Genome-Wide Transcription Factor Expression Profiling For Soybean Bacterial Leaf Pustule Using RNA-Seq.

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Transcription factors (TFs) are DNA-binding proteins and important regulators of gene expression. TFs interacted with other transcriptional regulators facilitate the activation and repression of genes. After the completion of soybean genome sequencing using a soybean cultivar (Glycine max var Williams 82), SoyDB, a knowledge database for all the TFs in soybean genome, was developed by database of plant transcription factor, G. max unigene, soybean EST, and genome research soybean gene indices.

Recently, next generation sequencing technologies have been applied to the development of RNA-seq techniques for sequencing cDNA from various organisms. The RNA-seq is a revolutionary approach to characterization of transcriptomes. This method provides quantification of gene expression, the discovery of novel transcribed regions, and the identification of the alternative splice events or new candidate genes.

Here, we describe an application of the RNA-seq using Illumina GA II to study genome wide TF expression profiling for soybean bacterial leaf pustule (BLP), which is one of the serious diseases of soybean in Korea. We used near isogenic lines constructed by backcross using BLP-susceptible Taekwangkong and BLP-resistant SS2-2. Short read mapping analysis and quantification of the transcriptome between BLP-susceptible Taekwangkong and BLP-resistant Taekwangkong-near isogenic line (TN) by RNA-seq was performed. The differentially expressed TF genes were classified between Taekwangkong and TN at different time period of 0, 6, and 12 hour after inoculation using SoyDB.

Transcription factors (TFs) are DNA-binding proteins, in which their interactions with other transcriptional regulators facilitate the transcriptional activation or repression of genes. Among the several TFs function, TFs related to pathogen in plant are one of the important agriculture traits of improvement of productivity. A database of TFs with their function and roles in soybean is needed. As the completion of soybean genome sequencing using a soybean cultivar (Glycine max var Williams 82), SoyDB, a knowledge database for all the TFs in soybean genome, was developed. Until the development of next generation sequencing (NGS) technologies such as Roche (454 GS-FLX), Illumina (Genome Analyzer II), and ABI (AB SOLiD), Microarray, EST sequencing, and qRT-PCR are the representative methods for the genome wide analysis of gene expression profiling. However, these methods have several limitations, which include reliance on existing information about genome sequence, the detection of RNA splice patterns, and previously unmapped genes. Using NGS technologies, it is possible to identify entire plant genome sequencing. This technology has been applied to the development of RNA-seq techniques for sequencing cDNA from various organisms. The RNA-seq is a revolutionary approach to characterization of transcriptomes. This method provides quantification of gene expression, the discovery of novel transcribed regions, and the identification of the alternative splice events or new candidate genes.

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