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Genetic variability studies for morpho-physiological characters in soybean (*Glycine max* L. Merill)

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Abstract

Soybean production and productivity mainly depends upon the improved high yielding cultivars. Screening of diverse genotypes for yield and yield contributing traits is the first step in any crop improvement programme from available germplasm stock. Fifty-four soybean germplasm lines were evaluated for assessment of genetic variability among twenty morphological and physiological characters using Randomized Block Design during Kharif season, 2024 with two replications at Soybean Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (MS). The mean sum of squares due to treatments were found significant for all twenty traits among the accessions. Significant variability was recorded in mean performance for traits under study, which indicates that the germplasm lines showed high level genetic diversity to be used for further breeding programme for development of elite cultivars. The phenotypic variance values were slightly higher than the corresponding genotypic variance values for all twenty traits. High GCV & PCV were noted for average growth rate 30 DAS (74.86 and 74.89), average growth rate 60 DAS (37.79 and 37.81) and seed yield per plant (35.40 and 35.49). Whereas, moderate, for number of pods per plant (27.19 and 24.71), AGR 90DAS (22.26 and 22.46), RGR 60 DAS (19.96 and 19.99) and NAR 30 DAS (20.06 and 20.35) NAR 60 DAS (25.27 and 29.37) and NAR 60 DAS (18.57 and 24.32). All the quantitative traits under investigation showed the high Heritability with range from 63.60 (chlorophyll content) to 98.70 (number of pods per plant). Heritability of 98.70 % was maximum for number of pods per plant followed by 100 seed weight (98.70), harvest index (98.50) and leaf area 30 DAS (97.91). High h^2 (heritability) coupled with with high GA (genetic advance) was observed for number of pods per plant, AGR 30 DAS, AGR 60 DAS, AGR 90 DAS and seed yield per plant. It is showing that these traits are governed by additive gene action and there is huge scope for genetic improvement by simple selection. The variability studies indicated that the high estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for number of pods per plant and seed cotton yield per plant. Modearate phenotypic coefficient of variation and genotypic coefficient of variation were observed for days to 50% flowering chlorophyll content leaf area, AGR, RGR, and NAR. High heritability observed for the almost all the characters. The number of pods per plant, AGR, RGR and seed yield per plant per plant shows high heritability coupled with high genetic advance over mean indicating the preponderance of additive gene action in the inheritance of these traits. Genetic variability parameters were studied in fifty-four soybean genotypes raised during *kharif* 2024-2025 at Soybean Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in randomized block design with two replications. The high degree of variability observed among genotypes for different yield contributing traits could be utilized in the breeding program for the improvement of soybean.

Keywords: Genotypes, genetic variability, soybean, characterization, heritability, genetic advance

