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Genetic variability analysis in soybean genotypes based on yield and yield contributing traits

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Abstract
In the present experiment fifty soybean genotypes including five checks were evaluated for fourteen quantitative characters. Analysis of variance indicated that mean sum of square due to genotypes were found significant for all the traits. The phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV) indicating the influence of environment in the expression of the traits under study. The high values of PCV and GCV were observed for number of seeds per plant followed by seed yield per plant, biological yield, pod bearing length, number of pods per plant and plant height. Days to maturity exhibited low GCV and PCV. High estimate of heritability coupled with high genetic advance as percent of mean were observed for number of seeds per plant, biological yield, pod bearing length, seed yield per plant, number of pods per plant, plant height and 100 seed weight.

Keywords: Soybean, genetic variability, heritability, genetic gain

Introduction
Soybean [*Glycine max* (L.) Merrill] is an important oilseed crop in the world also called as "Golden bean" or "Miracle Crop" of 20th century. Soybean is a self-pollinated crop (2n=2x=40) and belongs to family Fabaceae. Soybean plant is well known for its rich nutrition as it contains 38-42% of high-quality protein and 17-21% oil, comprising 85% polyunsaturated fatty acid with two essential fatty acids. Soybean protein is rich in valuable amino acid lysine (5%) in which most cereals are deficient. Soybean meal is a valuable ingredient in formulated feeds for poultry and fish. Considering the nutritional important of vegetable soybean, efforts are being made to increase the production of soybean varieties. In order to increase yield, assessment of genetic variability is prerequisite since it is the source of variation and perform selection in any breeding programme. However, when it is considered along with heritability becomes more valuable to observe response to selection than the heritability estimates alone. Present of large amount of variability in any genetic material indicates the scope for further improvement of the crop (Baig *et al*., 2018) [1]. Hence, the present investigation was carried out to study genetic variability for quantitative traits in soybean germplasm. The important genetic variability parameters include heritability (h2), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and expected genetic advance.

Materials and Methods
The present investigation was laid out in a Randomized Block Design with two replications during *kharif* 2021 at the experimental farm of AICRP on soybean, Indira Gandhi Krishi Vishwavidyalaya, Raipur. The experimental material consists of fifty soybean germplasm lines including five checks *viz*., CG Soya-1, RSC 10-46, JS335, JS 97-52, NRC 37. The observations were recorded for 14 different characters, *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod bearing length, number of seeds per pod, number of seeds per plant, 100 seed weight (g), biological yield, seed yield per plant, harvest index, oil content (%) and protein content (%). The genotypic and phenotypic coefficient of variation were estimated as per the formula suggested by Sivasubramanian and Menon (1973) [20]. Heritability in broad sense was calculated as per the formula suggested by Burton (1952) [4]. The expected genetic advance was estimated as suggested by Johnson *et al.* (1955) [9].

Result and Discussion

The analysis of variance was undertaken for all the characters under study and presented in Table 1. The analyzed result revealed that mean sum of square due to genotypes were found significant for all the traits under study, which indicated the presence of high phenotypic variability among the genetic materials. Similar results were recorded by Chandrawat *et al*. (2017) [6], Joshi *et al*. (2017), Neelima *et al*. (2018) [16], Pawar *et al*. (2020) [17] and Sonkamble *et al*. (2020) [21].

The estimate of component of variation including genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for all the traits under study are presented in Table 2. The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation indicated that the values of PCV were higher than GCV for all the characters, indicating the influence of environment in the expression of the characters studied. Narrow differences observed between the PCV and GCV in certain cases indicated that these characters were less influence by the environment. The similar results were confirmed by Bhakuni *et al*. (2017) [3], Neelima *et al*. (2018) [16], Jain *et al*. (2018) [8] and Pawar *et al*. (2020) [17].

Highest GCV and PCV values were observed for number of seeds per plant followed by seed yield per plant, biological yield, pod bearing length, number of pods per plant and plant height. The Similar results for the characters namely plant height, seed yield per plant and number of pods per plant were obtained by Chandel *et al*. (2013) [5], Mahbub *et al*. (2015) [15] and Neelima *et al*. (2018) [16]. Koraddi and Baswaraja (2019) [12] and Ghodrati (2013).

Low GCV and PCV values were observed for number of seeds per pod, days to maturity, protein content, days to 50% flowering and oil content. Similar results was reported by Chandrawat *et al*. (2017) [6] for days to 50% flowering and for days to maturity. Chandel *et al*. (2013) [5] and Puspa Reni *et al*. (2013) were reported similar results for days to maturity, oil and protein content.

The heritability estimates were high for all the characters under study (Table 2), which ranges from 61.8% to 99.08%. Highest heritability values were observed for protein content, 100 seed weight, oil content, days to maturity, number of seeds per plant, plant height, days to 50% flowering, pod bearing length, number of pods per plant, biological yield and seed yield per plant. Kumar *et al*. (2014) reported high heritability for the characters biological yield and seed yield per plant. Pawar *et al*. (2020) [17] observed the similar results for the number of pods per plant, plant height and days to 50% flowering. While moderate heritability was observed for the characters *viz*., number of primary branches per plant, number of seeds per pod and harvest index which is found similar with the finding of Kuswantoro *et al*. (2018) [14] for number of branches per plant.

