ABSTRACT

Ten soybean [Glycine max (L.) Merrill] cultivars and eighteen soybean accessions from AVRDC Soybean Germplasm Collection were used to study genetic variation using morphological characters, RAPD and AFLP Techniques. Thirty RAPD, 10-15 nucleotide primers with more than 4 bands per primer and 10 AFLP combinations were selected and used to study genetic variation among soybean samples. 206 RAPD markers and 437 AFLP markers were produced. Polymorphic Information Contents (PICs) ranged from 0.00-0.50 with 60.81% of total markers were in the range of 0.00-0.05. Mean PIC was 0.12. Genetic similarity estimated by Sneath and Sokal (1973) ranged from 0.87-0.96. The NTSYSpc2.02i analysis based on similarity coefficient could identify soybean cultivars into 5 distinct groups; sj.1, sj.2, sj.4, sj.5, cm.60, GC9984, ns.1, cm.2, kus20004, st.1, cm.3; GC2679, GC3318, GC7231, GC2796, GC4796, GC4637; GC9822, GC11254, GC10215, GC10950, GC10981, GC10992, GC1101, GC10848; st.2, GC4120 and pk462. Principal Component Analysis (PCA) was calculated using similarity matrix for 643 RAPD and AFLP markers to produce distribution pattern of 28 soybean cultivars. PCA1, 2 and 3 accounted for 27.17%, 12.28% and 11.56% of total variation, respectively. The distribution patterns confirmed UPGMA cluster analysis with same distinct subgroups produced. The morphological characters among samples were very similar and the data supported the information of
RAPD and AFLP techniques. The background genetic information will be useful for soybean improvement project in the future.