

GENETIC STUDIES OF F₂ POPULATION IN SOYBEAN

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ABSTRACT

Genetic study was conducted on 3 F₂ crosses of soybean (JS 335 × EC 34-01, JS 335 × EC 53-88-28, and JS 335 × *Glycine soja*) including one interspecific cross. The crosses along with parents were raised during *kharif* 2018-19 and data were recorded on seven quantitative characters *viz.*, days to first flower, plant height (cm), days to maturity, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g) and seed yield plant⁻¹ (g). Genotypic coefficient of variation was high for all characters except for days to first flower, days to maturity and 100 seed weight, where moderate to low GCV was recorded. The broad sense heritability was high for all characters under study except for days to maturity only in one cross where moderate heritability was recorded. The expected genetic advance among all F₂ population indicated significant progress under selection for plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹. Superior 30 individual plants were identified on the basis of high mean, GCV, heritability and genetic advance for economics traits *viz.*, seed yield plant⁻¹, number of pods plant⁻¹ and plant height. All crosses reported high mean, genotypic coefficient of variation, heritability and genetic advance as per cent of mean for plant height, number of branches plant⁻¹, number of pods plant⁻¹ and yield plant⁻¹, and hence would be useful for obtaining potential segregants with maximum number of branches plant⁻¹, plant height, number of pods plant⁻¹ and seed yield plant⁻¹. So, 30 single plants were selected on basis of these four traits at 5% selection intensity, which were suggested to be carried forward by plant to row method for exploiting improvement in the selected material.

(Key words: Soybean, genetic study, F₂ population, GCV, PCV, heritability, genetic advance, interspecific cross)

INTRODUCTION

Soybean being self-pollinated crop, naturally existing variation may not be sufficient to develop new varieties possessing different desirable characters. Due to autogamous nature of soybean, hybridization is difficult job but still it is cheap and effective source in creation of variability by using available germplasm. Hybridization leads to recombine the various desirable traits in one, followed by selection. Utilization of wild species for improving their cultivated counterparts is steadily increasing in various crops (Harlan, 1976). Exploitation of the wild progenitors is the most reasonable approach since a cultigens and its wild progenitor are genetically members of the same species and gene transfer between them is a relatively simple task.

An important source of genetic diversity that has been employed effectively in a variety of breeding programmes is that provided by wild relatives of crop plants for gene exchange with the soybean and therefore potentially useful for broadening the germplasm base of the crop.

Preliminary investigations have shown that the wild species carry resistance to diseases such as soybean rust, root rot, color rot, yellow mosaic virus and powdery mildew. Physiological traits exhibited by wild material such as drought tolerance, salt tolerance and day neutrality also may be of potential use (Hymowitz *et al.*, 1977). It is very important to orient the soybean breeding programme to develop new varieties with high yield potential, wider adaptability, disease resistance and high oil content. Presence of variability is the prerequisite for crop improvement and segregating generation obtained by hybridization between distant parents is one of the popular sources of increasing variability and its assessment is one of important programmes. Lande *et al.* (2018) and Kankal *et al.* (2018) in F₂ generation provide an active breeding material from which desirable plants may be selected. There have been varying reports about the reliability of early generation selection. Therefore, present study was planned to genetic studies of F₂ population in soybean.

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MATERIALS AND METHODS

This experiment was conducted during year 2018-19 at the Research Farm of Agricultural Botany section, College of Agriculture, Nagpur. The experimental material consists of three F_2 crosses selected on the basis of yield and its contributing characters and their four parents *viz.*, JS 335, EC 34-01, EC 53-88-28 and *Glycine soja*. The present research work is the continuation of previous F_1 study carried out during *kharif* 2017. The experimental material sown in non-replicated with ten rows having twenty plants each of F_2 population and one row of each parent. The data recorded on each and every plant of F_2 and five plants of parents on seven quantitative characters *viz.*, days to first flower, plant height (cm), days to maturity, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g) and seed yield plant⁻¹(g). Estimation of genetic parameter carried out as per Burton (1953), Allard (1960) and Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Data regarding variability, heritability and genetic advance estimated for seven quantitative traits of three F_2 crosses are presented in table 1. Days to first flower showed low variability as low values were reported for genotypic coefficient of variation and phenotypic coefficient of variation. Low difference between genotypic coefficient of variation and phenotypic coefficient of variation indicates that this character is least influenced by the environment. Neelima *et al.* (2018) and Shrivastava *et al.* (2018) also observed low variability for days to flower in their studies. High heritability with moderate genetic advance as per cent of mean was indicating less influenced of environment but governed by both additive and non additive gene action. Ali *et al.* (2016), Ekka and Lal (2016) and Shrivastava *et al.* (2018) were also reported high heritability with moderate genetic advance as per cent of mean in their studies. Cross JS 335 × EC 53-88-28 showed high heritability accompanied with low genetic advance as per cent of mean indicating that this character governed by the non additive gene action and resemblance due to influence of environment. Aditya *et al.* (2011) and Sana *et al.* (2017) also reported similar results and concluded ineffectiveness of selection for days to first flower in F_2 generation of soybean.

