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Soybean (*Glycine max*) Transcriptome Analysis by RNA-sequencing

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[Introduction]

Soybean [*Glycine max* (L.) Merr.] is the most widely grown grain legume in the world. It provides an important source of protein and oil for humans and animals. The purpose of this study is (1) to provide transcriptome information with genome and metabolite information of Korean soybean core collection obtained from previous research through transcript analysis in 50 accessions, and (2) to analyze patterns of expression genes through transcript analysis at immature seed of 10 and 30 days after flowering, which is the seed development stage in soybean growth.

[Materials and Methods]

A total of 50 accessions with genetic diversity were selected based on genome and metabolite analysis results from 430 Korean soybean core collection. Each RNA samples obtained from immature seed of 10 and 30 days after flowering, consisting of three independent biological replicates in 50 accessions. We were performed RNA sequencing on a total of 300 RNA samples.

[Results and Discussion]

We confirmed 27,576 significant genes with satisfies $|fc| \geq 2$ and $raw.p < 0.05$ conditions in at least one of total comparison pairs. Of the 50 accessions, CRS39 showed the highest 10,413 genes, whereas CRS6 showed the least 18 genes. In gene ontology enrichment analysis, the biological processes associated with the DEGs mainly focused on translation and carbohydrate metabolic process. The molecular function of the DEGs were structural constituent of ribosome and oxidoreductase activity. The cellular components mainly included chloroplast and ribosome. In differentially expressed genes (DEGs) analysis, there were no genes that commonly increased expression more than 2-fold (up-regulated) between 10 and 30 days after flowering in 50 accessions. However, 44 genes showed commonly increased expression more than 2-fold in 49 accessions except CRS6. In addition, only one gene showed commonly decreased expression more than 2-fold (down-regulated) in 50 accessions, whereas 89 genes showed commonly decreased expression more than 2-fold in 49 accession except CRS6. In the case of CRS6, a reanalysis of the transcript is necessary to confirm whether it is indeed a specific accession or the analysis is wrong.

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