Introduction

Soybean (*Glycine max* L.) is a major oilseed crop of Fabaceae family and also known as ‘Wonder bean” and known as miracle of the 21st century’ (Bairagi *et al*. 2023; Mishraand Patidar 2023) [3, 34]. About thirty species (perennial) are reported in subgenus of glycine having valuable characters for breeder, with a center of diversity in Australia and found in different habitats *viz*. rocky outcrops, temperate etc. (Chung and Singh, 2008) [9]. Worldwide, among oilseeds, soybean is main oilseed crop due to its 25% share to the edible oil production at global level and abundant source of protein in formulated animals feed. Every year, after processing, around 85% of the soybean in the world is used as soybean meal (by product of oil extraction) and oil. Maximum oil (95%) is used in eating purposes and remaining for industry purposes like in making of soaps and biodiesel (Verma and Chandrakar 2023) [50]. The USA, Argentina, China and Brazil are top countries in production of soya (Bairagi *et al*., 2023) [3]. It has significant share as edible oil in diet of peoples of India and cultivated in Madhya Pradesh, Karnataka, Andhra Pradesh, Maharashtra, Rajasthan, and Chhattisgarh during kharif season (Bairagi *et al*., 2023) [3]. Soybean is a one important crop for prosperity of farmers in India due to enhancement in income by export of its de-oiled cake (Dhurwey *et al*., 2019) [13]. In India, Madhya Pradesh is known as soya state and has ranked first in production due to large area coverage. Low productivity and yield of it in relation may be due to unavailability of high yielding genotypes and use of their poor-quality seeds, narrow genetic base of genotypes which are used for cultivation, lack of irrigation and poor management practices (Nair *et al*., 2023) [35]. Genetic variability analyses in available genetic material or genotypes are a primary requirement for start any breeding programme of a crop and for decide selection strategy (Koraddi and Basavaraja, 2019) [29]. Both, h2 and GA are known as valuable selection parameters (Singh and Narayanan, 1997) [44]. Heritability (h2) may be dividing as broad sense (h2bs) and narrow sense (h2ns) heritability respectively (Holland *et al*., 2003) [18]. Broad sense heritability (h2bs) gives information on the genetic variation in relation to total variation (genetic plus environment) in plant population taken for study of a particular trait (Holland *et al*., 2003; Visscher *et al*., 2008) [18, 51]. GA values show the mode of gene action of quantitative characters and assists in use of appropriate techniques for crop improvement (Singh and Narayanan, 1997) [44]. Thus, values of h2 along with values of GA are more precise and fruitful in predicting the gain under selection than individual focus on the parameters for selection of different characters. The present experiment of the genetic component responding yield and quality attributing traits included for evaluation of different genotypes.

Materials and Methods The present experiment was laid out with fifty-four entries in two replications using randomized block design at Soybean Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (MS) during the Kharif season of 2024-2025. The genotypes were planted each in two rows with spacing 45 cm (between two rows) 45 cm and 5 cm (between plants). Recommended package practices were followed for healthy growth of plants.

Experimental Material

Seed of fifty-four diverse germplasm of soybean were procured Soybean Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (MS) and listed in Table 1. The data for all the characters was recorded on five plants in each replication.

Table 1: Details of germplasm accessions used in this study

Sr. No.	Name of Germplasm	Sr. No.	Name of Germplasm	Sr. No.	Name of Germplasm
1	IC 0243770	20	EC 389155	39	EC771186
2	EC0550830	21	EC0309543	40	IC24075
3	IC 0100445	22	EC389165	41	IC0620493
4	EC 0109543	23	IC 0501548	42	EC771200
5	EC 0325113	24	EC 39777	43	EC771161
6	EC 333868	25	EC771199	44	EC241778
7	IC 0501559	26	EC 0057044	45	IC0198918
8	IC 0243776	27	EC39821	46	IC0042151
9	IC 0243607	28	IC 0411903	47	IC 0021749
10	EC 0456617	29	EC 771156	48	EC0542433
11	EC 0457145	30	EC 99990	49	IC0567510
12	EC 0118307	31	EC0528655	50	EC0014425
13	EC 0294384	32	IC 0243577		Checks
14	IC 0243606	33	IC 0118482	1	JS20-94(CH)
15	EC242004	34	IC 0243091	2	JS 20-98(CH)
16	EC03251042	35	EC103154	3	JS 22-12 (CH)
17	EC 0018596	36	IC 0243755	4	JS 335(CH)
18	IC 0567496	37	EC0333881		
19	IC0243121	38	IC0024060		

Quantitative characters for recording observations

Randomly Five plants, from each replication in an accession were selected for observe data. The tagged selected individual plant observations were noted for *viz*; days to 50% flowering, days to maturity, plant height, number of pods per plant, chlorophyll content, 100 seed weight, absolute growth rate (30, 60 & 90 days after sowing), net assimilation rate (30, 60 & 90 days after sowing), relative growth rate (30, 60 & 90 days after sowing), seed yield per plant.

Statistical analysis

The mean performance selected plants were statistically analyzed for variability. To test the significance of differences among the genotypes, the ANOVA was according to Bairagi *et al*. (2023) [3] and by methods of Panse and Sukhatme (1967) [38].

