



Evaluation of soybean (*Glycine max*) germplasm for some important morphological traits using multivariate analysis

KSHITIZ KUMAR PAWAR¹, N R RANGARE² and A K SINGH³

Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed- to- be University,
Allahabad, Uttar Pradesh 211 007

Received: 16 March 2012; Revised accepted: 13 February 2014

Key words: D², Genetic divergence, Multivariate analysis, Variability

Soybean [*Glycine max* (L.) Merrill] is a papilionoid legume that has a fairly wide range of adaptation involving a wide array of climatic, soil and growth conditions though it is mostly grown on rainfed land. It is now cultivated throughout East and South East Asia for food, animal feed and medicine. Improvement of yield, oil content in soybean is attributed to increased use of genetically diverse parents in breeding programme. However, in case of Indian soybean varieties, a narrow genetic base has been observed. This is probably due to use of same parents for evolving new varieties. Hence, knowledge of genetic divergence in the available cultivars is of immense importance for selecting the parents to be used in hybridization programme for obtaining desirable genetic recombination's (Rajesh *et al.* 2004, Veni *et al.* 2008 and Kayande *et al.* 2009). Mahalanobis D² statistic described by (Rao 1952) is a powerful tool used to quantify the degree of genetic divergence between the genotypes and relate cluster pattern with geographic origin. The objective of this study was to determine genetic variability and genetic diversity from the available germplasm.

The present experiment was conducted at the field experimentation centre, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, UP during *khari*f 2010-11. The material used in the study comprised of 42 genotypes of soybean procured from Directorate of Soybean Research, Indore, MP were planted in randomized block design with three replications. The experimental plot comprised 3 rows each of 3 meter in length. Row to row and plant to plant spacing was maintained at 45 and 10 cm. From each genotype five plants were randomly taken from each replication and observations were recorded for days to

50 percent flowering, number of pods/plant, pod length, number of branches/plant, plant height, days to maturity, number of grains/pod, 100-grain weight, grain yield/plant, biological yield, harvest index and oil content. The estimates of variance and genetic divergence were computed using genetic model of INDOSTAT software.

The analysis of variance due to genotypes showed significant difference, this revealed that the great variation among the genotypes for all the character under study. Phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect to all the characters (Table 1). The characters pods/ plant, number of branches/plant, grain yield/ plant and harvest index showed high PCV and GCV, while plant height and 100-grain weight showed moderate PCV and GCV values, whereas days to 50 per cent flowering, pod length, days to maturity, and oil content showed low PCV and GCV, further grains/ pod showed low GCV and moderate PCV (Karnwal *et al.* 2009, Burli *et al.* 2010 and Almeida *et al.* 2011).

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Johnson *et al.* 1955). High heritability accompanied with high genetic advance for number of pods/plant, number of branches/plant, plant height, 100-grain weight, grain yield/ plant, biological yield/plant and harvest index indicates that most likely the heritability is due to additive gene effect and selection may be effective for improvement of these characters. High heritability with moderate genetic advance was observed for days to 50% flowering and number of grains/pod, indicate that these characters were less influenced by environment but governed by additive and non-additive gene action and selection for such traits may not be rewarding. High heritability coupled with low genetic advance was observed for days to maturity, indicates non-additive type of gene action. Moderate heritability coupled low genetic advance was observed for pod length and oil content, indicates the character were highly influenced by environmental effect and need to be tested under diverse environments for effective selection (Bhushan *et al.* 2006, Gupta and Punetha 2007). (Table 1).

¹Ph D Scholar (email: kshitizpawar@hotmail.co.in), Department of Genetics and Plant Breeding, ³Principal Scientist (email: akspbrewa@rediffmail.com), Department of Plant Breeding and Genetics, College of Agriculture, Rewa, JNKVV, Jabalpur, Madhya Pradesh 486 001; ²Assistant Professor (email: nrrangare@yahoo.co.in), Department of Genetics and Plant Breeding, College of Agriculture, Janjgir-Champa, IGAU, Raipur, Chhattisgarh 495 668

Table 1 Estimation genetic parameters for different characters in 42 genotypes of soybean

