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Research Article

Devising selection strategy for increase in sesame yield based on variability heritability and genetic advance studies

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Abstract

The study on ten sesame entries was conducted during Kharif 2017 and 2018 at National Agricultural Research Centre, Islamabad, Pakistan. The results of two years indicated highly significant differences among the genotypes for all the traits showing presence of high degree of variability which could be utilized for sesame crop improvement. Genotypic and phenotypic coefficients of variation (GCV and PCV) were maximum for seed yield followed by pods and branches per plant. Heritability (broad sense) was high (0.69 to 0.97) for all the traits indicating large proportion of the total variance was because of high genotypic variance due to which influence of environment was less on these traits thus having high heritable variation. There were least differences between GCV and PCV values along with high heritability estimates for all the traits indicating less influence of environment. Hence, direct selection is recommended for the improvement. High values of genetic advance as percent of mean for branches per plant, pods per plant and seed yield showing that yield increase through selection can be achieved up to a level of 12.52%, 21.86% and 23.87% respectively. Branches per plant, pods per plant and seed yield showed high heritability coupled with high GA% values, indicating that additive genes control these traits and direct selection based on phenotypic performance would be helpful for the improvement in the sesame crop. Therefore, efforts should be focused on these traits for devising selection strategy for increase in sesame yield on the basis of phenotypic performance.

Keywords: Genetic Advance; Heritability; Pakistan; Sesame; *Sesamum indicum* L.; Variability

Introduction

Sesame (*Sesamum indicum* L.) belongs to family *Pedaliaceae.* It is one of the oldest oilseed crops. It is mainly cultivated in Asia, Africa, and South America and more than 80% of the sesame producing area is in the developing countries. Seed is the main purpose for its cultivation. Its oil contents range from 40-60% and protein content 22% **[1]**. Sesame oil is highly stable because of the presence of antioxidants lignans such as sesamin, sesamolin, and sesaminol. These compounds have antioxidant, antiaging, antihypertensive, anticancer, cholesterol lowering, and antimutagenic properties **[1]**. Sudan leads in sesame production with 981,000 tons, followed by Mynamar (768,858 tons), India (746,000 tons), Nigeria (572,761 tons), and Tanzania (561,103 tons) (FAOSTAT, 2018). During 2017-18, sesame was cultivated in Pakistan on 82,700 ha with total production of 35,400 tons and national average yield of 428 kg/ha (Agricultural Statistics of Pakistan, 2017-18).

Availability of narrow genetic variability hampers sesame breeders for the development of new and superior crop varieties. The understanding of the genetic variability of available gene pool will help in devising selection strategy for the development of high yielding varietiesfor raisingsesame production. Therefore, the present study was planned for devising selection strategy in sesame breeding for increased yield based on understanding variability, heritability and genetic advance as percent of mean for some quantitative traits.

Materials and Methods

The experimental materials comprised of ten sesame genotypes sown in randomized complete block design with three replications during Kharif 2017 and 2018 at National Agricultural Research Centre, Islamabad, Pakistan. Each experimental unit consisted of 4 rows of 5 meter length with row spacing of 45cm. Data were recorded on days to flower initiation, days to flower completion, days to maturity, plant height, number of branches per plant, number of pods per plant and seed yield (kg/ha). The data collected were subjected to Analysis of Variance (ANOVA) and Least Significant Difference (LSD) by Statstix 8.1 software. Follow Singh and Chaudhry **[2]** to calculate of estimates of genotypic and phenotypic variances (GV and PV). Genotypic and phenotypic coefficients of variation (GCV and PCV) and broad sense heritability (H_{bs}) were computed as Burton **[3]**. Estimates of heritability high (>50%), medium (20-50%) and low (<20%) were calculated as suggested by Stansfield **[4]**. Genetic advance (GA) at 5% selection intensity and genetic advance as percent of mean (GA %) were determined following Johnson *et al.* **[5]** formula consequently employed by Allard **[6].**

Results and Discussion

Analysis of variance over mean data of 2017 and 2018 indicated highly significant differences among the genotypes for all the traits under study showing presence of high degree of variability in the genotypes which could be utilized for sesame crop improvement. Coefficient of variation (CV%) for these traits ranged from0.42 to 4.56% (Table 1). Jamir *et al.* **[7]**, Patidar *el al.* **[8]**, Pavani *et al.***[1]** and Sirisha *et al.* **[9]** reported significant differences among genotypes for the traits under study.

