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Genetic variability studies in early generation lines of Soyabean (*Glycine max* (L.) Merrill.) for yield and its contributing traits

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Abstract
Eleven line from F_4 generation of crosses and their subsequent F_5 generation of soybean (*Glycine max* (L.) Merrill.) were evaluated in split plot design with two replications for variability, heritability and genetic advance during *Kharif* 2017 and 2018. The analysis of variance for all nine traits unveiled presence of highly significant variations among the treatments in both F_4 and F_5 generations, which showed presence of variability among the material used for the experiment. The variability estimates calculated showed higher PCV values over GCV in both the generations. The highest PCV value was recorded for seed yield in F_4 generation, whereas highest value for PCV in F_5 generation was observed for seed yield efficiency, suggesting good amount of variability. High PCV coupled with high GCV indicate the presence of wider adaptability for these traits in the genotypes studied, suggested the less influence of environment in the expression of characters. All the traits under investigation were found to be highly heritable, as majority of them showed high values of heritability (broad sense) estimates. In F_4 generation, highest value of heritability estimate was recorded for seed yield per plant, whereas in F_5 generation highest value was recorded for dry matter weight per plant. High heritability coupled with high genetic advance as percent of mean indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection.

Keywords: Genetic variability, heritability, genetic advance and soybean

Introduction
A great crop given to humanity by nature, soybeans (*Glycine max* (L.) Merrill) is one of the richest sources of both protein and oil. It has chromosomal number 2n=40 and is a self-pollinated crop that belongs to the Leguminosae family. Soybean is the most significant crops that can potentially meet the rising global demand for food and forage. Because of its flexibility and widespread use as a food crop for human nourishment, a source of protein for animals, a medicinal plant, and most recently, an industrial crop, soybean has spread far beyond its native land of origin (Alghamdi, 2004) [2]. Soybean is the cheapest, richest, and most convenient source of high-quality protein. Because of its many uses for both food and industry, soybean is referred to as a "wonder crop". Its protein is complete and contains all nine essential amino acids, earning it the nickname "Miracle bean" from a nutritional standpoint (Quayam *et al.* 1985) [14]. Soybean seed contains about 20.5% carbohydrates, 20% oil with poly unsaturated fatty acids, particularly Omega 6 and Omega 3 fatty acids, 4.5% minerals, 3.7% fiber, 8.1% water, and 43.2% protein.

Genetic variability is the basic requirement for crop improvement as this facilitates selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in breeding material and its heritability. Hence, in present investigation an attempt was made to assess the variability of seed yield and yield contributing traits, along with indices of variability i.e., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_{bs}), genetic advance (GA) and genetic advance as percent of mean (GAM). This study will facilitate an understanding behind the expression of character and role of environment.

Materials and Methods
Experimental material and filed layout: The study was conducted at N.E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar,

Udham Singh Nagar during *kharif* 2017 and 2018. The experimental material used in the study included ten F_4 crosses and each cross contained 5 lines of high yielding, 5 line of low yielding and 5 lines of bulk which were planted in split plot design with two replications and for next generation from each of 10 crosses, 5 most superior plants from high yielding group, 5 most inferior plants from low yielding group and seed from bulk lines were bulked and planted in split plot design with two replications in next season (ten F_5 crosses and each cross contained 5 lines of high yielding, 5 lines of low yielding and 5 lines of bulk along with two checks). The observations for the study of the characters *viz*. Pant height (cm), Number of nodes per plant, Number of primary branches per plant, Number of pods per plants, Number of seeds per pod, Dry matter weight per plant g), Harvest index (%), Seed yield per plant (g) and Seed yield efficiency (%) were recorded on five randomly selected plants from each row.

