

Phylogenomic-aided Identification and Characterization of Cell Wall Reassembly and Degradation Gene Families in Soybean, a Bioenergy Legume

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[Introduction]

Recently, the focus of biofuel industry has been shifted towards generation of second-generation bioethanol to overcome the future fuel demands. Second-generation biofuel production targets plant biomass which is the most abundant organic raw material. Soybean (*Glycine max* (L.) Merrill) is a promising biomass resource for second-generation biofuels. However, an optimized and enough bioethanol production from soybean is yet to be achieved. Despite the utility of soybean cellulosic biomass and post-processing residues in biofuel generation, there is no comprehensive information available on cell wall loosening and degradation related gene families.

[Materials and Methods]

The present study focused on mining publically available soybean genome for identification and comprehensive analysis of gene families involved in soybean cell wall loosening and degradation. Phylogenetic analysis, physical mapping of genes, duplication analysis, synteny analysis and gene co-expression analysis was done to get insight into evolution, functional relationship, and transcriptional association and coordination. To further aid future molecular breeding and biotechnological applications, all the identified genes were subjected to predict the presence of SSR markers and miRNA target sites. Furthermore, publically available microarray datasets for various soybean plant developmental stages, anatomical parts as well as under different biotic and abiotic stresses were analyzed to study the expression potential of all gene families involved in CWRD. Finally, gene co-expression networks were studied to visualize transcriptional coordination within studied gene families.

[Results and Discussions]

Comprehensive genome-wide analysis of gene families involved in cell wall modifications is an efficient stratagem to find new candidate genes for soybean breeding for expanding biofuel industry. We report the identification of 505 genes distributed among 12 gene families related to cell wall loosening and degradation. 1,262 tandem duplication events contributed towards expansion and diversification of studied gene families. We identified 687 Simple Sequence Repeat markers and 5 miRNA families distributed on 316 and 10 genes, respectively. Publically available microarray datasets were used to explore expression potential of identified genes in soybean plant developmental stages, 68 anatomical parts, abiotic and biotic stresses. Co-expression networks revealed transcriptional coordination of different gene families involved in cell wall loosening and degradation process.

[Acknowledgements]

This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2015R1D1A1A09060925).

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