

Assessment of Genetic Variability in Soybean (*Glycine max* L., Merrill)

Vijay Bairagi^{1*}, Sheshnath Mishra², Ramraj Sen³, Saurabh Dixit⁴ and Dinesh Baboo Tyagi⁵

¹M.Sc. Scholar, Department of Genetics and Plant Breeding,
Mandsaur University, Mandsaur (Madhya Pradesh), India.

²Assistant Professor, Department of Genetics and Plant Breeding,
Mandsaur University, Mandsaur (Madhya Pradesh), India.

³Research Associate at IARI -SKAF-CORC,
Sipani Krishi Anusandhan Farm, (Changli) Mandsaur (Madhya Pradesh), India.

⁴Assistant Professor, Department of Horticulture,
Mandsaur University, Mandsaur (Madhya Pradesh), India.

⁵Director, Faculty of Agriculture Sciences,
Mandsaur University, Mandsaur (Madhya Pradesh), India.

(Corresponding author: Vijay Bairagi*)

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ABSTRACT: Among the farmers, it is always demand of high yielding varieties. Development of high yielding varieties is routine activities which involve identification of superior plants through selection and development of new varieties by breeder. In now a day due to climate change, continuous breeding efforts with identification of new lines for development of high yielding varieties is essential to overcome climate change effects in form of decline in yield production of present high yielding cultivars due to these changes. Thirty two soybean genotypes were evaluated for ten morphological characters during *Kharif* season, 2022 in Randomized Block Design with three replications at IARI-SKAF-CORC, Changli, Mandsaur. Analysis of variance depicted significant differences among the accessions for all the traits. The estimated value of phenotypic variance was higher than the corresponding genotypic variance for all the ten traits. PCV and GCV were moderate to low for all characters. GCV recorded was the highest for number of pods per plant (36.44%) followed by grain yield (33.98%), number of pods per cluster (22.91%) and plant height (17.51%). High PCV coupled with high GCV for number of pods per plant, grain yield, number of pods per cluster, plant height and numbers of primary branches per plant show presence of wider adaptability for these traits in the genotypes due to the less effect of environment in the expression of traits. Number of pods per plant (97.27%) had the highest heritability followed by grain yield (95.91%), number of pods per cluster (93.01%), plant height (88.34%), number of primary branches per plant (86.58) and 100 seed weight (83.04%). High heritability coupled with high genetic advance as percent of mean was observed for number of pods per plant, grain yield, number of pods per cluster, plant height and number of primary branches per plant indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection. Considering genetic variability emphasis should be given on number of pods per plant, grain yield, number of pods per cluster, plant height and number of primary branches per plant during breeding program to improve seed yield of soybean.

Keywords: Genetic Variability, Soybean, Genotypes, PCV, GCV, Genotypic Variance, Heritability.

INTRODUCTION

Pulses are considered important food crops due to good source of vegetable dietary protein (Guleria *et al.*, 2019). Among the pulses, soybean is the most widely grown leguminous crop worldwide and considered as oilseed crop due to presence of high vegetable oil content. It is a self-pollinating annual legume having the chromosome number of $2n = 2x = 40$. This belongs to the family Fabaceae and subfamily Faboideae (Jain *et al.*, 2017).

Soybean is known as golden bean due to its nutritional values and health benefits. World production data of soybean (2019-2020) reported that Brazil rank was first

in soybean production (114.27 million tonnes) followed by United States of America (96.79 million tonnes) and Argentina (55.26 million tonnes) which contributed to 34.25, 29.01 and 16.56 per cent respectively. In 2019-20, India occupied fourth rank in area (11.34 million hectares) and fifth in production (11.22 million tons) worldwide. Madhya Pradesh is leading state in India in both area and production. Other soybean producing states are Maharashtra, Rajasthan, Karnataka and Telangana. According to the first advance estimates 2021-22 of Ministry of Agriculture, Soybean production is estimated at 127.20 lakh tonnes as compared to 128.97 lakh tonnes in 2020-21 (Source:

MoA&FW New Delhi; <https://agricoop.nic.in>). It occupies a very important position among grain legumes because of its highest protein content in seeds (30-45%) and rich oil contents (15-24%) in comparison to others grain legumes (Akram *et al.*, 2011; Guleria *et al.*, 2019). Among a series of routine activities in the crops improvement program, selection is the most important step for identify high yielding genotypes (Sulistyo *et al.*, 2018). The effectiveness of selection is calculated by the selection criteria like GCV, heritability, genetic advance, correlation and path analysis used. Analysis of selection parameters can be done in various ways. Collection of information on genetic parameters such as heritability may be used as selection criteria (Sulistyo *et al.*, 2018).

