



Genetic variability estimates in induced population of sesame (*Sesamum indicum*)

T BEGUM¹ and T DASGUPTA²

Institute of Agricultural Science, Calcutta University, Kolkata 700 019

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ABSTRACT

An investigation was carried out to study the nature and magnitude of induced genetic variability in sesame (*Sesamum indicum* L.). Seeds of three sesame genotypes, Rama, SI 1666 and IC 21706 were treated with three doses of γ -rays (200 Gy, 400 Gy and 600 Gy) and four concentrations of ethyl methane sulphonate (0.5%, 1.0%, 1.5% and 2.0%), separately. Mutant generations from M₁ to M₂ were raised to study the extent of variability, heritability and genetic advance in mutant populations. Mutations surpassed the magnitude of variability over control population in both the generations. Genotypic and phenotypic variances were higher for sterility% and 1000-seed weight in both M₁ and M₂ generations. With regardless of the genotype, M₁ generation professed maximum genotypic and phenotypic coefficients of variability (GCV and PCV) for number of seeds per capsule. On the contrary, in M₂ generation induced populations of all the three genotypes engendered maximum GCV and PCV for seed yield per plant. High heritability for sterility percentage and 1000-seed weight coupled with high genetic advance inferred that additive gene effects were important in determining these characters and could be improved through mass selection.

Key words: Genetic advance, Genotypic variance, Heritability, Induced mutation, Phenotypic variance, Sesame

Success in any breeding programme depends on the magnitude of genetic variability present for the different characters in a population. The extent of variability is measured by genotypic and phenotypic coefficients of variability (GCV and PCV) which provides information about relative amount of variation in different characters. Selection exercised for a long period in local varieties has nearly exhausted the natural variability of any crop. Mutation breeding is one of the effectual tools to create the latent variability. It has been successfully employed in oilseed crops like sesame (*Sesamum indicum* L.) (Begum and Dasgupta 2010, 2011, 2014). Since yield and its component traits are polygenic in nature, information on the extent of heritable portion of induced variability is meaningful for evolving improved varieties. The importance of genetic components of variance for predicting the response in selection have already been reported earlier (Labana *et al.*

1980, Ali 1985, Naazar *et al.* 2003, Larik *et al.* 2009, Siddiqui *et al.* 2009).

The genetic variability in terms of variances and coefficients of variability are not sufficient for determination of amount of heritable variability. The estimate of heritability acts as a predictive tool in expressing the reliability of phenotypic values. It indicates the relative degree to which a particular trait is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent of possible improvement through selection. Since heritability is also influenced by environment, the information on heritability alone may not suffice in pinpointing characters enforcing selection. Therefore, estimation of heritability coupled with genetic advance is also needed to assess the heritable portion of total variation and genetic gain expected for effective selection. Heritability with genetic advance is of more value in predicting the effect of selection. Such estimates facilitate the evaluation of genetic and environmental effects, thereby aiding in selection. Estimates of heritability can be used to predict genetic advance under selection, so that the breeder can anticipate improvement from different types and intensities of selection. It is interesting to fathom the upshot of mutations on genetic variability, heritability and genetic advance of characters. Albeit induced genetic variability, heritability and genetic advance for seed yield and its important attributes, viz.

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¹Research Associate (email: tamina@live.in), Central Research Institute for Jute and Allied Fibres (ICAR), Barrackpore, Kolkata 700 120; ²Professor and Head, Department of Genetics and Plant Breeding (tapashdg@rediffmail.com). Present address: Marie Curie International Fellow, School of Biological Science, University of Aberdeen, Aberdeen AB24 3UU, UK

number of capsules/plant, plant height and number of branches/plant under various mutagenic treatments have been reported (Begum and Dasgupta 2014), such kind of study for other polygenically inherited traits is quite scanty in sesame.

Under this genesis, the present investigation was formulated to assess the extent of genetic variability of sesame mutants in M_1 and M_2 generations along with non-treated control populations with particular references to genetic selection parameters for polygenically inherited traits excluding three important yield components, viz. number of capsules/plant, plant height and number of branches/plant as reported by Begum and Dasgupta (2014).