Table 1: Analysis of variance for seed yield and its traits in Soybean germplasm

Sl. No.	Characters	Replication	Treatment	Error
	Degree of freedom	1	49	49
1	Days to 50% flowering	6.76	18.09**	1.025
2	Days to maturity	0.04	43.63**	1.162
3	Plant height (cm)	35.153	514.10**	27.034
4	Number of primary branches per plant	0.661	1.759**	0.316
5	Number of pods per plant	89.586	982.01**	64.897
6	Pod bearing length	23.99	450.64**	26.92
7	Number of seeds per pod	0.002	0.012**	0.002
8	Number of seeds per plant	8.988	6847.98**	205.157
9	Hundred seed weight (g)	0.049	6.93**	0.06
10	Biological yield (g)	0.072	408.01**	27.295
11	Seed yield per plant (g)	1.316	74.23**	10.503
12	Harvest index (%)	53.159	117.51**	27.743
13	Oil content (%)	0.038	4.654**	0.063
14	Protein content (%)	0.013	8.09**	0.038

* Significant at 5%, **Significant at 1%

Table 2: Estimates of variability parameters for fourteen different characters of soybean genotypes

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	h^2 %	GA	GA as percent of mean (%)
			Max	Min					
1	Days to 50% flowering	43.96	52	37.5	6.65	7.03	89.28	5.69	12.94
2	Days to maturity	96.1	108.5	83.5	4.79	4.92	94.81	9.24	9.62
3	Plant height (cm)	53.37	123.5	33.665	29.24	30.82	90.01	30.49	57.14
4	Number of primary branches per plant	4.29	6.83	2.5	19.81	23.75	69.56	1.46	34.03
5	Number of pods per plant	71.07	117.16	17	30.13	32.19	87.60	41.29	58.09
6	Pod bearing length	45.31	109.83	25.33	32.12	34.10	88.73	28.24	62.33
7	Number of seeds per pod	2.437	2.58	2.25	2.82	3.42	68.12	0.12	4.79
8	Number of seeds per plant	144.61	314	26.83	39.85	41.06	94.18	115.22	79.67
9	100 seed weight (g)	12.33	15.76	5.82	15.04	15.17	98.28	3.79	30.71
10	Biological yield (g)	40.01	77.66	12.5	34.18	36.87	87.46	26.58	66.43
11	Seed yield per plant	16.52	28.5	4.33	34.26	39.39	75.21	10.08	61.03
12	Harvest index (%)	42.79	58.23	21.83	15.66	19.92	61.80	10.85	25.36
13	Oil content (%)	19.18	22.45	17.20	7.89	8.00	97.32	3.08	16.05
14	Protein content (%)	38.52	41.17	32.80	5.21	5.23	99.08	4.11	10.68

High genetic advance as percent of mean was observed for the characters viz., number of seeds per plant followed by biological yield, pod bearing length, seed yield per plant, number of pods per plant, plant height, number of primary branches per plant, 100 seed weight and harvest index while moderate genetic advance as percent of mean was recorded for oil content, days to 50% flowering and protein content. Low genetic advance as percent of mean was observed for number of seeds per pod and days to maturity. High heritability coupled with high genetic advance as percent of mean was observed for number of seeds per plant, biological yield, pod bearing length, seed yield per plant, number of pods per plant, plant height and 100 seed weight indicating the presence of additive gene action, therefore these traits can be used for direct selection in yield improvement program. This findings are accordance with Baraskar *et al*. (2014), Chandrawat *et al*. (2017) [6] and Joshi *et al*. (2018) [10] for plant height, number of pods per plant and seed yield per plant. Kumar *et al*. (2018) [13] recorded the similar result for biological yield, seed yield per plant, number of pods per plant and 100 seed weight. Chandel *et al.* (2013) [5] observed similar findings for pods per plant. High heritability coupled with moderate genetic advance as percent of mean was observed for oil content, days to 50% flowering and protein content. Similar results were obtained by khan *et al*. (2011) [11] and Chandel *et al*. (2013) [5] for days to maturity. Results indicate that these characters were less influence by environment and governed by both additive and non-additive gene action. The characters days to maturity showed high heritability with low genetic advance as percent of mean, suggesting that the expression of these character may be due to non-additive gene action. So selection for this traits were not rewarding in yield improvement program. Similar results were obtained by Neelima *et al*. (2018) [16] and Vart *et al*. (2005) [22].

High genetic advance was observed for number of seeds per plant followed by number of pods per plant, plant height, pod bearing length, biological yield similar results was observed by Pawar *et al.* (2020) [17]. Koraddi and Baswaraja (2019) [12] also recorded the high genetic advance for plant height and number of pods per plant. The genetic advance was found to be moderate for harvest index, seed yield per plant, days to maturity and days to 50% flowering. The same result was reported by Mahbub *et al.* (2015) [15] for moderate heritability in days to 50% flowering and for days to maturity. While low genetic advance was observed with the traits like number of seeds per pod followed by number of primary branches per plant, oil content, 100 seed weight and protein content. The similar results were reported by Ramteke *et al.* (2010) [19], Chandel *et al.* (2013) [5] and Mahbub *et al*. (2015) [15] were comparable with the findings of present investigation.

Conclusion

Analysis of variance revealed the presence of huge amount of phenotypic variability among the materials under study. The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. High estimates of heritability coupled with high genetic advance as percentage of mean were observed for number of seeds per plant, biological yield, pod bearing length, seed yield per plant, number of pods per plant, plant height and 100 seed weight, indicating the present of additive gene action and thus selection could be effective for these traits in any crop improvement programme.

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