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Genome-wide characterization of the *Brassica rapa* genes encoding serine/arginine-rich proteins: regulation of alternative splicing events by abiotic stress and hormone treatments

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Alternative splicing (AS) of precursor messenger RNAs (pre-mRNAs) diversifies the transcriptome and proteome of eukaryotes by generating different isoforms from the same gene loci. The serine/arginine-rich (SR) gene family members are one of many splicing factors involved in the AS of pre-mRNAs. A whole genome triplication recently occurred in Chinese cabbage (*Brassica rapa subsp. pekinensis*) after its speciation from *Arabidopsis thaliana*. Thus, we investigated the B. rapa SR (BrSR) gene family regarding its evolutionary dynamics, AS patterns, and expression levels in young seedlings treated with abiotic stresses and phytohormones. A comparative genomic analysis employing synteny, non-synteny, and homolog searches identified 25 *BrSR* genes at 18 loci and three *BrSR*-like genes at two loci. Most of these loci contained singletons (n = 13), while seven loci carried paralogs. All of the duplicated pairs between and within *A. thaliana* and *B. rapa* were under purifying selection pressure. The expansion of the *BrSR* gene family was the result of segmental duplications only. Additionally, the *BrSR* AS pattern depended on seedling age. The AS patterns of 64% (18 of 28) and 39% (11 of 28) of the *BrSR* genes were altered in response to abiotic stresses and phytohormones, respectively. Among the analyzed abiotic stresses, heat and cold treatments induced the biggest AS changes, followed by salt stress. BrSCL1 and BrRS3 were expressed as a single transcript in all analyzed samples. Of the seven *BrSR* paralogous pairs, only one (i.e., *BrSR*-like1:*BrSR*-like2) exhibited similar AS patterns in all tested samples, suggesting that the remaining six pairs may have undergone sub- and/or neo-functionalizations.

Biography

Soo In Lee has his expertise in genomics and evolution of family genes from Brassica rapa. He is studying characterization and expression pattern of genes about RNA-binging proteins (serine/arginine-rich proteins) related abiotic stress in Brassica rapa.

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