Genetic variability and correlation analysis in soybean (*Glycine max* (L.) Merrill) genotypes

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Abstract
The present investigation was carried out at V.C.S.G. Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri, Tehri Garhwal, Uttarakhand, India during *Kharif* 2015. The experiment consisted of 20 genotypes along with two checks namely PS-1347 and PS-1092 in Randomized Block Design. The analysis of variance showed highly significant differences for all the characters which indicate that bountiful variability present among the genotypes. The values of PCV were higher than of GCV, but the difference was closer between these two estimates for all the characters means less influenced due to environmental factors. High heritability was observed for yield and contributing characters. The high magnitudes of genetic advance observed for pod length, High heritability along with high genetic advance was observed for pod length, causes additive gene action. The seed yield per plant showed highly significant and positive correlation with plant height, number of cluster per plant, number of pods per plant, number of seeds per pod and 100 seed weight. The genotypes having high variability can be used in soybean breeding and high heritability along with high genetic advance favours for selection in crop improvement programme. Positive correlation of the characters with seed yield is so meaningful for improving yield.

Keywords: soybean, analysis of variance, heritability, genetic advance and correlation

Introduction
Pulses provides good source of vegetable dietary protein that's why it is an important food crop worldwide (Peerzada, *et al.,* 2014) [35]. Soybean is one of the most important oilseed crops in the world (Adoloju *et al.,* 2009) [3]. The center of origin of soybean is China. It has been cultivated in China for more than 4,000 years (Hymowitz, 1970) [25]. Soybean belongs to the genus *Glycine* which is divided into two subgenera such as *Glycine* and *Soja*, taxonomically. The cultivated soybean (*Glycine max* (L.) Merril) with the chromosome number 2n=40, comes under the subgenus *Soja* (Moench), which is aptly called as 'Golden Bean' or 'Miracle Crop' of the 20th century (Adoloju *et al.,* 2009) [3]. Soybean is a wonderful crop gifted by nature to mankind (Mahbub *et al.,* 2015) [31]. It enriches the soil by nitrogen fixation symbiotically. In the international world trade markets, soybean is ranked first in world among the major oil crops such as rapeseed, groundnut, cottonseed, sunflower, linseed, sesame and safflower (Chung and Singh, 2008) [19].
Soybean seeds have the highest protein content (30-45%) of all food crops and also contains a considerable oil content (15-24%) comprising high percent of unsaturated fatty acids (Akram *et al.,* 2011) [4], carbohydrate (24-26%) (Gowda and Kaul, 1982) [24] and ash (5%) (Kjaer, 2013) [29]. The oil contains 85% unsaturated fatty acids which is free from cholesterol, along with ample mineral elements, thus it is highly desirable for human diet (Antalina *et al.,* 2000) [7]. Soybean seeds also contain a good considerable amount of other nutrient elements like calcium, phosphorus, iron, carotene and vit-B_1, vit B_2 and vit-C (Gopalan *et al*., 1971) [23]. Soybean raw protein primarily contain legume proteins, which belongs to the globulin family of seed storage proteins called legumins (11S globulin fraction) and vicilins (7S globulin), or in case of soybeans, glycinin and beta-conglycinin. Soybeans also contain biologically active or metabolic proteins, such as enzymes, trypsin inhibitors, hemagglutinins, and cysteine proteases. Soybean consists of 8% seed coat or hull, 90% cotyledons and 2% hypocotyl axis or germ, approximately (Kjaer, 2013) [29]. Soybeans raw oil contains 20% fat and the major unsaturated fatty acids includes poly-unsaturated α-linolenic acid (Omega-3) (7-10%), and linoleic acid (Omega-6) (50-60%) and the mono-unsaturated oleic acid (20-25%).

It also contains the saturated fatty acids, stearic acid (3-7%) and palmitic acid (5-10%) (Choi and Rhee, 2006) [18].

Plant breeding programme is one of the attempts to improve yields through genetic improvement of plant. Selection, germplasm collection and hybridization followed by selection are the steps to achieve superior genotypes. Among a series of routine activities the selection is the most important step for obtaining high yielding varieties. Selection criteria are the effectiveness of selection determination (Sulistyo, *et al.,* 2018) [38]. Determining selection criteria can be done in various ways such as information on genetic parameters and knowledge of correlation (Arsyad *et al.,* 2009) [9]. The aim of this study was to analysis the heritable agronomic traits and yield contributing character in soybean genotypes.

