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## Inheritance Pattern of Cotton Seed Oil In Diverse Germplasm of *Gossypium hirsutum* L.

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**Abstract:** Genetic analysis of  $F_1$  and  $F_2$  data obtained by crossing eight parents in diallel fashion was made following simple additive dominance model, in order to study the type of gene action controlling variation in oil content in *Gossypium hirsutum* L seed. The parents and 56 hybrids differed significantly from each other for oil content. Estimation of genetic components of variation showed that non additive genes controlled oil content in  $F_1$  generation and the genes with additive properties appeared to be important in  $F_2$  generation, with varying degrees of dominance in both the generations. Dominance acted towards the parents with higher oil content. Depending upon the magnitude of additive gene effects estimates of heritability in narrow sense were moderate in  $F_1$  and high in  $F_2$ . The presence of additive genes effects and high estimate of heritability of oil content in  $F_2$  generation suggest that prompt and effective progress in oil content may be made following recurrent selection method.

Key words: Diallel cross; oil content; heritability; additive genes

### Introduction

Edible oil obtained from oil and non oil crops is insufficient to meet the increasing demand in the country. The gap between demand and supply is filled through import of edible oil by spending a huge amount of foreign exchange each year. Therefore in these circumstances, the plant breeders are obliged to look for new genetic resources, and to exploit the available germplasm through selection and breeding. Seed of hirsutum species in addition to giving fibre, also yields considerable amount of edible oil, as a by product and contributes substantially to the total local oil production (Khan et al., 1995). Despite the availability of the potential source of oil, the cotton breeders did not take much interests to exploit it through further breeding as they did to improve fibre yield and its properties. It is recently, keeping in view the magnitude of the problem of oil supply to the growing population, the breeders turned their attention to study this aspect of cotton plant vigorously. The work on genetics of oil content in cotton seed is not extensively done in the domain of cotton breeding, only few reports exist in the literature. The studies of Kohel (1980), Bhale et al. (1989), Dani (1991) and Khan et al. (1995) showed that cotton varieties differed for oil content. Other workers reported that variation in oil content was heritable, and both additive and dominance properties of genes influenced the trait (Sokolova et al., 1982; Dani and Kohel, 1989; Wang and Li, 1991). A recent study on inheritance of oil content in cotton seed showed the preponderance effects of additive genes, and thus estimate of heritability was high (Azhar and Ajmal, 1999). In the present work a sample of parents differing for oil content was taken and crossed to study the genetic basis of variation in oil content, its heritability and response to selection in segregating generation of Gossypium hirsutum L. The data were analysed following popular diallel technique developed by Hayman (1954 a, b) and Jinks (1954).

#### **Materials and Methods**

The plant material used in the present study was developed by crossing eight cultivars/lines of *Gossypium hirsutum* L in all possible combinations. The eight parents namely BJA, Reba-B50, A89/FM, Changmiah (exotics), CIM250, S12, NIAB78 and AUH50 (local) were taken from the gene pool maintained in the department.

The eight parents were planted in earthen pots in glasshouse, and crossed when they started to flower. The buds were emasculated and pollinated by hand and all necessary precautions were taken to avoid contamination of the genetic material. A large number of pollination were made to produce sufficient quantity of  $F_1$  seed. The 1/2 of the seeds of 56 hybrids and their parents were planted in single row plot to produce  $F_2$  seed and the other 1/2 was kept to develop  $F_1$ generation next year. When plants of F1 generation started to flower, they were covered with glassine bags to effect self pollination and the selfed seed was used to generate F<sub>2</sub> generation. Both the  $F_1$  and  $F_2$  populations were grown together in the field following randomized complete block design with 3 replications. The seeds of 56 F<sub>1</sub> hybrids and 8 parents were spaced at the distance of 30 cm within the row and 75 cm between the rows, and thus there were 12 plants in a row. In the same way  $64 F_2$  entries were planted in a plot measuring  $3.3 \times 6 \text{ m}^2$ , having 96 plants, of each family in each replication. One plant on either end of each row of both the populations was left as non experimental. At maturity all the produce of seed cotton of each plant in each family was picked and ginned to get sample of cotton seed. Α representative sample of seeds of each genotype was taken to determine oil content by "Wide Line" Nuclear Magnetic Resonance-4000.

