PB-035

Genetic Diversity of the Rice Heading Date Gene (*Ghd7*) Using Genotyping Array

Myeong-Hyeon Min[1][§], Kyu-Won Kim[2][§], Jungrye Nam[2], Sook Hee Yoon[2], Kyaw Myo Aung[1], Thant Zin Maung[1], Aueangporn Somsri[1], Luqi Hu [1], Do Hyun Kim[1], Beak Gi Hwan[1], Chang-Ho Kim[1], Myoung-Jun Jang[1], Jae Yoon Kim[1], Tae-Seok Oh[1], Yong-Jin Park[1,2]*

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea

[§]Both authors contributed equally to this work.

[Introduction]

The rice heading date 7 gene (*Ghd7*) is an important regulator of heading date. We extracted integrated high quality SNP/indel variant sites from 4835 accessions and profiled genetic diversity of *Ghd7*. The haplotypes will be employed in a *Ghd7* diversity study to improve the breeding of new varieties of rice.

[Materials and Methods]

A total of 4835 rice samples were collected from the world, we used IRGSP 1.0 as a reference genome for variation calling of those samples, including cultivar 3769 accessions, landrace 304 accessions, weedy 522 accessions and wild 240 accessions, identified the DNA genotyping chip containing 581,006 markers and 620,852 probes to detect nucleotide variants (SNPs / indels) as well as the absence/presence of genes. The haplotyping of *Gn1a* were purified from genotyping array.

[Results and Discussion]

Total of 4835 accessions had 115 haplogroups. *Ghd7* was located on chromosome 7, and a total of 30 mutations were confirmed in 2 exons. This allowed us to gather information on its genetic diversity, enabling more systematic identification of varieties associated with starch content.

[Acknowledgement]

*Corresponding author: Tel. 041-330-1213, E-mail. yjpark@kongju.ac.kr