Character	Replication (df=02)	Genotypes (df=41)	Error (df=82)	Range	GCV(%)	PCV(%)	h ²	GA%	CV	SEm±	CD(P=0.05)
Days to 50 % flowering	9.15*	43.93*	0.55	39.00-57.00	8.01	8.16	96.29	16.20	1.57	0.43	1.21
Number of pods/plant	9.46	3546.70*	5.93	53.80-205.13	33.57	33.65	99.5	68.98	2.38	1.41	3.96
Pod length	0.09	0.17*	0.06	3.32-4.42	5.40	8.74	38.15	6.87	6.87	0.14	0.41
Number of branches/plant	0.04	5.20*	0.05	3.13-8.40	24.47	24.85	96.94	49.62	4.34	0.13	0.38
Plant Height	3.62	249.50*	1.43	41.93-95.33	14.98	15.11	98.3	30.60	1.97	0.69	1.95
Days to maturity	0.05	49.60*	1.62	90.33-117.33	4.00	4.19	90.78	7.84	1.27	0.74	2.07
Number of grain/pod	0.08*	0.15*	0.02	1.78- 2.68	9.31	11.16	69.55	15.99	6.16	0.08	0.23
100 grain weight	0.45	4.75*	0.26	5.72- 10.80	14.32	15.55	84.71	27.14	6.08	0.30	0.84
Grain yield/plant	0.08	61.73*	0.67	5.00- 25.60	30.91	31.42	96.78	62.64	5.64	0.48	1.34
Biological yield/plant	2.50	329.21*	5.42	15.33- 58.33	26.86	27.53	95.22	54.00	6.02	1.34	3.78
Harvest index %	205.99*	268.18*	3.73	16.96- 56.75	24.25	24.76	95.94	48.93	4.99	1.12	3.14
Oil content	0.54	1.87*	0.79	15.19- 18.99	3.38	6.04	31.23	3.89	5.01	0.51	1.45

*: significant, **: highly significant

Success of any crop improvement programmes mainly depends on amount of diversity available in the crop. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. All the 42 genotypes were grouped into 7 clusters based on D² analysis. Cluster IV was the biggest with 13 genotypes followed by cluster I with 10 genotypes, cluster II contains 8 genotypes, the cluster VI contains 5 genotypes, and cluster V contains 4 genotypes. The remaining clusters III, VII were all solitary each containing single genotype (Table 2). The average D² values ranged from 0.00 to 15964.43. Intra cluster distance exhibited a range of 0.00 to 774.50 and inter cluster distance ranged from 898.25 to 15964.43 (Table 3). From the present investigation, it was clear that I comprising are the most divergent cluster. Cluster III showed maximum inter cluster distance with four clusters, whereas cluster VII was farthest with two clusters. Therefore, it can be concluded that the genotypes present in these clusters can be utilized for successful hybridization programme. Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank (Table 4). It has been observed that oil percent was highest contributor towards divergence followed by pods/plant, plant height, days to 50% flowering, grain yield/plant and 100-grain weight. While, grains/pod was the least contributor towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations (Gohil *et al.* 2007, Kayande *et al.* 2009 and Santoset *et al.* 2012). Further, analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence. The variation observed in cluster mean also points to the degree of variability (Veni *et al.* 2008 and Peluzio *et al.* 2012). The cluster means from various characters are presented in (Table 4). The cluster VII had the highest mean values for plant height (95.33 cm), 100-grain weight (10.28 g), grain yield/plant

Table 2 Distribution of 42 soybean genotypes into different clusters

Clusters	Number of genotypes	Name of the genotypes
I	10	RKS 63, KS 103, HIMSO 1680, JS(SH) 2003-8, AMS-MB-5-19, JS 20-29, NRC 86, AMS 243, SL- 525, Dsb 18.
II	8	VLS 77,AMS-MB-5-18, DS 15-2, TS 10, PS 1480, VLS 76, NRC 87, KDS 344.
III	1	JS 20-34
IV	13	PS 1476, PS 1477, NSO 81, NRC 88, KBS 8, CSB 08-08, PS- 1042, Bragg, JS 20-30, MASU 449, SL 871, KSO 245, MASC 1336.
V	4	NRC 85, DS 27-11, MASC 1336, MAUS 453.
VI	5	SL 778, Dsb 20, MACS 1311, RKS 61, BAUS 40
VII	1	CSB 08-09

Table 3 Average intra and inter cluster D² value of 42 soybean genotypes

Clusters	I	II	III	IV	V	VI	VII
I	(430.37)	898.25	3045.25	1002.96	1145.61	3134.68	5921.48
II		(493.93)	1460.97	2476.71	2557.43	5566.58	8952.11
III			(0.00)	6012.06	6144.11	10439.62	15964.43
IV				(432.80)	909.26	1919.72	3459.92
V					(358.03)	1154.80	2941.93
VI						(774.50)	1852.84
VII							(0.00)