Materials and Methods

The present investigation was carried out during *Kharif* 2015 at research block of crop improvement, VCSG, Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri, Tehri Garhwal, Uttarakhand, India. The experiment consisted of twenty genotypes along with two checks (PS-1347 and PS-1092) in Randomized Block Design. The entries were sown in two rows of three meter length adopting inter row spacing of 45 cm and intra row spacing of 15 cm. The other practices were followed as in recommended package for healthy crop. The data were recorded on five randomly selected competitive plants in each replication and each genotype for eleven characters *viz.,* days to 50% flowering, plant height (cm), no. of primary branches, no. of secondary branches, no. of clusters per plant, no. of pods per plant, pod length (cm), no. of seeds per pod, days to maturity, 100 seed weight (g) and seed yield per plant (g). The analysis of variance was analyzed by the formula given by Cochran and Cox (1992) [20], heritability (Allard, 1960) [5], genetic advance (Allard, 1960; Burton and Devane, 1953) [5, 14], correlation analysis (Searle, 1961) [37] and coefficient of variation (Burton and Devane, 1953) [14].

Result and Discussion
Analysis of Variance

The results of analysis of variance for Randomized Block Design for eleven characters of twenty soybean genotypes including two cheeks have been presented in Table 1. The mean sum of squares due to genotypes were showed highly significant difference for all the characters, it indicates that the sufficient variability present among the genotypes. Substantial variations in soybean have been also reported by Karad *et al.,* (2005) [27], Reni and Rao (2007) [36], Aditya *et al.,* (2011) [2], Dilnesaw *et al.,* (2013) [21] and Osekita and Olorunfemi (2014) [34].

Genetic components

Computation of genotypic, phenotypic an environmental variances, genotypic coefficient of variance (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were statistically worked out to understand the nature and extent of variability in expression of different characters prevailed in population and that led to facilitate selection for various traits for indentifying desired genotypes suitable for hills. The genetic variability in different field parameters presented in Table 2. The estimates of phenotypic (PCV) and genotypic coefficient (GCV) of variation indicated that the values of PCV were higher than of GCV, but the difference was closer between these two estimates for all the cases. These indicated that greater role of

genetic components and expression of characters under study was less influenced due to environmental factors. Similar results were reported by Karnwal and Singh (2009) [28] and Baraskar *et al.,* (2014) [13]. The perusal of the data revealed that higher PCV and GCV were recorded for seed yield per plant followed by number of primary branches, number of secondary branches, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and 100 seed weight indicated that selection with these characters may be good approach for enhancing seed yield of the genotypes. These findings of the present investigation agree with the earlier report for pod length, number of seeds per pod and 100 seed weight by Mahbub *et al.,* (2015) [31], for plant height, number of pods per plant, number of clusters per plant, 100 seed weight and seed yield per plant by Baraskar *et al.,*(2014) [13], for number of pods per plant by Mahajan *et al.,* (1994) [30] and Gohil *et al.,* (2007) [22], for seed yield per plant by Gohil *et al.,* (2007) [22], for plant height, pods per plant and yield per plant by Karad *et al.,* (2005) [27] and Reni and Rao (2007) [36].

Heritability and genetic advance

It is not possible to determine the extent of variation which is heritable through genotypic coefficient of variation alone. For the prediction of genetic advance for any quantitative characters and exercising selection procedure the knowledge of heritability helps to plant breeder (Baraskar *et al.,* 2014) [13]. The genotypic coefficient of variation together with heritability estimate would give the best picture expected for selection than the heritability value alone (Burton, 1952) [15].

According to MacWhirter (1979) [33] heritability estimates can be divided into three categories which are low heritability ($h^2 < 0.2$), medium heritability ($0.2 > h^2 < 0.5$), and high heritability ($h^2 > 0.5$). The estimates of heritability (Table 2) were observed to be high for yield and its contributing characters. This indicated that selection based on phenotypic levels would be useful for the improvement of the traits. Earlier workers also reported high magnitude of heritability for yield and its contributing characters (Bangar *et al.,* 2003; Malik *et al.,* 2006; Chandrawat *et al.,* 2017) [12, 32, 16].

