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De Novo Assembly and Characterization of the Transcriptome during Seed Development, and Generation of Genic-SSR Markers in Pomegranate (Punica granatum L.)

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Abstract : Pomegranate (Punica granatum L.) is known to be one of the oldest edible fruit tree species, with a wide geographical global distribution. Fruits from the two defined varieties (Hicaznar and 33N26) were taken at intervals after pollination and fertilization at different sizes. Seed samples were used for transcriptome sequencing. Primary sequencing was produced by Illumina Hi-Seq™ 2000. Firstly, we had raw reads, and it was subjected to quality control (QC). Raw reads were filtered into clean reads and aligned to the reference sequences. De novo analysis was performed to detect genes expressed in seeds of pomegranate varieties. We performed downstream analysis to determine differentially expressed genes. We generated about 27.09 gb bases in total after Illumina Hi-Seq sequencing. All samples were assembled together, we got 59,264 Unigenes, the total length, average length, N50, and GC content of Unigenes are 84.547.276 bp, 1.426 bp, 2,137 bp, and 46.20 %, respectively. Unigenes were annotated with 7 functional databases, finally, 42.681(NR: 72.02%), 39.660 (NT: 66.92%), 30.790 (Swissprot: 51.95%), 20.212 (COG: 34.11%), 27.689 (KEGG: 46.72%), 12.328 (GO: 20.80%), and 33,833 (Interpro: 57.09%) Unigenes were annotated. With functional annotation results, we detected 42.376 CDS, and 4.999 SSR distribute on 16.143 Unigenes.

Keywords : next generation sequencing, SSR, RNA-Seq, Illumina
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