Research Paper

Genetic analysis of yield and yield components in long duration pigeonpea [Cajanus cajan (L.) Millsp.]

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ABSTRACT

Six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of eight crosses having one row each of P_1 , P_2 and F_1 ; two rows each of B_1 and B_2 and six rows each of F_2 were grown in Compact Family Block Design with three replications in *kharif*, 2003-04 at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The estimates of six parameters model revealed the significant contribution of both additive and dominance gene effects in most of the traits studied. In general, for days to maturity, number of secondary branches, pods per plant and seed yield per plant, the relative contribution of dominance gene effect was even higher than those of additive gene effect. The epistatic gene effects were found to play an important role for the inheritance of almost all the characters in variable number of crosses.

Key words : Pigeonpea, Generation mean analysis, Additive, Dominance.

INTRODUCTION

India, a major pulse producing country, accounts roughly 33 per cent of the total world production. Pulses are grown both during kharif and rabi seasons. Out of the total area and production under pulses, the area of *kharif* and rabi pulses accounts 45 and 55 per cent, respectively (Singh, 1988).In India, pigeonpea is the second most important pulse crop after chickpea and is being widely grown in the country. Virtues like its resilience under rainfed conditions, nitrogen fixing ability and high protein content make this crop a mainstay for sustainable agricultural production under different agro-climatic situations. The major constraints that limit the production of pigeonpea are non-availability of quality seeds of improved varieties in adequate quantity, poor crop management, biotic and abiotic stresses prevalent in the pigeonpea growing areas, besides socio-economic factors. Quantitative traits, such as yield, are characterised by continuous distribution. Inheritance of such characters is governed by genes which have small, similar and cumulative effects. Non-heritable agencies also influence the phenotypic expression of these characters. The choice of an appropriate breeding method for improvement of quantitative characters also depends largely on the nature of gene action. The objective of the present investigation is to characterize the gene effects following generation means analysis.

MATERIALS AND METHODS

Six generations $(P_1, P_2, F_1, F_2, B_1 \text{ and } B_2)$ of eight crosses (Bahar x MA 98 SD 74, Bahar x MAL 8, Bahar

x Pusa 9, ICPL 7035 x MA 98 SD 74, ICPL 7035 x MAL 8, ICPL 7035 x Pusa 9, MA 98 PTH 1 x ICPL 84023 and DA x ICPL 84023) were grown in kharif, 2003-04 at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. One row each of P_1 , P_2 and F_1 ; two rows each of B_1 and B_2 and six rows each of F_2 were grown in Compact Family Block Design with three replications. Data were recorded on ten randomly selected plants from each row excluding border plants. Each row was consisted of 4m length and row to row and plant to plant distance being 75 and 25 cm, respectively. All the agronomic practices were followed to raise a good crop. For each family the plot means values in each generation were averaged over replication to obtained generation means. These generations mean formed the basis of calculation of various genetic parameters. The means, variance, variances of mean and standard errors of each of the six generations were estimated. Analysis of data was performed following six parameter model (Hayman, 1958, Jink and Jones, 1958).

RESULTS AND DISCUSSION

Estimation of relative magnitude of various gene effects including epistasis is of great importance in formulating the appropriate breeding procedure for further improvement. Additive and dominance gene effects are also likely to be biased in the presence of epistasis (Hayman, 1958). For those crosses, where scaling test indicates the presence of epistasis, six parameter models gives the estimates of major genetic components (with

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