

GENETIC ANALYSIS FOR QUANTITATIVE TRAITS IN SESAME [*SESAMUM INDICUM* **L.]**

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Abstract

Nine sesame genotypes and their 36 F_1 diallel hybrids and 36 F_2 s were evaluated in four different environments to study the gene action for seed yield per plant and its attributes. The additive as well as dominant components were significant for seed yield per plant and its component traits with few exceptions in different environments, revealing equal importance of both additive as well as non-additive genetic effects for the traits studied. However, in most of the traits including seed yield per plant, the relative magnitude of dominance components were found to be higher than additive components in all four environments, indicates that studied characters were mostly under the control of dominance variance. The average degree of dominance $(H_1/D)^{1/2}$ indicated, in general, over dominance type of gene action in all four environments for all the traits studied. The estimates of H₂/4H₁ indicated considerable degree of gene symmetry over all the loci for the traits studied. The estimates of KD/KR ratio was more than unity indicated the excess of dominant alleles in parents in most of the characters in all the environments. In general, narrow sense heritability was found for all the traits, indicating comparatively more role of dominance gene effects in the expression of seed yield and its attributes.

Introduction

Sesame (*Sesamum indicum* L. Family: Pedaliaceae) is one of the oldest oilseed crops grown throughout the tropical and sub-tropical regions of the world. Sesame oil is considered as the queen of high quality vegetable oil (44-58% of dry seed weight) for human consumption as it contains high levels of unsaturated fatty acids and antioxidants e.g., sesamol, sesamin, sesamolin and sesaminol (Nupur *et al.,* 2010). India is the second largest producer of sesame in the world but suffers a serious setback in terms of productivity (368 kg/ha) as compared to world average (489 kg/ha). Low productivity of sesame in India is mainly due to cultivation of varieties with poor yield potential and inconsistent yield performance under varied environmental conditions. Hence, there is a need to augment the productivity of crop through crop improvement programme.

Component of genetic variation analysis is the primary step in the selection of an appropriate breeding

methodology. Sesame predominantly a self pollinated crop, therefore, breeders, essentially will require a programme which will follow the accumulation of fixable genes in homozygous lines. Hence, the understanding of different type of gene action *viz*., additive, dominance and epistasis is pre-requisite to frame effective breeding programme. In this context, the study was undertaken to estimate the nature of gene action for different quantitative characters through genetic component analysis of F₁ and F₂ of a 9 \times 9 diallel analysis of sesame.

Materials and Methods

The experimental material comprised of nine sesame genotypes and their 36 F_1 diallel hybrids and 36 F_2 s were evaluated in a Randomized Block Design with three replications in four different environments [two locations, Junagadh and Nana Kandhasar and two dates of sowing, February 20 and March 10, 2016 at Junagadh and February 22 and March 12, 2016 at Nana Kandhasar] during *summer* 2016-2017. Each entry was sown in single **Author for correspondence :* row of 3.0 m length with a spacing of 45 cm between row and 15 cm between plants within the row. Five competitive plants per genotype in each replication in each environment were selected randomly for recording observations on different characters *viz*., days to flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, height to first capsule (cm), length of capsule (cm), width of capsule (cm), number of capsules per leaf axil, number of seeds per capsule, 1000 seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index $(\%)$ and oil content $(\%)$. Genetic components of variance were computed by employing diallel cross method suggested by Hayman (1954) as well as Jinks (1954) as described in detail by Mather and Jinks (1982) and Singh and Chaudhary (1985).

