

**PB-60**

## **Establishment and Utilization of Genetic Resource Population Data for Rice Molecular Breeding**

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### **[Introduction]**

Plant genetic resources are basic materials for crop improvement and biotechnology research. To develop varieties of rice with several special traits, the use of more diverse genetic resource populations is required. As Korea's bio-research policy shifted to data-based research, the necessity of collecting, and using genetic resources, and securing genetic data expanded. Accordingly, by registering data from CNDH and SNDH, genetic populations of rice collected in this laboratory, it is intended to increase the utilization of rice molecule breeding as basic data that can contribute to solving food problems in the future.

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

The Cheongcheong/Nagdong double haploid (CNDH) population was the result of anther culture from the F1 cross between 'Cheongcheong' and 'Nagdong'. The Samgang/Nagdong double haploid (SNDH) population was the result of anther culture from the F1 cross between 'Samgang' and 'Nagdong'. CNDH and SHDH population data were registered in the national data station systems (Station-B) based on NCBI.

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

CNDH and SNDH genetic map based on the genetic resource population data collected in this laboratory. polymorphism analysis for each population was conducted on various traits of rice by analyzing QTL involved in specific traits of rice. Genetic maps created using genetic resource populations can be used to increase selection efficiency by using markers associated with major genes when selecting traits involved in polygene and can be used to shorten the breeding cycle and genome editing. The rice genetic resource data registered in the national data station system (Station-B) by bio-data engineers can be used by everyone. By sharing genetic data, the industrial utilization of genetic resources will increase and it is expected to be useful in rice molecular breeding research.

### **[Acknowledgement]**

This work was supported by the National Research Foundation of Korea Grant funded by the Korean Government (NRF-2021M3E5E6022715).

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