MATERIALS AND METHODS

Three diverse sesame genotypes namely Rama, SI 1666 and IC 21706 were selected for the study. One physical mutagen, viz. gamma (γ)-rays and one chemical mutagen, viz. ethyl methane sulphonate (EMS) were used separately to induce mutation. Well filled dry seeds (10-12% moisture content) of each genotype were exposed to 200 Gy, 400 Gy and 600 Gy doses of gamma-rays. Irradiation was done at the rate of 30 Gy per minute with a ^{60}Co source in the gamma garden of Central Research Institute for Jute and Allied Fibres (Indian Council of Agricultural Research), Barrackpore, Kolkata, West Bengal, India. Three hundred seeds were treated for each irradiation dose. On the contrary, four concentrations of EMS, 0.5%, 1.0%, 1.5% and 2.0%, were used. For each EMS dose, 150 seeds were treated for six hours, then laved under running tap water and sown immediately in the field after surface drying with filter paper. Thus, a total of eight treatments (control; 200 Gy, 400 Gy and 600 Gy doses of gamma-rays; 0.5%, 1.0%, 1.5% and 2.0% concentrations of EMS) were used for each genotype.

The treated seeds were planted during 2004-05 at Agricultural Experimental Farm of Calcutta University, Baruipur, West Bengal, India representing alluvial part of coastal South Bengal having the latitude and longitude of 22°21'56" N and 88°26'14" E, respectively. The treated plants thus raised were designated as M_1 plants and subsequently M_2 plants were grown during 2005-2006. The spacing between row-to-row and plant-to-plant was kept at 35 cm and 10 cm, respectively. A randomized block design was followed with three replications. Normal cultural practices were followed during the entire growing period. In both the generations observations were recorded for 11 quantitative characters, viz. sterility percentage, days to 1st flowering, flower duration, plant height (cm), number of branches/plant, number of capsules/plant, capsule length (cm), number of seeds/capsule, 1000-seed weight (g), days to maturity and seed yield/plant (g). As the genetic variability estimates for seed yield, number of capsules/plant, plant height and number of branches/plant in induced population of sesame were reported by Begum and Dasgupta (2014), the remaining traits were considered for the present investigation. The average data were subjected to statistical

analysis to estimate genetic parameters like components of variance, co-efficient of variation, heritability and genetic advance for both control and mutant populations in both M_1 and M_2 generations. Genetic parameters were computed following the methods suggested by Singh and Chaudhary (1979).

RESULTS AND DISCUSSION

The effect of mutations on genetic variability was conspicuous. Both the genotypic and phenotypic variances and consequently genotypic and phenotypic coefficient of variations appeared to tally closely with each other for majority of characters in control and mutagen treated populations of three genotypes. In both generations phenotypic variance for characters was higher than genetic variance both in control and mutagen treated population of three genotypes indicating the role of environmental variance in the expression of characters (Tables 1, 2 and 3). The present report corroborates the findings of Ali *et al.* (2003) in winter rapeseed, Larik *et al.* (2009) in sorghum, Islam *et al.* (2010) in ber and Sumathi *et al.* (2010) in pearl millet. Genetic estimates computed through variance component method evinced that wider range of genotypic and phenotypic variance subsisted among the traits of mutants. There was a considerable increase in variance in mutant populations for all the traits under study. Similar observation was reported by Siddiqui *et al.* (2009) in rapeseed. Irrespective of the genotypes in M_1 generation maximum genotypic (253.00) and phenotypic (265.98) variances recorded for sterility percentage, while in M_2 generation both the variances were highest for seed yield per plant in mutant population of IC 21706. Irrespective of the genotypes an increase in genotypic and phenotypic coefficient of variation (PCV) over respective control population indicated that mutation induced reasonably wider variability in all the treated population. In M_1 generation sterility percentage, number of seeds per capsule and seed yield recorded significantly and consistently very high GCV and PCV compared to respective control population, whereas only seed yield per plant exhibited similar result in M_2 generation. Out of 8 quantitative characters in M_1 generation both GCV (74.85) and PCV (77.95) were highest for seed yield per plant in mutant population IC 21706 albeit sterility percentage, and number of seeds per capsule recorded higher GCV and PCV in treated population of all the three genotypes. On the other hand, lower GCV and PCV was observed consistently for capsule length in mutant population of three genotypes. Kamala (1990) observed very high genotypic and phenotypic variance for seed yield followed by capsules per plant and seeds per capsule in sesame.