Results and Discussion

The genetic components of variance were worked out from the diallel cross data of F_1 s and F_2 s of individual environments Table 1, as suggested by Hayman (1954) as well as Jinks (1954) and as described in details by Mather and Jinks (1982) and Singh and Chaudhary (1985). Validity of hypothesis according to Hayman (1954) was tested by t^2 values. Non-significance values of t^2 for all the characters in individual environments except for days to flowering in E_1 , E_2 and E_3 of F_2 population, number of capsules per plant, number of seeds per capsule and length of capsule in E_3 of F_2 population, width of capsule in E_3 and E_4 of both F_1 and F_2 population, number of capsules per plant, number of seeds per capsule and length of capsule in E_3 of F_2 population, width of capsule in E_3 and E_4 of both F_1 and F_2 population, number of capsules per leaf axil in all four environments of F_2 and E_1 , E_2 and E_3 of F_1 population, 1000 seed weight in E_3 of F_1 population, seed yield per plant in E_2 of F_1 population, biological yield per plant in all the environments of F_1 and E_2 and E_3 of F_2 population, harvest index in E_3 and E_4 of F_1 and E_1 and E_4 of F_2 population and oil content in all four environments of F_2 population, suggested the adequacy of additive - dominant model to explain the variation in almost all the traits studied except for the above listed characters in the respective environment for respective population for which the t^2 was significant.

The additive (D) as well as dominant $(H_1$ and $H_2)$ components were significant for plant height, number of branches per plant, number of capsules per plant, height to first capsule, length of capsule, width of capsule, number of capsule per leaf axil, 1000 seed weight, seed yield per plant and biological yield per plant in all four environments of both the generations, except for dominance components (H_1, H_2) in environment E_2 of F_1

in plant height, for additive component in E_4 environment of both F_1 and F_2 population in number of capsules per plant, for additive effects in E_3 in F_1 population in width of capsule, for additive component in E_1 , E_2 and E_4 of F_1 population and in E_2 of F_2 population in seed yield per plant, and for additive component in E_1 and E_2 of F_1 population in biological yield per plant. For days to flowering, variances due to additive (D) and dominance effects (H_1) were significant in all the environments and generations and variances due to dominance components (H_2) were significant in E_1 , E_2 and E_4 of F_2 generations; for days to maturity, variances due to additive (D) effects were significant in all the environments and generations, variances due to dominance effects (H_1) were significant in all the environments of F_2 generation, and in environment E_2 of F_1 generation, and dominance components (H_2) were significant in E_2 of F_1 s and in E_1 and E_4 of F_2 generations; for number of seeds per capsule, estimates of additive (D) and dominance effects (H_1, H_2) H_2) were significant in all the environments of both the populations, except for E_3 in both the population; for harvest index, genetic component for additive (D) effect was significant in E_3 of segregating population, while dominance components $(H_1 \text{ and } H_2)$ were significant in all the environment of both F_1 and F_2 population; and for oil content, additive (D) and dominance effects $(H_1$ and $H₂$) were non-significant in all the environments of both the generations, except for D component in E_2 in F_1 s and for dominance components $(H_1 \text{ and } H_2)$ in E_1 and E_2 of F_2 s.

These results revealing equal importance of both additive as well as non-additive genetic effects for the traits studied. However, the relative magnitude of dominance components was, in general, found to be higher than additive components for all the traits studied, indicated the predominance of dominance components in the genetic expression, means the preponderance of dominance gene action. Significance of additive gene effects in sesame has been reported for seed yield per plant by Reddy *et al.,* (2015), Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for days to flowering by Lavanya *et al.,* (2006), Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for days to maturity by Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for plant height by Reddy *et al.,* (2015) and Vekaria *et al.,* (2015); for number of branches per plant by Lavanya *et al.,* (2006) and Vekaria *et al.,* (2015); for number of capsules per plant by Lavanya *et al.,* (2006) and Reddy *et al.,* (2015); for number of seeds per capsule by Reddy *et al.,* (2015); for height to first capsule and number of capsules per leaf axil by Vekaria *et al.,* (2015); and for capsule length and 1000 seed weight by Napit

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and Arjaria (2016).

