



Study on genetic variability, heritability and genetic advance in Soybean [*Glycine max* (L.) Merrill]

Ravindra Kumar Jain^{*1}, Arunabh Joshi¹, Hem Raj Chaudhary², Abhay Dashora² and Champa Lal Khatik³

Department of Molecular Biology and Biotechnology, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur-313 001, Rajasthan, India

Received: 30-03-2017

Accepted: 09-08-2017

DOI: 10.18805/LR-3874

ABSTRACT

Soybean, an important legume crop, serves as a good source of protein and oil with tremendous ability to fix atmospheric nitrogen for soil improvement. To study the genetic variability, genotypic, phenotypic and environmental coefficient of variation, broad sense heritability and genetic advance in soybean, a field experiment was conducted during *Kharif* 2013. The experiment, laid out in a randomized block design (RBD) with three replications, comprised of 24 genotypes and observations on 9 traits of soybean were recorded. In this experiment, analysis of variance indicated that significant variation were present among the different genotypes of the soybean for all the traits under study. The highest genotypic (GCV) and phenotypic coefficient of variation (PCV) were exhibited by the test weight, number of pods per plant, harvest index and plant height. The PCV was found higher than GCV which indicates the important role of environment in the expression of the characters. High heritability and high genetic advance were observed in the test weight, number of pods per plant, harvest index and plant height. The combination of the high heritability and high genetic advance provide the clear image of the trait in the selection process for crop improvement programme.

Key words: Crop improvement, Genetic advance, Genetic variability, GCV, PCV, Soybean.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is known as “Golden Bean” and “Miracle Crop” of the 21st century because of its multiple uses. It contains a high amount of quality protein (42 per cent) and 20 per cent oil (Gopalan *et al.*, 1994) rich in lysine and vitamins A, B and D. Taxonomically, soybean belongs to the order *Fabales* the family *Fabaceae*, the subfamily *Faboideae* and the genus *Glycine*. It is a diploidized allotetraploid ($2n = 40$) and autogamous plant. It has a fairly wide range of adaptation involving a wide array of climatic, soil and growth conditions (Kumar *et al.*, 2015).

For protein sources, soybean can be used in different ways such as soy milk, soy meat, snaps, tofu etc. For oil source, some products have been produced from soybean oil, such as cooking oil, margarine, cosmetics, biodiesel etc. Soybean oil in various more refined forms has vital chemical uses in varnishes, paints, lubricants, pharmaceuticals, sealants and soaps. Soybean meets the nutritional needs of humans and other animals (He and Chen, 2013; Malek *et al.*, 2014; Ghosh *et al.*, 2014). It contains numerous compounds that can act as antioxidants and are beneficial to human health, as they diminish the risk of many diseases (Kumar *et al.*, 2014). Besides fixing the atmospheric

nitrogen, this crop has the ability to grow in a range of environments, to reduce soil erosion, to suppress weeds and to suit inter as well as sequential cropping pattern.

The knowledge of genetic variability existing within the different parameters contributing to yield is an important criterion for yield enhancement but in highly self-pollinated crops like soybean, natural variation is narrow resulting in limited scope for selection opportunity. Genetic diversity analysis provides the insight for selection of appropriate parents for combining new alleles for the trait in a crop improvement programme (Rani *et al.*, 2016). For the effective selection of superior genotype to use in hybridization programme for the development of superior varieties, proper study of genetic variability due to genetic and non-genetic causes and other genetic parameters is necessary (Prasad *et al.*, 2012). It is desirable for plant breeder to know the extent of relationship between yield and its various components, which will inevitably facilitate selection of desirable characteristics (Jain *et al.*, 2015). Large variability in the initial breeding material ensures better chances of producing new desired forms of a crop (Raturi *et al.*, 2014).

Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are useful

*Corresponding author's e-mail: rjjainravindra@gmail.com

¹Department of Molecular Biology and Biotechnology and Plant Breeding and Genetics, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur-313 001, Rajasthan, India, ²Agriculture Research Station, Kota, Agriculture University, Kota- 324 001, Rajasthan, India, ³Plant Breeding & Genetics, Rajasthan College of Agriculture, MPUAT

biometric tools for measuring genetic variability (Aditya *et al.*, 2011). Hence, characterizing the genetic background of soybean and determining breeding values should be done before carrying out any improvement programme (Agong *et al.*, 2001).