In M_2 generation highest PCV (129.43) was observed for seed yield per plant in the mutant population of IC 21706. On the other hand, GCV was very less in days to maturity in the mutant population of all the three genotypes. Minimum PCV was recorded for days to maturity in the mutant population of Rama and IC 21706, while in the treated population of SI 1666 capsule length evinced lowest

PCV. Similar to the present finding, Govindarasu *et al.* (1997) reported that γ -rays had resulted in increased genetic variability for the traits plant height, number of seeds per capsule and 1000-seed weight and seed yield in M_2 generation in sesame, but it varied depending upon the variety, character and mutagenic dose. Such increased genetic variability for quantitative characters through mutagenic treatment of varieties was also reported in earlier studies in sesame (Kamala 1990). The enhanced genetic variability observed for seed yield and its component characters indicated the scope for effective selection.

Heritability of control population for most of the characters in general was slightly lower or at parallel with the mutant population irrespective of the genotypes. In general, heritability (%) in broad sense for most of the characters was consistently high in mutant population of all the genotypes in both generations. Such estimates were likely to be inflated because of the presence of different interaction, so only estimate above 80 was considered somewhat reliable. It was noted that most of the characters in M_1 generation consistently recorded above 80% heritability in the mutant population of the three genotypes except capsule length in SI 1666 where below 80% heritability was observed. Such a high heritability estimates in M_1 population was also observed by Kamala (1990) in sesame and Larik *et al.* (2009) in sorghum. Heritability estimates and genetic advance for capsule length was reduced as compared to other characters in all the mutant population. This would suggest that even in M_1 generation different genetic parameters were greatly influenced by treatments and the genotypes responded differently in their response to mutagens. This demonstrated that mutagenic treatments, viz. γ -rays and EMS influenced polygenetically controlled metric characters and the effects were more pronounced in one genotype than other. High heritability combined with high genetic advance was observed for sterility percentage and 1000-seed weight professing the lesser influence of environment in expression of these characters and preponderance of additive gene action of their inheritance, hence amenable for selection. Contrary to it, high heritability coupled with low genetic advance was recorded for capsule length and seed yield per plant indicating prevalence of non-additive gene action for these traits, hence heterosis breeding would be recommended for these traits. These results confirm the findings of Senthamizh Selvi *et al.* (2007).

In M_2 generation above 80% heritability was observed for sterility% and 1000-seed weight in the treated population of all genotypes. Apart from these characters above 80% heritability was also recorded for days to 1st flowering and days to maturity in the treated population of Rama, while mutant population of SI 1666 exhibited above 80% heritability for flower duration, capsule length, days to maturity and seed yield per plant. On the other hand, above 80% heritability was also noticed for days to 1st flowering, flower duration and number of seeds per capsule in the treated population of IC 21706. Such high heritability

indicates the scope of genetic improvement for superior plants with high yield and its components by selection in these populations. Ramanathan (1983) also reported high heritability for pod yield at 400 Gy and 40 mM of EMS treatment in M_2 generation in groundnut suggesting the scope of selection. Interestingly, irrespective of the genotypes sterility percentage and 1000-seed weight engendered high heritability along with high genetic advance indicating confirming the results of M_1 generation. Apart from these characters, high heritability coupled with high or moderate genetic advance was recorded for days to 1st flowering and number of seeds per capsule in mutant population of Rama; flower duration in treated population of SI 1666; days to 1st flowering, flower duration and number of seeds per capsule in induced population of IC 21706 indicating preponderance of additive gene action or coupled action of both additive and non-additive factors. The increased heritability and genetic advance in the treated populations of the present study are in conformity with the results obtained by Chavan and Chopde (1982), Sarwar *et al.* (2008) and Boranayaka *et al.* (2010) in sesame. Interestingly, Begum and Dasgupta (2014) observed that the traits plant height, number of branches/plant, number of capsules/plant and seed yield/plant would offer good scope of selection in the early mutant generations of sesame. Thus the present study clearly indicates that apart from those yield components (Begum and Dasgupta 2014) days to 1st flowering, flower duration, number of seeds per capsule and seed yield provide a good selection base as they professed high values of heritability coupled with high genetic advance. Emphasis should be given on these characters for formulating reliable selection indices for isolation of the promising micro-mutant lines to refurbish high yielding mutant varieties of sesame.

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