

Genetic Diversity and Relationship in Soybean MDP (Mutant Diversity Pool) Revealed by TRAP and TE-TRAP Markers

Dong-Gun Kim^{1,2}, Chang-Hyu Bae² and Soon-Jae Kwon^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Republic of Korea, ²Department of Life-resources, Graduate School, Sunchon National University, Suncheon 59722, Republic of Korea

Mutation breeding is the useful tool to improve agronomic traits in various crop species. Soybean is most important crop and is rich in protein and oil contents. Despite of the importance as economic value and various genetic resource of soybean, there have been limited studies of genetic relationship among mutant resources through radiation breeding. In this study, the agronomical phenotype for selecting various genetic resources was evaluated in 528 soybean mutant lines. As a result, 210 soybean mutants with their original cultivars were selected with various traits. We named 210 selected lines as Mutant Diversity Pool (MDP). The genetic diversity and the relationship of the MDP were investigated using TRAP and TE-TRAP markers. In TRAP analysis, sixteen primer combination (PC)s were used and a total of 551 fragments were amplified. The highest (84.00%) and the lowest (32.35%) polymorphism levels were showed in PC MIR157B+Ga5 and B14G14B+Ga3, respectively. The mean of PIC values was 0.15 ranging from 0.07 in B14G14B+Sa12 to 0.23 in MIR157B+Sa4. Phylogenetic and population structure analysis indicated that the 210 MDP lines dispersed to four groups among the wild types and their mutants. The highest genetic diversity among populations was observed between lines Paldal and 523-7 ($F_{st}=0.409$), whereas the lowest genetic diversity was between population KAS360-22 and 94seori ($F_{st}=0.065$). AMOVA showed 11.583 (21.0%) and 43.532 (79.0%) variations in inter and intra mutant population, respectively. Overall, the genetic similarity of each intra mutant populations was closer than that of inter mutant population. A total of 408 fragments were amplified in the 210 MDP using twelve PCs of TE-TRAP markers that were obtained from a combination of three TIR sequence of transposable elements (MITE-stowaway; M-s, MITE-tourist; M-t, PONG). The highest (77.42%) and the lowest (56.00%) polymorphism levels were showed in PONG+Sa4 and PONG+Sa12, respectively. The mean of PIC values was 0.15 ranging from 0.09 in M-s+Sa4 and M-s+Ga5 to 0.21 in M-t+Ga5. AMOVA of M-s showed 2.209 (20%) and 8.957 (80%) variations in inter and intra mutant population, respectively. AMOVA of M-t showed 2.766 (18%) and 12.385 (82%) variations in inter and intra mutant population, respectively. AMOVA of PONG showed 3.151 (29%) and 7.646 (71%) variations in inter and intra mutant population, respectively. According to our study, the PONG had higher inter mutant population and lower intra mutant population. This mean was that for aspect of radiation sensitivity, M-s and M-t showed higher mobility than that of PONG. Our results suggest that the TRAP and the TE-TRAP markers may be useful for assessing the genetic diversity and relationship among soybean MDP and help to improve our knowledge of soybean mutation/radiation breeding.

(Corresponding author) E-mail: soonjaekwon@kaeri.re.kr Tel: 063-570-3310