

Assessment of Genetic variability and Character Association for Morpho-physiological Attributes and Seed Yield in Sesame

Abu Saleh Nizamuddin Ahmed*, Subrat Das, Daizi Durba Saharia, Manoj Kumar Sarma, Manash Protim Nath and Jugal Chandra Talukdar

Department of Plant Breeding and Genetics, BN College of Agriculture, Assam Agricultural University, Biswanath Chariali (Assam), India.

(Corresponding author: Abu Saleh Nizamuddin Ahmed*)

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ABSTRACT: In Assam Sesame (*Sesamum indicum* L.) is grown as a minor oilseed crop and it occupies only 3.8 % of the total area under oilseed crops in the state. Considering the enormous gap between the potential and realized yields, there is ample scope for enhancement of its productivity through breeding efforts. Therefore, a study was carried out to assess the genetic variability and character association for twelve morpho-physiological traits including seed yield in 32 sesame genotypes of Assam, India. Genotypic and phenotypic coefficient of variation (GCV & PCV) was recorded highest for biological yield and capsules per plant. All other traits under study except days to maturity, harvest index and relative leaf water content exhibited moderate values of GCV and PCV. Heritability estimates were observed above 80 per cent for all the traits except seed yield, plant height and primary branches per plant. Seed yield per plant exhibited a lower magnitude of GCV, heritability and genetic advance. Comparatively a higher magnitude of GCV coupled with higher heritability and genetic advance as per cent of mean was observed for harvest index, biological yield and capsules per plant. Selection for these traits would, therefore, be meaningful. Correlation estimate revealed that the characters viz., days to maturity, plant height, number of primary branches per plant, number of capsules per plant, leaf area index, relative leaf water content, chlorophyll content and harvest index exhibited a significant positive correlation with seed yield. Path coefficient analysis revealed that the characters viz., days to maturity, plant height, number of primary branches per plant, number of capsules per plant, leaf area index, relative leaf water content, total chlorophyll content, biological yield and harvest index had a positive direct effect on seed yield, while days to 50 per cent flowering and 1000- seed weight showed a negative direct effect. Hence, direct selection for the traits showing a positive direct effect would bring about improvement in seed yield in sesame.

Keywords: Genetic variability, Genetic diversity, character association, morpho-physiological traits, Sesame.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is the oldest oilseed crop known to man. It is regarded as the “Queen of oilseeds” because of its excellent quality of edible oil (Biswas *et al.*, 2018). Sesame is extensively cultivated in tropical to temperate regions in the world. It is the fifth most important edible oilseed crop in India. Even though the crop originated in Africa, India is considered to be the major centre of genetic diversity (Maiti *et al.*, 2012). In India sesame is cultivated in an area of 17.30 lakh hectares with a productivity of 431 kg/ha and production of 7.46 lakh MT (FAOSTAT, 2018). Sesame seed contains 50 % oil, 23 % protein and 15 % carbohydrate along with a high amount of calcium, phosphorous and oxalic acid (Abhijatha *et al.*, 2017). Sesame oil is very stable due to the presence of powerful antioxidants viz., sesamin, sesamol and sesamol which confer resistance to the oxidative

deterioration (Pathak *et al.*, 2014). Amongst all the edible oils, the antioxidant content is reported to be highest in sesame oil (Cheung *et al.*, 2007). Despite having the largest area under cultivation and being one of the largest producers in the world, its production is still very low in India. The crop is grown marginally in the state of Assam and therefore, very less attempt for improvement has been made in sesame in this region despite having indigenous landraces throughout the region. The study of variability and character association for yield and yield contributing traits is the prerequisite for any crop improvement programme. Thus, to understand the nature and magnitude of genetic variance and character association the present study was undertaken in a set of 32 sesame accessions considering 12 morpho-physiological traits associated with seed yield in sesame.