Table 2: Analysis of variance for morphophysiological characters in Soybean

Sr. No.	Characters	Mean sum of squares		
		Replication (1)	Treatment (53)	Error (53)
1	Days to 50% flowering	2.08	18.62**	3.11
2	Days to maturity	2.37	18.82**	2.12
3	Plant height (cm)	2.43	23.78**	2.04
4	Chlorophyll content	0.13	39.06**	8.68
5	Number of pods per plant	0.45	163.52**	15.36
6	Leaf area (30 DAS)	0.09	0.45*	0.09
7	Leaf area (60 DAS)	0.15	1.50*	0.35
8	Leaf area (90 DAS)	0.09	0.36**	0.05
9	100 seed weight (g)	0.07	1.39**	0.09
10	Harvest Index	0.12	11.27**	1.82
11	AGR (30 DAS)	0.09	0.29**	0.04
12	AGR (60 DAS)	0.01	0.17*	0.03
13	AGR (90 DAS)	0.02	1.50*	0.30
14	NAR (30 DAS)	0.01	0.15*	0.03
15	NAR (60 DAS)	0.06	0.21*	0.04
16	NAR (90 DAS)	0.02	0.39**	0.05
17	RGR (30 DAS)	0.01	0.04*	0.02
18	RGR (60 DAS)	0.01	0.22**	0.04
19	RGR (90 DAS)	0.01	0.42**	0.05
20	Seed yield per plant (g)	0.52	14.65**	1.37

*, ** significant at 5 and 1 percent level, respectively.

Heritability and expected genetic advance

The heritability in broad sense and expected genetic advance was analyzed as described by Bairagi *et al*. (2023) [3]. The broad sense heritability estimates were measured as low (70%) suggested by Robinson (1949) [40].

Results and Discussion

Mean performance and range of different characters

The analysis of variance for fourteen characters studied is presented in. The mean sum of squares due to treatments were found highly significant for all the characters studied. Which reveals significant differences among the germplasm lines studied for all the characters studied.

The magnitude of variability was in decreasing sequence for remaining traits *viz*., Plant height (cm), days to 50% flowering, days to maturity, 100 seed weight (gm), leaf area and harvest index. These findings are supported by Jain *et al*., (2017) [20]; Broyles *et al*., (2014) [6]; Khan *et al*., (2022) [27] and Gilles *et al*., (2022) [16]. Mean performance that having significant variability for all the nine traits shows that the genotypes have enough exploitable level of genetic variability to be utilized for further breeding of suitable cultivars or pre-breeding lines (James *et al*., 2015; Zhang and Boahen, 2010) [22, 52]. These variations in mean values of genotypes might come from variations either in genetic or environmental factor under (Roth *et al*., 2020) [41].

The germplasm line IC 198918 recorded maximum 46 days to 50% flowering, whereas minimum of 32 days were noted in EC 528655. The mean for days to 50% flowering was 38.6 days. The check JS 335 recorded maximum 105 days to attain maturity, whereas minimum of 93 days to maturity were noted in EC 0528655. The mean for days to maturity was 98.05 days. The germplasm line IC 0243606 recorded maximum chlorophyll content of 47.55, whereas lowest chlorophyll content of 39.47 was recorded in the germplasm line IC 0100445. The germplasm lines EC 39821 and IC 0411903 recorded maximum number of pods per plant (46), whereas minimum of 13 number of pods per plant were recorded in germplasm line EC 241778.

At 30 DAS, the mean value was 4.65 (dm^2) with range of 3.85 to 5.55 dm^2. The germplasm IC0243606 recorded significantly highest leaf area (5.55dm^2). While the germplasm lines EC0057044 and EC39821 recorded lowest leaf area (3.85 dm^2). At 60 DAS, the leaf area ranged from 8.10 to 10.60 (dm^2) With mean leaf area of 9.74 dm^2. The germplasm line IC0411903 recorded significantly highest leaf area (10.60 dm^2). While the germplasm IC0100445, recorded lowest leaf area (8.10 dm^2). At 90 DAS, the mean leaf area recorded was (4.29dm^2). It ranged from 3.25 to 5.35 dm^2. The germplasm EC0118307 observed highest for leaf area /plant (5.35). While, the lowest value for leaf area recorded in germplasm EC389165 (dm^2).

