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Comparative transcriptome analysis of flower heterosis in two soybean F1 hybrids by RNA-seq

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Heterosis has been widely exploited as an approach to enhance crop traits during breeding. However, its underlying molecular genetic mechanisms remain unclear. Recent advances in RNA sequencing technology (RNA-seq) have provided an opportunity to conduct transcriptome profiling for heterosis studies. We used RNA-seq to analyze the flower transcriptomes of two F1 hybrid soybeans (HYBSOY-1 and HYBSOY-5) and their parents. More than 385 million high-quality reads were generated and aligned against the soybean reference genome. A total of 681 and 899 genes were identified as being differentially expressed between HYBSOY-1 and HYBSOY-5 and their parents, respectively. These differentially expressed genes (DEGs) were categorized into four major expression categories with 12 expression patterns. Furthermore, gene ontology (GO) term analysis showed that the DEGs were enriched in the categories metabolic process and catalytic activity, while Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis found that metabolic pathway and biosynthesis of secondary metabolites were enriched in the two F1 hybrids. Comparing the DEGs of the two F1 hybrids by GO term and KEGG pathway analyses identified 26 common DEGs that showed transgressive up-regulation, and which could be considered potential candidate genes for heterosis in soybean F1 hybrids. This identification of an extensive transcriptome dataset gives a comprehensive overview of the flower transcriptomes in two F1 hybrids, and provides useful information for soybean hybrid breeding. These findings lay the foundation for future studies on molecular mechanisms underlying soybean heterosis.