Table 4 The cluster mean values, percent contribution of 12 characters

Clusters	I	II	III	IV	V	VI	VII	Contribution (%)
Days to 50% flowering	46.23	48.00	39.00	47.74	47.83	47.80	57.00	2.67
Pods/plant	90.78	82.04	66.00	87.26	136.15	166.75	155.23	22.65
Pod length	3.68	3.63	3.46	3.64	3.65	3.70	3.64	0.00
Branches/plant	5.20	4.20	3.13	5.73	4.48	7.41	6.43	2.32
Plant height	57.54	58.47	41.93	61.87	62.83	62.59	95.33	6.62
Days to maturity	99.53	102.29	90.33	100.43	98.25	99.60	102.66	0.58
Grains/ pod	2.29	2.31	2.46	2.26	2.08	2.46	2.32	0.12
100 grain weight	8.18	8.84	8.67	8.71	8.22	8.18	10.28	0.35
Grain yield/ plant	12.60	10.86	8.40	17.96	12.67	17.12	21.79	2.44
Biological yield/plant	34.06	25.20	15.33	45.71	41.83	49.33	58.33	0.00
harvest index	37.07	43.50	56.75	39.77	30.81	34.59	37.42	0.58
Oil content	17.78	18.18	17.99	17.42	17.98	17.76	17.95	61.67

(21.79 g), biological yield/plant (15.33 g), and genotypes in cluster VI highest mean values for number of pods/plant (166.75), pod length (3.70), number of branches/plant (7.41) similarly, genotypes includes in cluster III highest mean values for number of seed/pod (2.46), harvest index (56.75 %), and less to number of days for 50 % flowering (39.00 days), days to maturity (98.25 days) whereas the cluster II recorded highest mean values for oil content was (18.18 %). The genotypes included in these clusters may be utilized in future breeding programme to enhance the yield and its components.

SUMMARY

Based on the results obtained in present study, it is advocated that the genotypes namely MACS 1201, SL 788 and MASU 449 were identified as the best genotypes for grain yield. The cluster VII (CSB 08-09) and VI (SL 778, Dsb 20, MACS 1311, RKS 61, BAUS 40) was most diverse to each other. Hence, crossing between these cluster would help to accumulate favorable and desirable alleles for further improvement in grain yield and its component in soybean.

REFERENCES

- Almeida R D de, Peluzio J M and Afferi F S. 2011. Genetic divergence among soybean cultivars, under irrigated conditions, in south Tocantins State. *Revista Ciencia Agronomica* **42**(1): 108–15.
- Bhushan Bhairav, Sharma S P and Ranwah B R. 2006. Genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *National Journal of Plant Improvement* **8** (1) : 94–5.
- Burli A V, Dodake S S, Kamble A B and Gare B N. 2010. Genetic variability, heritability and correlation in soybean. *Journal of Maharashtra Agriculture University* **35**(2): 331–4.
- Gohil, V N, Mehta D R and Pandya H M. 2007. Genetic divergence in soybean (*Glycine max* (L.) Merrill.). *Legume Research* **30**(3) : 224–6.
- Gupta A K and Punetha H. 2007. Genetic variability studied for quantitative traits in soybean [*Glycine max* (L.) Merrill]. *Agriculture Science Digest* **27**(2): 140–1.
- Johnson H W, Robinson H F and Comstock R E. 1955. Estimates of genetic and environmental variability in soybeans. *Journal of Agronomy* **47**: 314–8.
- Karnwal M K and Singh Kamendra. 2009. Studies on genetic variability, character association and path coefficient for seed yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Legume Research* **32**(1): 70–3.
- Kayande N V and Patil S P. 2009. genetic divergence in soybean [*Glycine max* (L.) Merrill]. *International Journal of Plant Science* **4** (1): 218–20.
- Peluzio J M, Pires L P M, Cancellier L L, Afferi F S, Colombo G A, Teixeira Junior T, and Ribeiro G R dos S. 2012. Genetic divergence among soybean cultivars in irrigated lowland in the State of Tocantins. *Ciencia Rural* **42**(3): 395–400.
- Rajesh S, Hooda J S, Vashishtha R D and Malik B P S. 2004. Genetic divergence in soybean [*Glycine max* (L.) Merrill]. *Annals of Biology* **20**(1): 17–21.
- Rao C R. 1952. *Advanced Statistical Methods In Biometrical Research*, pp 357–69. John Wiley And Sons, New York.
- Santos E R, Dos Barros, Capone H B, Melo A, Cella A V, Santos A J da S and Dos W R. 2012. Genetic divergence between soybean genotypes based on quality of seeds. *Revista Brasileira de Ciencias Agrarias* **7**(2): 247–54.
- Veni B K, Rani B P and Ramana M V. 2008. Genetic divergence studies in soybean [*Glycine max* (L.) Merrill]. *Soybean Research* **6**: 77–80.