

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.912.017>

Correlation Studies in F₃ Segregating Generations of Soybean

Pradnya P. Bambodkar^{1*}, Ritik D. Bisane¹, Shubhangi K. Maraskole²,
Vasant S. Pawar¹ and Sandeep R. Kamdi¹

¹Section of Agriculture Botany, COA Nagpur, Dr. Panjabrao Deshmukh Krishi Vidyapeeth
Akola, India

²Agricultural Botany Section, Dr. Balasaheb Sawant Konkan krishi Vidyapeeth,
Dapoli, Dist. Ratnagiri, India

*Corresponding author

ABSTRACT

Keywords

Soybean,
Correlation,
Yield

Article Info

Accepted:
04 November 2020
Available Online:
10 December 2020

Eight F₃ populations and one check (JS 335) of soybean were evaluated at the experimental farm of Agricultural Botany Section, College of Agriculture Nagpur during Kharif 2018-19 using randomized block design with 3 replications. The objectives of the study were to investigate the correlations among seven characters of soybean which will be used for the selection of seed yield in early generations. The data regarding seven characters viz., days to first flower, plant height, days to maturity, number of branches plant⁻¹, number of pods plant⁻¹, hundred seed weight and seed yield plant⁻¹ were evaluated for phenotypic- genotypic correlations. Yield plant⁻¹ showed highly significant positive phenotypic and genotypic correlations for the number of pods plant⁻¹ ($r_g=0.840^{**}$, $r_p=0.645$) and 100 seed weight ($r_g=0.877^{**}$, $r_p=0.738^{**}$) which indicates the importance of these characters during selection in the breeding program.

Introduction

Soybean [*Glycine max* (L.) Merrill.] is an important global legume crop that belongs to the family Leguminoceae and subfamily Papilionoideae. Soybean has 20 chromosome pairs ($2n = 40$) and is a self-fertile species with less than 1% outcrossing (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 oil is

utilized as an edible oil for human consumption throughout India. It is one of the most common vegetables cooking oil used in food processing industries. 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). Soybean is recognized for its benefits to human health such as the cholesterol lowering effect of protein as approved recently by the United States Food and Drugs Administration. Consumption of soybean-based foods may also reduce the risk of colon cancer, possibly due to the presence of

sphingolipids (Symolon *et al.*, 2004). Research is underway to ascertain the possible benefits of soybean in other areas of human health such as cancer, osteoporosis and postmenopausal discomfort (Krishna, 2001).

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) as compared to other countries (world average 2.2 t/ha). The versatile nature of this crop, its increasing contribution to industrial, agricultural and medicinal sectors and the wide yield gap indicate the necessity of identifying and developing high yielding soybean cultivars suitable for food processing and human consumption (Fasoula and Boerma, 2007).

Grain yield, an extremely complex trait, is the result of the expression and association of several plant growth components. Associations between these traits can be evaluated by correlation analysis, which helps in the simultaneous selection for more than one character (Akhtar *et al.*, 2010; Sathya and Jebaraj, 2013; Semahegn and Tesfaye, 2016). The degree of relatedness between important plant traits is an index that can be used to predict yield responses concerning changes associated with a particular character (Malek *et al.*, 2014). So, for soybean, identification of key characters associated with yield and other contributing components is important for maximizing yields (Aditya *et al.*, 2011; Meitei *et al.*, 2014; Jain *et al.*, 2015). Correlation studies enable the breeder to study the strength of the relationship between various characters as well as the magnitude and direction of changes expected during selection. This investigation provides information that could lead to the development of desirable genotypes in future breeding programmes.

Materials and Methods

The experimental material comprised of eight F₃ crosses selected on the basis of yield performance of F₂ obtained from Indian institute of soybean research Indore and one check JS-335. The list of selected eight crosses is given below in table 1.

During *kharif* 2018, seeds from each cross (8 crosses) of F₂ generation along with a check (JS-335) were sown to raise F₃ generation using a randomized block design with 3 replications. Each plot comprises five rows of each F₃ population and one row of the 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. The sowing was undertaken on the fertile and well-leveled piece of land at the research farm of Agricultural Botany Section, College of Agriculture Nagpur. Total 20 plants were chosen randomly from each of 8 F₃ population and 5 selected plant 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).

Phenotypic and genotypic correlation coefficients between characters were computed by utilizing respective components of variance and covariance by the following formula suggested by Miller *et al.*, (1958).

$$r_{xy} = \frac{\text{Covariance } x, y}{\sqrt{(\text{Variance } x) (\text{Variance } y)}}$$

where,

r_{xy} = Correlation coefficient between character x and y,

To test the significance of correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at t-2 d. f. at two levels of probability, viz., 5% and 1%.

