GENETIC ANALYSIS OF SEED YIELD AND ITS COMPONENTS OVER ENVIRONMENTS IN SESAME (Sesamum indicum L.)

ABSTRACT

Key words: Combining ability, heterobeltiosis, inbreeding depression, standard heterosis, sesame, stability

The present investigation entitled “Genetic analysis of seed yield and its components over environments in sesame (Sesamum indicum L.)” was carried out with a view to estimate heterosis and inbreeding depression, combining ability and gene action, genetic components of variance, genotype x environment interaction and stability parameters for seed yield per plant and 14 different quantitative traits in sesame. The experimental materials comprised of 82 entries (Nine parents AT 164, AT 238, AT 255, AT 282, AT 345, China, Nesadi Selection, GT 1 and GT 10, their 36 F1s developed through half diallel mating design, their 36 F2 segregating populations and one standard check variety GT 3) were evaluated in a Randomized Block Design with three replications over four environments during summer 2016 at two locations, Sagadividi Farm, Department of Seed Science and Technology, College of Agriculture, JAU, Junagadh and Krishi Vigyan Kendra, JAU, Nana Kandhasar. At each location, two environments were created by different date of sowing as E1 = February 20, 2016 and E2 = March 10, 2016 at Sagadividi Farm (L1) and E3 = February 22, 2016 and E4 = March 12, 2016 at KVK, Nana Kandhasar (L2). Five competitive plants per genotype in parents, F1 and standard check, and 20 competitive plants in F2, 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 (%). The data were analyzed for heterosis and combining ability (Method-II, Model-I of Griffing, 1956a), while the genetic components of variation were estimated according to Hayman (1954) and G x E interactions and stability parameters were calculated following the model of Eberhart and Russell (1966).

The analysis of variance pooled over environments revealed significant differences among genotypes, parents, F1s and F2s for all the characters. The comparison of parents vs. hybrids (F1) was found significant for all the characters, except for number of branches per plant, number of seeds per capsule, 1000 seed weight and oil content, while the comparison of parents vs. F2 was found significant for all the characters, except for height to first capsule, length of capsule and width of capsule, which, in general, revealed the existence of heterosis and inbreeding depression. Mean squares due to F1s vs. F2s were significant for all the characters, also suggesting presence of considerable amount of inbreeding depression in F2 generation.

On pooled basis, fifteen hybrids over better parent and one hybrid over standard check variety exhibited significant and positive heterosis. None of the cross combination noted significant and positive standard heterosis in E3 and E4 environment, while AT 238 × AT 345 (15.48 %), AT 282 × GT 10 (14.83 %) and AT 238 × GT 1 (13.28) in E1; AT
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238 × AT 345 (41.23 %), AT 282 × GT 10 (26.64 %), AT 238 × GT 1 (24.73 %) and AT 164 × AT 238 (18.45 %) in F₂ and AT 238 × AT 345 (11.69 %) on pooled basis were the best significant and positive cross combinations with respect to standard heterosis for seed yield per plant. Total of 13, 1, 8, 9 and 1 cross combination noted significant and desirable inbreeding depression for height to first capsule, width of capsule, number of capsules per leaf axil, number of seeds per capsule and seed yield per plant, respectively. These crosses had possibilities of desirable segregants in F₂ population.

On pooled basis, significant difference of gca and sca indicated that both additive and non-additive gene effects played an important role in the genetic control of the traits under study. The variance ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ was less than unity for all the characters, except for days to maturity in both the generations; for oil content in F₁ generation; and for 1000 seed weight in F₂ generation indicates the preponderance of non-additive gene action for almost all the characters under investigation, which suggested that the best cross combinations might be selected on the basis of sca for further tangible advancement in sesame. Preponderance of non-additive gene action for seed yield and its components and inbreeding depression could be utilized advantageously for improving yield through heterosis breeding. As sesame is self-pollinated crop, the genetic variability resulting from additive effects can be effectively utilized through selection followed by hybridization in segregating generations. It is, therefore, suggested that biparental mating, intermating of elite segregants and selection at later generations should be followed which meets the requirement of utilizing both types of gene actions.

The parents AT 238 and AT 345 in F₁ and AT 238, AT 345 and GT 10 in F₂ were found good general combiners for seed yield per plant. On the basis of significant positive sca effects for seed yield per plant on pooled basis, AT 238 × GT 1 (2.76), AT 282 × GT 10 (2.61) and AT 164 × AT 238 (2.57) in F₁ generation and AT 238 × GT 1 (1.84), AT 164 × AT 238 (1.79) and AT 255 × Nesadi Selection in F₂ generation, were three best hybrids. These best specific crosses of F₁ generation involved good x good or good x average or average x good or poor x poor general combiners.

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 $H_2/4H_1$ 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.

A single parent AT 345 and 11 hybrids (AT 238 x AT 345, AT 282 × GT 10, AT 164 × AT 238, AT 345 × China, AT 255 × Nesadi Selection, AT 345 × GT 10, China × GT 10, Nesadi Selection x GT 1, AT 255 x GT 10, AT 255 x GT 1 and AT 282 × AT 345) expressed their stability across the environments for seed yield per plant due to their high seed yield per plant, non-significant regression coefficient (b) and deviation from linear regression ($S^2_d$). Cross AT 238 x AT 345 (9.35 g) ranked first with respect to seed yield per plant manifested significant heterosis over better parent as well as standard check (GT 3) along with significant and positive sca effects in both F₁ and F₂ generation and stability for seed yield per plant, days to flowering, days to maturity, number of capsules per plant, length of capsule, number of seeds per capsule and test weight, could be exploited for improvement in seed yield of sesame.