



Genetic variability, heritability and correlation studies in soybean (*Glycine max*)

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ABSTRACT

Genetic variability parameters and correlation among 11 quantitative traits were studied in 219 soybean working collection during *kharif* 2014-15 at Bengaluru. Analysis of variance revealed significant differences among the 219 accessions for all the quantitative characters studied except for the seed size. Among the traits, number of clusters per pod exhibited highest estimate of phenotypic coefficient of variance (PCV) (37.04) and genotypic coefficient of variance (GCV) (36.94) followed by 100-seed weight (g) (PCV=31.96, GCV=31.46) and number of branches per plant (PCV=29.56, GCV=29.18). Heritability was highest (>70%) for all the characters studied. High heritability coupled with high genetic advance as per cent mean was recorded for plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, pod length (cm), seed size (cm) and 100-seed weight (g). Hundred seed weight (g) exhibited highly significant and positive correlation with seed size (cm) (0.68) and pod length (cm) (0.17). A very wide range of variability was observed for 11 qualitative traits in the working collection and this can be potentially used for the improvement of soybean for yield and related traits.

Key words: Genetic variability, Heritability, Quantitative traits, Soybean

Soybean (*Glycine max* (L.) Merrill, 2n=40) is considered as a 'miracle legume' of the 21st century as it contains high amount of quality protein (42%) and oil (20%). It belongs to family Fabaceae. An improvement in yield and quality of self-pollinated crops like soybean is effected mainly through selection of genotypes with desirable characters from the germplasm or by creating variation through recombination and/or induced mutagenesis followed by selection. The basic requirement for adopting a suitable breeding method is sound knowledge of the genetic make-up of the characters and their expression in different genetic backgrounds.

The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a crop improvement programme and knowledge of certain genetic parameters is essential for proper understanding followed by their manipulation during plant breeding. Genetic parameters such as GCV, PCV, heritability and GA are useful biometric tools for determination of genetic variability. The grain yield is a complex character, quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield per se may not be much rewarding unless other yield attributing traits are taken into consideration. Correlation study provides a measure of association between

characters and helps to identify important characters to be considered while making elucidates selection. Knowledge of correlation between grain yield and other characters is helpful in selection of suitable plant type. The present study was aimed at understanding the extent of genetic variability and nature of correlations among a set of eleven traits including yield.

MATERIALS AND METHODS

The study comprised 219 accessions that were partly provided by AICRP on Soybean, UAS, Bengaluru. The accessions were field evaluated in Augmented Block Design at the College of Horticulture, GKVK campus, Bengaluru during *kharif* 2014-15. Three checks, Karune, a released vegetable type soybean from UAS, Bengaluru and two genotypes, viz. AGS 432 and AGS 433 were used in the experiment. Each accession was sown in a ridge of four meter length spaced 45 cm apart with intra row spacing of 20 cm. All the necessary requirements of the crop such as irrigation and inter cultural operations were undertaken as per the package of practices. Observations were recorded on five competitive plants randomly selected for plant height (cm), number of branches/plant, number of clusters/plant, number of pods/cluster, number of seeds/pod, pod length (cm), seed size (cm) and 100-seed weight. While data on days to 50% flowering, days to R6 stage and days to maturity were recorded on plot basis. The mean values over replications were subjected for analysing various parameters.

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The genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation and heritability were estimated as suggested by Singh and Choudhary (1979), while genetic advance was computed as per the procedure of Johnson *et al.* (1955). The data were also analysed for estimating the correlation coefficient (Al-Jibouri *et al.* 1958) for grain yield and its component characters.

The data for qualitative traits like plant growth habit, shape of lateral leaflet, size of lateral leaflet, branching pattern, stem colour, intensity of leaf colour, flower colour, pubescent colour, pubescent density, pubescent type and seed shape were recorded.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the accessions for all the quantitative traits studied except seed size (cm) indicating the presence of adequate variability which can be exploited through selection (Table 1). The genotype GC-9901-35 yielded highest 100-seed weight (31.00 g), followed by Karune and AGS 432 (31.50 g). EC-25768 showed good performance due to more plant height (51.50 cm) and number of branches per plant (14.00). Least days to 50% flowering, R6 stage as well as days to maturity were recorded in the genotype Karune (97 days), followed by AGS 432 (99 days). However, highest pod length was observed in IC-501592 (3.50 cm) followed by IC-501195 (3.20 cm). This variability among genotypes can be used for exploiting these traits directly or through recombination breeding.