**Statistical Analysis:** Before analysing the data following diallel technique, the data were subjected to ordinary analysis of variance technique, in order to determine whether the genotypic differences for oil content were significant. Only significant genotypic differences allow the use of Hayman-Jinks method of genetic analysis.

The simple additive dominance model of genetic analysis requires the computation of the variance of the components of each array (V<sub>r</sub>), the co-variance of all the offspring included in each parental array with the non recurrent parent (W<sub>r</sub>) and variance of the parental means (V<sub>0L0</sub>). The second degree statistics necessary to calculate includes means of array variances (V<sub>1L1</sub>), the variances of means of arrays (V<sub>0L1</sub>) and the means of array co-variances (W<sub>0L0</sub>). These statistics are used for the estimation of four genetic components of variation, D (additive effects of genes), H<sub>1</sub> and H<sub>2</sub> (dominance effects of genes) and F, which provides an estimate of the



Fig. 1: Wr/Vr graph for oil content

relative frequency of dominant to recessive alleles in the parental lines and the variation in dominance over the loci. Hence F will be positive, whenever the dominant alleles are more frequent than the recessive alleles, irrespective of whether or not the dominant alleles have increasing or decreasing effects. In following the additive-dominance model, reciprocal F1 families have identical expectations and are generally averaged before computing these statistics, hence halving the environmental component, E (Mather and Jinks, 1982). For calculating the genetic parameters in F<sub>2</sub> population the formulae used in F<sub>1</sub> were modified as proposed by Verhalen and Muuray (1969) and Verhalen et al. (1971). The adequacy of simple additive-dominance model to account for the data was determined by joint regression analysis of variance (V,) and co-variance (W,). According to the suggestion of Mather and Jinks (1982), the regression co-efficient (b) must deviate significantly from zero, but not from unity, if all the assumptions underlying the genetic model were met.

#### Results

The mean values of oil content in 56  $F_1$  hybrids and 8 parents in  $F_1$  and  $F_2$  and  $V_r$  and  $W_r$  are given. The mean squares obtained from analysis of variance of oil content in both the populations are significant ( $p \le 0.01$ ), revealing significant differences among the hybrids and their parents. The significant genotypic differences allowed the use of simple additive-dominance model for analysing the data (the results of analysis of variance are not given here).

Regression analysis of V<sub>r</sub> and W<sub>r</sub> revealed that regression coefficients (b) for F<sub>1</sub> (0.602 $\pm$ 0.170) and F<sub>2</sub> (0.991 $\pm$ 0.066) deviated significantly from zero, and are equal to unity. The unit slopes of regression lines suggested that inter-allelic interaction was not present and all the assumptions underlying the Hayman-Jinks method were met (Mather and Jinks, 1982).

Although in  $F_1$  generation components D,  $H_1$  and  $H_2$  are positive and significant, the magnitude of H<sub>1</sub> and H<sub>2</sub> is greater than that of D. This indicated that the genes with dominance properties were important controlling oil content, whilst in F<sub>2</sub> generation, greater magnitude of D revealed the presence of the genes with additive effects. The degree of dominance was partial as  $\sqrt{(H_1/D)}$  is less than 1 in F<sub>1</sub> and F<sub>2</sub>, and this was verified by the slopes of regression lines in Fig. 1a and Fig. 1b. As  $H_1$  and  $H_2$  in  $F_1$  generation are equal in their magnitude, and thus equal distribution of gene frequencies was indicated and this claim was further strengthened by the ratio of  $H_2/4H_1$  which is 0.23 and is almost equal to 0.25. With unequal gene distribution in the parents this ratio would have been less than 0.25, which occurred in case of F<sub>2</sub> generation (0.19). Although value of F in F<sub>1</sub> generation is low and non significant, the positive sign of F indicate that there were more dominant genes than recessives in the parents, but this value in F<sub>2</sub> is high and This claim is supported by the ratio of significant.  $\sqrt{(4DH_1)}$ +F/ $\sqrt{4DH_1}$ -F. The positive value of h<sup>2</sup> indicated the trend of the dominance towards the parents having high oil content in cotton seed. The ratio of 1/2 F/([D(H1-H2)] indicated the extent to which the level of dominance varied from one locus to another, and exceedingly low estimate of the ratio in F<sub>1</sub> (0.0015) suggests that dominance existed at some loci and not at others, whilst high estimate in  $F_2$  (0.96) suggests that level of dominance was constant at all loci. The estimate of narrow sense heritability of oil content in F1 material is 53%, whilst in F<sub>2</sub> the estimate is 100%. An examination of Fig. 1a reveals that cultivar S12 being nearer to the point of origin carried the maximum number of dominant genes, and by contrast the two exotics, Reba-B50 and A89/FM possessed the maximum number of recessive genes for oil content. The remaining lines/cultivars lying in between the two groups, were intermediate with respect to the distribution of the aenes.