Aditya *et al.* (2011) studied genetic parameter and correlation of eight quantitative traits including grain yield in thirty one soybean genotypes. They reported that seed yield per plant exhibited highest estimate of PCV (47.74) and GCV (41.83) followed by dry matter weight per plant and number of pods per plant. Heritability was highest for three characters i.e., days to 50 per cent flowering, number of primary branches per plant and 100 seed weight (91%). High heritability coupled with high genetic advance was reported for number of pods per plant and dry matter weight per plant. Similarly Naik *et al.* (2016) evaluated 225 soybean genotypes for variability parameters. Significant variability (5%) was recorded among genotypes for agronomic and seed quality parameters. Number of pods per plant (23.76%), test weight (21.61%), seed yield per plant (28.07%), final germination (36.7%), seed coat permeability (30.09%), electrical conductivity (40.09%) and germination reduction (40.03%) showed high phenotypic and genotypic coefficient of variation, heritability and genetic advance. Pallavi *et al.* (2018) studied 24 genotypes of soybean reported that variability was maximum for seed yield/ha, pods/plant and Plant height. High (>20%) phenotypic variance was observed for traits namely plant height, pods/plant, seed yield/ha and Germination % respectively. High heritability (60%) was recorded for days to 50% flowering, pods/plant, seed yield/ha, germination %, seedling length, seedling dry weight whereas High heritability coupled with high genetic advance was recorded for seedling dry weight, Seed Yield/ha and clusters/plant. Neelima *et al.* (2018) assessed the genetic variability in 124 diverse soybean germplasm accessions. The data showed that values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters under study. The magnitude of heritability was observed to be high for all the characters under study. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for plant height, number of branches per plant, number of pods per plant and seed yield per row. Koraddi *et al.* (2019) evaluated 13 genotypes of soybean for variability, heritability and genetic advance. Result of analysis of variance revealed highly significant differences among the genotypes for the all the

characters. The range was maximum for plant height (39.27-77.73) followed by number of pods per plant (35.87-61.40). The genotypic coefficient of variation and phenotypic coefficient of variation were high for pod weight per plant followed by seed yield per. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height (cm), number of pods per plant, number of seeds per pod, pod weight per plant, 100 seed weight, biomass and seed yield per plant.

The present investigation was undertaken with an aim to characterize *Glycine max* L., Merrill genotypes at morphological level with the objectives to estimate genetic parameter of variability for yield and yield related traits. On the basis of findings, superior and genetically diverse entries were identified for future improvement programmes.

MATERIAL AND METHODS

Collection of germplasm. The present investigation was carried out at Sipani Krishi Anusandhan Farm, (Changli) Mandsaur. The material was collected from the IARI - Sipani Krishi Anusandhan Farm, Collaborative Outstation Research Centre, Sitamau Road (Changli), Mandsaur (M.P.) –India. Thirty two soybean genotypes were sown in the *kharif* season 2022 with three replications in Randomized Block Design. For grow healthy crop, all the recommended package and practices were followed. Row to row and plant to plant spacing was 45 cm and 10 cm. Each accession was sown in six rows having four meter length. To observe data, ten individual plants from each genotype and each replication was randomly selected and tagged. Data was recorded on whole plot basis for days to 50% flowering where as for plant height, Days to 50% Flowering, Days to 50% Pod Initiation, Plant Height (cm), Number of Nodes/Plant, Number of Pods/Cluster, Number of Pod/Plant, Days to Maturity (days), Grain yield (Kg), Number of Primary Branches/plant, 100 Seed Weight (gm), Flower color, Pubescence Appearance, Leaf Shape, Plant Structure.