Estimates of genetic parameters, viz. genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance along with mean and range of different characters are presented in Table 1. A considerable range of variation was observed for all the characters under study. Generally, phenotypic coefficient of variation revealed relatively high values in comparison to corresponding genotypic coefficients of variation for all the characters, indicating the effects of environment in expression of traits. The range of PCV was observed from 3.43 to 37.04% for the traits under study which provides a picture of the extent of phenotypic variability in the population. The PCV was noted high for the characters like number of clusters/plant (37.94%), 100-seed weight (31.95%), number of branches/plant (29.56%), and plant height (28.32%), number of pods/cluster (24.92) and seed size (22.79%). Moderate PCV values observed for number of seeds per pod (18.70%) and pod length (16.02%). Rest of the characters showed low values of PCV. Genotypic coefficient of variation, which expresses the picture of the extent of genetic variability in the population, ranged from 3.32 to 36.94%. The GCV was noted high for the characters like number of clusters/plant (36.04%), 100-seed weight (31.45%), number of branches/plant (29.17%), plant height (28.24%), number of pods/cluster (24.12) and seed size (22.52%). Moderate GCV values observed for number of seeds per pod (16.33%) and pod length (14.72%). These findings are in agreement with Vidya *et al.* (2002), Islam *et al.* (2011) and Nagy *et al.*

Table 1 Analysis of variance (ANOVA) and estimates of genetic variability for eleven quantitative traits in soybean germplasm field evaluated during 2014-15 at Bengaluru

Source of variation	Df	Mean Sum of Squares										
		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
Blocks	5	0.139	0.189	1.423*	0.000	0.056	0.090*	2.322	1.567	0.316	0.139	0.293
Entries	218	82.694**	5.307**	86.023**	0.585**	0.261**	0.168**	12.943**	17.481**	17.498**	0.017	45.052**
Checks	2	40.815**	0.389	15.056**	2.000**	1.389**	0.684**	4.056	85.167**	14.889**	0.151	0.368
Varieties	215	75.795**	4.977**	75.851**	0.543**	0.244**	0.152**	11.789**	12.450**	13.906**	0.015	28.429**
Checks vs. Varieties	1	1649.821**	86.205**	2414.821**	6.684**	1.551**	2.507**	278.926**	963.68**	794.88**	0.224	3708.292**
Error	10	0.413	0.122	0.389	0.000	0.056	0.023	2.522	3.033	0.825	0.276	0.837
CV (5%)		29.03	30.49	37.98	24.85	19.14	16.38	7.99	4.80	3.53	12.91	31.69

*Significant @ 5% probability level, **Significant @ 1% probability level. X1: Plant height (cm), X2: Number of branches per plant, X3: Number of clusters per plant, X4: Number of pods per cluster, X5: Number of seeds per pod, X6: Pod length (cm), X7: Days to 50 per cent flowering, X8: Days to maturity, X9: Seed size (cm), X10: 100-seed weight (g).

(2013). Thus, these traits further provided an opportunity for genetic improvement. The phenotypic and genotypic coefficient of variation indicated that number of clusters/plant, 100-seed weight, number of branches/plant, plant height (cm), number of pods/cluster, seed size, number of seeds per pod and pod length were found to be important characters. The difference between PCV and GCV values was low for all the characters studied, suggesting minimal influence of environment on the expression of the character.

Genetic coefficient of variation along with heritability estimates would provide clear picture on the efficiency of the selection (Burton 1952). The estimate of broad sense heritability was the highest for all the characters studied (Table 1). The values were especially high for days to maturity (93.73%), number of branches/plant (91.40%), 100-seed weight (90.88%), number of clusters/plant (90.46%), number of pods/cluster (90.00%), plant height (89.42%), pod length (84.39%), seed size (81.62%), days to 50% flowering (77.60%), days to R6 stage (74.54 %) and number of seeds/pod (76.20%). Similarly, high heritability values for 100-seed weight, days to maturity and number of branches/plant was reported by Aditya *et al.* (2011). In the present investigation, all the traits under the study showed high magnitude of heritability in broad sense (70%), suggesting that the highly heritable characters were least affected by environmental variations and selection for these characters based on phenotypic performance may be more effective for soybean improvement.