MATERIAL AND METHODS

The experiment material for the present investigation consisted of 32 sesame genotypes collected from Regional Agricultural Research Station, Shillongani, Assam. The investigation was carried out during the *Kharif* season 2019 at the experimental field and laboratory of the Department of Plant Breeding and Genetics and the Institutional Biotech Hub, Biswanath College of Agriculture, AAU, Biswanath Chariali. The experimental site lies in the North Bank Plain Zone of Assam at a latitude and longitude of 26°42'N and 93°30'E, respectively along with a mean altitude of 105 m above mean sea level. The soil of the experimental site was sandy loam with a pH of 5.5. The sesame genotypes were sown in a Randomized Complete Block Design (RCBD) with three replications. Each plot consisted of three rows of three meters in length with a spacing of 15 cm between plants and 30 cm between rows. The observations were recorded on days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches/plant, number of capsules/plant, 1000- seed weight (g), leaf area index, relative leaf water content (%), total chlorophyll content (mg/g fresh wt.), biological yield (g), harvest index and seed yield/plant (g). The data obtained were subjected to analysis of variance following the standard protocol given by Panse and Sukhatme (1967). Estimation of genetic parameters of variation was estimated as per Singh & Choudhury (1988). The standard methods of Burton and Devane (1953), Lush (1945) and Johnson *et al.*, (1955) were used to estimate the variability parameters, heritability and genetic advance. Both genotypic and phenotypic coefficients of correlation

between all pairs of characters were determined by using variance and covariance components as suggested by Al-Jibouri *et al.* (1958). Path coefficients were calculated as suggested by Wright (1921); Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters under study which indicated that the genotypes under study had considerable variability and of worthwhile for carrying out further crop improvement attempts. The genetic parameters of variation for the 12 traits under study are presented in Table 1, Fig 1, 2. In the present study, the phenotypic coefficient of variation (PCV) was observed higher than the corresponding genotypic coefficient of variation (GCV) with a narrow difference for all the traits. This indicated that the variability amongst these traits was mostly contributed by genetic factors. Similar results were also reported by Revathi *et al.* (2012); Abate and Mekbib (2015); Meenakumari and Ganesamurthy (2015); Bamrotiya *et al.* (2016). It also indicates that there is scope for improvement of this character (Kiruthika *et al.*, 2017). Moderate to higher magnitude of genotypic (GCV) and phenotypic coefficient of variation (PCV) were recorded for all the characters under study except days to maturity and relative leaf water content. These results corroborate with the findings of Abhijatha *et al.* (2017); Bharathi *et al.* (2014); Singh *et al.* (2018) for number of capsules per plant; Hika *et al.* (2015) for biological yield.

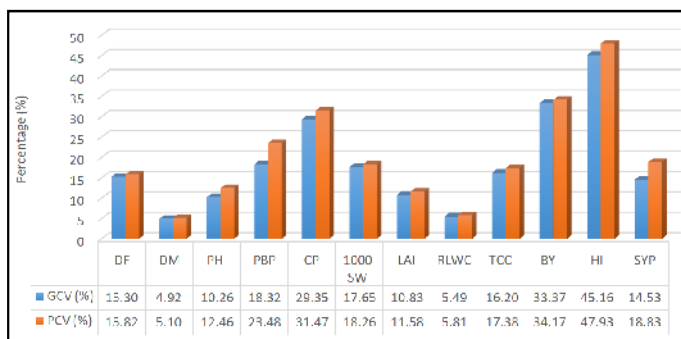


Fig. 1. GCV (%) and PCV (%) for various characters of sesame genotypes.

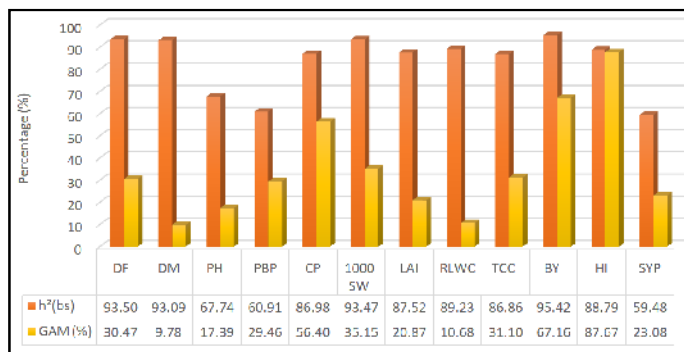


Fig. 2. Heritability (%) and genetic advance as per cent of mean (%) for various characters of sesame genotypes.