Experimental Site. The field experiment was undertaken at IARI-SKAF-CORC, Collaborative Outstation Research Centre, Sitamau Road (Changli), Mandsaur (M.P.) 458001, Mandsaur situated in North Eastern part of Madhya Pradesh state, is located at an elevation of 379.50 meter above mean sea level on latitude of 24007' North and longitude of 75006' East. The climate of the region is sub-humid type with an average rainfall of about 883 mm and soil of area is sandy-loam in nature. Crop was raised during *Kharif* - 2022-23.

Experimental Material. In the present investigation seed of thirty two diverse genotypes/varieties of *Glycine max* L. Merrill were procured from different geographical sources listed in Table 1.

Statistical Analysis. ANOVA for estimating variability was worked out as suggested by Panse and Sukhame (1984).

The coefficient of variation (CV): CV was calculated by the formulae suggested by Burton (1952).

Heritability in the broad sense: Heritability in broad sense was estimated as per the following formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance was carried out for ten characters to test the differences between the genotypes. The results of analysis of variance for ten characters of thirty two soybean genotypes including two checks have been shown in Table 2. The analysis of variance predicted that the mean sum of square due to genotypes was highly significant for ten traits indicated the presence of higher amount of variability among the genotypes. Similar results in soybean have been also reported by Karad *et al.*, (2005); Reni and Rao (2007); Aditya *et al.* (2011); Dilnesaw *et al.* (2013); Osekita and Olorunfemi (2014).

The estimates of mean performance is presented in Table 3. Wide range of variability was found among the tested genotypes for the 10 traits (Table 3). Data of range shows enough scope for bringing about improvement in the desire direction. The mean value of the character days to 50% flowering varied from 31.33 to 45.00 days with the grand mean of 38.79 days. On the basis of mean performance, accessions 'SKAF-6017', 'SKAF-6035', 'SKAF-409', 'SKAF-6038', 'SKAF-2007' were the earliest to days to 50% flowering (31.33 days) while 'SKAF-Exo-99' were late to days to 50% flowering (45.00 days.). The entries *viz.*, 'SKAF-4067' gave lowest Days to 50% Pod Initiation (40.67 days) whereas the entry 'NRC-86' most delayed Days to 50% Pod Initiation (60.00 days). The lowest plant height was produced by 'SKAF-7T' (38.37 cm) while highest plant height was produced by the accession 'SKAF-6038' (87.17 cm). The maximum number of nods/plant was depicted by the genotype 'SKF-547' (14.33) whereas lowest by 'SKF-7T' (7.33). Number of pods per cluster is important trait in soybean as yield pertaining to it by increasing more number of pods per cluster. Number of pods per cluster varied from 2.33 to 4.67 with a grand mean value of 3.50. Maximum numbers of pods were recorded in 'SKF-Exo-142', 'SKF-470', 'SKF-403', 'SKF-221', 'SKF-547', 'NRC-181', and 'SKF-BS-6' (4.67) respectively whereas genotype 'JS-95-60', 'SKF-6038' (2.33) gave less number of pods. Significant differences among genotypes for number of pods per plant were recorded. Number of pods per plant varied from 22.00 to 91.67 with a grand mean of 41.35. The accession 'SKF-470' exhibited highest Number of pods/plant (91.67) followed by 'SKF-470' (74.00) and 'NRC-86' (61.00) while accession 'SKF-616' (22.00) showed the lowest Number of pods/plant. The mean value of maturity varied from 81.67 to 110.00 days with the grand mean of 88.66 days. The earliest maturity was found in the accession 'SKF-409' (81.67 days) whereas late maturity was present in 'JS-335' (110.00). Number of primary branches per plant is important trait in soybean as yield pertaining to it by increasing more number of grain per branch. Number of primary branches per plant varied from 4.67 to 9.33 with a grand mean value of 7.14. Maximum numbers of primary branches was

recorded in 'SKF-75-46' (9.33) whereas genotype 'SKF-340' (4.67) gave less number of primary branches. The values test weight (100 seed weight) ranged from 7.33 to 12.90 gm weight with a grand mean of 9.82 gm weight. The genotypes 'NRC-86' had highest 100 seed weight (12.90 gm), respectively while it was lowest in 'SKAF-208' (7.33). The mean grain yield per plot was 1051.05 Kg with a range of 552.33 kg to 1800.33 kg. The genotype 'SKF-623' (1800.33 kg) showed highest grain yield followed by 'SKF-470' (1695.00) and 'SKF-Exo-142' (1597.67) respectively. A total of thirty two genotypes of soybean were evaluated under field condition for grain yield/plot, of which fifteen genotypes depicted more grain yield/plot (kg) than grand mean.

