

System's identification and Characterization of Cell Wall Loosening Related Genes in *Glycine max*: A Resource for Second-Generation Bioethanol

Sung-June Chu¹, Muhammad Amjad Nawaz¹, Hafiz Mamoon Rehman¹, Mawra Nadeem¹, Seung Hwan Yang¹ and Gyuhwa Chung^{1*}

¹Department of Biotechnology, Chonnam National University, Chonnam 59626, Korea

[Introduction]

Energy output from soybean can be enhanced by considering its potential to be used as a promising biomass resource for generation of second generation (2G) biofuel. Despite the utility of soybean cellulosic biomass and post-processing residues in biofuel generation, there is no comprehensive information available on cell wall loosening related gene families. A major constraint in 2G biofuel generation is recalcitrance. To achieve enhanced lignocellulosic biomass with softened cell walls and reduced recalcitrance, it is important to identify genes involved in cell wall polymer loosening.

[Materials and Methods]

We performed genome-wide identification and characterization of cell wall loosening related genes. For this we mined publically available soybean genome to identify the putative cell wall loosening related genes based on gene models in Arabidopsis. We then performed phylogenetic analysis, structure analysis, physical chromosome mapping, duplication and synteny analysis. We also identified SSR repeats to aid molecular and biotechnological applications of our results. We studied the digital expression of identified genes and co-expression networks.

[Results and Discussions]

We report identification of 130 genes distributed among 3 gene families related to cell wall loosening. Extensive segmental duplication and two rounds of whole genome duplications contributed towards expansion and diversification of studied gene families. We identified 88 Simple Sequence Repeat markers and 3 miRNA families distributed on 59 and 4 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.

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*Corresponding author: Tel. +82-61-659-7302, E-mail, chung@chonnam.ac.kr