

**PB-023**

## Phenotypic Characterization of Ac/Ds Mediated Mutant Pool in Rice.

Seung Uk Ji<sup>1</sup>, So-Young Kim<sup>1</sup>, Min Kang<sup>1</sup>, Gang-Seob Lee<sup>1\*</sup>

<sup>1</sup>National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea

Rice is one of the world's most important crops, particularly in Asia, for human consumptions. Rice consumption has been increased due to versatility of nutrients and tastes. In addition, Rice has taken a role of model plant since the small size of the genome was completely sequenced (Jun et al. 2002, Feng et al. 2002). To increase higher yield potentials of crops, the discovery of novel genes and the construction of QTL maps should be essential projects in genomic researches.

Currently, various insertional mutants are used for rice functional genomics. The insertional mutant pool of this research is stable knockout population for various screening studies. Through this research program, insertion sites of more than 33,157 Ds lines were exploited and their information has been released via a database.

Through this research program, phenotypic and agronomical characteristics of the population will be open for public and be expected to be useful in isolating agronomically important genes. Currently, genomic resequencing strategy becomes very powerful in isolating rice genes. Our genetic materials will serve perfectly for the resequencing project in the near future. Ultimate goals are to supply genetic materials and informations essential for functional analysis of rice genes and for breeding using agronomically important genes.

\*Corresponding author: Tel. 063-238-4791, E-mail. kanglee@korea.kr