

Studies on the Construction of Mutant Diversity Pool (MDP) lines, and their Genomic Characterization in Soybean

Dong-Gun Kim¹, Sang Hoon Kim¹, Chang-Hyu Bae² and Soon-Jae Kwon^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Korea

²Department of Life Resources, Graduate School, Sunchon National University, Suncheon 59722, Korea

Mutation breeding is useful for improving agronomic characteristics of various crops. In this study, we constructed soybean Mutant Diversity Pool (MDP) from 1,695 gamma-irradiated mutants through two selection phases over M_1 to M_{12} generations; we selected 523 mutant lines exhibiting at least 30% superior agricultural characteristics, and, second, we eliminated redundant morphological phenotypes in the M_{12} generation. Finally, we constructed 208 MDP lines and investigated 11 agronomic traits. We then assessed the genetic diversity and inter-relationships of these MDP lines using target region amplification polymorphism (TRAP) markers. Among the different TRAP primer combinations, polymorphism levels and PIC values averaged 59.71% and 0.15, respectively. Dendrogram and population structure analyses divided the MDP lines into four major groups. According to an analysis of AMOVA, the percentage of inter-population variation among mutants was 11.320 (20.6%), whereas mutant inter-population variation ranged from 0.231 (0.4%) to 14.324 (26.1%). Overall, the genetic similarity of each cultivar and its mutants were higher than within other mutant populations. In an analysis of the genome-wide association study (GWAS) using based on the genotyping-by-sequencing (GBS), we detected 66 SNPs located on 13 different chromosomes were found to be highly associated with four agronomic traits: days of flowering (33 SNPs), flower color (16 SNPs), node number (6 SNPs), and seed coat color (11 SNPs). These results are consistent with those previously reported for other genetic resource populations, including natural accessions and recombinant inbred line. Our observations suggest that genomic changes in mutant individuals induced by gamma rays occurred at the same loci as those of natural soybean population. This study has demonstrated that the integration of GBS and GWAS can serve as a powerful complementary approach to gamma-ray mutation for the dissection of complex traits in soybean.

*(Corresponding author) soonjaekwon@kaeri.re.kr, Tel: +82-63-570-3312