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Research Note

Assessment of genetic variability, heritability and genetic advance in soybean genotypes

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Abstract
Forty soybean genotypes were evaluated for two consecutive years *kharif* 2018 and 2019 to determine genetic variability, heritability (h^2) and genetic advance (GA) for yield and other yield attributing traits. The pooled analysis of variance revealed significant variation among year and treatment for all characters studied. The interaction of year x treatment also showed a significant difference for most of the traits. RVSM2011-35 recorded the highest mean performance of seed yield/plant and a high value of oil content over the two years indicating that the genotype was found to be promising and could be recommended for Assam. In the case of oil content, NRC 148 showed the highest mean value and also a high value of mean seed yield/ plant over the two years. Range estimation showed wide values for most of the traits except plant height, the number of branches and pods/plant in comparison with the check. The estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation indicated that the values of PCV were slightly higher than GCV. The highest values of GCV and PCV were observed for seed yield/plant, the number of seeds/pod and oil content. Higher values of heritability ($h^{2)}$ coupled with high genetic advance (GA) were recorded for seed yield/plant, the number of seeds/pod, oil content, the number of branches, days to 50% flowering, plant height, the number of pods/plant, and 100 seed weight, suggesting that these characters could easily be modified or improved through simple selection.

Key words: *Glycine max*, genotypes, genetic variability, genetic advance, heritability, soybean

Soybean is considered as a wonder crop due to its dual qualities viz., high protein (40-44%) and oil content (20%) (Baraskar *et al*., 2014). Improvement of its genotypes can be done through selection. The success of the breeding programme relies on the variability present in the breeding material (Manju Devi and Jayamani, 2018) For the selection to be effective, the variability must be heritable in nature. The present study was undertaken to assess and estimate the magnitude and nature of variation among 40 genotypes of soybean with respect to various yield attributing characters.

The present investigation was conducted at the Instructional cum Research farm, Assam Agricultural University, Jorhat during *kharif* , 2018 and 2019. The experiment consisted of 40 genotypes which were evaluated in randomized block design with three replications. The genotypes were obtained from the All India Coordinated Research Project on Soybean. Three check varieties namely JS335, JS93-05 and BRAGG were also evaluated along with 40 genotypes. Care was taken to raise a healthy crop using recommended packages and practices. Five plants per replication per genotype were randomly selected and data of days to 50% flowering, days to maturity, plant height, number of branches/plant, number of pods/plant, number of seeds/pod, pod length, 100-seed weight, oil content and seed yield/plant were recorded at appropriate stages. Observations on days to 50 % flowering and days to maturity were recorded on a plot basis. Pooled analysis of variance and coefficients of variance was computed according to formulae given by Lush (1940) and Chaudhary and Prasad (1968) for the observed characters. GCV and PCV were computed according to Burton and Devane (1953). Broad sense heritability was estimated based on the ratio of genotypic variance and was expressed in percentage (Hanson *et al*., 1956). GA was computed according to the formula given by Johnson *et al.* (1955).

The pooled analysis of variance revealed that mean squares due to genotypes were significant for all the traits indicating varietal differences for all the characters studied (**Table 1**). Earlier, significant variability was also reported by Khurana and Sandhu (1972), Shwe *et al*. (1972) and Chandrawat *et al*. (2017). Years were also found significantly different except for a number of seed/ pod, pod length and oil content. The year x treatment interaction was also found significant for most of the traits except plant height, the number of seed/pod, pod length, 100 seed weight and oil content. The non-significant difference of the interaction effect for some traits indicated that the performance of the genotypes with respect to these traits was consistent across the year. Replication within a year showed non-significant values for all the traits. RVSM2011- 35 recorded the highest value of seed yield/plant over the two years indicating that this genotype is promising and could be recommended for Assam. The oil content was also moderately high for this genotype. However, in the case of oil content, NRC 148 showed the highest value over the two years with a comparatively high value for seed yield/plant (**Table 2**).

The analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic variance in the collection and hence the range of variation was also assessed as shown in **Table 3**. Range observed for all the characters under study showed a significant and a wide range of variation for most of the traits except for plant height, number of branches, pods/plant in comparison with the checks. To estimate the genetic nature of the traits under study PCV and GCV, h^2 and GA as per cent of the mean were estimated. For all the characters, PCV was slightly greater than the GCV but the difference was closer between these two estimates for all the cases. These indicated that the greater role of genetic components and expression of characters under study was less influenced due to environmental factors. Higher GCV and PCV were recorded for seed yield/ plant, the number of seeds/pod, and oil content. Higher PCV and GCV values for seed yield/plant was also recorded by Ramana *et al*. (2000), Hina Kausar (2005) Aditya *et al*. (2011) and Chandrawat *et al*. (2017).