Table 1: Parameters of genetic variation for morpho-physiological traits and seed yield in sesame.

| Characters | Mean | SE(m) | Range | | CV (%) | GCV (%) | PCV (%) | h ² (bs) | GAM (%) |
|------------|--------|-------|--------|--------|--------|---------|---------|---------------------|---------|
| | | | Min. | Max. | | | | | |
| DF | 38.01 | 0.89 | 30.30 | 55.30 | 4.03 | 15.30 | 15.82 | 93.50 | 30.47 |
| DM | 84.77 | 0.66 | 78.00 | 93.60 | 1.34 | 4.92 | 5.10 | 93.09 | 9.78 |
| PH | 126.15 | 5.15 | 101.40 | 149.00 | 7.08 | 10.26 | 12.46 | 67.74 | 17.39 |
| PBP | 4.24 | 0.36 | 2.77 | 5.71 | 14.68 | 18.32 | 23.48 | 60.91 | 29.46 |
| CP | 56.99 | 3.74 | 27.00 | 94.90 | 11.36 | 29.35 | 31.47 | 86.98 | 56.40 |
| 1000 SW | 2.46 | 0.07 | 1.68 | 3.06 | 4.67 | 17.65 | 18.26 | 93.47 | 35.15 |
| LAI | 3.55 | 0.08 | 2.92 | 4.17 | 4.09 | 10.83 | 11.58 | 87.52 | 20.87 |
| RLWC | 84.75 | 0.93 | 77.30 | 92.30 | 1.91 | 5.49 | 5.81 | 89.23 | 10.68 |
| TCC | 1.64 | 0.06 | 1.23 | 2.19 | 6.30 | 16.20 | 17.38 | 86.86 | 31.10 |
| BY | 42.50 | 1.79 | 22.50 | 67.10 | 7.31 | 33.37 | 34.17 | 95.42 | 67.16 |
| HI | 22.12 | 2.05 | 12.90 | 40.10 | 16.05 | 45.16 | 47.93 | 88.79 | 87.67 |
| SYP | 8.14 | 0.56 | 5.32 | 10.74 | 11.99 | 14.53 | 18.83 | 59.48 | 23.08 |

DF - Days to 50 % flowering; DM - Days to maturity; PH - Plant height(cm); PBP - No. of primary branches/plant; CP - No. of capsules/plant; 1000 SW - 1000 seed weight(g); LAI - Leaf area index; RLWC - Relative leaf water content (%); TCC - Total chlorophyll content(mg/g fresh weight); BY - Biological yield(g); HI - Harvest index (%); SYP - Seed yield per plant (g).

Manjeet *et al.* (2020) for harvest index. This information on the coefficient of variation suggested the presence of sufficient variability among the genotypes evaluated under the present study, which can be utilized for the genetic improvement of sesame through selection.

The mere presence of genetic variation is not useful unless the heritable fraction of genetic variation is not known. Johnson *et al.* (1955) suggested that heritability and genetic advance calculated together are more useful for predicting the outcome of selection for superior individuals rather than information on heritability and genetic advance calculated alone. Thus, for selection to be effective, the high heritability of a character should be accompanied by a high genetic advance (as *per cent* mean).

In this investigation, high heritability estimates (> 80%) were observed for all the traits under study except seed yield, plant height and primary branches per (Kiruthika *et al.*, 2018). High heritability coupled with moderate to high genetic advance was observed for all the traits except days to maturity, plant height, primary branches per plant, relative leaf water content and seed yield which demonstrates the presence of additive gene effect indicating the effectiveness of selection for improvement of these traits. Seed yield per plant exhibited a lower magnitude of GCV and heritability (Bedawy *et al.*, 2018). This may be due to the higher influence of the environment on the expression of yield and the complex nature of it being influenced by many other component traits. Overall it appeared that harvest index, biological yield and capsules per plant had a higher magnitude of GCV, heritability and genetic advance as *per cent* of the mean, which indicated selection will be most effective for obtaining genetic gain for these traits (Mustafa *et al.*, 2015).

