

Genetic Variation of Korean Soybean Cultivars using Genome-Wide 202 InDel Markers

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[Introduction]

Soybean [*Glycine max* (L). Merr.] is a widely cultivated crop plants in the world. Knowledge of chromosomal constitution of modern soybean ancestors will complement plant breeding efforts to improve the agronomic and economic characteristics of soybean.

[Materials and Mehtods]

For this study, variation block (VB)-based comparison using genome-wide insertion/deletion (InDel) markers was used on a diverse panel of 147 soybean accessions to assess the impact of chromosomal changes during modern breeding.

[Results and Discussions]

Results showed that in ‘Daepoong’, there were identical variation patterns of the examined InDels that consistently appear in the genome parts arising from parental varieties. This indicates that soybean chromosomes in descendants should be all determined by genetic reshuffling of VBs inherited from parental chromosomes. The phylogenetic tree and structure analysis of the accessions through the 202 InDels separated the accessions into four subgroups that corresponded to two soybean landraces (‘Jangdanbackmok’ and ‘Keunolkong’), and two introduced cultivars (‘Williams’ and ‘Essex’). Gene introgression revealed by the structure analysis corresponds to the reality that a limited number of landraces and elite varieties was introduced and used as donors for breeding soybean cultivars in the pedigree analysis. In addition, VBs became more reshuffled over time as a result of the breeding process. This shows that breeding parents with new VB-types should be introduced for improving the end-use value of soybean. Therefore, their clustering using the 202 VB-specific InDels is strongly influenced by the difference in breeding ancestors among the subgroups, which resulted in the change in the reshuffling patterns of the soybean cultivars. This indicates that the 202 InDel markers are highly useful for genetic study in analyzing the reshuffling patterns of the parental genomes in the descendant.

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