The performance of sesame genotypes for yield and agronomic traits over mean data of 2017 and 2018 is given in (Table 2). Days to flowering initiation ranged from 41 days (SG-52 and SG-175) to 44 days (SG-11, SG-21, SG-58 and SG-93) with a mean value of 43 days. Only two genotypes (SG-52 and SG-175) initiated flowering (41 days) earlier than check TS-5 (43 days). The range of days to flower completion 69 days (SG-50, SG-93, SG-174 and SG-175) to 72 days (SG-21 and SG-99) having mean value of 70 days. Two entries (SG-21 and SG-99) had longer days to flowering completion period (72 days) compared tocheck TS-5 (71 days). Days to maturity varies from 99 days (SG-50, SG-52, SG-93 and SG-175) to 104 days (TS-5) showing mean value of 100 days. All the entries matured earlier than check TS-5 ranging from 99 to 101 days.

Plant height ranged from 112 cm (TS-5) to 123 cm (SG-11) with mean value of 118 cm. All the entries were taller than check TS-5 (112 cm) and had a range of 115 to 123 cm. Maximum number of branches per plant (4.1) was recorded in SG-50 and minimum (3.2) in

SG-99 possessing a mean value of 3.6 branches per plant. SG-50, SG-11, SG-21, SG-52, SG-174 and SG-175 had more branches per plant compared to check TS-5 (3.5) with a range of 3.6 to 4.1 branches per plant. Number of pods per plant varies from 47 (SG-93) to 68 (SG-11) showing a mean value of 56 pods. Four genotypes had more pods per plant viz. SG-11, SG-21, SG-174 and SG-50 with a range of 56 to 68 pods per plant than check TS-5 (55 pods). Seed yield of these ten genotypes had a range of 533 kg/ha (TS-5) to 828 kg/ha (SG-11) having a mean value of 703 kg/ha. All the genotypes were better in seed yield compared to check TS-5 (533 kg/ha) and had a range of 606 to 828 kg/ha.

The values of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (H_{bs}) and genetic advance as percent of mean (GA%) are given in (Table 3). GCV and PCV were found maximum for seed yield followed by pods per plant and branches per plant while minimum for days to maturity. Anbanandan **[10]** reported high GCV and PCV for branches per plant, pods per plant and seed yield. Jamir *et al.* **[7]** reported high GCV and PCV values for branches per plant, pods per plant and seed yield. Pavani *et al.* **[1]** reported high GCV and PCV values for branches per plant and pods per plant.

Heritability (broad sense) ranged from 0.69 to 0.97 and was high for all the traits indicating that large proportion of the total variance was because of the high genotypic variance due to which influence of environment was less on these traits thus having high heritable variation. These traits possessing high heritability, consequently, may respond more effectively to phenotypic selection. Anbanandan **[10]** reported high heritability estimates for branches per plant, pods per plant and seed yield. Pavani *et al.* **[1]** reported high heritability values for days to flowering, plant height, branches per plant and pods per plant. Jamir *et al.* **[7]** and Sirisha *et al.* **[9]** reported high heritability values for days to flowering, days to maturity, branches per plant, pods per plant and seed yield.

Furthermore, it was found that there were fewer differences between GCV and PCV values alongwith high heritability estimates for all the traits in this study. These results indicatedthat there would be less influence of environment on these traits. Hence, direct selection is recommended for the improvement. Anbanandan **[10]** reported similar results for branches per plant, pods per plant and seed yield. Pavani *et al.* **[1]** was of same view for branches per plant and pods per plant. Jamir *et al.* **[7]** and Sirisha *et al.* **[9]** also reported similar results.

High values of genetic advance as percent of mean were observed in branches per plant, pods per plant and seed yield showing that yield increase through selection can be achieved up to a level of 12.52%, 21.86% and 23.87% respectively within the tested materials. Jamir *et al.* **[7]** reported that sesame crops improvement was possible up to 85%. Pavani *et al.* **[1]** reported up to 47% improvement in the sesame crop. Sirisha *et al.* **[9]** reported that improvement in sesame crop was possible up to 74%.

