

Study of gene action in cotton [*Gossypium hirsutum* (L.)]

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SUMMARY

Genetic components of variance and related statistics for eight quantitative character's viz seed cotton yield/plant (g), lint yield/plant, boll number per plant, boll weight (g), ginning percentage, halo length (mm), seed index (100 seed weight) and earliness index were estimated from F₁ generation derived from 7 x 7 diallel cross excluding reciprocals. The results revealed that dominant component (H₁ and H₂) was more prevalent than additive component (D) for most of the characters excepts seed index. Heritability in narrow sense was higher for seed index and ginning percentage, while it was moderate for boll count and mean fibre length and it was low for characters like boll weight, seed cotton yield and earliness index.

Key words : Diallel, Additive component, Dominant component, Heritability.

Cotton [*Gossypium hirsutum* (L.)] is one of the important commercial crop of India. It is basically cultivated for its fibre which is used universally as textile raw material. Cotton seed is crushed as textile raw material. Cotton seed is crushed to get its oil for human consumption and left out cakes used as a cattle feed. Millions of people depend on cotton cultivation, trade, transportation, ginning and processing for their livelihood. In addition to low ginning outturn presently released hybrids and varieties has inferior fibre qualities. This was mainly because of the breeding strategies of the breeders to evolve hybrids and varieties of cotton having medium staple length. Owing to the demand of cultivators mill owners for high ginning hybrid or variety having medium to long staple length the cotton breeders are actively engaged in breeding such kinds of hirsutum cotton hybrids and varieties suitable for rainfed cultivation.

MATERIALS AND METHODS

The experiment consisted eight cotton genotypes and their twenty one F₁'s (excluding reciprocals) grown during *kharif* season of 1999-2000. The experiment was conducted at the field of cotton Research Scheme, Marathwada Agriculture University, Parbhani. The seven parents with their twenty one hybrids and two checks were planted in randomized block design with three replications under rainfed conditions. Each genotype was sown in a single row in each replication. The row length was 4.8 m. The spacing was 90 cm between rows and 60 cm between plant to plant, respectively. Recommended cultural practices and plant protection measures were adopted and efforts were made to keep the experimental

plot free from weeds. Observations were recorded on five randomly selected plants per genotypes in each replication. Different genetic components were estimated as per the procedure of Hayman (1954). Heritability estimates in narrow sense were calculated as per Mather and Jinks (1971).

RESULTS AND DISCUSSION

Estimates of genetic components of variation along with ratio of genetic components for different quantitative characters are presented in Table 1. The estimates of additive component (D) were significant for lint yield/plant, boll number per plant, ginning percentage, halo length and seed index. The dominance components (H₁ and H₂) were significant for almost all the characters except boll weight. High magnitude of H₁ reflected non-additive gene effects for all these characters in F₁ generation. The higher value of H₁ component over H₂ component showed unequal distribution of genes among the parents. The positive value of F for seed cotton yield / plant was due to the presence of dominant genes which were more frequently distributed among the parents. The estimates of h² were significant for all the characters except seed index and earliness index. The non-significant values of E component indicated that the effect of environment was negligible in the expression of these characters.

The average degree of dominance (H₁/D)^{0.5} revealed the presence of over dominance for all the traits studied. The value of (H₂/4H₁) was less than its expected value i.e. 0.25 for all the traits which indicated the symmetrical distribution of positive and negative genes among the parents. The value of (KD/KR) was observed greater

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