

M-155

Genome-wide comparative analysis of DNA methylation between soybean cytoplasmic male-sterile line NJCMS5A and its maintainer NJCMS5B

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DNA methylation is an important epigenetic modification. It can regulate the expression of many key genes without changing the primary structure of the genomic DNA, and plays an important role in the growth and development of the organisms. Although genome-wide DNA methylation maps have been reported in many organisms, the DNA methylome of the soybean cytoplasmic male-sterile (CMS) line has few related studies. In the study, we apply DNA methylation sequencing on flower bud of the soybean CMS line *NJCMS5A* and its maintainer *NJCMS5B* for the first time. A total of 3,527 differentially methylated regions (DMRs) and 485 differentially methylated genes (DMGs), including 353 high-credible methylated genes, 56 methylated genes coding unknown protein and 76 novel methylated genes with no known function were identified. Among them, 25 DMRs were validated that the genome-wide DNA methylation profile results were reliable through bisulfite treatment, and 9 DMRs were confirmed the relationship between methylation and gene expression by qRT-PCR. Finally, 14 key DMGs which participated in pollen and flower development were identified as potentially related to CMS in soybean.