In F<sub>2</sub> all the 8 cultivars/lines formed a cluster away from point of origin (Fig. 1b). Comparing the position of the array points, Reba-B50 and NIAB78 are closer to the origin than A89/FM and CIM250 and thus contained the maximum number of dominant genes, and the later carried maximum number of recessive genes for the character.

#### Discussion

To effect rapid improvement in oil content in seed of *hirsutum* species through conventional breeding methods, the availability of two components is essential. Firstly, there must be variation present in the breeding material and secondly this variation must involve a significant genetic component. Ordinary analysis of variance revealed that 56 hybrids and their parents differed significantly from each other for oil content. Analysis of diallel cross data following Hayman-Jinks approach described the genetic basis of variation and

estimates of heritability of oil content.

Although both additive and dominance properties of genes appeared to be important in affecting the variation in oil content, the genes acting non additivity showed preponderance influence on the genetic control  $F_1$  generation. However, in segregating population (F2) variation was controlled largely by additive gene effects. The degree of dominance was partial in both the generations (Fig. 1) and direction of dominance was towards the parents having high oil content. Previous reports on the inheritance of oil content revealed the presence of both types of gene effects, for example, Kohel (1980) and Pulatov and Gubanova (1986) reported that oil content was additively controlled, whilst studies of Bhale et al. (1989), Dani and Kohel (1989) and Wang and Li (1991) showed that the character was controlled by non-additive gene effects. The plant character which involves significant additive genetic component had been suggested to be less complex in its inheritance (Azhar and McNeilly, 1988). These results suggests that the segregating population is amenable to selection, and rapid improvement in oil content may easily be achieved.

Previous genetic experiments on oil content in cotton seed are not extensively done, therefore evidences about the estimates of heritability of the character is not sufficiently available to support the magnitude of heritability reported here. Only one study that exists indicated that the cotton seed oil in hirsutum species was controlled largely by additive gene effects, and estimates of heritability was 100% (Azhar and Ajmal, 1999). However genetic studies carried out on rapeseed (Hu, 1998; Gupta and Labana, 1988) and Pearl millet (Bharaj et al., 1989) revealed that oil content in these crops was mainly additively influenced and therefore estimates of narrow sense heritability were moderate to high. Therefore on the basis of magnitude of additive gene effects in the genetic control of oil content, moderate estimate of heritability in F1 and high in F2 generation are justified. The greater magnitude of heritability in  ${\sf F}_2$  population may be a result of greater gene expression in segregating generation and/or due to smaller environmental component, a suggestion given by Saranga et al. (1992). However it had been stated that these estimates ae subject to environmental variation, and therefore must be interpreted and used with great care while making selection of desired plants from segregating generation (Falconer and Mackey, 1996). Nonetheless modest estimates of heritability in F1 and high in F<sub>2</sub> suggest that significant advance in oil content may be achieved by using single plant and recurrent selection method, as suggested previously (Azhar and Ajmal, 1999). The estimates of heritability may be used to predict genetic advance of oil content in the  $F_2$  and  $F_3$  generations.

The expected genetic gain in  $F_2$  generation (R) may be expressed as selection differential (S) ×  $h_{ns}^2$  (Falconer and Mackey, 1996). Selection differential for oil content was estimated as the difference between overall mean of the population and mean of the superior hybrids selected from that population. The value of the response for oil content in the  $F_2$ genetic material is R=0.637, and therefore expected genetic gain is 22.47. Similarly response (R) to selection for oil in the  $F_3$  population is 0.756, and the expected genetic gain is 21.29. The information on the inheritance pattern of oil content, gained from the present study, may not be interpreted for general use in the breeding programme, because the sample of the parents used in the crossing programme did not represent whole of the cotton germplasm. Therefore it is suggested that this information must be substantiated by involving a representative sample of large number of genotypes in hybridisation programme.

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