Low GCV and PCV were observed for pod length and days to maturity. The low GCV estimates for days to maturity was reported by Sharma *et al*. (1983). The difference between PCV and GCV was very small for oil content, the number of pods/plants and pod length indicating a lesser influence on the environment. Thus, selection based on the phenotypic performance of these characters would be effective to bring about considerable improvement.

The estimates of h^2 have a greater role to play in determining the effectiveness of a selection of a character provided, it is considered in conjugation with the predicted GA as suggested by Panse and Sukhatme, (1967). The amount of h^2 permits a greater degree of success in selection. A highly heritable character is more suitable for selection because it indicates a greater correspondence between genotype and phenotype.

A high h^2 was observed for all the traits indicating the scope for improvement by adopting simple selection procedures. Among all, the highest values were found for oil content, pods/plant, pod length, the number of seeds/ pod, and seed yield/plant (**Table 3**). Similar results have been reported for the tnumber of seeds/pod (Konwar and Talukdar, 1984), seed yield/plant (Malhotra,1973) and the number of pods/plant (Perraju *et al*.,1982).

The expected genetic advance gives a quantitative measure of the degree of advancement that can be achieved through a given selection procedure as it takes into account the intensity of selection (i), phenotypic

Table 1. Pooled analysis of variance for quantitative traits in soybean

Sources of variation	df	Days to 50% flowering	Days to maturity	Plant height	Number of branches	Pods/ plant	Number of seeds/ pod	Pod length	100seed weight	Oil content	Seed yield/ plant
Year	1	1,255.83**	2,106.33**	75,161.20**	6,383.95**	24,732.04**	0.08	0.00	226.56**	0.04	2,242.74**
Replication within year	4	7.00	12.35	10.34	0.05	0.18	0.04	0.00	0.12	0.01	1.48
Treatment	39	349.32**	412.53**	185.96**	14.71**	144.61**	2.20**	0.39**	25.79**	80.77**	151.13**
Year x treatment	39	18.14**	45.03**	7.59	0.54**	18.76**	0.05	0.00	0.21	0.00	11.37**
Pooled error	156	9.77	13.53	8.94	0.16	0.07	0.03	0.00	0.98	0.00	0.77

**significant at 1 % probability level

Table 2. Mean performance of soybean genotypes for different yield and its attributing traits