According to Baraskar *et al.,* (2014) [13] genetic advance estimates can be divided into three classes which are high (>20%), moderate (10-19%) and low (<10%). The magnitudes of genetic advance were observed to be high for pod length, moderate for number of primary branches and number of secondary branches whereas other characters showed low genetic advance as per cent of mean. The magnitude of high genetic advance is useful in identification and selection for appropriate characters. The results are in agreement with those reported by Bangar *et al.,* 2003[12]; Gohil *et al.,* 2007[22]; Karnwal and Singh, 2009[28]; Baraskar *et al.,* 2014 [35].

The genetic architecture of the population can be measured by the idea of estimates of heritability and genetic advance (Baraskar *et al.,* 2014) [13]. High heritability along with high genetic advance was observed for pod length which indicates the presence of additive gene action for improvement of this trait by various selection methods. The moderate genetic advance accompanied with high heritability were observed for number of primary branches and number of secondary branches which indicates the presence of both additive and non-additive gene action for these traits. High heritability coupled with low genetic advance found for other characters, which clearly indicates the presence of non-additive gene action and selection is not rewarding for such traits. For such types of traits the recombination breeding and recurrent

selection may be used for population improvement. Such kind of information was also reported in soybean for different characters by Chandrawat *et al.*, 2017 [16].

Correlation analysis

The degree of association among different characters can be measured by correlation coefficient, which is an important statistical constant. A mazy character that is grain yield is depends upon the other agronomic traits. Therefore study of the relationship of the characters with yield and each other become more important in crop improvement programme. It is very essential to find out the relative contribution with the yield of the other characters so as to give weightage during the selection (Baig *et al.*, 2017) [10]. Grain yield greatly affected by erratic environment. Moreover, during inheritance grain yield is an intricate and may involve several related traits (Balla and Ibrahim, 2017) [11]. In the present study, simple correlation coefficient (Table 3) was computed among the 11 characters. The seed yield per plant showed highly significant and positive correlation with plant height, number of clusters per plant, number of pods per plant, number of seeds per pod and 100 seed weight. The results are in accordance with the findings for plant height, number of pods per plant and 100 seed weight by Baig *et al.*, 2017[10]. for number of pods per plant, plant height and 100 grain weight by Amarnath *et al.*, 1990 [6]; for number of pods per plant by Taware *et al.*, 1995 [39], and *Inderjit and Phul*, 1999 [35]; for number of seeds per pod and 100 seed weight by Chavan *et al.*, 2016 [17]; for plant height and number of pods per plant by Bala *et al.*, 2017 [11]; for 100 seed weight by Arsad *et al.*, 2006 [8].

This indicates that seed yield per plant increases potentially with the tall plants that bear substantially number of clusters per plant, high number of pods per plant, high number of seeds per pod and higher 100 seed weight. These traits, besides being correlated with seed yield per plant, were highly heritable and highly correlated with each other. Thus, if they proved to be controlled by a few number of genes, selection for their combination should be unpretentious (Balla and Ibrahim, 2017) [11]. The pleiotropy or genetic linkage, or may be due to developmental induced relationships between components have been attributed for such kind of associations that were only indirectly consequences of gene action (Adam, 1967) [1].

Conclusion

Based on the result, the characters having high heritability followed by high genetic advance can be used in soybean breeding programme because selection favours in the positive direction to obtain high yield. The characters having high heritability alone can also be used in breeding programme for improving yield. The selection criteria should be for plant height, number of cluster per plant, number of pods per plant, number of seeds per pod and 100 seed weight because of high heritable and high correlation among them in soybean.

