

PERFORMANCES OF DIFFERENT BREEDING METHODS BASED ON THE ESTIMATED GENETIC PARAMETERS IN F4, F5 AND F6 GENERATION ADVANCEMENTS OF COWPEA (*VIGNA UNGUICULATA* (L). WALP)

M.C. MILLAWITHANACHCHI¹, V. A. SUMANASINGHE², A.P. BENTOTA¹
B.N. SAMARANAYAKE¹ AND N.T. PRATHAPASINGHE¹

¹*Grain Legumes & Oil Crops Research & Development Center,
Angunakolapellassa, Sri Lanka*

²*Faculty of Agriculture, University of Peradeniya, Sri Lanka*

INTRODUCTION

Knowledge about the relative efficiency of different breeding methods may greatly help plant breeders in selecting a better method to be adopted in a particular crop (Adnan *et al.*, 2011). In cowpea cultivation of Sri Lanka there are farmer grown cultivars with some good attributes such as drought tolerance, better taste, elasticity of growth pattern according to the rainfall changes, yet the yield performances were at poor level. So there is a demand for high yielding cowpea varieties with better adaptability. (Millawithanachchi *et al.*, 2012).

Hence, an efficient breeding method to develop adaptable cowpea varieties for the farmer field conditions is required. Therefore, this study was conducted with the objectives of comparing three breeding methods at F4, F5 and F6 generations based on the mean performance and genetic parameters and other selected traits using two cross combinations of cowpea.

F3, F4, F5 and F6 generations were advanced with a series of trials following pedigree method (PM), modified bulk method (MB) and Single Seed Descent (SSD) method using two cross combinations of four distinct parents of cowpea, CP19 X Waruni (cross 01) and CP20 X CP22 (cross 02) at the Grain Legumes and Oil Crops Research and Development Centre (GLORDC) at Angunakolapellassa, Sri Lanka starting from 2011 *yala*. From F2 to F5 in PM 100 progeny lines were derived from respective previous population following within and between line selections. SSD method followed for the two populations from F2 to F4 and F5 generations were established as the progeny lines in both crosses. In modified bulk method (MB) F3 and F4 bulk populations were established with the bulked seed samples from superior 5% of selected plants of the F2 and F3 respectively. Hundred plants were established as lines in the F5 generation selected from F4. Ten best lines of each F5 generation of three breeding methods belong

to two crosses were selected based on the visual selections by breeders and farmers. The ten best lines selected from each of the three breeding methods along with the parents of the relevant crosses and three standard checks were evaluated for their performance. Two separate experiments were conducted for the two crosses. Each experiment was laid out in a RCBD with three replicates, at GLORDC.

Data were recorded on plant height at maturity, number of peduncles per plant, number of pods per plant, number of seeds per pod, average length of pod, hundred seed weight and yield per plant in F4, F5 and F6 generations. Phenotypic (V_p) and Genotypic (V_g) variances and the Genotypic (GCv) and phenotypic (PCv) coefficients of variation, heritability broad sense (H_b) and genetic advance (GA) were estimated separately for each selection method per each cross at F4, F5 and F6 populations.

Results indicated that for the plant height character SSD populations have retained more genetic variability in F4 and F5 compared to those developed by other two methods due to less selection pressure on the SSD population than the pedigree and MB method populations. In F6 PCv and GCv were reduced in SSD compared to the other two methods due to the selection pressure at F5 generation. High level of GCv and PCv of plant height indicated that it is highly variable character. Though it has recorded high H_b , due to low to moderate nature of GA fixable additive gene effects are low for this character. The results with higher GCv , PCv H_b and GA at early generations indicate considerable proportion of additive or additive x additive gene effects exist for pods per plant character and additive effects of this character can be fixed by early selection. According to Kurer, 2007, pods per plant is the major component of seed yield among many components. This trait can be improved by simple selection. SSD method recorded the highest variability for pod length character with higher GCv , PCv and H_b and other two methods recorded moderate to low GCv , PCv and high H_b in early generations. Seeds per pod, GCv , PCv and H_b were high to moderated for all the methods in F4. At F6 level SSD method recorded low GCv and moderate PCv . MB and pedigree methods recorded moderate GCv while H_b was high for pedigree and SSD methods.

PCv and GCv of seed weight were moderate for all the methods and high H_b s were recorded by all the methods at F4. All the methods recorded low GA values. SSD has recorded the highest values for GCv , PCv and H_b with higher GA as % of mean for yield per plant while pedigree and MB methods recorded moderate values for GCv and PCv and higher values for PCv in F4 and similar pattern for SSD in F5. The other two methods recorded low GCv and high PCv along with low GA . For the yield per ha character SSD was the highest variability recorder for GCv , PCv in F6 for both crosses.

According to genetic parameters of the 3 methods the highest variation was observed with SSD method due to low selection pressure incurred compared to that in the other two methods at F2, F3 and F4 levels. At F6 level evaluations with equal number of lines per method at same trial, SSD selected lines performed as well as those from other two methods and resulted in better GA values than with the other two methods. Therefore, SSD can be identified as a better method with low cost compared to the other two methods tested.

Highest variation was observed with SSD method in F4 and F5 generations due to low selection pressure exerted on SSD populations. SSD selected lines also performed well and resulted in better GA values in comparisons to other two methods at F6 generation. Since the SSD method has not reduced the GA up to F6 level, SSD can be identified as a better method with low cost compared to the other pedigree and modified bulk methods to advance cowpea populations without losing genetic variability at early generations.

REFERENCES

- Adnan Kanbar, Katsuhiko Kondo and H.E. Shashidhar. 2011. Comparative efficiency of pedigree, modified bulk and single seed descent breeding methods of selection for developing high-yielding lines in rice (*Oryza sativa* L.) under aerobic condition. *Electronic Journal of Plant Breeding*, 2(2): 184-193.
- Kurer, S. 2007. Genetic Variability Studies in F2 and F3 generations of cowpea. (*Vigna unguiculata* (L.) Walp). MSc. Thesis. Department of genetics and Pant Breeding. University of Agricultural Sciences, Dharwad.
- Millawithanachchi, M.C., Bentota, A.P., Weerasinghe, P. Saranasinghe, S.N.K. Prathapasinghe, N.T. and Kumri, R.A.C. (2012). Cultivation of Rainfed cowpea [*Vigna unguiculata* (L.) Walp] in the Monaragala district of Sri Lanka: status, constraints and breeding requirements. *Annals of the Sri Lanka Department of Agriculture*. Vol.14.