As shown in the table 1, high F_2 variance, GCV, PCV, heritability and genetic advance indicating effectiveness of selection for plant height in the crosses. Low difference between the GCV and PCV indicates least influence of environment. High heritability coupled with high genetic advance indicating the predominance of additive gene action. This suggests the amenability of plant height through selection. Humstoe *et al.* (2017), Neelima *et al.* (2018), Santoshkumar *et al.* (2018) and Shrivastava *et al.* (2018) also reported high F_2 variance, GCV, PCV, heritability and genetic advance indicating effectiveness of selection for plant height.

Genotypic coefficient of variation and phenotypic coefficient of variation for days to maturity were low for all the crosses. F_2 variances calculated varied from low to high among the crosses. Shrivastava *et al.* (2018), Santoskumar *et al.* (2018), Neelima *et al.* (2018) and Mesfin (2018) also reported low GCV and PCV for days to maturity. Low heritability coupled with low genetic advance as per cent of mean in certain cross which was in accordance with Lyimo *et al.* (2017), whereas high heritability coupled with moderate to low genetic advance as per cent of mean also reported in some crosses. Similar results were reported by Ali *et al.* (2016), Chandrawat *et al.* (2017), Desissa (2017) and Shrivastava *et al.* (2018). They showed significant role of non-additive gene action and significant role of environment influencing this character. Hence, selection is not effective for early maturing plant in F_2 generation.

All the crosses exhibited high GCV, PCV, heritability and genetic advance for number of branches plant⁻¹. This indicates that there is a lesser influence of environment and exhibits additive gene action in the expression of this character which is amenable for selection. Chandrawat *et al.* (2017), Humstoe *et al.* (2017), Mesfin (2018) and Neelima *et al.* (2018) also observed high GCV, PCV, heritability and genetic advance for number of branches plant⁻¹.

Highest GCV and PCV indicated the existence of substantial variability for number of pods plant⁻¹. Low differences between PCV and GCV for this trait indicated the lower influence of environment and reflect on reliability of selection based on phenotypic performance. High heritability coupled with high genetic advance as per cent mean was observed indicates the lesser influence of environment in expression of this characters and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for this character would be effective. Similar findings of high GCV, PCV, heritability and genetic advance for number of pods plant⁻¹ reported by Chandrawat *et al.* (2017), Lyimo *et al.* (2017), Humstoe *et al.* (2017), Shrivastava *et al.* (2018) and Neelima *et al.* (2018).

Moderate values of GCV and PCV indicate that there was presence of substantial variation for 100 seed weight. Minimum difference between GCV and PCV showed least influence of environment on this character. Hakim *et al.* (2014), Ekka and Lal (2016), Lyimo *et al.* (2017), and Santoskumar *et al.* (2018) also reported moderate values of GCV and PCV for this trait. High heritability coupled with high genetic advance as per cent of mean recorded in all of these crosses indicates the prevalence of additive gene action in their inheritance, since amenable for the simple selection by visual means. Similar findings were also observed by Mehta, (2016), Chandrawat *et al.* (2017), Humstoe *et al.* (2017), Neelima *et al.* (2018), and Shrivastava *et al.* (2018). They had also reported high heritability and genetic advance which were supported to the present finding.

Highest genotypic coefficient of variation and heritability coupled with high genetic advance as per cent