Results and Discussion

Knowledge of the relationship among plant characters is useful while selecting traits for yield improvement. The correlation coefficient was worked out among seven characters for the year 2018 to find out the

association of seed yield plant⁻¹ with its components at genotypic (r_g) and phenotypic (r_p) levels and are presented in table 2.

The data given in table 2 revealed that in general, genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlation coefficients for most of the characters. This indicates a greater contribution to the genotypic factor in the development of the character associations.

Table.1 List of F₃ crosses used for study

Sr. No.	Crosses
1.	Cat 3293 × NRC 2
2.	Cat 3293 × JS 90-41
3.	JS 97-52 × NRC-37
4.	JS 97-52 × DSb 1
5.	JS 97-52 × Ankur
6.	JS 97-52 × 104-31 [F ₆ (JS 97-52 × JS90-41)]
7.	KDS 726 × BNS 5
8.	PS 1556 × RSC 10-46

Table.2 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seven characters in F₃ generation of soybean

Characters		Days to first flower	Plant height (cm)	Days to maturity	Number of branches plant ⁻¹	Number of pods plant ⁻¹	100 seed weight (g)
Seed yield plant ⁻¹ (g)	r_g	0.178	0.738**	-0.324	0.572**	0.840**	0.877**
	r_p	0.218	0.374	-0.204	0.374	0.645**	0.738**
Days to first flower	r_g		0.242	0.053	0.038	0.091	0.333
	r_p		0.182	0.062	0.051	0.107	0.277
Plant height (cm)	r_g			-0.272	0.172	0.370	0.633**
	r_p			-0.233	0.314	0.273	0.374
Days to maturity	r_g				-0.743**	-0.335	-0.714**
	r_p				-0.575**	-0.256	-0.564**
No. of branches plant ⁻¹	r_g					0.540**	0.504*
	r_p					0.616**	0.428*
Number of pods plant ⁻¹	r_g						0.536**
	r_p						0.509*

*Significant at 5% level of probability; **Significant at 1% level of probability

The seed yield plant⁻¹ had highly significant and positive correlation with plant height ($r_g=0.783$) and number of branches plant⁻¹ ($r_g=0.572$) at genotypic level and number of pods plant⁻¹ ($r_g=0.840$, $r_p=0.645$) and 100 seed weight ($r_g=0.877$, $r_p=0.738$) at both genotypic and phenotypic levels.

Days to first flower ($r_g =0.178$, $r_p =0.218$) showed positive but non significant association with seed yield plant⁻¹ whereas days to maturity ($r_g=-0.324$, $r_p =-0.204$) had negative and nonsignificant association with seed yield plant⁻¹ at both genotypic and phenotypic levels. Similar results were observed by Sadat *et al.*, (2010), Patil *et al.*, (2011) and Guleria *et al.*, (2018). In contrast, the negative correlation of seed yield plant⁻¹ with days to maturity was reported by Akram *et al.*, (2015).

The days to first flower had positive but non significant association at genotypic and phenotypic level with plant height ($r_g=0.242$, $r_p=0.182$), days to maturity ($r_g=0.053$, $r_p=0.062$), number of branches plant⁻¹ ($r_g=0.038$, $r_p=0.051$), number of pods plant⁻¹ ($r_g=0.091$, $r_p=0.107$) and 100 seed weight ($r_g=0.333$, $r_p=0.277$).

Plant height exhibited a highly positive and significant correlation with 100 seed weight ($r_g=0.633$) at the genotypic level whereas positive but non-significant ($r_p=0.374$) association at the phenotypic level. Days to maturity exhibited negative and non-significant association ($r_g=-0.272$, $r_p=-0.233$) with plant height (cm) at both levels.

The positive but non significant association was exhibited by the number of branches plant⁻¹ ($r_g=-0.314$, $r_p=0.172$) and the number of pods plant⁻¹ ($r_g=0.370$, $r_p=0.273$) at genotypic and phenotypic levels.

The days to maturity exhibited highly significant but negative correlation at genotypic and phenotypic levels with the number of branches plant⁻¹ ($r_g=-0.743$, $r_p=-0.575$) and 100 seed weight ($r_g=-0.714$, $r_p=-0.564$).

The negative and non-significant association was exhibited by the number of pods plant⁻¹ ($r_g=-0.335$, $r_p=-0.256$) with days to maturity at both genotypic and phenotypic levels.

The number of branches plant⁻¹ exhibited a highly significant and positive association with the number of pods plant⁻¹ ($r_g=0.540$, $r_p=0.616$) at genotypic and phenotypic levels and significant and positive association with 100 seed weight ($r_g=0.536$, $r_p=0.509$) at both the levels.