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches	Pod per plant	Number of seed per pod	Pod length (cm)	100 seed weight(g)	Oil Content (%)	Seed yield/ plant(g)
DS3109	36	82	37.07	7.6	37	1	3.24	12.36	16.14	4.65
NRC146	25.5	71	50.35	8.87	43.8	1.4	3.48	13.78	15.17	8.62
PS1634	42.5	88	38.16	10.33	45.37	1.67	3.54	14.04	17.41	10.79
JS21-71	37.5	83	49.72	7.23	35.67	0.93	3.18	14.17	15.1	4.79
MACS1566	40.5	88	56.58	6.6	32.5	0.87	2.95	15.72	16.17	4.48
SL1191	29	72.5	48.96	7.9	39.77	1.07	3.34	12.53	17.18	5.42
HIMSO1688	26.5	71	53.35	6.87	34.5	0.87	3.15	14.42	15.17	4.35
VLS95	39	83	46.36	8.07	38	1.07	3.27	15.44	16.55	6.33
RSC11-17	42	89.5	51.88	9.63	46.73	1.93	3.63	11.14	15.24	10.26
MAUS734	36.5	79	44.75	8.3	41.8	1.2	3.39	12.14	16.21	6.21
DSB33	37.5	83.5	45.15	11.37	48.53	2.53	3.81	14.87	20.72	18.49
NRC138	28	73	39.45	8.57	41.4	1.13	3.37	12.30	22.26	5.89
JS21-72	46.5	91.5	55.5	8.3	43.57	1.27	3.45	16.53	15.71	9.24
PS1637	39	81.5	53.26	10.43	47.9	2.2	3.73	15.26	15.7	16.30
AUKS176	46.5	88	46.18	7.37	36.2	1	3.22	13.14	16.14	4.82
VLS63	38	80	51.04	10.83	48.2	2.47	3.78	13.72	16.16	16.58
GJS3	39	81.5	48.33	8.07	43.5	1.33	3.47	13.37	16.1	7.87
NRC139	42.5	87.5	52.96	7.07	33.97	0.87	3.11	15.17	15.28	4.49
DS3110	31	74	45.04	10.9	48.03	2.27	3.75	15.03	15.96	16.59
SL1171	35	80.5	44.13	9	44.13	1.47	3.49	13.60	24.61	8.98
MACS1620	48.5	95.5	51.43	10.83	47.3	2	3.66	19.25	15.73	18.37
MAUS732	45.5	95.5	46.64	8.07	43.17	1.2	3.42	17.56	16.26	9.32
KS113	47	98	48.98	9.77	45.6	1.73	3.56	11.98	25.74	9.64
PS1092	45.5	87.5	52.29	10.77	47.63	2.13	3.70	15.89	25.03	16.45
NRC148	43	90.5	52.59	10.57	47.47	2.07	3.69	19.2	25.79	19.00
RSC11-15	51	99.5	49.58	7.7	40.03	1.13	3.35	12.76	16.4	5.91
RVS2011-10	50	98	43.72	9.13	44.43	1.53	3.51	12.67	25.7	8.82
HIMSO1689	48.5	95.5	42.19	10	45.07	1.6	3.53	14.33	15.51	10.48
CAUMS1	43.5	83.5	42.93	11.5	49.67	2.67	3.95	12.12	15.72	16.30
RVSM2011-35	49	93.5	36.14	12.03	49.87	2.73	4.02	14.69	16.66	20.23
VLS97	51	101	50.19	11	50.07	2.8	4.05	11.62	16.93	16.54
TS59	49	95.5	37.45	8.73	38.4	1.07	3.29	13.09	17.55	5.44
RVS2007-4	51	77	40.71	10.33	46.57	1.87	3.61	10.36	22.77	9.30
KDS1073	41	85	54.56	6.6	37.3	1	3.25	11.24	16.46	4.25
NRCSL2	49	93	38.95	9.33	44.73	1.53	3.52	11.53	17.45	8.08
KDS1009	41	87.5	41.37	11.73	48.97	2.6	3.88	12.78	15.47	16.59
BAUS100	43.5	93	45.30	9.87	46.07	1.8	3.58	11.35	15.21	9.58
CHECKS										
BRAGG	28	79	52.07	10.7	45.87	1.8	3.56	12.08	17.58	10.15
JS335	33	85	46.32	10.83	48.88	2.6	3.84	11.7	25.58	15.12
JS9305	26.5	75.5	52.36	10.63	42.17	1.2	3.40	13.14	23.21	6.77
SE(m)	1.26	1.53	1.24	0.16	0.11	0.05	0.01	0.41	0.02	0.42

Table 3. The estimates of variability for quantitative characters in soybean

Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (%)	GA (%)
Days to 50% flowering	25.50-51	40.56	18.55	19.31	92.24	36.70
Days to maturity	71-101	85.91	9.48	9.97	90.41	18.58
Plant height (cm)	36.14-56.58	47.10	11.52	12.39	86.47	22.07
Number of branches	6.6-11.73	9.33	16.68	16.99	96.82	33.81
Pod/ plant	32.50-50.07	43.49	11.28	11.29	99.84	23.22
Number of seeds/pod	0.87-2.80	1.64	36.82	37.21	97.91	75.07
Pod length(cm)	2.95-4.05	3.51	7.23	7.27	98.77	14.80
100 seed weight(g)	10.36-19.25	13.70	14.82	15.72	88.83	28.77
Oil content (%)	15.10-25.79	18.14	20.22	20.22	99.98	41.65
Seed yield/plant (g)	4.25-20.33	10.28	48.60	49.12	97.90	99.07

genetic deviation of the characters (p) and heritability (h^2). A character with high genetic advance and h^2would thus predict the greater potential for effective genetic selection in a breeding programme. The traits with high GA and h^2 indicating the influence of additive gene effects. Improvement for such characters could easily be achieved through a simple selection scheme like mass selection without progeny testing.

In the present study, high estimates of GA were found for seed yield/plant, the number of seeds/pod, oil content, days to 50% flowering, the number of branches, 100 seed weight, pods/plant, and plant height. Similar results of higher values of GA for days to 50% flowering, seed yield/plant and plant height were observed Parameshwar, (2006); the number of branches, the number of pods/plant by Karad *et al*. (2005), the number of seeds/pod by Hina Kausar, (2005), oil content by Harer and Deshmukh (1992) and 100 seed weight by Chandrawat *et al*. (2017).