In crop species, phenotypes are controlled mainly by genetic make-up of such crops coupled with the kinds of environment where they are being grown as well as the interactions between the genotypes and the environments (Ajayi *et al.*, 2014). It is therefore necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance (Athoni and Basavaraja, 2012). However, inheritance of quantitative character is often influenced by variation in other characters which may be due to pleiotrophy or genetic linkage (Harland, 1939). Hence, knowledge of association between yield and its components obtainable through estimation of genotypic and phenotypic correlations helps in a great deal to formulate selection strategies to develop suitable genotypes (Athoni and Basavaraja, 2012). Correlation study provides a measure of association between characters and helps to identify important characters. Associations between many yield-contributing characters 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 present research programme was imitated to understand the genetic variation of different Soybean

[*Glycine max* (L.) Merrill] genotypes for yield and related traits.

MATERIALS AND METHODS

The field study was conducted at Agriculture Research Station (ARS), Kota, Agriculture University, Kota (Rajasthan) to analyze the genetic variability, genotypic, phenotypic and environmental coefficient of variation, broad sense heritability and genetic advance during *Kharif*, 2013. Twenty four genotypes of soybean were procured from ARS, Kota. Source and pedigree of the material are given in Table-1.

The field experiment was laid out in randomized block design (RBD) with three replications. Twenty four genotypes were planted with a spacing of 30 cm row to row and 10 cm plant to plant distance. Fertilizers were applied (40 kg N/ha, 40 kg P₂O₅/ha 40 kg K₂O/ha and 30 kg S/ha) at the time of sowing. All the recommended agronomical practices and plant protection measures were adopted to raise the healthy crop.

At maturity five competitive plants were randomly selected from each replication of each genotype for recorded observation, except for days to 50 per cent flowering and days to maturity observation recorded on plot basis. The procedure adopted for recorded observations / data on different characters are as follow: Plant height (cm), Days to 50 per cent flowering, Days to maturity, Number of branches per plant, Number of pods per plant, Number of seeds per pod, Seed yield per plant (g), Test weight (g) and Harvest index (%).

Table 1: Pedigree and source of 24 genotypes of *Glycine max* L. Merrill

Genotypes	Pedigree	Source
KDS-726	JS-93-05 X EC-241780	SANGLI (MH)
PS-1539	PS-1024 X JS-335	PANTNAGAR
DS-3050	DT-23 X DT-227	DELHI
SL-983	SL-525 X PK-1368	LUDHIANA
DS-2961	MO-74 X JS-335	DELHI
RKS-109	RKS-224 X PK-1024	KOTA
SL-955	SL-599 X PK-1283	LUDHIANA
DS-3047	DT-23 X DT-27	DELHI
AMS-1001	Mutant of JS-93-05	AMARAWATI
JS-20-79	JS-97-52 X JS-(15) 90-5-12-1	JABALPUR
MACS-1419	EC-391343 X MACS-450	PUNE
NRC-98	Ankur X PK-1024	INDORE
RVS-2002-4	JP-120 X JS-335	SIHORE
KDS-722	AMS-99 X EC-241780	SANGLI (MH)
MAUS-609	Himso-1563 X MAUS-71	PARBANI
NRC-107	Mutant of NRC-37	INDORE
MACS-1410	MAUS-144 X MACS-450	PUNE
JS-20-53	JS-97-52 X JS-20-02	JABALPUR
PS-1543	PS-1029 X JS-335 X PS-1241	PANTNAGAR
Himso-1685	H-330 X HARDEE	PALAMPUR
RVS-2002-22	NRC-37 X JS-39-05	SIHORE
RKS-111	RKS-45 X RKS-24	KOTA
BAUS-27	PK-472 X L-119	RANCHI
RSC-10-17	MAUS-144 X RAUS-5	RAIPUR

The data were subjected for analysis of variance by Panse and Sukhatme (1985). The genotypic and phenotypic coefficient was calculated by Kwon and Torrie (1964) technique. The genetic advance in percentage of mean was calculated by using Falconer (1989) formula.

RESULTS AND DISCUSSION

24 soybean genotypes with 9 traits have been selected to study the genetic variability, GCV, PCV and environmental coefficient of variation.

It is clear from Table-2 that significant variations were present between the genotypes for all the recorded traits. This variation is very important for the plant breeder and selection is effective when magnitude of variability in the breeding population is too enough. Table-3 depicted that the observation between the genotypes were highly significant for all the recorded traits. Genotypic variance, phenotypic variance and environmental variance, genotypic coefficient of variation, phenotypic coefficient of variation and environmental coefficient of variation, broad sense heritability and response to the selection for nine recorded traits were shown in Table-4.

