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Transcriptome analysis of dwarf soybean derived from crossing of *G. max* and *G. soja*

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Soybeans are known as the most widely used legume crops in the world, and the crops provide an abundant source of oil and protein-rich food for human. Soybean growth is one of the most important traits for high yield breeding development. We selected normal and dwarf phenotype soybeans, which are F4 recombinant inbred lines (RIL) from a cross between *G. max* (Peking, female) and soybean *G. soja* (male), and compared the gene expression associated with growth type. Whole transcriptome sequence was generated by Illumina HiSeq2500 sequencing platform. A total of more than thousand genes were identified to be highly differentially expressed between normal and dwarf mutant lines. We performed Gene Ontology analysis separately in two groups that were divided into more and less expressed in dwarf phenotype. The dwarf phenotype showed less expression of photosynthesis- and protein biosynthesis-related genes than normal phenotype. Interestingly, plastid-related genes are rarely expressed in the dwarf phenotype. Given that chloroplast, one kind of plastids, performs photosynthesis in plants, the dwarf phenotype seems to have low photosynthetic efficiency. Sucrose and other metabolites produced by the photosynthesis process have been found to interact with hormones to regulate and integrate many plant metabolic processes. In addition, various ion transports-related genes also showed low expression in dwarf phenotype. We expect that these candidate genes will be useful for subsequent studies on plant growth.

Biography

Chanseok Shin is an Associate Professor in the Department of Agricultural Biotechnology at Seoul National University. His research is interested in studying the regulation of gene expression in eukaryotes, especially focusing on the regulatory roles of non-coding RNAs including microRNAs and long non-coding RNAs.

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