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Registration of Two Rice Populations Derived from *indica-japonica* Cross Based on QTL Analysis

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[Introduction]

Rice is One of the most important crops worldwide and provides food for nearly 50% of the world's population. *Indica* and *japonica* are the predominant sub-species of cultivated rice in Asia, however the two varieties have very different biological and ecological characteristics. In recent years, many *indica-japonica* rice hybrids have been developed and planted widely in China for their super-high yield potential. As crop improvement and biotechnology research increases, the use of more diverse rice genetic resource populations is required. Accordingly by registering data from the Cheongcheong/Nagdong double haploid (CNDH) and the Samgang/Nagdong double haploid (SNDH), developed in this laboratory, it is intended to support genomics-assisted rice breeding.

[Materials and Methods]

The cultivars Cheongcheong(IT228761, *indica*-type), Nagdong(IT006182, *japonica*-type) and Samgang(IT221837, *indica*-type) were used as the parents of the double haploid (DH) population. CNDH composed of 120 lines and SNDH composed of 113 lines were the result of anther culture from the F₁ cross. CNDH and SNDH population survey trait data were registered in the national data station system (Station-B) based on NCBI.

[Results and Discussion]

The CNDH and SNDH developed double haploid (DH) mapping populations using japonica and indica rice varieties and released at Kyungbook National University in August 2021 have been used to identify genomic regions associated with phenotypic 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 breeding cycle and genome editing. These mapping populations and related datasets provide important insights into the rice varieties and facilitates the practical use in rice breeding.

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