Table 1. Estimation of genetic parameters of each F₂ population of soybean

Cross No.	Parameters	Days to first flower	Plant height (cm)	Days to maturity	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)
C1	Mean	44.23	44.17	102.47	4.38	56.62	9.76	10.82
	Range	35-56(21)	21-71 (50)	95-119 (24)	2-8 (6)	16-79 (63)	6.9-14.2 (7.3)	3.3-15.9 (12.6)
	VF ₂	14.55	119.90	32.86	2.27	258.21	3.61	10.24
	GCV (%)	8.15	24.04	5.39	32.86	27.67	18.92	29.13
	PCV (%)	8.62	24.79	5.59	34.40	28.38	19.46	29.59
	Heritability (%)	89.3	93.98	92.85	91.21	95.01	94.53	96.90
	GA	7.02	21.20	10.96	2.83	31.45	3.70	6.39
	GAM	15.88	48.00	10.70	64.64	55.55	37.90	59.08
	Mean	44.48	34.88	94.08	3.92	49.13	9.72	9.74
	Range	39-48(9)	14-63 (49)	88-97 (9)	2-6 (4)	10-74 (64)	5.8-13.3 (7.5)	2.8-16.4 (13.6)
C2	VF ₂	6.46	140.58	5.67	2.04	288.73	3.01	14.30
	GCV (%)	5.17	32.56	1.47	34.08	33.66	17.56	37.58
	PCV (%)	5.71	33.99	2.53	36.50	34.58	17.86	38.82
	Heritability (%)	81.8	91.78	33.65	87.16	94.74	96.69	93.71
	GA	4.28	22.42	1.65	2.57	33.16	3.46	7.30
	GAM	9.63	64.26	1.75	65.53	67.49	35.57	74.93
	Mean	46.37	32.44	95.15	4.73	51.87	8.73	9.38
	Range	41-57 (16)	20-46 (26)	91-103 (12)	2-7 (5)	13-68 (55)	5.8-11.4 (5.6)	2.1-15.3 (13.2)
	VF ₂	15.73	64.02	10.13	1.85	219.57	1.50	10.4
	GCV (%)	8.31	22.38	3.01	26.72	27.34	13.87	33.42
C3	PCV (%)	8.55	24.66	3.35	28.73	28.57	14.02	33.78
	Heritability (%)	94.44	82.33	80.76	86.47	91.60	97.93	97.85
	GA	7.71	13.57	5.30	2.42	27.96	2.47	6.39
	GAM	16.64	41.83	5.57	51.18	53.91	28.28	68.10

C1= JS 335 × EC 34-01

C2= JS 335 × EC 53-88-28

C3= JS 335 × *Glycine soja*

Table 2. List of superior individual plant selected from three F₂ crosses

Sr. No.	Single plant selected in F₂	Seed yield plant⁻¹ (g)	Number of pods plant⁻¹	Number of branches plant⁻¹	Plant height (cm)
1.	C1-47	15.9	76	6	43
2.	C1-17	15.3	66	5	44
3.	C1-30	15.2	79	6	51
4.	C1-21	15.2	76	8	46
5.	C1-57	14.9	76	5	45
6.	C1-51	14.9	58	6	58
7.	C1-45	14.8	72	6	34
8.	C1-53	14.8	62	5	45
9.	C1-7	14.7	67	5	55
10.	C1-41	14.4	74	6	52
11.	C2-11	16.4	69	6	47
12.	C2-36	15.2	74	5	36
13.	C2-44	15.1	74	5	39
14.	C2-51	15.1	74	5	63
15.	C2-21	14.9	69	5	26
16.	C2-25	14.8	61	6	47
17.	C2-14	14.6	71	6	36
18.	C2-41	14.5	61	6	47
19.	C2-7	13.9	74	6	44
20.	C2-16	13.8	62	3	26
21.	C3-38	15.3	66	7	43
22.	C3-31	14.2	68	6	41
23.	C3-49	13.8	65	6	40
24.	C3-30	13.3	61	6	32
25.	C3-36	13.2	63	5	42
26.	C3-42	13.2	65	5	39
27.	C3-33	12.9	61	6	46
28.	C3-34	12.8	65	5	41
29.	C3-7	12.4	68	7	41
30.	C3-20	11.9	62	5	34

mean was observed for seed yield plant⁻¹ which indicated less influence of environment in expression of character and prevalence of additive gene action in their inheritance. Naturally, selection based on phenotypic observations for this character would be effective indicated the existence of substantial variability for this character. It also indicated greater scope for selection to improve upon this character. Low differences between PCV and GCV for this trait indicates the lower influence of environment and reflect on reliability of selection based on phenotypic performance. Earlier worker Mehta, (2016), Lyimo *et al.* (2017), Humstoe *et al.* (2017), Neelima *et al.* (2018) and Shrivastva *et al.* (2018) had also reported high GCV, heritability and genetic advance which were supported to the present finding.

All crosses reported high mean, genotypic coefficient of variation, heritability and genetic advance as per cent of mean for plant height, number of branches, number of pods plant⁻¹ and yield plant⁻¹, and hence would be useful for obtaining potential segregants with maximum number of branches plant⁻¹, plant height, number of pods plant⁻¹ and seed yield plant⁻¹. So, 30 single plants were selected on basis of these four traits at 5% selection intensity (Table 2.) which were suggested to be carried forward by plant to row method for exploiting improvement in the selected material.

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Rec. on 20.07.2019 & Acc. on 31.07.2019