At 30 DAS, the mean dry matter ranged from 3.79g to 5.09g with mean of 4.43g. The germplasm IC 0021749 recorded significantly highest dry matter 5.09g. While the genotype EC0325113 recorded lowest dry matter 3.79g. At 60 DAS, the mean dry matter varied from range 12.72 to 24.57 g with mean value of 17.94 g. The germplasm line IC0567496 observed significantly highest value of 24.57g. While, the germplasm EC 333868 observed lowest mean dry matter 12.72 g. At 90 DAS, the mean dry matter varied from 35.48 to 57.92 g with mean of 47.25 g. The germplasm IC0243606 recorded significantly highest dry matter i.e. 49.60 g while the germplasm IC0567496 recorded lowest dry matter 31.20 g.

The range for 100 seed weight varied from 9.25g to 12.61g with mean value 12.85g. The germplasm EC0542433 observed highest mean value of 100 seed weight (12.61g), Whereas the germplasm EC0309543 recorded lowest 100 seed weight (9.25g). The highest harvest index was observed in germplasm IC 24075 (46.55 %) whereas, lowest was recorded in germplasm EC 0550830 (35.30%) respectively. The mean value of harvest index was 40.63 %.

The highest seed yield per plant was recorded in germplasm IC0411903 (12.36 g). Whereas, the lowest seed yield per plant was observed in the germplasm EC0542433 3.45 (g). The mean value for seed yield per plant was 7.63 g.

At 30 DAS, the mean absolute growth rate ranged from 0.068 to 1.388 with a mean of 0.509. The germplasm line EC 771199 recorded significantly highest absolute growth rate (1.388) while lowest absolute growth rate (0.068) was recorded by the germplasm line EC 0550830. At 60 DAS, the absolute growth rate ranged from 0.273 to 2.005 with a mean of 0.787. The germplasm EC771199 recorded significantly highest absolute growth rate (2.005), while the germplasm lines EC0109543 and EC0325113 recorded lowest absolute growth rate of (0.273). At 90 DAS, the absolute growth rate ranged from 0.735 to 2.064. The germplasm EC771161 recorded significantly highest absolute growth rate (2.064). While the germplasm EC 0457145 recorded lowest absolute growth rate (0.735) with the mean value 1.254.

At 30 DAS, Maximum relative growth rate recorded by germplasm line IC0021749 (0.059), while minimum relative growth rate recorded in germplasm line IC0501559 (0.038) with the mean value of (0.050). At 60 DAS, minimum value of relative growth rate was recorded in the germplasm line EC 333868 (0.041), however maximum relative growth rate was observed in germplasm line EC 0333881 (0.098). The mean value for 60 DAS, relative growth rate is (0.098). At 90 DAS, the mean relative growth rate ranged from 0.015 to 0.046 with a mean value of (0.032). The check JS 335 recorded significantly highest relative growth rate of (0.046), whereas the germplasm line EC 0325113 recorded lowest relative growth rate (0.015).

At 30 DAS, the mean net assimilation rate ranged from 0.031 to 0.059 with a mean of 0.043. The germplasm EC389165 and IC0411903 recorded significantly maximum net assimilation rate (0.059), while the germplasm EC241778 and EC0014425 recorded minimum net assimilation rate (0.031). At 60 DAS, the highest net assimilation observed in germplasm line EC 0109543 (0.262), whereas lowest net assimilation was observed in germplasm line EC 389155 (0.069). The mean net assimilation rate at 60 DAS was (0.116). At 90 DAS, the net assimilation rate ranged from 0.133 to 0.387 with a mean value of 0.205. The germplasm line IC 0243770 recorded significantly highest net assimilation rate of (0.387), whereas the germplasm line EC771200 recorded lowest net assimilation rate (0.133).