Estimates of variability parameters for all the 10 characters are presented as Table 4. The data showed that the PCV was higher than of GCV, but the difference was closer between these two estimates for all the ten characters taken for study. These indicated that characters under study were less influenced due to environmental factors because of more impact of genetic components rather than phenotypic components. Similar finding were also obtained by Karnwal and Singh (2009); Baraskar *et al.*, (2014); Neelima *et al.* (2018). PCV and GCV both of them were higher for character Grain Yield (34.70; 33.98 %), Number of pods per plant (36.95; 36.44%) and Number of pods per cluster (23.76; 22.91%) respectively. Similarly high PCV and GCV for number of pods per plant was reported by Aditya *et al.* (2011) and for seed yield by Koraddi *et al.* (2019).

Selection is preferred for those characters which show eighty percent or more heritability (Singh, 1990). High heritability was observed for all the characters taken under present investigation except days to maturity. High heritability was observed for number of nodes per plant (82.86%), 100 seed weight (83.04%), number of primary branches per plant (86.58), plant height (88.34%), number of pods per cluster (93.01%), grain yield (95.91%) and number of pods per plant (97.27%) respectively. The data showed that the recorded heritability of these traits was mainly under genetic control. Therefore these characters are less influenced by the environment and the possibility of progress from selection. Similar results were also reported by Ramteke *et al.* (2010) for plant height and biomass per plant, Aditya *et al.* (2016) for number of primary branches per plant and 100 seed weight, Pallavi *et al.* (2018) for pods per plant and seed yield and grain yield per hectare, Neelima *et al.* (2018) for plant height, number of branches per plant, number of pods per plant and seed yield per row, Koraddi *et al.* (2019) plant height (cm), number of pods per plant, Moderate heritability values (40-80%) were observed for days to maturity (51.45%) and days to 50% pod initiation (73.47%). Similar results were reported by other workers (Zinaw *et al.*, 2013; Reni and Rao 2007). It has been suggested that high heritability along with high genetic advance are more fruitful in predicting the gain under selection than heritability values alone in selecting best plants (Johnson *et al.*, 1955). The

maximum genetic advance as percentage of mean was recorded for the trait number of pods per plant (74.03%). High heritability coupled with high genetic advance as percent of mean recorded for number of pods per cluster (93.01% and 45.52%), grain yield (95.91% and 68.55%) and number of pods per plant (97.27% and 74.03%) respectively. Similar finding was reported by Aditya *et al.* (2016) for number of pods per

plant, Neelima *et al.* (2018) for number of pods per plant and seed yield. High heritability along with high genetic advance as percent of mean of characters namely number of pods per cluster, grain yield and number of pods per plant is due to additive gene effects and selection might be effective for these characters (Rahman *et al.*, 2016).

Table 1: Name of 32 genotypes of *Glycine max* L. Merrill used for study.

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1.	SKF-7T	8.	SKF-403	15.	SKF-6128	22.	SKAF-Exo-99	29.	SKAF-616
2.	SKF-340	9.	SKF-6017	16.	SKF-601	23.	JS-95-60 ©	30.	Kuber
3.	NRC-86	10.	SKF-6035	17.	SKF-449	24.	SKAF-208	31.	Chamtkar
4.	SKF-Exo-142	11.	SKF-206	18.	SKF-75-46	25.	SKAF-409	32.	JS-335 ©
5.	SKF-470	12.	SKF-221	19.	NRC-181	26.	SKAF-Exo-131		
6.	SKF-2012	13.	SKF-547	20.	SKAF-623	27.	SKAF-6038		
7.	SKF-6125	14.	SKF-535	21.	SKAF-BS-6	28.	SKAF-2007		

Table 2: Analysis of variance (mean sum of squares) for ten characters in soybean under field condition.

