

GENETIC VARIABILITY STUDIES IN F₃ SEGREGATING GENERATIONS IN SOYBEAN FOR YIELD AND ITS COMPONENTS

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ABSTRACT

The genetic analysis in F₃ crosses in soybean was undertaken with a view to estimate genetic parameters and to identify potential F₃ crosses at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. Eight F₃ crosses and check (JS 335) were raised during *kharif* 2018 in Randomized Block Design in three replications and data were recorded on seed yield and its contributing traits. Analysis of variance revealed the presence of significant genetic variability in all crosses as highly significant values for mean squares due to genotypes were observed for all the seven traits studied. Genetic parameters estimated revealed the influence of additive gene action for characters *viz.*, number of pods plant⁻¹, seed yield plant⁻¹ and number of branches plant⁻¹ as high heritability coupled with high genetic advance were recorded for these traits and hence, suggested the use of these characters for selection to improve further. Among the eight crosses studied, JS 97-52 x NRC 37, JS 97-52 x 104-31 and Cat 3293 x NRC 2 were identified as potential F₃ crosses on the basis of high mean, genotypic coefficient of variation, heritability and genetic advance for characters like seed yield plant⁻¹, number of pods plant⁻¹ and number of branches plant⁻¹ and were suggested to carry over by single seed descent method to identify potential segregants.

(Key words: Genetic variability, F₃ segregating generations, soybean, yield components, heritability, genetic advance)

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill.] is an important global legume crop which belongs to the family Leguminosae and subfamily Papilionoideae. Soybean has 20 chromosome pairs (2n = 40) and is a self-fertile species with less than 1% out crossing (Shurtleff and Aoyagi, 2007).

It is the most popular and fascinating crop with innumerable possibilities of improving agriculture and supporting industries. Soybean plays an important role in world agriculture because of its oil content and protein. Soybean can be processed easily and give different products. They include soya milk, soya flour, soya cheese, soya nut, soya curd and tofu (soya Paneer).

The contribution of India in the world soybean area is 10%, but the contribution to total world soybean grain is only 4% indicating the poor levels of productivity of the crop in India (1.1 t ha⁻¹) as compared to other countries (world average 2.2 t ha⁻¹). The versatile nature of this crop, its increasing contribution to industrial, agricultural and medicinal sectors and the wide yield gap indicates the necessity of identifying and developing high yielding

soybean cultivars suitable for food processing and human consumption (Fasoula and Boerma, 2007).

To evolve a variety having high yield combined with good yield contributing characters require the information on the nature and magnitude of variation in the available material. All this information has a practical utility in a segregating population, where selection is actually practiced. The continuous improvement of soybean depends on the information about genetic variability, genetic parameters and their application, that assists the breeders in reliable selection process. Estimation of genetic parameters allows breeder to define best strategy to be adopted in the improvement of given population (Santos *et al.*, 1995 and Lande *et al.*, 2018). The present study was designed to estimate genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h²), expected genetic advance (GA) that may be used as selection tools in future breeding programme.

MATERIALS AND METHODS

The experimental material comprised of eight F₃ crosses selected on the basis of yield performance of F₂

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obtained from Indian Institute of Soybean Research Indore and one check JS-335. During *kharif* 2018, seeds from each cross (8 crosses) of F_2 generation along with check (JS-335) were sown at research farm of Agricultural Botany Section, College of Agriculture, Nagpur to raise F_3 generation using randomized block design with 3 replications. Each plot comprised five rows of each F_3 population and one row of check (JS-335) spaced 45 cm apart with an intra-row spacing of 10 cm. All the cultural practices were followed to raise a good crop. Total 20 plants were chosen randomly from each of 8 F_3 population and 5 selected plants in check variety during *kharif* 2018 for recording observations on days to first flower, days to maturity, plant height (cm), number of primary branches plant^{-1} , number of pods plant^{-1} , 100 seed weight (g) and seed yield plant^{-1} (g).

The analysis of variance was done as suggested by Panse and Sukhatme (1954). The genotypic and phenotypic coefficients of variation were worked out according to the method given by Burton and Devane (1953). Heritability in broad sense and expected genetic advance on the basis of per cent of mean were worked out according to the method given by Hanson *et al.* (1956) and Johnson *et al.* (1955) respectively.

RESULTS AND DISCUSSION

The mean sum of squares due to replication was non-significant for all the studied character while, the variation due to genotypes was significant for all the characters under study both at 5 and 1 per cent probability levels (Table 1). Shivkumar (2008) and Mukesh *et al.* (2009) observed the similar results and reported the highly significant variations among the genotypes for all the characters studied.

The characters under investigation were analyzed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as per cent of mean (Table 2).