Statistical and genetic analysis
Means of the observations recorded for various characters were subjected to the following statistical/biometrical analyses for drawing appropriate conclusion from the present investigation. The analysis of variance for each character was carried out for the randomized complete block design as suggested by Fisher (1946). Genotypic and phenotypic components of variance were calculated using following formulae (Burton and De Vane, 1953). Genotypic, phenotypic and environmental coefficients of variability were derived for each character studied (Singh and Chaudhary, 1977).
Heritability coefficient (h^2) was ratio of genotypic variance to phenotypic variance was calculated as follows (Hanson *et al.* 1956)

$$h^2 = \frac{\sigma 2g}{\sigma 2p} X\ 100$$

Genetic advance (GA) for each character studied was calculated as given by (Johnson *et al.* 1955) [9].

$$GA = h^2\ KP$$

Were,
K = Selection differential which is equal to 2.06 at 5% intensity of selection (Lush, 1949).
Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{X} X100$$

Were,
X = general mean of the character

Results
Genetic variability parameters
Effectiveness of selection largely depends on presence of genetic variability. Heritability is used to get the index variation governed by genetic cause or which are transmissible to offspring. Heritability helps to judge how much importance should be given to particular trait during selection.
The mean sum of squares due to treatment was found to be significant for all the characters studied, while the mean sum of squares due to replication for all the characters were found

to be non-significant. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV) for various characters were also recorded. The results of estimates indicated that variability is largely due to genotypic differences. Hence, selection for the character should be effective.
The values of estimates of phenotypic coefficients of variation, genotypic coefficients of variation, range, mean along with values of heritability, genetic advance and genetic advance as percent mean were also calculated for all characters studied are tabulated for F_4 and F_5 in Table 1 and Table 2 respectively for both generations. The results obtained showed that the values for PCV were higher that of both GCV and ECV for all the characters studied in F_4 and F_5 generations. The GCV and PCV values were divided into three groups Low (0-10%) Moderate (10-20%) and High (20% and above) (Sivasubramanian and Menon 1973) [16].

Phenotypic coefficient of variation (PCV)
The study revealed that phenotypic coefficient of variation (PCV) estimates in both generations have moderate to high values for the majority of the characters under study. PCV value for seed yield per plant was highest with 43.44% followed by seed yield efficiency (39.62%), dry matter weight per plant (33.9%), number of pods per plant (33.48%), harvest index (28.92%) and number of primary branches per plant (20.47%). Moderate value of PCV was recorded for plant height (19.93%) and number of nodes per plant (16.23%) whereas, low value was recorded for number of seeds per pod (5.64%) (Table 1). In F_5 generation highest values was recorded for seed yield efficiency (33.21%) followed by seed yield per plant (27.57%),dry matter weight per plant (26.94%), numbers of pod per plant (23.78%), number of primary branches per plant (21.67%) and harvest index (21.26%), while moderate to low PCV was observed for plant height (16.4%), number of nodes per plant (8.75) and number of seeds per pod (4.55%) got lowest values for PCV as mentioned in the Table 1.

Genotypic coefficient of variation (GCV)
The values recorded for estimates of GCV showed similar trends like PCV. High values of genotypic coefficient of variation were observed and presented in Table 1 and Table 2 for F_4 and F_5 generations, respectively. In F_4 generation highest value of estimates of GCV was recorded for seed yield (43.21%) followed by seed yield efficiency (39.07%), dry matter weight (33.64%), number of pods per plant (32.43%), harvest index (28.92%), numbers of primary branches per plant (20.04%) and moderate to low values of estimates were recorded for plant height (19.8%), numbers of nodes (15.93), while GCV value for number of seeds per pod (5.1) found to be lowest. In F_5 generation high value was recorded for seed yield efficiency (32.14%) followed by seed yield per plant (26.98%), dry matter weight (26.39%), number pods per plant (23.12%), harvest index (20.52%) and number of branches (20.54%), while moderate value was observed only for plant height (16.04%) and low value were recorded for number of nodes per plant (8%) and number of seeds per pod (3.96%).

Environmental coefficient of variation (ECV)
Results obtained showed low value of environmental coefficient of variation in comparison to genotypic and

phenotypic coefficients of variation for all traits under investigation in F_4 and F_5 generations. The highest value in F_4 of ECV per cent estimates was recorded for number of pods per plant (8.34%) followed by seed yield efficiency index (4.49%), dry matter per plant (4.21%), number of nodes (3.1%), number of seeds per pod (2.41%) and for plant height (2.28%) was recorded to be lowest in F_4 generation. Low value of estimates of environmental coefficient of variation showed that trait is stable towards the influence of environment. In F_5 generation as earlier generation low values for environmental coefficient of variation were recorded whereas highest value was recorded for seed yield efficiency (8.38%) followed by number of branches per plant (6.9%), seed yield (5.69%), harvest index (5.56%), number of pods per plant (5.53%), dry matter weight (5.38%), number of nodes per plant (3.55%), plant height (3.43%) and lowest value was recorded for number of seeds per pod (2.24%) as mentioned in Table 1 and 2 for F_4 and F_5 generations, respectively.

