Annals of Sri Lanka Department of Agriculture 2016. 18: 70 - 73

ESTIMATION OF PHENOTYPIC DIVERSITY OF CHILLI (*CAPSICUM* SPP.) GERMPLASM IN SRI LANKA

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EXTENDED ABSTRACT

Chilli (*Capsicum* Spp.) is an important cash crop with high market value for its taste, aroma and pungency. A wide range of genotypic variability exists in this crop (Nandi, 1992; Munshi and Behera, 2000). This variability can be utilized for crop improvement programs. Chilli is a diploid (2n=24) species and genetically self-pollinated plant. However, 2 to 96% out-crossing has been observed under open pollination (Hasanuzzaman *et al.*, 2012). There are approximately 25 species within the genus *Capsicum,* five of which have been domesticated. The most widely grown and economically important species is *Capsicum annuum.* The four other domesticated species are *C. baccatum, C. pubescens, C. chinense* and *C. frutescence.* Study of genetic diversity within available genetic resources is essential to understand the evolutionary and genetic relationship among accessions. A wide diversity exists in morphological traits such as fruit shapes in chilli, both within and between species. Study of genetic diversity within available genetic resources is essential to understand the evolutionary and genetic relationship among accessions. Characterized and evaluated genotypes are essential for an effective breeding program to incorporate desired traits. Germplasm resource contains unique traits/genes that can be utilized for further crop improvement. Exploration, collection and evaluation of germplasm are the quickest and simplest method for acquiring the desired ones for future breeding programmes.

Therefore, in this field study thirty eight chilli (*Capsicum spp.*) genotypes were evaluated to assess genetic diversity of *Capsicum* spp. in a Randomized Complete Block Design with two replications during *Yala* 2015 and *Maha* 2015/16 seasons at the Field Crops Research and Development Institute (FCRDI), Mahailluppallama. Fourteen morphological characters were recorded, namely, number of days to 50% flowering, plant height (cm), plant breadth (cm), mature leaf length (cm), mature leaf width (cm), pod length (cm), pod girth (cm), pericarp thickness (mm), number of pods per plant, individual pod weight (g), number of seeds per pod and pod yield (t/ha).Analysis of variance, Multivariate data analytical methods *viz.* principal component and cluster

analysis and Pearson correlation coefficient was performed to estimate phenotypic diversity of chilli genotypes accounting fourteen morphological traits.

Out of 38 genotypes with 14 morphological traits, the highest variation was observed in pods per plant followed by seeds per pod and days to 50% flowering. Moderate variation was observed in plant height and plant breadth. Lowest variation was observed in pericarp thickness of the pods. Analysis of variance revealed significant differences at 0.05% probability level among different genotypes in days to 50 % flowering, plant height, plant breadth, number of pods per plant, individual pod weight, seeds per pod and yield scored. Principal component analysis quantifies each trait to calculate the Principal Components (PCs) which help in describing grouping of variables.

The first principal component (PC1) is related to mature leaf length, leaf width, pod length, pod weight and yield. It explained 39% of total variability. The second principal component (PC2) is related to pod width, pericarp thickness and secondary branches explained 15% of total variability. The third principal component (PC3) is related to morphological characters such as number of primary branches, number of pods per plant and yield. These four components explained more than 75% of total variability among the chilli genotypes evaluated. Leaf characters (length and width), pod length, pod width and yield were recorded higher magnitudes (above 0.35) for the PC1. Leaf characters were positively correlated with PC1. Furthermore, pod width, pericarp thickness were negatively correlated with a high magnitude for PC2 while pods per plant were recorded high positive magnitude for PC2.

The phenotypic tree derived based on Pearson distance explain the relative positions of chilli genotypes scored on morphological traits. At 40 similarity levels, there were six clusters with three main clusters and minor clusters. Germplasm of *Capsicum annuum* was grouped in to I, II and III clusters. In first cluster, variety MI2 stayed separately. In second cluster Hot Beauty having foreign origin stayed distantly to others. At this similarity level, MI Waraniya1and ICPN 987.5 lines were grouped together which possess same morphological characters like long pod character. *Capsicum chinense* and *C. frutescence* lines were clustered separately at cluster IV and V. The line of kochchi 13 which belongs to *C. frutescence* was stayed separately at cluster VI. It has shown unique characteristic and genetically distance to others.

The derived phenotypic tree revealed that there is a genetically distinctness of parents. Genetic diversity within closely located genotypesis lower than that of distantly located genotypes. The distance parents with different genetic constitution can be utilized for future breeding programmes. In intra-specific crosses of *C. annuum,* germplasm of cluster I (MICH 3, Galkiriyagama selection and MI2) could be used with germplasm of cluster II (KA2, Arunalu, MI Hot *etc.*) and cluster III (MI Waraniya1and ICPN 987.5 lines). For inter-specific crosses the germplasm of cluster I, II and III which belong to *C. annuum* could be combined with germplasm of cluster IV, V and VI which belong to *C. chinense* and *C. frutescence* to have new genetic makeup.

The first two major principal components that accounts 54% of the total variance were plotted to observe the relationship between clusters in a Score Plot. All genotypes in cluster I were grouped together in score plot. Germplams of cluster II were closely stayed in the score plot except variety PC 1. Genotypes of cluster IV showed a close relationship. Genotypes of minor cluster of III *i.e.* MI Waraniya 1 and ICPN 985.7 were stayed closely. Minor clusters of V *i.e.* Kochchi 7 and Kochchi 15 were also stayed closely. Results of score plot confirm the pattern found in cluster analysis. Thus, there is a potential of utilizing such variability in future chilli crop improvement programmes. Pearson correlation coefficient were shown significant positive correlations between leaf related characters, plant breath, pod width, pericarp thickness, secondary branches per plant, weight per pod and yield with most of morphological traits.

Yield is complex character influenced by a number of other component characters (Jose and Khader, 2002). Weight per fruit and number of fruits per plant are the most important components of yield. Thus, in the process of selection, emphasis should be given to those characters. Other yield components that can be used to improve yield are plant width, fruit length, fruit diameter, days to fruit set and fruit density. (Ahamed and Hurra, 2000). Higher phenotypic and genotypic coefficients of variation were observed for leaf area, fruits per plant, fruit weight, fruit length, fruit girth and yield per plant. High heritability coupled with high genetic advance observed in these characters implies their potential for crop improvement through selection process.

Principal component analysis and cluster analysis have given comparable results for 38 chilli germplasm and score plot has confirmed the aforesaid results. Therefore, estimation of diversity with respective to quantitative traits such as plant breath, leaf characters, pod length, pod width, pericarp thickness, pod weight, secondary branches per plant and yield will help to identify parental materials for future chilli crop improvement programmes. High genetic variation can be created with more genetic distant parents in order to achieve maximum heterosis.

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