The trait seed test weight exhibited the highest genotypic and phenotypic variance i.e. 104.03 and 43.26 respectively and followed by the number of pods per plant that have genotypic variance 64.94 and phenotypic variance 95.08. Lowest genotypic and phenotypic variance was recorded for the traits of number of seeds per pod and number of branches per plant i.e. 0.05 and 0.03 for number of seed and 0.14 and 0.18 for number of branches respectively (Table-4). The coefficient of phenotypic, genotypic and environmental variance was also calculated for all the traits under study. The genotypic coefficient of variance was range from 12.78 % (number of seeds /pods) to 98.76% (seed test weight). Maximum genotypic coefficient of the variation was observed for the seed test weight (98.76%) followed by the

number of pods per plant (95.08%). Phenotypic coefficient of variation was observed for the number of pods per plant (63.82%) followed by the seed test weight (63.69%). In general, estimate of phenotypic coefficients of variance (PCV) was slightly higher than their corresponding genotypic coefficient of variance (GCV) indicating the important role of environment in the expression of the characters. The highest genotypic and phenotypic coefficient of variation observed for the traits seed test weight, number of pods per plant, harvest index and seed yield per plant. It indicates that selection can be applied on the traits to isolate more promising line. Similar trends of results were also reported by Aditya *et al.*, (2011), Akram *et al.*, (2016), Athoni and Basavaraja, (2012) in soybean. The traits such as number of seeds per pod and number of branches per plant exhibited low PCV and GCV which indicated that the breeders should go for source of high variability for these traits to make improvement.

In a population, observation is due to both factors *i.e.* genetics and environmental, whereas genetic variability is the only heritable from generation to next generation so the heritability alone does not give an idea about the expected gain in the next generation, but it has to be considered in conjunction with the genetic advance. The traits those exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such traits are controlled by the additive gene and less influenced by the environment (Panse and Sukhatme, 1995). The broad sense heritability was higher for all the recorded traits. For efficient selection we cannot solely believe on heritability. The combination of high heritability with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable genotypes. High heritability was observed in traits *viz.*, number of seeds per pod, plant height, days to maturity, harvest index and

Table-2: Mean and Range performance of the traits among the *G. max* genotypes

Traits	Minimum	Maximum	Average performance
Days to 50% Flowering	30.67	48.67	41.25
Days to Maturity	88.33	105.00	98.11
Plant Height (cm)	39.69	56.75	49.69
No. of Branches/Plant	5.33	8.00	6.88
No. of Pods/Plant	59.00	90.00	71.83
No. of Seeds/Pod	2.33	3.67	2.94
Test Weight (g)	95.87	143.73	106.66
Seed Yield/Plant (g)	17.02	30.08	22.98
Harvest Index (%)	32.96	58.28	42.59

Table-3: Analysis of variance of the different characters among the genotypes of the *G. max*

Source of Variation	Degree of Freedom	Days to 50% Flowering	Daysto Maturity	Plant Height	No. of Branches/Plant	No. of Pods/Plant	No. of Seeds/Pod	Test Weight	Seed Yield/Plant	Harvest Index
MSS	23	27.08*	57.90*	69.14*	1.35*	217.65*	0.19*	337.85*	45.29*	118.28*
Error	46	3.240	9.028	13.227	0.135	22.846	0.049	25.763	3.242	14.552

** Highly Significant at 0.01% level * Significant at 0.05% level.

Table-4: Mean Sum of squares, genotypic, phenotypic and environmental variance and coefficient of variation, broad sense heritability and response to selection.

Characters	G.Variance	GCV %	P.Variance	PCV %	E Variance	ECV%	H ² (%)	GA	GA as %age of Mean
Days to 50% Flowering	7.95	3.73	43.89	30.07	3.24	28.03	46.92	18.52	44.89
Days to Maturity	16.29	8.44	40.75	29.33	9.02	30.32	51.79	29.27	29.83
Plant Height (cm)	18.64	10.62	61.25	46.23	13.22	51.58	56.97	34.44	69.30
No. of Branches/Plant	0.41	0.18	24.24	16.16	0.135	14.00	44.44	3.96	57.47
No. of Pods/Plant	64.94	29.26	95.08	63.82	22.84	56.39	45.06	50.83	70.77
No. of Seeds/Pod	0.05	0.03	12.78	10.49	0.049	12.91	67.36	2.07	70.28
Test Weight (g)	104.03	43.26	98.76	63.69	25.76	49.14	41.59	59.38	55.68
Seed Yield/Plant (g)	14.02	5.75	78.81	50.48	3.24	37.89	41.04	21.51	95.30
Harvest Index (%)	34.58	16.38	90.91	62.56	14.55	58.97	47.36	38.99	93.18

Table- 5: Potential donor genotypes for yield and other recorded traits.