Significance of non-additive gene effects in sesame has been reported for seed yield per plant by Swain *et al*., (2001), Sedeck and Shafie (2013), Reddy *et al.,* (2015), Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for days to flowering by Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for days to maturity by Vekaria *et al.,* (2015) and Napit and Arjaria (2016); for plant height by Reddy *et al.,* (2015) and Vekaria *et al.,* (2015); for number of branches per plant by Lavanya *et al.,* (2006) and Vekaria *et al.,* (2015); for number of capsules per plant by Lavanya *et al.,* (2006) and Reddy *et al.,* (2015); for number of seeds per capsule by Reddy *et al.,* (2015); for height to first capsule by Vekaria *et al.* (2015) and for number of capsules per leaf axil by Vekaria *et al.,* (2015).

The preponderance of dominance components was reported by many workers in the past. Swain *et al*., (2001) observed the preponderance of non-additive genetic variance for seed yield per plant, capsules on main stem, capsules per plant, capsule length and 1000 seed weight; Mothilal and Manoharan (2005) for plant height, number of capsules per plant and seed yield per plant; El-Bramawy and Shaban (2008) for days to 50 % flowering, plant height, number of branches per plant, number of capsules per plant, 1000-seed weight, oil content and seed yield per plant; Mishra *et al*., (2009) for 1000 seed weight, fruiting branches per plant, capsules per plant, single plant yield and oil content; Sakhiya (2013) for days to flowering, days to maturity, plant height, height to first capsule, number of branches per plant, length of capsule, width of capsule, number of capsules per plant, number of capsules per leaf axil, number of seeds per capsule, 1000-seed weight and seed yield per plant; Reddy *et al.*, (2015) for plant height, number of capsules per plant, number of seeds per capsule, test weight and seed yield per plant; and Vekaria *et al.,* (2015) for days to 50 per cent flowering, days to maturity, plant height, height to first capsule, number of branches per plant, number of internodes per plant, number of capsules per plant, number of capsules per leaf axil and oil content;

The average degree of dominance $(H_1/D)^{1/2}$ indicated over dominance type of gene action all four environments for all the traits studied except for days to flowering in environment E_2 and E_4 of F_2 generation; for plant height E_2 in F_1 generation; for number of branches per plant in all four environments of F_2 and E_1 , E_3 and E_4 of F_1 generation; for length of capsule E_1 and E_2 of F_2 generation; for width of capsule E_1 of F_2 generation; and for oil content E_2 of F_1 generation. Thus, on the basis of present study, it is evident that characters studied are

Table 1 continued...

under the control of non-additive gene action. Over dominance for seed yield per plant and important yield components in sesame was reported earlier by Swain *et al*., (2001), Mothilal and Manoharan (2005), El-Bramawy and Shaban (2008), Sakhiya (2013), Sedeck and Shafie (2013), Reddy *et al.,* (2015), Mishra *et al.,* (2016), Napit and Arjaria (2016), Tripathy *et al.,* (2016a and 2016b) and Abd El-Kader *et al.,* (2017).

The distribution of genes with positive and negative effects (H_2/H_1) in the parents was observed nearly symmetrical in both F_1 s and F_2 s in all the environments for seed yield per plant and all the characters studied, indicating considerable degree of gene symmetry over all the loci for the studied traits. Symmetrical distribution of positive and negative genes was reported for different traits in sesame, *viz*., Swain *et al*., (2001) for 1000 seed weight, days to maturity, branches per plant, capsules on main stem, capsules per plant and seed yield; Tripathi and Hasan (2004) for 1000 seed weight, days to maturity, branches per plant, capsules on main stem, capsules per plant and yield per plant; and El-Bramawy and Shaban (2008) for 1000 seed weight, fruiting branches per plant, capsules per plant, single plant yield and oil content.