Genotypic (GCV%) and phenotypic coefficient of variation (PCV%): Results of yield and related characters for GCV & PCV in Table 3 reported that the values of PCV were more than the values of GCV, which showing that GCV and PCV could express variability among genotypes. Similar results were found by Neelima *et al*., 2018 [36]; Shilpashree *et al*., 2021 [42] and Bairagi *et al*., 2023 [3]. The high genotypic and phenotypic coefficient of variation was observed for AGR 30 DAS (74.86 and 74.89) followed by seed yield per plant (gm) (35.40 and 35.49), AGR 60 DAS (37.79 and 37.81), NAR 60 DAS (25.27 and 29.37), number of pods per plant (27.19 and 24.71) and harvest index (5.82 and 7.86) respectively. The above results indicated the presence of substantial amount of genetic variability for the traits, which exhibited less influence of environment on the expression of these traits. Similar results for different characters have also been reported by Drabo *et al*., (2013) [14]; Machado *et al*., (2017) [31]; Kasper *et al*., (2019) [25]; Zida *et al*., (2021) [53] and Bairagi *et al*., 2023 [3].

Whereas, moderate GCV & PCV were recorded for days to 50% flowering (10.27 and 10.28), chlorophyll content (9.87 and 12.37), RGR 60DAS (19.96 and 19.99) and leaf area 30 DAS (10.12 and 10.23). Low GCV & PCV were recorded for chlorophyll content (9.87 and 12.37), RGR 30 DAS (8.81 and 8.96), 100 seed weight (7.68 and 7.73), harvest index (5.82 and 7.86), plant height (4.53 and 4.93), leaf area 60 DAS (4.97 and 5.28) and days to maturity (3.27 and 3.28). The results are in accordance with the reports of King and Purcell, (2001) [28]; Aditya *et al*., (2011) [1]; Baraskar *et al*., (2014) [4]; Thai *et al*., (2019) [48] and Bairgi *et al*. (2023).

Heritability (%) in broad sense

According to Lush (1940) [30] heritability may be grouped in broad sense and narrow sense. The estimation of heritability in broad sense reported that all eight traits depicted the high heritability (Table 3). It varied from 98.70 (100 seed weight) to 63.60 (chlorophyll content). The character, 100 seed weight revealed maximum (98.70 %) heritability followed by harvest index 98.50 %), number of pods per plants (98.41), leaf area 30 DAS (97.90), seed yield per plant (95.55), days to maturity (92.30), days to 50% flowering (91.25). Visscher *et al*., 2008 [51]; Aditya *et al*., (2011) [1]; Shilpashree *et al*., (2021) [42] and Bairagi *et al*. (2023) [3] found in support with current finding. High heritability indicated that expression of character namely 100 seed weight, number of pods per plants, leaf area, RGR, plant height, days to 50% flowering, harvest index, seed yield per plant (gm), days to maturity and number of pods per plant was least influenced by the environment.

Table 3: Parameter of genetic variability parameters for morphophysiological characters in Soybean