Yield of any crop is a complex trait which is influenced by many component traits (Yol *et al.*, 2012). Although the parameters of variation indicate the selection efficiency of the individual traits, to bring about improvement in yield, the nature of the influence of individual traits on the seed yield needs to be understood. Character association studies reveal the nature and magnitude of the *inter se* association of the component traits as well as their association with seed

yield. This information on the magnitude and direction of association of the component characters with seed yield and also inter association among them would prove to be very useful in formulating an effective breeding programme for improvement of seed yield (Jogdhande *et al.*, 2017; Manisha *et al.*, 2018).

Such studies are required for simultaneous improvement of many characters or a single complex character like the yield on the assumption of correlated response to selection. An attempt was, therefore, made to estimate the genotypic and phenotypic correlation coefficients between seed yield and the component characters and also amongst the components to acquire adequate information on this aspect.

Seed yield per plant exhibited a highly significant association in the positive direction with days to maturity, plant height, number of primary branches per plant, number of capsules per plant, 1000-seed weight, leaf area index, relative leaf water content, total chlorophyll content and harvest index (Table 2). Similar results were also reported by Sikarwar (2002); Lal *et al.* (2016) in the case of days to maturity; Singh *et al.* (2018); Pawar *et al.* (2002) in the case of plant height; Teklu *et al.* (2017); Satankar *et al.* (2019) in case of number of primary branches per plant; Manjeet *et al.* (2019); Saxena and Bisen (2016) in case of number of capsules per plant; Satankar *et al.* (2019); Manjeet *et al.* (2019) in case of 1000 seed weight; Kumar *et al.* (2013); Panda (2017) in case of leaf area index; Panda (2017) in case of relative leaf water content and total chlorophyll content; Bamrotiya *et al.* (2016); Manjeet *et al.* (2019) in case of harvest index. In the present study, a highly significant negative correlation was observed for seed yield per plant with days to 50 *per cent* flowering. The results conform with those reported by Satankar *et al.* (2019); Manjeet *et al.* (2019).

Inter se correlation coefficients among the component characters revealed that those characters that were positively correlated with seed yield per plant, also showed positive association among themselves, and the character, days to 50 *per cent* flowering which was negatively correlated with seed yield per plant, also showed a negative association with the characters positively associated with seed yield. Interestingly, days to flowering exhibited a negative association with

days to maturity. It was because the plants which started flowering earlier continued to flower much longer time being indeterminate in nature (Uzun *et al.*, 2013). These observations indicated that plants with early flowering and later in maturity are likely to produce more plant height, more number of primary branches per plant, more number of capsules per plant, high 1000 seed weight, high leaf area index, high relative leaf water content, high total chlorophyll content and high harvest index. This indicated, that longer flowering duration is associated with higher yield and yield attributes. These findings are supported by the works of Yol *et al.* (2010); Vanishee *et al.* (2011); Hika *et al.* (2014). Therefore, selection based on these characters could result in further yield improvement.

Simple correlation indicates the association between two traits. Yield being a complex trait being governed by many other independent traits, it would be more meaningful to partition the simple correlation into its direct and indirect components through path analysis. Path coefficient analysis devised by Wright (1921) is a

convenient way to carry out the partitioning of the total correlation coefficients into their direct and indirect effects.

The phenotypic path matrix is presented in Table 3. The path analysis revealed that the characters, days to maturity, plant height, number of primary branches per plant, number of capsules per plant, leaf area index, relative leaf water content, total chlorophyll content, biological yield and harvest index had a positive direct effect on seed yield, while days to 50 per cent flowering and 1000- seed weight showed a negative direct effect. Similar results were reported by Singh *et al.* (2018) in case of plant height; Manjeet *et al.* (2019) in case of biological yield and harvest index; Kehie *et al.* (2020) in case of days to 50 per cent flowering and 1000- seed weight. Thus character showing a positive direct effect on seed yield may be expected to show yield promising results from direct selection (Abate *et al.*, 2021). Negative associations shown by the traits on seed yield may be broken by recombination breeding through hybridization followed by segregation and selection.