The estimates of KD/KR ratio was more than unity indicated the excess of dominant alleles in parents for all the characters studied in all the environments of both the generations, except for days to flowering, days to maturity and 1000 seed weight in all environments of F_2 ; for plant height in E_3 of F_2 ; number of branches per plant in E_1 , E_3 and E_4 of F_2 ; and for number of seeds per capsule in E_1 , E_3 and E_4 of both the populations; which indicated more number of dominant genes than recessive genes in the parents. The present findings are in accordance with those of Sedeck and Shafie (2013) for seed yield per plant and plant height; Reddy *et al.,* (2015) for number of capsules per plant, number of seeds per capsule and seed yield per plant; Mishra *et al.,* (2016) for number of seeds per capsule; and Tripathy *et al.,* (2016a and 2016b) for seed yield and oil content.

Knowledge of number of gene groups which exhibit dominance and are responsible for particular trait is important for the genetic progress through selection. In the present investigation, the ratio of h^2/H_2 , estimating the number of gene groups indicated that there was one group of genes responsible for days to flowering in all the environments of F_2 and E_1 , E_3 and E_4 of F_1 ; for days to maturity in E_2 , E_3 and E_4 of F_1 and E_1 , E_2 and E_3 of F_2 ; for plant height in E_1 , E_3 and E_4 of F_1 s and E_2 of F_2 ; for number of branches per plant in E_3 of F_2 ; for number of capsules per plant in E_2 of F_2 ; for length of capsule in E_1

and E_2 of F_1 ; for width of capsule in E_1 and E_2 of both the populations; for number of seeds per capsule in E_1 , E_2 and E_4 of F_1 and E_4 of F_2 ; for 1000 seed weight in E_1 of F_2 ; for seed yield per plant in E_1 and E_4 of F_1 ; for biological yield per plant in E_1 , E_2 and E_4 of F_1 and in E_3 of F_2 ; for harvest index in E_3 of F_2 ; and for oil content in E_2 of F_1 population. For all the remaining environments of respective generations, more than one gene group controlled the particular trait. Reddy *et al.,* (2015) for number of plant height, capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant; and Tripathy *et al.,* (2016a and 2016b) for oil content, reported that these characters were under the control of at least single group of genes; while Tripathy *et al.,* (2016a and 2016b) reported that a number groups of genes showing dominance controlling for seed yield per plant in sesame. However, this parameter (h^2/H_2) can be underestimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes is correlated (Jinks, 1954) or when complementary gene interaction occur (Mather and Jinks, 1982).

According to Robinson (1966), placed the heritability estimates in cultivated plants in following categories: low (5 to 10 per cent), medium (10 to 30 per cent) and high (30 to 60 per cent). Looking into account this classification for present study, it was observed that high estimates of narrow sense heritability were depicted for days to flowering in E_1 of F_1 ; and for width of capsule in all the environment of F_i ; while medium estimates of heritability were noted for width of capsule in E_1 and E_2 of F_2 ; and for number of capsules per leaf axil E_1 and E_2 of F_1 and E_1 , E_3 and E_4 of F_2 . Low estimates of heritability were observed in all the remaining environments of respective generations for the studied traits. In general, narrow sense heritability was found for all the traits, indicating comparatively more role of dominance gene effects in the expression of seed yield and its attributes. It is therefore, suggested that selection should be delayed to advanced generations and some sort of intermating may be employed in early generations followed by pedigree method with careful progeny tests in advanced generation to achieve better success. The single seed descent method would be useful to maintain high variability for exercising selection in later generation. Low estimates of heritability for seed yied and its components in sesame were reported by Hoballah (2001), Aladji Abatchoua *et al.,* (2014) and Reddy *et al.,* (2015).

Conclusion

Magnitude of dominance components were found to

be higher than additive components in all four environments, indicates that characters studied including seed yield per plant were under the control of dominance variance. The average degree of dominance $(H_1/D)^{1/2}$ indicated, in general, over dominance type of gene action in all four environments for all the traits studied, suggested that heterosis breeding may be effective for improvement of traits studied.

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