Higher values of h^2 coupled with high GA were recorded for seed yield/plant, the number of seeds/pod, oil content, the number of branches, days to 50% flowering, plant height, the number of pods/plant, and 100 seed weight, suggesting that these characters could easily be modified or improved through simple selection. Similar results for days to 50% flowering and the number of branches were observed by Chandrawat *et al*. (2017), the number of pods/plant by Parameshwar (2006) and Chandrawat *et al*. (2017) and the number of seeds/pods by Hina Kausar (2005).

REFERENCES

Aditya, J.P., Bhartiya, P., Bhartiya, A. 2011. Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill). *Journal of Central European Agriculture*, **12**(1): 27-34. [Cross Ref]

Baraskar, V.V., Kachhadia, V. H., Vachhani, J. H., Barad H. R., Patel M. B. and Darwankar M. S., 2014. Genetic variability, heritability and genetic advance in soybean [Glycine max (L.) Merrill]. *Electronic Journal of Plant Breeding*, **5**(4): 802-806.

Burton, C.W. and Devane, E.H. 1953. Estimating heritability in tall Festuca (Restuca arundinaceae) from donor material. *Agronomy journal*, **45**: 1476-1481. [Cross Ref]

Chandrawat, K.S., Baig, K, S., Hashmi, S., Sarang, D. H., Kumar, A. and Dumai, K. 2017. Study on genetic variability, heritability and genetic advance in soybean. *Int. J. Pure App. Biosci.,* **5** (1): 57-63. [Cross Ref]

Chaudhary, L.B. and Prasad, B. 1968. Genetic variation and heritability of quantitative characters in Indian mustard (*Brassica juncea*). *Indian journal of Agricultural science,* **124**(1):48-55.

Hanson, G. H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal*., **48**:268-272. [Cross Ref]

Harer, P.N. and Deshmukh, R.B. 1992. Genetic variability, correlation and path coefficient analysis of soyabean [*Glycine max* (L.) Merrill]. *J. of Oilseed Res*., **9**: 65 – 71.

Hina Kausar, J. 2005. Genetic investigation in segregating population of soybean [*Glycine max* (L.) Merrill]. M.Sc. (Agri.) Thesis. University of Agricultural Science, Dharwad.

Johnson, H.W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environment variability in soybeans. *Agronomy Journal*.,**47**: 314-318. [Cross Ref]

Karad, S.R., Harer, P.N., Kadam, D.B. and Shinde, R.B. 2005. Genotypic and phenotypic variability in soybean [*Glycene max* (L.) Merrill].*J. Maha. Agric. Univ.,* **30**(3): 365-367 (2005).

Khurana, S.R. and Sandhu, R.S. 1972. Genetic variability and interrelationship among certain quantitative traits in soybean [*Glycine max*(L) Merrill]. *J.Res*. **9**:520-527.

Konwar, B.K. and Talukdar, P. 1984. Environmental influence on the estimates of genetic parameters in Soybean. *J. Res. Assam Agril. Univ*., **5**(2): 135-142.

Lush, J.L., 1940. Inter size correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production,* **33**: 293-301

Malhotra, R.S. 1973. Genetic variability and discriminant functions in Soybean. *Madras Agric. J*., **60**: 225-228.

Manju Devi, S. and Jayamani, P. 2018. Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding,* **9** (2): 476-481. [Cross Ref]

Panse, V.C. and Sukhatme, P.V. 1967. Statistical methods for agricultural workers ICAR Publication. New Delhi, 259.

Parameshwar, M.G. 2006. Genetic investigations in soybean [*Glycine max* (L.) Merrill]. *M. Sc. (Agri.) Thesis.* University of Agricultural Sciences, Dharwad.

Perraju, P., Mishra, Y., Sharam, S.M. and Tawar, M.L. 1982. Correlation response in Soybean,. *J NKVVRes. J*., **16**(2): 105-111. [Cross Ref]

Ramana, M. V., Pramilarani, B. and Satyanarayana, A. 2000. Genetic variability, correlation and path analysis in soybean. *Journal of Oilseed Research*., **17**(1): 32-35.

Sharma, S.M., Raw, S.K. and Goswami. U. 1983. Genetic variation, correlation and regression analysis and their implications in selection of exotic soybean. *Mysore J. agric.sci*., **17**(1) : 26-30.

Shwe, U.H., Murty, B.R., Singh, H.B. and Rao, U.M.B. 1972. Genetic divergence in recent elite strains of soybean and groundnut in India. *Indian J. Genetics*., **32**: 285-298.