High heritability (broad sense) *per se* is not an index of high genetic gain. Therefore, it should be accompanied by high GA% when describing the genetic parameters in any crop as cautioned by Kadir *et al.* **[11]**. In present study, branches per plant, pods per plant and seed yield showed high heritability coupled with high GA% values, indicating that additive genes control these traits and direct selection based on phenotypic performance would be helpful for the improvement in the sesame crop. Jamir *et al.* **[7]** reported that branches per plant, pods per plant and seed yield are under the influence of additive genes and improvement is possible through selection based on these traits. Patidar *et al.* **[8]** reported that improvement in sesame crop is possible through selection based on traits having highly heritability and high genetic advance as per cent of mean. Pavani *et al.* [1] reported that direct selection based on pods per plant is possible. Sirisha *et al.* [9] reported that branches per plant, pods per plant and seed yield had high heritability and high genetic advance as percent of mean estimates showing the role of additive gene action for these traits which could be exploited by simple selection.

Table 1. Mean Squares for yield and agronomic traits over mean data of 2017 and 2018

Source of variation	df	Days flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Seed Yield (kg/ha)
Replication	2	0.03333	0.63333	0.7000	2.7000	0.01233	20.833	4012.9
Genotypes	9	3.02222**	4.84815**	6.4037**	30.8148**	0.16626**	112.681**	20374.8**
Error	18	0.25556	0.33704	0.18148	8.4037	0.0227	6.759	474.5
CV%		1.17	0.82	0.42	2.46	4.18	4.56	3.10

** = Highly significant at 1% level of probability

Table 2. Mean performance of sesame genotypes for yield and agronomic traits over mean data of 2017 and 2018

Genotypes	Days flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Seed Yield (kg/ha)
SG-11	44	71	101	123	3.7	68	828
SG-21	44	72	101	122	3.7	64	752
SG-50	43	69	99	117	4.1	56	681
SG-52	41	70	99	119	3.7	52	606
SG-58	44	71	100	118	3.4	54	709
SG-93	44	69	99	117	3.2	47	759
SG-99	43	72	100	118	3.5	55	736
SG-174	43	69	100	115	3.6	57	707
SG-175	41	69	99	119	3.6	51	720
TS-5	43	71	104	112	3.5	55	533
Mean	**43**	**70**	**100**	**118**	**3.6**	**56**	**703**
Minimum	**41**	**69**	**99**	**112**	**3.2**	**47**	**533**
Maximum	**44**	**72**	**104**	**123**	**4.1**	**68**	**828**
LSD (5%)	**0.87**	**0.99**	**0.73**	**4.97**	**0.3**	**4.46**	**37.37**

Table 3. Estimates of genetic parameters for yield and agronomic traits in sesame genotypes over mean data of 2017 and 2018

Genetic parameters	Days flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Seed Yield (kg/ha)
Genotypic variance (GV)	0.92	1.50	2.07	7.47	0.05	35.31	6633.43
Phenotypic variance (PV)	1.18	1.84	2.26	15.87	0.07	42.07	7107.93
Genotypic coefficient of variation % (GCV)	2.23	1.75	1.44	2.32	6.08	10.61	11.59
Phenotypic coefficient of variation % (PCV)	2.52	1.94	1.50	3.38	7.38	11.58	11.99
Heritability ($H_{(bs)}$)	0.88	0.90	0.96	0.69	0.82	0.92	0.97
Genetic advance (GA)	1.98	2.53	2.97	5.63	0.45	12.24	167.78
Genetic advance as percent of mean (GA%)	4.60	3.61	2.97	4.77	12.52	21.86	23.87

Conclusion

Identification of superior genotypes is prerequisite to achieve progress from selection. From the results of this study, it is observed that branches per plant, pods per plant and seed yield are under the control of additive genes as they had high values of heritability coupled with genetic advance as percent of mean, hence, provide a good selection base. Therefore, efforts should be focused on these traits for devising selection strategy for increase in sesame yield on the basis of phenotypic performance.

Authors' contributions

Conceived and designed the experiments: MA Khan, Performed the experiments: MA Khan, N Nawaz & Tahira, Analyzed the data: MA Khan, N Nawaz & Tahira, Contributed materials/ analysis/ tools: N Nawaz & Tahira, Wrote the paper: MA Khan

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