. rapa*, *B. oleracea* and *R. sativus* lines. From database searches in the 5′-flanking region, these repeats and a putative pollen-specific sequences were not also found in the 5′-flanking region of *B. oleracea* and *R. sativus* lines. Moreover other common repeat or palindromic sequence was not found in these sequences.

Acknowledgements: This work was supported by a grant from BioGreen 21 Program, Development Administration, Republic of Korea

* *Corresponding author* : Ill-Sup Nou, TEL: 061-750-3249, E-mail: nis@sunchon.ac.kr