In general, PCV values were higher than that of GCV and ECV, whereas GCV values were slightly lower than PCV. The environmental coefficient of variation was negligible in comparison to contribution of GCV towards PCV, which showed minimal environment influence with genetic factors having major role in governing character so, substantial increment can be gained through selection.

Malek *et al.* (2014) [12] also reported slight difference in the values of GCV and PCV estimates. Sureshrao *et al*. (2014) [17] also reported high values of estimates of GCV and PCV for number of pods per plant while lowest value was recorded for seeds per pod similar to present investigation. Kumar *et al.* (2014) [10] also documented moderate values for plant height. Similar results were also documented by Datt *et al. (*2011) [5], Jain *et al.* (2015) [8] and Manav and Arora (2017) [13]. This suggested that selection on the basis of phenotypic performance should be effective enough to bring about considerable improvement of these characters (Aditya *et al.,* 2011) [1].

Heritability and genetic advance
Heritability can be understood as degree of variation which is accountable to genetic causes in total variation in population or phenotypic variation, it plays a significant role in determining the chances of transmissibility of a trait from parents to its progeny (Comstock and Robinson., 1948) [4] suggested that use of heritability along with the estimates of genetic advance would be more appropriate to use in selection programs rather than heritability alone.

The values of estimates of heritability can be classified in three groups as indicated by Rabinson *et al.* (1949) [15]. Where, traits having values 60% or above were considered as high, with values of 30% to 60% as moderate and below 30% were considered as less heritable.

A critical account of the values of estimates of heritability is mentioned in Table 1 and Table 2 for F_4 and F_5 generations, respectively. The results of the study for F_4 generation, traits like seed yield per plant, plant height and number of seeds per pod were found be nearly equal with high heritability value of 98.91%, 98.69% and 98.46%, respectively, followed by harvest index (97.59%), seed yield efficiency (97.27%),

number of nodes per plant (96.35%), number of pods per plant (93.79%), number of primary branches (93.37%) and lowest for number of seeds per pod with 81.72% heritability. Similar to F_4, high values of estimates of heritability were obtained in F_5 generation for all the traits under study with highest for dry matter weight per plant (96.01%) followed by seed yield per plant (95.74%), plant height (95.62%), number of pods per plant (94.59%), seed yield efficiency (93.64%), harvest index (93.16%), number of primary branches (89.87%), number of nodes per plant (83.58%) and lowest for number of seeds per pod (75.7%).

Genetic advance as per cent mean (GAM) was also grouped into three categories, as traits having values of estimate 20% or above were considered as high, traits with GAM 10% to 20% as moderate and values below 10% were considered as low (Johnson *et al.,* 1955) [9]. In F_4 generation it was highest for seed yield per plant (88.52%) followed by seed yield efficiency (79.39%), dry matter weight per plant (68.75%), number of pods per plant (64.69%), harvest index (58.14%), plant height (40.52%), number of primary branches per plant (39.9%) and number of nodes per plant (39.9%) presented in Table 1. In F_4 generation the estimates of genetic advance expressed as per cent of mean was observed to be highest for seed yield per plant which showed additive gene action was majorly involved in expression of these traits. Hence, selection based on phenotypic criteria was effective in segregating generation. Whereas low values for genetic advance over mean was recorded for number of seeds per pod (9.5%). However, in the next generation (F_5 progenies) highest value was observed for seed yield efficiency (64.06%) followed by seed yield per plant (54.37%), dry matter weight per plant (53.27%), number of pods per plant (46.33%), number of branches per plant (40.12%), harvest index (40.8%), plant height (32.31%) while, moderate value was observed for number of nodes per plant (15.07%) and number of seeds per plant (7.09%), which was been mentioned in the Table 2.