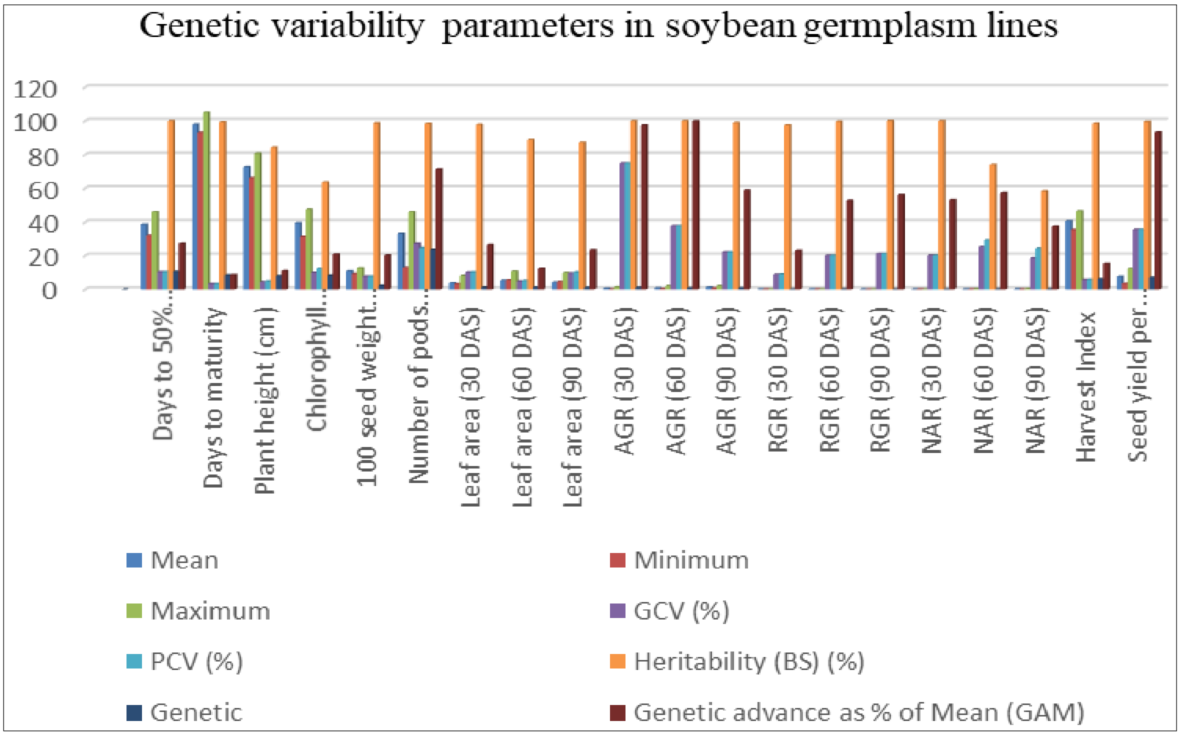
Sr. No.	Characters	Mean	Minimum	Maximum	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic advance (GA)	Genetic advance as % of Mean (GAM)	Genotypic Variance (GV)	Phenotypic Variance (PV)
1	Days to 50% flowering	38.6	32	46	10.27	10.28	99.90	10.47	27.12	15.74	15.75
2	Days to maturity	98.05	93	105	3.27	3.28	99.30	8.43	8.60	10.28	10.35
3	Plant height (cm)	72.70	66.20	80.75	4.53	4.93	84.21	7.98	10.97	10.87	12.91
4	Chlorophyll content	39.47	31.37	47.55	9.87	12.37	63.60	8.21	20.79	15.18	23.87
5	100 seed weight (g)	10.85	9.25	12.61	7.68	7.73	98.70	2.18	20.14	0.69	0.70
6	Number of pods per plant	33.12	13.00	46.00	27.19	24.71	98.41	23.58	71.20	81.10	82.42
7	Leaf area (30 DAS)	3.85	3.25	8.10	10.12	10.23	97.90	1.23	26.45	0.22	0.22
8	Leaf area (60 DAS)	5.35	5.55	10.60	4.97	5.28	88.90	1.21	12.39	0.23	0.26
9	Leaf area (90 DAS)	4.29	4.65	9.74	9.52	10.21	87.00	1.00	23.43	0.16	0.19
10	AGR (30 DAS)	0.50	0.06	1.38	74.86	74.89	99.91	1.00	97.56	0.14	0.14
11	AGR (60 DAS)	0.78	0.27	2.00	37.79	37.81	99.91	0.78	99.77	0.08	0.08
12	AGR (90 DAS)	1.25	0.73	2.06	22.26	22.26	98.91	0.73	58.78	0.07	0.07
13	RGR (30 DAS)	0.05	0.04	0.05	8.81	8.96	97.60	0.01	23.08	0.02	0.02
14	RGR (60 DAS)	0.05	0.04	0.09	19.96	19.99	99.60	0.03	52.60	0.05	0.07
15	RGR (90 DAS)	0.03	0.01	0.04	21.28	21.28	100.00	0.02	56.18	0.04	0.08
16	NAR (30 DAS)	0.043	0.031	0.059	20.06	20.06	99.90	0.02	52.93	0.05	0.03
17	NAR (60 DAS)	0.12	0.07	0.26	25.27	29.37	74.00	0.06	57.41	0.04	0.06
18	NAR (90 DAS)	0.21	0.13	0.38	18.57	24.32	58.30	0.07	37.46	0.01	0.02
19	Harvest Index	40.63	35.30	46.55	5.82	5.86	98.50	6.21	15.26	5.59	5.68
20	Seed yield per plant (g)	7.63	3.45	12.36	35.40	35.49	99.5	7.11	93.22	7.30	7.34