Table 1: Analysis of Variance (ANOVA) for yield and contributing characters in soybean genotypes

| Source of variance | df | Means sum of square |
		50% flowering	Plant height (cm)	No. of primary branches	No. of secondary branches	No. of clusters/ plant	No. of pods/plant	Pod length (cm)	No. of seeds /pod	Days to maturity	100 seed weight (g)	Seed yield/ plant (g)
Replication	1.0	0.0313	0.2563	0.0020	0.0013	0.0094	0.6922	0.0811	0.0063	2.0875	0.0010	6.5918
Treatment	19.0	17.12**	44.29**	2.41**	1.97**	14.66**	56.34**	0.30**	0.14*	11.02**	10.40**	43.88**
Error	19.0	1.28	0.81	0.09	0.10	0.52	1.24	0.007	0.05	0.80	0.80	2.65
GM		86.83	77.12	5.92	8.93	10.07	24.81	3.57	2.28	137.57	10.26	15.91
Sem		080	0.64	0.23	0.23	0.51	0.79	0.060	0.16	0.63	0.63	1.15
CD at 5%		2.38	1.89	0.65	0.68	1.51	2.33	0.18	0.48	1.87	1.88	3.41
CD at 1%		3.25	2.58	0.89	0.91	2.07	3.19	0.24	0.65	2.56	2.56	4.66
CV		1.31	1.17	5.23	3.57	7.17	4.50	2.39	9.99	0.65	8.74	10.23

* and ** are significant at 1 and 5 per cent respectively

Table 2: Estimation of variance and genetic parameters of different characters in soybean genotypes

S.N.	Characters	General Mean	Vg	Vp	Ve	GCV	PCV	ECV	Heritability (h²)%	Genetic advance as % of mean
1.	50% flowering	86.82	17.120	18.407	1.287	4.765	4.941	1.306	93.008	1.07
2.	Plant height (cm)	77.11	44.298	45.110	0.812	8.630	8.709	1.168	98.199	1.27
3.	No. of primary branches	5.922	2.413	2.508	0.095	26.224	26.740	5.227	96.212	16.24
4.	No. of secondary branches	8.927	1.975	2.076	0.101	15.740	16.139	3.559	95.134	10.65
5.	No. of clusters/plant	10.07	14.664	15.185	0.521	38.020	38.685	7.167	96.568	9.58
6.	No. of pods/plant	24.80	56.342	57.586	1.244	30.260	30.590	4.495	97.839	3.94
7.	Pod length (cm)	3.570	0.304	0.311	0.007	15.440	15.627	2.343	97.654	27.38
8.	No. of seeds / pod	2.282	0.149	0.669	0.520	16.914	19.64	9.992	74.129	9.80
9.	Days to maturity	137.56	11.023	11.824	0.801	2.413	2.499	0.650	93.225	0.67
10.	100 seed weight (g)	10.25	10.404	11.206	0.802	31.441	32.631	8.734	92.843	5.83
11.	Seed yield/plant (g)	15.91	43.888	46.539	2.651	41.634	42.872	10.232	94.303	9.20

Where,
Vg = Genotypic variance, Vp = Phenotypic variance, Ve = Environmental variance, GCV= Genotypic coefficient of variation,
PCV= Phenotypic coefficient of variation and ECV =Environmental coefficient variation

Table 3: Estimation of simple correlation coefficient among different characters in soybean

S. N.	Character	Days to maturity	Plant height (cm)	No. of primary branches	No. of secondary branches	No. of clusters /plant	No. of pods / plant	Pod Length (cm)	No. of seeds /pod	100 seed weight (g)	Seed yield/ plant (g)
1.	50% flowering	0.088	0.235	-0.119	0.476*	0.232	0.118	0.288	0.286	0.213	0.016
2.	Days to maturity		-0.341	-0.197	-0.101	-0.348	-0.288	-0.101	-0.156	-0.087	-0.123
3.	Plant height (cm)			0.087	0.527**	0.877**	0.876**	0.873**	0.642*	0.881**	0.801**
4.	No. of primary branches				0.586*	0.379	0.050	-0.136	0.313	0.369	-0.191
5.	No. of secondary branches					0.560*	0.386	0.451	0.644*	0.666*	0.413
6.	No. of clusters/plant						0.861**	0.568*	0.644*	0.912**	0.868**
7.	No. of pods/plant							0.613*	0.654*	0.876**	0.972**
8.	Pod length (cm)								0.583*	0.682*	0.518
9.	No. of seeds / pod									0.810**	0.735**
10.	100 seed weight (g)										0.914

*and ** are significant at 1 and 5 per cent respectively

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