ANALYSIS OF GENETIC DISTANCE AMONG COMMON BEAN USING MORPHOLOGICAL AND MOLECULAR MARKERS

K.M.A.N. Kulathunga[1], H.M.P.S. Kumari[2], M.C.M. Zakeel[1] and L.K.W. Wijayaratne[1]

[1]Department of Plant Sciences, Faculty of Agriculture, Rajarata University of Sri Lanka, Puliyankulama, Anuradhapura, Sri Lanka

[2] Biotechnology Division, Horticultural Crop Research and Development Institute, Gannoruwa, Peradeniya, Sri Lanka

Common bean, is a king of vegetable with a higher farmer and consumer demand, in Sri Lanka. Information on genetic diversity of local common bean genotypes is scanty, posing a great impediment for crop improvements. This research assessed the genetic diversity among different genotypes of common bean in Sri Lanka, based on the genetic distances obtained by morphological and simple sequence repeats (SSRs) markers, and also identified the most distinguished line or lines from farmer selections for further improvements. Thirteen genotypes, comprise of five Department of Agriculture (DOA) recommended varieties (*Lanka butter, KWG, Bandarawela Green, Balangoda Nil* and *Kappetipola Nil*) and eight farmer selections (*Mandaramnuwara Kalu; MNK, Mandaramnuwara Sudu; MNS, Mandaramnuwara Sudu selected; MNSS, Mandaramnuwara Kalu; MNKa, Bandarawela Kalu; BWK, Bandarawela Kaha; BWKa, Galpalama Kalu; GPK, Galpalama Kaha; GPKa*) were evaluated using 32 SSR primer pairs and 30 morphological traits. SSR marker analysis revealed that approximately 57% of the amplified products showed polymorphism, indicating a considerable variation at the DNA level. Sixteen primers showed diversity in common bean, mapping a total of 100 amplifications with an average of 8.3 bands per primer. The minimum genetic distance among the study population (0.03) was found between two farmer selections whereas the maximum distance (0.49) was in between two DOA recommended varieties. Common bean varieties could be distinguished at the genetic distance of 0.17 according to the genetic distance analysis of DOA recommended varieties. Cluster analysis of SSR data revealed eight major clusters at 19.98 with three separate clusters formed by farmer selections. All DOA recommended varieties formed separate clusters. *Kappetipola Nil* formed a cluster, closer to all farmer selections whereas *Lanka butter* formed a cluster far away from the rest of the genotypes. The cluster analysis of morphological traits showed farmer selections getting clustered with some DOA recommended varieties, perhaps due to higher degree of morphological similarities among farmer selections and some DOA recommended varieties. Therefore, SSR markers could successfully be used to distinguish common bean varieties in Sri Lanka and three clusters of farmer selections could be used as three different lines in future breeding and varietal improvement programmes.

Keywords: Common bean, DOA recommended varieties, Farmer selections, Genetic distance, SSR markers