Source of variation	df	Days to 50% Flowering	Days to 50% Pod Initiation	Plant Height (cm)	No. of Nods /Plant	No. of Pods /Cluster	No. of Pod/Plant	Maturity (days)	N/o Primary Branches/Plant	100 Seed Weight (g)	Grain Yield (kg)
Repl	2	2.18	0.95	9.46	0.03	0.00	1.29	35.57	0.02	0.06	2303.42
Treat	31	79.68**	91.29**	356.57**	7.28**	1.98**	687.54**	80.44**	4.69**	6.34**	388062.52**
Error	62	6.05	9.81	15.02	0.47	0.05	6.38	19.25	0.23	0.40	5439.46
Total	95	29.99	36.21	126.36	2.68	0.68	228.55	39.56	1.68	2.33	130229.38

Table 3: Mean performance.

Sr. No	Genotypes	Days to 50% Flowering	Days to 50% Pod Initiation	Plant Height (cm)	No. of Nods /Plant	No. of Pods /Cluster	No. of Pod/Plant	Maturity (days)	N/o Primary Branches/Plant	100 Seed Weight (g)	Grain Yield (kg)
1.	SKF-7T	40.33	50.33	38.37	7.33	2.67	50.33	94.00	6.67	10.93	654.00
2.	SKF-340	42.67	54.33	52.23	9.33	3.67	50.33	92.67	4.67	8.71	845.33
3.	NRC-86	41.33	60.00	65.23	10.67	4.00	61.00	96.00	6.00	12.90	952.67
4.	SKF-Exo-142	42.33	51.67	77.23	12.00	4.67	91.67	94.67	8.33	10.61	1597.67
5.	SKF-470	35.00	45.33	70.40	11.67	4.67	74.00	83.67	8.00	7.51	1695.00
6.	SKF-2012	41.00	53.67	52.17	12.67	3.67	51.33	90.33	6.33	9.56	1398.33
7.	SKF-6125	32.00	41.33	65.67	8.33	2.67	31.00	84.67	6.00	10.00	557.00
8.	SKF-403	42.00	53.33	70.57	13.33	4.67	50.00	88.67	8.00	7.41	1285.00
9.	SKF-6017	31.33	42.33	65.77	9.67	3.67	38.00	88.33	7.67	8.74	955.00
10.	SKF-6035	31.33	41.33	62.67	10.00	2.67	40.00	86.33	5.67	9.56	1105.00
11.	SKF-206	32.00	47.67	70.63	10.67	3.67	25.33	91.00	5.33	11.02	605.00
12.	SKF-221	32.67	44.33	42.93	13.00	4.67	51.33	86.33	8.67	11.81	1550.33
13.	SKF-547	41.00	53.67	57.30	14.33	4.67	56.33	90.33	8.33	9.03	1496.67
14.	SKF-535	42.00	54.67	62.93	11.26	3.67	40.33	86.00	8.33	8.50	1154.33
15.	SKF-6128	41.67	55.67	52.20	11.33	2.67	31.00	90.00	6.33	10.36	747.67
16.	SKF-601	41.67	51.33	60.57	10.33	3.67	29.33	87.67	5.67	7.86	822.33
17.	SKF-449	44.33	54.33	55.23	10.33	3.33	26.67	88.00	5.67	9.91	604.33
18.	SKF-75-46	42.00	52.33	67.87	12.08	3.33	46.33	87.33	9.33	10.75	1347.67
19.	NRC-181	45.00	54.67	70.50	12.67	4.67	45.00	89.67	8.67	12.80	1155.00
20.	SKAF-623	32.00	41.67	72.50	12.33	4.33	48.00	84.67	6.67	9.54	1800.33
21..	SKAF-BS-6	44.67	51.33	70.67	11.33	4.67	44.67	84.67	7.67	10.25	1556.33
22.	SKAF-Exo-99	45.00	52.67	57.83	10.00	3.67	31.00	87.33	8.67	10.26	950.67
23.	JS-95-60 (Check)	31.67	41.67	40.67	10.33	2.33	26.67	88.67	8.00	11.51	1143.33
24.	SKAF-208	42.00	52.33	42.80	10.00	3.67	34.67	90.33	6.33	7.33	850.33
25.	SKAF-409	31.33	42.00	52.83	10.67	2.67	36.33	81.67	8.33	9.34	955.67
26.	SKAF-Exo131	41.33	49.67	55.27	9.33	2.67	40.33	87.33	6.33	10.69	1096.00
27.	SKAF-6038	31.33	42.00	87.17	10.33	2.33	31.33	83.33	6.33	11.11	901.00
28.	SKAF-2007	31.33	40.67	62.23	11.00	2.67	26.67	82.33	7.67	10.34	746.67
29.	SKAF-616	41.00	51.67	57.53	8.33	2.67	22.00	87.33	8.67	9.36	649.00
30.	Kuber	41.67	51.00	60.63	11.00	2.67	25.67	86.00	7.33	10.03	703.67
31.	Chamatkar	43.33	53.67	62.27	8.67	2.67	27.67	87.67	5.33	9.03	552.33
32.	JS-335 (Check)	43.00	55.67	67.63	11.33	3.67	39.00	110.00	7.33	7.48	1200.00
	Mean	38.79	49.64	60.95	10.80	3.50	41.35	88.66	7.14	9.82	1051.05
	Min	31.33	40.67	38.37	7.33	2.33	22.00	81.67	4.67	7.33	552.33
	Max	45.00	60.00	87.17	14.33	4.67	91.67	110.00	9.33	12.90	1800.33
	SE(d) ±	2.01	2.56	3.17	0.56	0.18	2.06	3.58	0.39	0.52	60.22
	C.D. at 5%	4.02	5.12	6.34	1.12	0.36	4.13	7.18	0.79	1.04	120.67
	C.V. (%)	6.34	6.31	6.36	6.34	6.28	6.11	4.95	6.72	6.47	7.02

