

Genetic analysis of pod yield and its attributes in vegetable cowpea

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SUMMARY

The nature of gene action was studied for pod yield and eight other component traits in vegetable cowpea using 7 x 7 diallel fashion, excluding reciprocals. The preponderance of non-additive gene action was observed in the inheritance of days to 50 per cent flowering, days to first picking and seeds per pod. Whereas, the importance of both additive and non-additive gene action were noticed for pod yield per plant, leaf area, branches per plant, plant height, pods per plant and protein content. However, the magnitude of dominant gene action (H_1) was greater than their corresponding additive gene effects (D) for all the traits. This suggested that the dominant genes played a significant role in the control of all the characters. The average degree of dominance (H_1/D)^{0.5} was found to be in the range of over dominance for all the characters. The distribution of genes with positive and negative effects was either close to symmetrical or not too distant. Excess of dominant genes against one recessive gene was not very high as their ratio ranged between one or two only. One or two gene groups governed characters. Narrow sense heritability estimates were moderate for branches per plant and plant height, whereas they were low for rest of characters. JCPL 2000-10 x GC 4, JCPL 2000-10 x JCPL 2000-2 and GC 3 x GC 4 were the most promising on the basis of *per se* performance, SCA effects and heterosis, which are expected to throw transgressive segregates.

Key words : Cowpea, Diallel, Gene effects, *Vigna unguiculata*

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important quick growing legume crop capable of withstanding moderate drought conditions. Being a multipurpose crop, it is grown during rainy and summer seasons as a vegetable crop in most part of India and also for grain and fodder purposes. Green tender marketable pods of cowpea have excellent nutritive values for human diet. The success of any breeding programme depends upon the selection of parents together with the information of nature and magnitude of gene actions controlling various traits of importance. Diallel mating system extensively used for the estimation of gene action and combining ability is of immense value in identifying parents and crosses which are likely to yield maximum improvement for the characters under consideration. Besides high yield, correlated morphological traits are also important for harnessing the yield potential fully. In the past, improvement in autogamous crops in general and cowpea is particular, was achieved through conventional breeding procedures like selection from the naturally occurring variability or induced variability through hybridization following the traditional pedigree method of breeding. Therefore, the present study was undertaken

to elucidate the nature and magnitude of gene action involved in inheritance of pod yield and its components through diallel analysis in vegetable cowpea.

MATERIALS AND METHODS

The experimental material comprised of genetically diverse seven genotypes of cowpea, namely, JCPL 2000-7, JCPL 2000-10, GC-2, JCPL 2000-2, GC-3, GC-4 and Pusakomal and their 21 F_1 hybrids obtained through mating in a diallel fashion, excluding reciprocals. Both parents and hybrids were grown during *Kharif* 2001 in a Randomized Block Design with three replications. The parents and hybrids were planted in single row of 3.0 m length spaced at 60 x 30 cm. All the recommended agronomic practices were followed to raise good crop. Data were recorded on five random, competitive plants for each genotype, in each replication for various characters (Table 1). Observations on days to 50 per cent flowering and days to first picking were noted on plot basis. Observations for number of seeds per pod, number of primary branches per plant, plant height (cm) and leaf area (cm²) were recorded at last picking. Data on number of pods per plant and green tender pod yield per plant (g) was obtained for each picking and was summed over picking. The average values were computed. For protein content (%), the nitrogen was estimated in per cent on oven dry basis by using modified 'Kjeldhal method' (Jackson, 1973). The mean values were used for the analysis to determine genetic components of variation following Hayman (1954).

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