Heritability alone does not provide clue for genetic gain resulting from the best selected individuals. Burton (1952) suggested that h^2 , in combination with genetic advance (GA), was more reliable in predicting the effect of selection. The estimates of genetic advance (as percent of mean) ranged from 8.49 for days to maturity to 97.26

for number of clusters/plant (Table 1). Analysis of pooled data showed that estimates of GA (as percent mean) were high for number of clusters/plant (97.26%), 100-seed weight (91.73%), number of branched per plant (76.01%), plant height (74.34%) number of pods/cluster (63.66%) seed size (49.12%), number of seeds/pod (37.62%) and pod length (35.69%). Days to 50% flowering (15.97%) showed moderate estimates of GA (Table 2). Days to R6 stage and days to maturity had low GA. Similarly, in soybean, Basavaraja *et al.* (2005) reported high genetic advance coupled with high heritability for plant height, 100-seed weight, harvest index and daily production rate indicated heritable nature of variation and scope for selection for these traits among the vegetable soybean genotypes. The high heritability combined with high genetic advance as per cent mean is indicative of additive gene action and hence, selection based on these parameters would be more reliable (Johnson *et al.* 1955).

Hundred seed weight (g) exhibited highly significant and positive correlation with seed size (cm) (0.68) and pod length (cm) (0.17) (Table 3). It was evident that the traits were associated with grain yield and were inter-correlated among them. It indicates that the selection in any one of these yield attributing traits will lead to increase in the other traits, thereby finally enhancing the grain yield. Similar results were reported by Shrivastava *et al.* (1998) and Nagy *et al.* (2013). Seed with high 100-seed weight were larger. Hence, selection for traits like seed size and pod length also be given importance along with yield. Apart from that plant height is negatively correlated hence selection of dwarf plant also be given importance.

The wide variability for the entire 11 quantitative traits, viz. stem colour, and leaf colour, size of lateral leaflet, flower colour, shape of lateral leaflet, growth habit, branching

Table 2 Estimates of variability for selected quantitative traits among accessions of soybean germplasm field evaluated during 2014-15 at Bengaluru

Trait	Range		Mean	PCV (%)	GCV (%)	Heritability	GA	GA as % mean
	Min.	Max.						
X1	13.30	51.50	29.85	28.32	28.24	89.42	22.19	74.34
X2	3.00	14.00	7.33	29.56	29.17	91.40	5.57	76.01
X3	6.00	50.00	22.83	37.94	36.04	90.46	22.21	97.26
X4	2.00	5.00	2.97	24.92	24.12	90.00	1.89	63.66
X5	2.00	3.00	2.58	18.70	16.33	76.20	0.97	37.62
X6	1.70	3.50	2.37	16.02	14.72	84.39	0.84	35.69
X7	33.00	52.00	43.04	7.79	6.87	77.60	6.87	15.97
X7	62.00	82.00	73.78	4.67	4.04	74.54	6.79	9.20
X9	97.00	115.00	105.63	3.43	3.32	93.73	8.97	8.49
X10	0.60	1.00	0.76	22.79	22.52	81.62	3.74	49.12
X11	6.90	33.00	16.21	31.95	31.45	90.88	13.25	91.73

PCV (%) = Phenotypic Co-efficient of Variability, GCV (%) = Genotypic Co-efficient of Variability, GA = Genetic Advance

Table 3 Correlation co-efficient among selected quantitative traits for accessions of soybean germplasm field evaluated during *kharif* 2014-15 at Bengaluru

	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Seeds per pod	Pod length (cm)	Days to 50 % flowering	Days to R6 stage	Days to maturity	Seed size (cm)
Branches per plant	0.837**	1								
Clusters per pant	0.828**	0.826**	1							
Pods per cluster	0.239**	0.204**	0.242**	1						
Seeds per pod	0.160*	0.187**	0.161*	0.078	1					
Pod length (cm)	-0.077	0.051	-0.037	-0.004	-0.021	1				
Days to 50% flowering	0.126	0.097	0.124	0.202**	-0.042	-0.045	1			
Days to R6 stage	0.184**	0.152*	0.159*	0.201**	-0.003	-0.055	0.863**	1		
Days to maturity	0.152*	0.153*	0.122	0.186**	-0.019	-0.004	0.914**	0.924**	1	
Seed size (cm)	-0.133*	-0.036	-0.153*	-0.206**	-0.032	0.102	-0.160*	-0.229**	-0.215**	1
100-seed weight (g)	-0.171*	-0.039	-0.118	-0.172*	0.017	0.172*	-0.161*	-0.283**	-0.268**	0.682**

** Correlation is significant at $p \leq 0.01$, * Correlation is significant at $P \leq 0$.

pattern, pubescent colour, pubescent density, pubescent type and seed shape were also observed. Similar range of variability for leaf and seed characters was recorded by Basavaraja *et al.* (2005). High genetic variability and nature of correlations among the eleven traits in the working collection of germplasm would serve as basis in deploying specific accessions and formulation of strategies for further improvement of soybean.

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