PCV was higher than GCV for all the studied characters which indicates the effect of environmental variation. High values of GCV and PCV were observed for characters *viz.*, number of pods plant^{-1} , seed yield plant^{-1} and number of branches plant^{-1} which indicates the wide spectrum of genotypic variation for these traits. Moderate to high GCV and PCV was observed for plant height and the characters days to first flower and days to maturity revealed low GCV and PCV. These results are in agreement with experimental studies of many scientist. Patil *et al.* (2011) and Sawale *et al.* (2014) observed high values of GCV and PCV for seed yield plant^{-1} and pods plant^{-1} whereas low values of GCV and PCV for days to maturity and days to 50% flowering were reported by Patil *et al.* (2011) and Kankal *et al.* (2018).

GCV measures the amount of variation present in a particular character but it doesn't provide an idea about the proportion of heritable variation present in the total variation therefore, heritability estimates were calculated in the present study. In the present investigation heritability estimates were high for characters *viz.*, plant height, number of branches plant^{-1} , number of pods plant^{-1} and seed yield plant^{-1} in all the crosses whereas moderate to high values were recorded for days to first flower and days to maturity as categorized (Low <30%; Moderate 30-60%; high >60%) by Robinson *et al.* (1949) (Table 2).

High heritability coupled with high genetic advance observed for the traits *viz.*, plant height, branches plant^{-1} , pods plant^{-1} , 100 seed weight and seed yield plant^{-1} which indicates presence of additive gene action and offers the best possibility for improvement of these traits by various selection methods. High heritability coupled with low genetic advance found for traits days to first flower and days to maturity. This indicates the presence of nonadditive gene action and selection is not rewarding for this trait. Above results are in agreement with the experimental studies of Neelima *et al.* (2018) and Sabale *et al.* (2018), who also reported high values of heritability coupled with high genetic advance as per cent mean for plant height, number of branches plant^{-1} and number of pods plant^{-1} .

Seed yield plant^{-1} (12.32%), number of pods plant^{-1} (10.10%) and number of branches plant^{-1} (10.56%) exhibited moderate coefficient of variation whereas other characters exhibited low coefficient of variation. Hence, only number of branches plant^{-1} , number of pods plant^{-1} and seed yield plant^{-1} would be considered as objective of selection in this study. In all the above three characters high heritability was coupled with high genetic advance indicating the significance of additive gene action. Hence, above three characters *viz.*, seed yield plant^{-1} , number of branches plant^{-1} and number of pods plant^{-1} were considered for selection in this study.

F_3 populations JS 97-52 \times NRC 37, JS 97-52 \times 104-31 and Cat 3293 \times NRC 2 were observed to record high mean, GCV, heritability and genetic advance for all the three characters *viz.*, number of branches plant^{-1} , number of pods plant^{-1} and seed yield plant^{-1} (Table 2). These three crosses would be useful for obtaining potential segregants with high number of pods plant^{-1} , seed yield plant^{-1} and number of branches plant^{-1} . As the number of pods plant^{-1} and seed yield plant^{-1} being polygenic and highly influencing character early generation selection of individual plant in F_3 would be unreliable. It is therefore, advisable to delay the selection until the genes get stabilized. Hence, the three crosses identified from this study may be handled by single seed decent method (S.S.D.) to overcome the effect of non additive components by delaying the selection in early generation.

Table 1. Analysis of variance for different traits in F₃ generation of soybean

Source of Variation	d.f.	Mean sum of square						Seed yield plant ⁻¹ (g)
		Days to flower	Plant height (cm)	Days to maturity	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	
Replications	2	0.53	41.08	0.16	0.17	30.41	0.24	0.85
Genotypes	7	30.97**	98.20**	40.27**	0.94**	149.75**	1.33**	7.77**
Error	14	0.95	21.82	1.76	0.18	16.12	0.24	0.91

** Significant at 1% level of probability

Table 2. Estimates of genetic parameters in the F₃ generation of eight soybean crosses for different characters