Table 2: Phenotypic and Genotypic correlation coefficients among 12 quantitative traits in sesame.

| Traits | DF | DM | PH | PBP | CP | 1000 SW | LAI | RLWC | TCC | BY | HI | SYP (Phenotypic) |
|-----------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-----------------|------------------|
| DF | 1 | 0.8420** | 0.7549** | 0.7304** | -0.8031** | 0.8868** | 0.8497** | 0.8541** | 0.7965** | 0.1376 | -0.5483** | -0.8481** |
| DM | -0.8549** | 1 | 0.8090** | 0.7946** | 0.8863** | 0.9008** | 0.8607** | 0.8719** | 0.8961** | -0.3144 | 0.6334** | 0.855** |
| PH | -0.8087** | 0.8932** | 1 | 0.8104** | 0.8587** | 0.8416** | 0.824** | 0.8036** | 0.834** | -0.3232 | 0.6634** | 0.8494** |
| PBP | -0.8585** | 0.9152** | 0.8592** | 1 | 0.8222** | 0.8539** | 0.7824** | 0.7988** | 0.7857** | -0.2906 | 0.5998** | 0.8023** |
| CP | -0.8295** | 0.9277** | 0.9465** | 0.9571** | 1 | 0.8886** | 0.8251** | 0.8401** | 0.8985** | -0.4049** | 0.6839** | 0.8322** |
| 1000 SW | -0.9017** | 0.9173** | 0.9132** | 0.9856** | 0.9121** | 1 | 0.9099** | 0.8990** | 0.8843** | -0.3605* | 0.7250** | 0.8840** |
| LAI | -0.8647** | 0.8872** | 0.8509** | 0.8761** | 0.8455** | 0.9273** | 1 | 0.8798** | 0.8370** | -0.3123 | 0.6658** | 0.8552** |
| RLWC | -0.8647** | 0.8923** | 0.8393** | 0.9041** | 0.8507** | 0.9054** | 0.8904** | 1 | 0.8686** | -0.2446 | 0.6096** | 0.8748** |
| TCC | -0.8145** | 0.9345** | 0.8759** | 0.8892** | 0.9368** | 0.9036** | 0.8472** | 0.8797** | 1 | -0.3943* | 0.6962** | 0.8722** |
| BY | 0.1631 | -0.3526* | -0.4322* | -0.4176* | -0.4609** | -0.3934* | -0.3565* | -0.2781 | -0.4436* | 1 | -0.8494** | -0.2089 |
| HI | -0.5653** | 0.6630** | 0.7530** | 0.7237** | 0.7328** | 0.7538** | 0.6938** | 0.6195** | 0.7342** | -0.8810** | 1 | 0.6305** |
| SYP (Genotypic) | -0.9784** | 0.9884** | 0.8825** | 0.8821** | 0.9197** | 0.9980** | 0.9288** | 0.9458** | 0.9435** | -0.2965 | 0.6854** | |

Above diagonal: Phenotypic correlation coefficients Below diagonal: Genotypic correlation coefficients

[* Significant at 5%** Significant at 1%]

DF - Days to 50 % flowering; DM - Days to maturity; PH - Plant height(cm); PBP - No. of primary branches/plant; CP - No. of capsules/plant; 1000 SW - 1000 seed weight(g); LAI - Leaf area index; RLWC - Relative leaf water content(%); TCC - Total chlorophyll content(mg/g fresh weight); BY - Biological yield (g); HI - Harvest index (%); SYP - Seed yield per plant (g).

