

عنوان مقاله:

In-silico identification of SSRs based on RNA-sequencing data from fully open flowers of a frost-tolerant almond under frost stress

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خلاصه مقاله:

Spring frost injury is a major environmental limit for the productivity of stone fruits such as almond. Thus, it is important to screen and breed spring frost tolerant trees. Among molecular markers, SSR derived from EST sequences are more desirable for breeding programs. In our previous study, we employed a frost treatment for flowers of a frost-tolerant almond genotype at full blooming stage as the important phenological stage to study frost stress. The transcriptomes of the frost-treated and non-frost-treated flowers (after post-thaw period) were analyzed and compared by using next generation sequencing technology. A total of ۶۳۲۱۸ sequences were generated and analyzed using SSR-Locator. In total, ۲۶۸۰ SSRs were identified and ۲۶۰۱ of sequences contained SSRs. In ۱۱ sequences, there was more than one EST-SSRs. Among the potential EST-SSRs, five types of the motifs were identified; di-nucleotide and tri-nucleotide had the highest frequencies followed by penta-nucleotide, hexa-nucleotide and tetra-nucleotide repeats. Our study revealed that di- and tri-nucleotide motifs are more frequent. TA/TA and GA/TC were the most abundant di-nucleotide motifs while GAA, AAC and ACC were common in tri-nucleotide SSRs. GO annotation showed that the top GO terms associated with SSRs containing tri-nucleotide motif were involved in the regulation of transcription, regulation of cellular biosynthetic processes, regulation of gene expression, regulation of cellular processes, response to stress and response to stimulus. Our study is the first report on SSR development for fully open flowers of a frost-tolerant almond genotype

کلمات کلیدی:

almond, frost, fully open flowers, SSR, RNA-seq

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