

## **Identification of Soybean Cultivars bred in Gangwon-do using Soybean Barcode System**

Hwang-Bae Sohn<sup>1\*</sup>, Yun-Ho Song<sup>2</sup>, Su-Jeong Kim<sup>1</sup>, Su-Young Hong<sup>1</sup>, Yul-Ho Kim<sup>1</sup>

<sup>1</sup>Highland Agricultural Research Institute, National Institute of Crop Science, RDA, Pyeongchang-gun, 25342, KOREA

<sup>2</sup>Gangwondo Agricultural Research and Extension Services, Chuncheon-si, 24226, KOREA

### **[Introduction]**

The cultivation areas of soybean [*Glycine max* (L.) Merrill] cultivars bred in Gangwon-do have been increasing due to growing demand for well-being foods. Due to similar morphology of the cultivars, researchers have been focused on incorporating molecular markers for cultivar identification. Soybean barcode system is a useful tool for cultivar identification and diversity analysis, which could be used in seed production system of the soybean cultivars.

### **[Materials and Methods]**

We genotyped the cultivars by using 202 insertion and deletion (InDel) markers specific to dense variation blocks (dVBs) and examined their abilities of cultivar identification and diversity analysis through comparison with the database in soybean barcode system.

### **[Results and Discussions]**

The genetic homology of 'Cheonga', 'Gichan', 'Daewang', 'Haesal' and 'Gangil' to the 147 accessions was lower than 81.2%, demonstrating that these barcodes have potentiality in cultivar identification. Diversity analysis among 152 soybean cultivars revealed four subgroups and one admixture (major allele frequency <0.6). Among the accessions, 'Heugcheong', 'Hoban', 'Cheonga' were included in subgroup 1 and 'Gichan', 'Daewang', 'Haesal' and 'Gangil' in admixture. Especially, genetic regions of subgroup 3 and 4 in the admixture became more reshuffled for early maturity and environmental tolerance respectively, suggesting that soybean accessions with new dVB-types should be developed for improving the value of soybean products to end user. These results indicated that the two-dimensional barcodes of the soybean cultivars enable not only genetic identification but also managing of genetic resources through diversity analysis.

### **[Acknowledgements]**

This work was supported by a grant from Co-operative Research Program (Project No. PJ01125902) for Agriculture Science and Technology Development by Rural Development Administration, Republic of Korea.

\*Corresponding author Tel. +82-33-330-1870, E-mail. misson7@korea.kr