Characters	Potential Donors
Days to 50% Flowering	NRC-107, DS-2961, RVS-2002-22
Days to Maturity	NRC-107, BAUS-27, JS-20-53, RKS-111, RVS-2002-22
Plant Height (cm)	NRC-107, DS-2961,
No. of Branches/Plant	JS-20-79, RVS-2002-4, JS-20-53, BAUS-27
No. of Pods/Plant	PS-1539, NRC-98, SL-955, JS-20-53
No. of Seeds/Pod	JS-20-79, RVS-2002-4
Test Weight (g)	Himso-1685, PS-1539, KDS-726
Seed Yield/Plant (g)	Himso-1685, PS-1539, JS-20-79, PS-1543, JS-20-53, RVS-2002-4, SL-955, NRC-98
Harvest Index (%)	Himso-1685, PS-1539, PS-1543, JS-20-79

days to 50% flowering. High genetic advance was observed in traits *viz.*, seed test weight, number of pods per plant, harvest index, plant height and days to maturity. These traits are highly reliable during selection process of the genotypes. The genetic advance as percentage of mean for nine traits range from 29.83% (days to maturity) to 95.30% (seed yield per plant). The higher genetic advance as percentage of mean was recorded by seed yield per plant (95.30%), harvest index (93.18%), number of pods per plant (70.77%), number of seeds per pod (70.28%) and plant height (69.30%). In this experiment, some genotypes were identified as potential donors for the crop improvement of different traits (Table-5).

Several workers (Baraskar *et al.*, 2014; Chandrawa *et al.*, 2017; Malek *et al.*, 2014; Mishra *et al.*, 2015; and Reni and Rao, 2013) have also calculated genotypic and phenotypic components of variance, heritability and genetic advance for different yield characters in soybean and have revealed that selection was effective for a population with broad genetic variability and character with high heritability.

REFERENCES

- Aditya, J. P., Pushpendra, B. P. and Anuradha, B. (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.
- Agong, S. G., Schittenhelm, S. and Fried, W. (2001). Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* Mill.) germplasm. *Journal of Food Technology in Africa*, **6**(1): 13-17.
- Ajayi, A. T., Adekola, M. O., Taiwo, B. H. and Azuh, V. O. (2014). Character Expression and Differences in Yield Potential of Ten Genotypes of Cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of Plant Research*, **4**(3): 63-71.
- Akhter, T., Ivy, N. A., Rasul, M. G. and Mian, M. A. K. (2010). Variability and character association of reproductive traits in exotic rice germplasm. *Bangladesh Journal of Plant Breeding and Genetics*, **23**(1): 39-43

From the results of the present study, it can be concluded that direct selection can be done for most of the yield attributing traits since it exhibited high genetic variability and high range of variation. The phenotypic coefficient of variation was found higher than genotypic coefficient of variation which indicates the important role of environment in the expression of the characters. The highest genotypic (GCV) and phenotypic coefficient of variation (PCV) were exhibited by the test weight, number of pods per plant, harvest index and plant height which indicates the presence of wider variability for these traits in the genotypes studied. High heritability and high genetic advance were observed in the test weight, number of pods per plant, harvest index and plant height. The combination of the high heritability and high genetic advance provide the clear image of the trait in the selection process for crop improvement programme.

ACKNOWLEDGEMENT

Authors gratefully acknowledge the financial assistance from RKVY project "Validation of important crop varieties through DNA fingerprinting".