Sr. No.	F ₃ population	Days to first flower				Plant height (cm)				Days to maturity						
		Mean	GCV (%)	PCV (%)	h ² (%)	GAM	Mean	GCV (%)	PCV (%)	h ² (%)	GAM	Mean	GCV (%)	PCV (%)	h ² (%)	GAM
1	KDS 726 X BNS 5	42.77	5.19	5.67	83.80	9.79	53.28	18.66	20.61	81.92	34.79	98.48	2.25	2.63	73.64	3.99
2	JS 97-52 X NRC 37	41.67	6.63	7.03	88.92	12.89	63.36	15.01	16.72	80.56	27.75	97.58	2.81	3.12	81.01	5.21
3	PS 1556 X RSC 10-46	48.27	2.27	3.04	55.82	3.50	67.78	14.59	16.13	81.75	27.17	101.58	1.59	2.06	59.76	2.54
4	JS 97-52 X 104-31	48.36	2.30	3.06	56.46	3.56	58.38	20.78	22.27	87.09	39.94	99.02	2.83	3.13	81.68	5.27
5	Cat 3293 X JS 90-41	39.18	2.97	3.88	58.77	4.70	59.13	20.41	21.89	86.97	39.21	103.46	1.24	1.79	48.29	1.78
6	JS 97-52 X Dsb1	45.75	1.71	2.73	39.14	2.20	52.00	21.13	22.96	84.69	40.05	108.56	2.58	2.86	81.67	4.81
7	Cat 3293 X NRC 2	43.08	2.34	3.25	51.54	3.45	51.31	17.48	19.71	78.66	31.93	99.72	2.56	2.88	78.64	4.67
8	JS97-52 X Ankur	45.19	2.75	3.49	61.78	4.45	58.32	23.41	24.74	89.52	45.62	98.32	1.60	2.09	58.23	2.51
	SE _(m) ±	0.56					SE _(m) ±	2.70					SE _(m) ±	0.77		
	CD (5%)	1.68					CD (5%)	8.10					CD (5%)	2.31		
	CV (%)	2.20					CV (%)	8.06					CV (%)	1.32		

Table 2. Cont....

Sr. F ₃ population	Number of branches plant ⁻¹					Number of pods plant ⁻¹					100 seed weight (g)					Seed yield plant ⁻¹ (g)				
	Mean	GCV (%)	PCV (%)	h ² (%)	GAM	Mean	GCV (%)	PCV (%)	h ² (%)	GAM	Mean	GCV (%)	PCV (%)	h ² (%)	GAM	Mean	GCV (%)	PCV (%)	h ² (%)	GAM
1 KDS 726 X BNS 5	3.67	30.67	32.80	87.46	59.10	27.00	46.61	48.93	90.76	91.48	8.56	13.02	14.23	83.71	24.54	6.13	27.70	31.80	75.89	49.71
2 JS 97-52 X NRC 37	4.38	33.85	35.22	92.37	67.01	49.24	34.82	35.76	94.80	69.83	9.49	17.98	18.71	92.33	35.60	10.63	17.51	19.69	79.11	32.09
3 PS 1556 X RSC 10-46	3.64	31.59	33.68	87.97	61.04	40.16	34.61	36.02	92.30	68.49	8.95	16.21	17.11	89.69	31.62	8.59	19.49	22.45	75.38	34.85
4 JS 97-52 X 104-31	5.00	25.10	26.50	89.67	48.96	44.26	34.77	35.93	93.63	69.31	9.07	13.89	14.91	86.79	26.67	9.35	17.19	20.00	73.83	30.42
5 Cat 3293 X JS 90-41	4.10	31.81	33.46	90.38	62.29	36.54	46.25	47.54	94.66	92.70	7.60	14.22	15.62	82.86	26.66	6.91	27.14	30.47	79.33	49.79
6 JS 97-52 X Dsb1	3.14	28.47	31.54	81.50	52.95	35.50	33.83	35.67	89.95	66.09	7.74	15.22	16.49	85.15	28.92	7.00	22.87	26.64	73.68	40.44
7 Cat 3293 X NRC 2	4.08	27.58	29.49	87.50	53.15	46.58	36.59	37.59	94.74	73.37	8.39	13.07	14.33	83.26	24.57	7.37	32.05	34.58	85.91	61.20
8 JS97-52 X Ankur	4.22	39.48	40.75	93.86	78.79	38.49	40.37	41.69	93.74	80.51	8.05	14.29	15.54	84.57	27.07	6.13	32.92	39.16	84.14	67.88
SE_(m)±	0.25					SE_(m)±	2.32				SE_(m)±	0.28			SE_(m)±	0.55				
CD (5%)	0.75					CD (5%)	6.96				CD (5%)	0.84			CD (5%)	1.65				
CV (%)	10.56					CV (%)	10.10				CV (%)	5.80			CV (%)	12.32				

Table 3. Performance of selected F₃ population

Parameters	Characters	Cat 3293 × NRC 2	JS 97-52 × NRC 37	JS 97-52 × 104-31
Mean	Seed yield plant ⁻¹	7.37	10.63	9.35
	Number of pods plant ⁻¹	46.58	49.24	44.26
	Number of branches plant ⁻¹	4.08	4.38	5.00
GCV (%)	Seed yield plant ⁻¹	32.05	17.51	17.19
	Number of pods plant ⁻¹	36.59	34.82	34.77
	Number of branches plant ⁻¹	27.58	33.85	25.10
h ² (%)	Seed yield plant ⁻¹	85.91	79.11	73.83
	Number of pods plant ⁻¹	94.74	94.80	93.63
	Number of branches plant ⁻¹	87.50	92.37	89.67
GAM	Seed yield plant ⁻¹	61.20	32.09	30.42
	Number of pods plant ⁻¹	73.37	69.83	69.31
	Number of branches plant ⁻¹	53.15	67.01	48.96

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