The majority of the characters *viz.* plant height, number of primary branches per plant, number of pods per plant, dry matter weight per plant, seed yield per plant, harvest index and seed yield efficiency studied showed high heritability accompanied with high genetic advance in both the generations. These high values of estimates of heritability and genetic advance as percent over mean showed predominance of additive gene action in governing these traits, which showed substantial scope for improvement through selection in early generations of segregation. The results showed similarity to the findings of Gupta and Punetha (2007) [7]. They found highest heritability accompanied with high genetic advance for number of pods per plant and seed yield. Sureshrao *et al*. (2014) [17] documented lowest value of heritability for number of seeds per pod and high value of genetic advance as per cent of mean (GAM %) for number of pods per plant and lowest for number of seeds per pod. Dubey *et al*. (2015) [6] observed high value of heritability for maximum characters along with high values of genetic advance as per cent of mean for biological yield per plant, harvest index, number of seeds per plant, seed yield per plant and number of pods per plant. Similar results were also documented by Mahbub *et al.* (2015) [11] and Bisht (2018) [3].

Table 1: Range, general means (GM), standard error of mean (S.Em) and variability parameters in F₄ generation

Character	Range	GM	S.Em±	PCV (%)	GCV (%)	h² (%)	GA	GA value % mean
Plant height(cm)	43.77-64.05	52.82	0.85	19.93	19.8	98.69	21.42	40.52
Number of nodes per plant	12.18-16.72	14.45	0.32	16.23	15.93	96.35	4.66	32.22
Numbers of primary branches per plant	5.47-6.98	6.25	0.24	20.74	20.04	93.37	2.5	39.9
Number of pods per plant	61.51-96.29	74.11	4.36	33.48	32.43	93.79	47.87	64.69
Number of seeds per pod	2.11-2.33	2.2	0.04	5.64	5.1	81.72	0.21	9.5
Dry matter weight per plant(g)	31.32-50.81	43.21	1.29	33.9	33.64	98.46	29.72	68.75
Seed yield per plant(g)	7.06-17.97	13.70	0.44	43.44	43.21	98.91	12.15	88.52
Harvest index (%)	14.36-38.75	32.02	1.02	28.92	28.57	97.59	18.65	58.14
Seed yield efficiency (%)	17.23-65.92	49.84	2.31	39.62	39.07	97.27	39.66	79.39

GM= General mean, Sem= Standard error mean, P.C.V= Phenotypic coefficient of variation, G.C.V = Genotypic coefficient of variation, E.C.V= Environmental coefficient of variation, h2= Heritability.= Genetic advance, G.A.(%)= Genetic advance expressed as percent of mean

Table 2: Range, general means (GM), standard error of mean (S.Em) and variability parameters in F₅ generation

Character	Range	GM	S.Em±	PCV (%)	GCV (%)	h² (%)	GA	GA value % mean
Plant height(cm)	45.7-64.82	57.92	1.41	16.4	16.04	95.62	18.71	32.31
Number of nodes per plant	12.88-15.62	14.97	0.38	8.75	8	83.58	2.26	15.07
Numbers of primary branches per plant	3.57-6.30	5.29	0.26	21.67	20.54	89.87	2.12	40.12
Number of pods per plant	67.49-89.16	77.06	3.01	23.78	23.12	94.59	35.7	46.33
Number of seeds per pod	2.16-2.38	2.28	0.04	4.55	3.96	75.7	0.16	7.09
Dry matter weight per plant (g)	32.23-60.19	44.15	1.68	26.94	26.39	96.01	23.52	53.27
Seed yield per plant(g)	12.05-18.68	15.66	0.63	27.57	26.98	95.74	8.52	54.37
Harvest index (%)	27.02-43.10	36.3	1.43	21.26	20.52	93.16	14.81	40.8
Seed yield efficiency (%)	37.33-76.03	59.06	3.5	33.21	32.14	93.64	37.85	64.06

GM= General mean, Sem= Standard error mean, P.C.V= Phenotypic coefficient of variation, G.C.V = Genotypic coefficient of variation, E.C.V= Environmental coefficient of variation, h2= Heritability= Genetic advance, G.A.(%)= Genetic advance expressed as percent of mean

Conclusions

All the traits under investigation were found to be highly heritable, as majority of them showed high values of heritability (broad sense) estimates. In F₄ generation, highest value of heritability estimate was recorded for seed yield per plant, whereas in F₅ generation highest value was recorded for dry matter weight per plant. High heritability coupled with high genetic advance as percent of mean indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection.

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