Table 4: Genetic variability.

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)	% cont
Days to 50% Flowering	38.79	31.33	45.00	24.55	30.59	80.23	9.14	23.57	12.77	14.26	14.05
Days to 50% Pod Initiation	49.64	40.67	60.00	27.16	36.97	73.47	9.20	18.54	10.50	12.25	11.91
Plant Height (cm)	60.95	38.37	87.17	113.85	128.87	88.34	20.66	33.89	17.51	18.62	10.08
No. of Nods /Plant	10.80	7.33	14.33	2.27	2.74	82.86	2.83	26.16	13.95	15.33	11.95
No. of Pods /Cluster	3.50	2.33	4.67	0.64	0.69	93.01	1.59	45.52	22.91	23.76	9.43
No. of Pod/Plant	41.35	22.00	91.67	227.06	233.43	97.27	30.61	74.03	36.44	36.95	6.75
Maturity (days)	88.66	81.67	110.00	20.40	39.65	51.45	6.67	7.53	5.09	7.10	14.13
N/o Primary Branches/Plant	7.14	4.67	9.33	1.49	1.72	86.58	2.34	32.74	17.08	18.35	9.40
100 Seed Weight (g)	9.82	7.33	12.90	1.98	2.38	83.04	2.64	26.88	14.32	15.72	8.72
Grain Yield (kg)	1051.05	552.33	1800.33	127541	132980	95.91	720.48	68.55	33.98	34.70	3.60

CONCLUSIONS

The data of analysis of variance produced the presence of significant genetic variability among the genotype for all ten characters including seed yield. Estimates of genetic variability parameters showed that phenotypic coefficient of variation was higher than respective genotypic coefficient of variation. High GCV was recorded for character grain yield (33.98 %), number of pods per plant (36.44%) and number of pods per cluster (22.91%) respectively. This study depicted high value of heritability indicates that predominance of additive gene action and there is least influenced of environment in characters. Hence direct phenotypic selection would be followed for these traits in breeding program for develop high yielding traits. High heritability coupled with high genetic advance as percent of mean recorded for number of pods per cluster, grain yield and number of pods per plant respectively. High heritability along with high genetic advance as percentage of mean indicated that there is an additive gene action so that they are selectable traits for future breeding program.

FUTURE SCOPE

High heritability coupled with high genetic advance as percentage of mean indicated that there is an additive gene action so that they are selectable traits for future breeding program.

The genotype viz., 'SKF-623', 'SKF-470', 'SKF-Exo-142', 'SKF-BS-6' and 'SKF-121' were found high yielding based on their mean performance for seed yield per plot. Therefore these genotypes may be used in future for development of new cultivars with desirable yield contributing characters.

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Conflict of Interest. None.

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