Genetic advance as percent of mean

Genetic advance as percentage of mean was analyzed to know the genetic gain and presented in Table 3. The highest genetic advance as percentage of mean was noticed for AGR 60 DAS (99.77) followed by AGR 60 DAS (97.56), seed yield per plant (93.22), number of pods per plants (71.20), AGR 90 DAS (58.78), RGR 90 DAS (56.18), NAR 60 DAS (57.41), days to 50% flowering (27.12) and RGR 30 DAS (23.08). Similar findings were reported by Pimentel *et al*., 2005 [39]. Medium genetic advance as percentage of mean were expressed by plant height (10.97), leaf area 60 DAS (12.39) and harvest index (15.26).

Heritability and genetic advance are crucial genetic parameters for selection. The analysis of heritability may be used for the prediction of genetic gain, which shows the genetic improvement would be possible through selection of best genotype. Genetic advance is the improvement in the mean genetic value of selected plants over the parental population. Values of heritability for traits are valid for only one generation, genetic advance vary from generation to generation. Data of heritability in broad sense and genetic advance as percentage of mean of every character should always be considered and interpreted simultaneously to know the role of additive gene action (Holland *et al*., 2003 and Visscher *et al*., 2008) [18, 51]. Heritability and genetic advance were high for seed yield per plant followed by number of pods per plants, leaf area, RGR, AGR. NAR and days to 50% flowering. Jalata *et al*., 2010 [21]; Pimentel *et al*., 2005 [39]; Aditya *et al*., (2011) [1] for number of pods per plant; Shilpashree *et al*., (2021) [42] for plant height and number of pods per plant, Bairagi *et al*., (2023) [3] for number of pods per plants, plant height and primary branches per plant in number found in support with our finding.

Mass selection or pure line selection would be effective for days to 50% flowering, number of pods per plants, leaf area and seed yield per plant because these traits are showing high heritability and high genetic advance (Aditya *et al*., 2011; Barcchiya *et al*., 2018; Jandong *et al*., 2020) [1, 5, 23]. These traits indicated the presence of intermediate expression for both additive gene effects. Whereas, high heritability with low GA as percentage of mean were expressed by days to maturity and plant height. Similar results were also found by Kavera, (2008) [26] in groundnut and Malik *et al*., (2006) [32] in soybean respectively.



Conclusion

Significant amount of variation is found in mean performance of all the traits which indicates that the genotypes have significant amount of genetic variability. Which may be utilized in selection of elite genotypes for hybridization. Which will be helpful for isolation of transgressive segregants in variety development of soybean. High heritability and high genetic advance for seed yield per plant, number of pods per plants, leaf area, RGR, AGR, NAR and days to 50% flowering indicated the presence of additive gene action and less effect of environment in governing of these characters. So, simple selection would be effective for these traits for soybean improvement. The grain yield per plant (gm) was maximum for IC 0411903 (12.36 g) followed by EC 39821 (12.31g) and EC 39777 (12.11g) respectively, which indicated that these genotypes should be considered for hybridization programme during development of high yielding varieties in soybean.

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