

PB-9

Development of Korean Wheat Cultivar Identification System by SNP Marker Combination

Da Won Seo¹, Deok Ryong Koo¹, Ha Neul Lee¹, Ha Young chung¹, Jae Yoon Kim^{1*}

¹Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

[Introduction]

Wheat (*Triticum aestivum*) has been a major food crop for a long time and has been of direct benefit to mankind. In Korea, the self-sufficiency rate is very low due to the low quality and low production of wheat. A cultivation system through identification of wheat cultivars can increase self-sufficiency. Molecular markers are a useful research method for the early detection of various genetic factors of wheat cultivars. In this study, experiments were carried out new Korean cultivars marker using previously developed Korean cultivars marker. Our marker combination is a system that can further differentiate between new and existing Korean cultivars.

[Materials & Methods]

A total of 41 Korean wheat cultivars were added 9 to the 32 cultivars used in previous patents. The 41 Korean cultivars were grown under speed breeding conditions (22 degrees, 22/2 light/dark conditions). PCR analysis was performed by selecting primers with high reproducibility and accuracy based on prior patents. After selecting a primer set, cultivars were grouped for each primer. To develop new Korean cultivars markers, PCR amplification products were used and sequenced. High-Resolution Melts (HRMs) were analyzed based on the results of Single Nucleotide Polymorphism (SNP) differences.

[Result & Discussion]

The 9 Korean cultivars that were not previously performed were analyzed in the same way using existing markers. ‘Chokwang’, and ‘Yungkwang’ are clearly identified in KWSM 4, 7, 8, 10, 11, 12 markers. In addition, ‘Olmill’ confirmed that the sequence of the KWSM 4 marker amplification product was different from that of other Korean cultivars in analyzing the nucleic acid sequence. In particular, we developed a new marker by analyzing HRM using the SNP differences found in ‘Olmill’. This study provides the possibility of developing precise markers by use and agricultural characteristics. In addition, Accurate identification of wheat cultivars is expected to contribute significantly to agriculture by protecting Korea’s wheat genetic resources.

[Acknowledgements]

This research was carried out with the support of Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ0159642022) Rural Development Administration, Republic of Korea.

*Corresponding author: E-mail, jaeyoonkim@kongju.ac.kr Tel. +82-041-330-1203