

Conservation of bacterial disease resistance among homeologous chromosomal regions in soybean

Kyung Do Kim¹, Dong Hyun Kim¹, Jin Hee Shin¹, Kyujung Van¹, Suk-Ha Lee^{1,2,*}

¹Department of Plant Science and Research Institute for Agriculture and Life Science, Seoul National University, Seoul 151-921, Korea

²Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

Genome duplication is common in plants and many of modern diploid plants are in fact paleopolyploids possessing vestiges of multiple rounds of polyploidy. Soybean [*Glycine max* (L.) Merr.] is also considered as a paleopolyploid whose genome has gone through at least two rounds of polyploidy events. Many studies revealed the structure produced by a relatively recent polyploidy, but still few are reported regarding an ancient polyploidy due to high frequency of gene loss after duplication events. Bacterial leaf pustule (BLP), caused by *Xanthomonas axonopodis* pv. *glycines* (*Xag*), is a prevalent bacterial disease of soybean that has been reported in many soybean-growing regions of the world where high temperature and humidity prevail. In our previous study, we reported two homeologous regions of *Rxp* locus produced by recent duplication and their paralogous region in *Medicago truncatula*. Here, we report more comprehensive soybean genome structure anchored by *Rxp* genes and evolutionary history of *Rxp* regions from the most recent common ancestor legume through comparative genomics with *M. truncatula*. Despite the fact that dynamic structural changes in *Rxp* regions were considered in both soybean and *M. truncatula* after their divergence, not only genome structure and synteny, but also their functions were found to be highly conserved between four homeologous regions in soybean. At last, our data show that most of the multiple *Rxp* QTLs in different soybean linkage groups (LGs) are actually comprised of homeologous regions produced by two rounds of polyploidy events.

Proteomic Analysis of Stress Responses Protein in Wheat (*Triticum aestivum* L.)

Abu Hena Mostafa Kamal¹, Ki-Hyeon Kim¹, Kwang-Hyun Shin¹, Hyeong-Seok Seo¹, Dong-Hoon Shin¹, Lan-Seon Hong⁴, Cheol-Soo Park², Young-Keun Jong², Hwa-Young Heo³, Beom-Heon Song¹, Chul Won Lee¹, and Sun-Hee Woo^{1,*}

¹Department of Crop Science, Chungbuk National University, Cheongju 361-763, KOREA;

²Honam Agricultural Research Institute, Nat. Institute of Crop Science, Iksan 570-080, KOREA;

³Breeding Resource Development, National Institute of Crop Science, Suwon, 441-857, KOREA;

⁴CRIEF, Chungbuk National University, Cheongju 361-763, KOREA;

Abstract

Stress is one of the major causes for limiting crop productivity throughout the world. We carried out a comparative proteomic analysis of four wheat cultivars (two Korean; Keumgang, Jinpum and two Chinese; China-108, Yeonnon-78). MALDI-TOF/MS analysis and database searching of some of the identified proteins indicated which is the responsible for stress in wheat such as disease, salt, cold, pathogen, water and heat stress. Abscisic acid-inducible protein kinase, which is involved in water-stress responses. Heat shock protein plays a pivotal role in stress tolerance in wheat. Cold acclimation led to an accumulation of proline, a decrease in water content and an increase insoluble protein, especially in winter wheat. Ubiquitin are enhanced drought and salt tolerance in wheat. Salt stress in plants is due primarily to ion cytotoxicity involving alteration of cytosolic K⁺/Na⁺ ratios and osmotic stress that disrupts homeostasis and ion distribution in the cell and leading to denaturation of structural and functional proteins. Both wheatwin1 and wheatwin2 have specific antifungal activity toward the wheat-specific pathogenic fungi of wheat *Fusarium culmorum* and *Fusarium graminearum* of groups 1 and 2. Nucleotide binding leucine-rich repeat (NBS-LRR) proteins play an important role in plant immunity. In wheat, these resistance proteins recognize specific pathogen-derive effectors proteins. Recognition subsequently triggers a rapid and efficient defense response often associated with the hypersensitive response and other poorly understood processes that suppress the pathogen. In conclusion, our study provides new avenue into stress related proteins in wheat and demonstrates the advantages of proteomics analysis.

Acknowledgement: This work was supported by a grant from the BioGreen 21 Program (20070301034043), Rural Development Administration, Republic of Korea