



Genetic Architecture of Seed, Yield and Contributing Characters in Cowpea [*Vigna unguiculata* (L.) Walp.]

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Abstract: Genetic architecture studies for seed yield and contributing characters were studied using diallel cross method involving ten lines of cowpea through Hayman's diallel approach. The estimates of additive component as well as non-additive components were significant for most of the characters in both F_1 and F_2 generations. Average degree of dominance $(H_1/D)^{1/2}$ was found in the range of over dominance for all the characters in F_1 and F_2 generations except for days to 50 per cent flowering and branches per plant in F_2 generation. Asymmetrical distribution of positive and negative genes in the parental lines was observed from the estimate of $H_2/4H_1$ for all the characters in both the generations. The ratio of total number of dominant to recessive alleles in the parents (K_D/K_R) indicated unequal frequency of dominant and recessive genes with more number of dominant genes in most of the traits. The value of h^2/H_2 was low in most of the cases in both the generations, indicating that a few genes or group of genes generally controlled the inheritance of a particular character. Low value of heritability estimates was for plant height, pod length, 100-seed weight, protein content and harvest index in F_1 and F_2 generations indicated a major role of non-additive gene action in the inheritance of these characters studied and hence there are of limited scope for improvement in these characters through direct selection.

Keywords: Genetic architecture, Diallel, F_1 and F_2 generation, Non-additive, Seed yield, Cowpea