The number of pods plant⁻¹ had a significant and positive association with 100 seed weight ($r_g=0.536$, $r_p=0.509$) at both the genotypic and phenotypic levels.

In conclusions the selection for high yielding genotypes should focus on the strongly positively associated characters of crop plants on their yield. From the present investigation it can be concluded that in soybean, traits like the number of pods plant⁻¹, number of branches plant⁻¹, plant height and 100 seed weight showed positive correlation with yield. Hence these traits can be used as selection indices in soybean to bring about the improvement in yield.

References

- Aditya, J.P., B.P. Pushpendra and B. Anuradha, 2011, Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill), *J. Central European Agriculture*, 12(1): 27-34.
- Akhter, T., N.A. Ivy, M. G. Rasul and M.A.K. Mian, 2010, Variability and character association of reproductive traits in exotic rice germplasm, *Bangladesh J. Plant Breed. Genet.* 23(1): 39-43.
- Akram, S., B. M. N. Hussain, M. A. A. Bari, D. J. Burritt and M. A. Hossain. 2015. Genetic variability and association analysis of Soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. *Plant Gene and Trait*, 7: 1-11.

- Fasoula, V. A. and H. R. Boerma, 2007. Intra-cultivar variation for seed weight and other agronomic traits within three elite soybean cultivars. *Crop Sci.* 47: 367-373.
- Fisher, R. A. and F. Yates. 1938. Statistical tables for Biological Agricultural and Medicinal Research, 6th Edition, Longman Group Limited, England, pp. 37-38 & 134-139.
- Guleria, H., P. Kumar, B. Jyoti, A. Kumar, A. Paliwal and Arunima Paliwal. 2018. Genetic variability and correlation analysis in soybean (*Glycine max* (L.) Merrill) genotypes. *Int. J. Chemical Studies*, 7(1): 1928-1932.
- Jain S., S. C. Srivastava, K. S. Singh, Y. M. Indapurkarand B. K. Singh, 2015. Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Agricultural Research Communication Center, Legume Res.* 38(2): 182-184.
- Krishna, M. M. 2001. Health benefits and food application of isolated soy-protein. *India Soy. Forum*, 170-173.
- Malek M.A., M. Y. Raffi, M. S. S. Afroj, U. K. Nath and M. M. A. Mondol, 2014, Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. *The Scientific World Journal*, 1-12.
- Meitei K.M., G. C. Bora, J. S. Singh and K. A. Sinha, 2014. Morphology based genetic variability analysis and identification of important characters for tomato (*Solanum lycopersicum* L.) crop improvement. *American-Eurasian J. Agric. Environmental Sci.* 14(10): 1105-1111
- Miller P., Williams J., Robinson H., and Comstock R., 1958, Estimates of genotypic and environmental variances and co-variances in upland cotton and their implications in selection, *Agronomy Journal*, 50: 126-131.
- Patil, S. S., M. R. Naik, P. P. Patil and D. A. Shinde, 2011. Genetic variability, correlation and path analysis in soybean. *J. Legume Res.* 34 (1): 36-40.
- Sadat, H. A., G. A. Nematzadeh, N. B. Jelodar and O. G. Chapi. 2010. Genetic evaluation of yield and yield components at advanced generation in rapeseed (*Brassica napus* L.). *Afr. J. Res.* 5(15): 1958-1964.
- Sathya, R., and S. Jebaraj, 2013. Inter-Relationship and cause effect analysis among drought and physiological traits in three-line aerobic rice hybrids. *Plant Gene and Trait*, 4: 70-73.
- Semahegn Y., and M. Tesfaye, 2016. Characters associations and path analysis in safflower (*Carthamus tinctorious*) accessions. *Molecular Plant Breeding*, 7(31): 1-5.
- Shurtleff, W. and A. Aoyagi, 2007. The soybean plant: Botany, Nomenclature, Taxonomy, Domestication and Dissemination. *Soy info Center, California*. pp. 40.
- Symolon, H., E. M. Schmelz, D. L. Dillehay, A. H. Merrill, 2004. Dietary soy sphingolipids suppress tumorigenesis and gene expression in 1, 2-Dimethylhydrazine treated CF1 Mice and Apc (Min/+) Mice. *J. Nutr.* 134(5): 1157-1161.

How to cite this article:

Pradnya P. Bambodkar, Ritik D. Bisane, Shubhangi K. Maraskole, Vasant S. Pawar and Sandeep R. Kamdi. 2020. Correlation Studies in F₃ Segregating Generations of Soybean. *Int.J.Curr.Microbiol.App.Sci.* 9(12): 132-136. doi: <https://doi.org/10.20546/ijcmas.2020.912.017>