- Akram, S., Hussain, B. M. N., Al-Baril, M. A., Burritt, D. J. and Hossain, M. A. (2016). Genetic Variability and Association Analysis of Soybean [*Glycine max* (L.) Merrill] for Yield and Yield Attributing Traits. *Plant Gene and Trait*, **7(13)**: 1-11.
- Athoni, B. K. And Basavaraja, G. T. (2012). Association analysis, genetic variability and genetic diversity studies in soybean [*Glycine max* (L.) Merrill]. *Asian Journal of Bio Science*, **7(2)**: 114-118.
- 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.
- Chandrawat, K. S., Baig, K. S., Hashmi, S., Sarang, D. H., Kumar, A. and Dumai, P. K. (2017). Study on genetic variability, heritability and genetic advance in soybean. *Int. J. Pure App. Biosci.*, **5 (1)**: 57-63.
- Falconer, D. S. (1989). Introduction to Quantitative Genetics (3rd ed.). Logman Scientific and Technical, Logman House, Burnt Mill, Harlow, Essex, England.
- Ghosh, J., Ghosh, P. D. and Choudhury, P. R. (2014). An assessment of genetic relatedness between soybeans [*Glycine max* (L.) Merrill] cultivars using SSR markers. *American Journal of Plant Sciences*, **05**: 3089-3096.
- Gopalan, C., Ramashastry, B. V. and Balasubramanian, S. C. (1994). Nutritive Value of Indian Foods, *Indian Council of Medical Research*, pp. 24-26
- Harland, S. C. (1939). The genetics of cotton. Jonathan Cape, London (United Kingdom).
- He, F. J. and Chen, J. Q. (2013). Consumption of soybean, soy foods, soy isoflavones and breast cancer incidence: Differences between Chinese women and women in Western countries and possible mechanisms. *Food Science and Human Wellness*, **2**: 35-38.
- Jain, S., Srivastava, S. C., Singh, S. K., Indapurkar, Y. M. and Singh, B. K. (2015). Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill] *Legume Research*, **38(2)**: 182-184.
- Kumar, A., Pandey, A. and Pattanayak, A. (2015). Assessment of genotypic variation in soybean (*Glycine max*). *Legume Research*, **38(2)**: 174-177.
- Kumar, A. V., Kumar, S., Lal, K., Jolly, M. and Sachdev, A. (2014), Influence of gamma rays and ethylmethanesulphonate (EMS) on the levels of phytic acid, raffinose family oligosaccharides and antioxidants in soybean seeds of different genotypes, *Journal of Plant Biochemistry and Biotechnology*, **24**: 204-209.
- Kwon, S. H. and Torrie, J. H. (1964). Heritability and interrelationship of two soybean (*Glycine max* L.) genotypes. *Crop Science*, **4**: 196-198.
- Malek, M. A., Raffi, M. Y., Afroj, M. S. S., Nath, U. K. and Mondol, M. M. A. (2014), Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants, *The Scientific World Journal*, 1-12.
- Mishra, S., Pancheshwar, D. K., Singh, P. and Jha, A. (2015). Study of Genetic Variability in recently evolved genotypes of soybean [*Glycine max* (L.) Merrill]. *Trends in Biosciences*, **8(19)**: 5390-5393.
- Panes, V. G. and Sukhatme, P. V. (1995). Statistical Methods for Agricultural Workers (3rd ed.). ICAR, New Delhi.
- Panse, V. G., and Sukhatme, P. V. (1985). Statistical Methods for Agricultural Research Workers. Indian Council of Agricultural Research, New Delhi.
- Prasad, B., Bahuguna, A. and Shukla, D. K. (2012). Genotypic variation studies of perilla(*Perilla prutescens* L.) germplasm under north-west Himalayan agrisystem. *Environment and Ecology*, **30(4)**: 1235-1237.
- Rani, A., Kumar, V., Gill, B. S., Morya, V. and Rawal, R. (2016). Assessment of genetic diversity of soybean genotypes differing in resistance against yellow mosaic virus using simple sequence repeat markers. *Legume Research*, **39(5)**: 674-681.
- Raturi, A., Singh, S. K., Sharma, V. and Pathak, R. (2014). Genetic variability and interrelationship among qualitative and quantitative traits in mungbean. *Legume Research*, **37(1)**: 1 – 10.
- Reni, Y. P. and Rao, Y. K. (2013). Genetic Variability in Soybean [*Glycine max* (L) Merrill]. *International Journal of Plant, Animal and Environmental Sciences*, **3(4)**: 35-38.
- Sathya, R. and Jebaraj, S. (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 Tesfaye, M. (2016). Characters associations and path analysis in safflower (*Carthamus tinctorious*) accessions, *Molecular Plant Breeding*, **7(31)**: 1-5.