# IDENTIFICATION OF GENETIC DIST ANCE OF EXOTIC AND LOCALLY DEVELOPED MAIZE INBRED LINES

**J.A.U.C. Jayasooriya[1], S.K. Wasala[2], M.C.M. Zakeel[1]**

[1]*Department of Plant Sciences , Faculty of Agriculture, Rajarata University of Sri Lanka, Puliyankulama, Anuradhapura, Sri Lanka.*
[2]*Biotechnology Division, Plant Genetic Resour ces Center, Gannoruwa, Peradeniya Sri Lanka.*

Development of hybrid varieties is one of the strategies to increase the productivity and production of Maize *(Zea mays* L.) in Sri Lanka. Heterosis is an important aspect to measure the hybrid vigour. Genetic distance is a main factor, which affects on heterosis. Identification of suitable parents using molecular markers gives many advantages over morphological evaluation. This study was conducted at the Molecular Biology Laboratory of Plant Genetic Resources Centre, Gannoruwa to identify distant parents using Simple Sequence Repeats (SSR) primers. Genomic DNA was isolated from selected 23 inbred lines including exotic and locally developed lines using modified CTAB method. Molecular characterization was done using four SSR primers; *UMC1023, phi402893, phi112* and *phi041.* Amplified products were resolved in Polyacrylamide Gel Electrophoresis. Data were manually scored and analysis of genetic variation was carried out using the software POWEMARKER 3.1. Analysis revealed that polymorphism existed for all four SSR primers. Considerable genetic diversity was observed among the loci. Number of alleles per locus ranged from 2 to 3. Polymorphic information content (PIC) ranged from 0.24 *(phi112)* to 0.42 *(phi402893).* Gene diversity varied from 0.28 *(phi112)* to 0.46 *(phi402893).* Based on the values, it was found out that there was a high genetic diversity present within the tested inbred lines. Genetic distance was calculated based on Nei's genetic distance and phylogenetic tree was developed using Unweighted Pair Group Method with Arithmetic Mean (UPGMA). Tested 23 populations could be grouped into four clusters. Most of the exotic inbred lines got grouped into one cluster showing that there is shorter genetic distance present within the exotic lines. The genetic distance information obtained in this study will be useful to select better parents for development of maize hybrids with good performances.

*Key words:* Genetic distance, Maize hybrids, SSR mark