Table 3: Phenotypic path coefficients among 12 quantitative traits in sesame.

| Traits | DF | DM | PH | PBP | CP | 1000 SW | LAI | RLWC | TCC | BY | HI |
|------------------------|---------------|--------------|---------------|---------------|---------------|----------------|---------------|---------------|---------------|---------------|---------------|
| DF | -0.003 | 0.0025 | 0.0022 | 0.0022 | 0.0024 | 0.0026 | 0.0025 | 0.0025 | 0.0024 | -0.0004 | 0.0016 |
| DM | -0.0825 | 0.098 | 0.0793 | 0.0779 | 0.0869 | 0.0883 | 0.0844 | 0.0855 | 0.0878 | -0.0308 | 0.0621 |
| PH | -0.0608 | 0.0652 | 0.0806 | 0.0653 | 0.0692 | 0.0678 | 0.0664 | 0.0648 | 0.0672 | -0.026 | 0.0535 |
| PBP | -0.0683 | 0.0743 | 0.0758 | 0.0935 | 0.0769 | 0.0798 | 0.0732 | 0.0747 | 0.0735 | -0.0272 | 0.0561 |
| CP | -0.0442 | 0.0488 | 0.0473 | 0.0453 | 0.0551 | 0.049 | 0.0455 | 0.0463 | 0.0495 | -0.0223 | 0.0377 |
| 1000 SW | 0.1106 | -0.1124 | -0.105 | -0.1065 | -0.1108 | -0.1247 | -0.1135 | -0.1121 | -0.1103 | 0.045 | -0.0904 |
| LAI | -0.0465 | 0.0471 | 0.0451 | 0.0428 | 0.0452 | 0.0498 | 0.0547 | 0.0482 | 0.0458 | -0.0171 | 0.0364 |
| RLWC | -0.0878 | 0.0896 | 0.0826 | 0.0821 | 0.0863 | 0.0924 | 0.0904 | 0.1028 | 0.0893 | -0.0251 | 0.0627 |
| TCC | -0.2292 | 0.2578 | 0.24 | 0.2261 | 0.2585 | 0.2544 | 0.2408 | 0.2499 | 0.2877 | -0.1135 | 0.2003 |
| BY | 0.0926 | -0.2116 | -0.2175 | -0.1956 | -0.2725 | -0.2427 | -0.2102 | -0.1646 | -0.2654 | 0.6731 | -0.5718 |
| HI | -0.429 | 0.4956 | 0.519 | 0.4692 | 0.5351 | 0.5672 | 0.5209 | 0.4769 | 0.5447 | -0.6646 | 0.7824 |
| SYP | -0.8481 | 0.855 | 0.8494 | 0.8023 | 0.8322 | 0.884 | 0.8552 | 0.8748 | 0.8722 | -0.2089 | 0.6305 |
| Partial R ² | 0.0025 | 0.0838 | 0.0685 | 0.075 | 0.0458 | -0.1103 | 0.0468 | 0.0899 | 0.251 | -0.1406 | 0.4933 |

Residual effect = 0.307

DF - Days to 50 % flowering; DM - Days to maturity; PH - Plant height(cm); PBP - No. of primary branches/plant; CP - No. of capsules/plant; 1000 SW - 1000 seed weight(g); LAI - Leaf area index; RLWC - Relative leaf water content(%); TCC - Total chlorophyll content(mg/g fresh weight); BY - Biological yield (g); HI - Harvest index (%); SYP - Seed yield per plant (g).

CONCLUSION

From the above discussion, it is clear that considerable genetic variability existed among the genotypes under study and hence, there is ample scope for the selection

of promising lines that could be used as parents in further crossing programmes. The information on the nature and magnitude of genetic parameters indicated the effectiveness of the selection of the traits under

study. Further, the findings from the character association revealed the selection criteria to be adopted for improving seed yield and also to adopt recombination breeding to break the undesirable negative associations.

Abbreviations: FAOSTAT (Food and Agriculture Organization Corporate Statistical Database), MT (Metric Tonnes), RCBD (Randomized Complete Block Design), GCV (Genotypic coefficient of variation), PCV (Phenotypic coefficient of variation), GA (Genetic advance), Hbs (Heritability in the broad sense).

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Conflict of Interest. None.

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