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GENETIC DIVERSITY FOURTEEN SOYBEAN MUTANT LINES USING SSR MARKERS AND YIELD PERFORMANCE UNDER DRY LAND CONDITION

Development of drought-tolerant varieties is an effective alternative to overcome this abiotic stress. The objectives of this research were to evaluate the genetic diversity and relationship among soybean mutant lines using SSR markers and to select promising mutant lines with high yield under dry land condition. A total of 14 soybean mutant lines derived from induced mutation (Mutant A, B, C, D, E, F, G, H, Y, K, L, M, N, P) and two control varieties (R=Panderman and S=Muria) were used in present study. Those genetic materials were grown at Gunung Kidul and Bantul (country). Results revealed five mutant lines (E, B, G, P and Y) exhibiting a higher yield (2.63, 2.51, 2.32 t/h, respectively) than the control variety Panderman (2.05 t/h). These mutant lines exhibited significant differences in 100-seed weight (14.3, 14.5, 14.3 gr) number of pot fill (118, 116, 104) and number of seed per plant (215, 218, 205) as compared to national control drought tolerant variety (Dering: 14.1, 103.6 and 201.3). A wide genetic distance between soybean mutant accessions and their wild-type were observed by using 12 simple sequence repeats (SSR) markers. A total of 58 alleles with an average of 4.8 alleles per locus were detected. The polymorphic information content varied from 0.40 to 0.75 with an average of 0.53. The accessions were clustered into two groups according to their genetic background, namely group I (B) and group II (R= the Panderman). The highest genetic diversity value of 0.78 was shown by the Satt294 primers. Six informative markers (GMES3515, GAAT47, Satt009, Satt038, Satt294, and Satt431) provided polymorphic alleles between the parents and their mutants.

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