

## Genetic diversity, structure analysis and relationship in soybean mutants as revealed by TRAP marker

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Mutation breeding by radiation is useful for improving various crop species. Up to now, a total of 170 soybean mutant varieties have been released in the world, which is the second most registered varieties after rice. Despite the economic importance of soybean, there have been no TRAP marker system studies on genetic relationships between/among mutant lines. To develop a strategy of Mutant Diversity Pool (MDP) conservation, a study on the genetic diversity of 210 soybean mutant lines (8 cultivars and 202 mutants) was performed through a TRAP analysis. Sixteen primer combinations amplified a total of 551 fragments. The highest (84.00%) and lowest (32.35%) polymorphism levels were obtained with primers MIR157B + Ga5 and B14G14B + Ga3, respectively. The mean PIC values 0.15 varied among the primer combination ranging from 0.07 in B14G14B + Sa12 to 0.23 in MIR157B + Sa4. Phylogenetic, principal component analysis (PCA) and structure analysis indicated that the 210 lines belong to four groups based on the 16 combination TRAP markers. AMOVA showed 21.0% and 79.0% variations among and within the population, respectively. Overall, the genetic similarity of each cultivar and its mutants were higher than within other mutant populations. Our results suggest that the TRAP marker system may be useful for assessing the genetic diversity among soybean mutants and help to improve our knowledge of soybean mutation breeding.

Key words: Mutant Diversity Pool(MDP), TRAP marker, structure analysis

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