

**OB-02**

## **Assessment of the Genetic Diversity of Colored Rice Germplasms Using SSR Markers**

Jae-Ryoung Park<sup>1</sup>, Kyung-Min Kim<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Korea

### **[Introduction]**

Annual per capita rice consumption in Korea is steadily decreasing. However, the consumption of rice for processing is increasing due to the expansion of convenient meal replacement, and the cultivation of the processing industry. Accordingly, functional rice varieties have been newly developed and popularized. However, since the breeding materials used by the rice breeding companies are limited, so we predicted that the rice varieties will be very similar genetically, and there is a lot of seed disputes at present. Molecular markers can easily analyze the relationship of genetic resources with low cost, as well as analyze the genotype of genetic resources and the relationship with functional substances. Since SSR markers are excellent repeatable reproducibility and are co-dominant markers. In this study, we analyzed the genetic diversity of colored rice using SSR markers.

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

We analyzed the genetic diversity of colored rice (350 black rice and 150 red rice) collected from Korea and abroad using SSR markers. In order to select suitable SSR markers for evaluation of rice varieties, 436 SSR markers were applied to 11 rice varieties with different botanical characteristics such as 'Junnam'. 16 SSR markers with high polymorphism and excellent repeatability were selected. After that, we analyzed the population structure of colored rice genetic resources using computer program.

### **[Results and Discussion]**

When 16 SSR markers were used, a total of 409 alleles were amplified. 11 to 47 alleles were detected on chromosome and an average of 25.6 alleles were detected. The PIC values ranged from 0.855 to 0.964 and the average was 0.913, which was very high. Using the selected 16 SSR markers, the overall similarity index of genetic resources ranged from 0.04 to 1.00 and was divided into seven subgroups. The results of this study provide important information for breeding rice and it will be very useful to preserve various genetic resources.

### **[Acknowledgement]**

This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ0136472019), Rural Development Administration, Republic of Korea.

\*Corresponding author: Tel. +82-53-950-5711, E-mail, kkm@knu.ac.kr