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Genetic variability and character association studies for seed yield and component characters in soybean [*Glycine max* (L.) Merrill] under North-western Himalayas

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ABSTRACT

The present investigation was undertaken to assess the genetic variability and character associations for seed yield and component characters in 307 soybean germplasm lines. The lines were raised in augmented block design in four blocks during *kharif* 2014. Out of these, twenty seven promising genotypes were selected and forwarded for evaluation along with four checks in randomized block design with three replications at CSKHPKV, Palampur (H.P) during *kharif* 2015. The analysis of variance revealed the presence of sufficient genetic variability in the breeding material. High PCV and moderate GCV were recorded for harvest index and biological yield/plant. High heritability coupled with high genetic advance were observed for harvest index followed by biological yield /plant, seed yield /plant, number of pods/plant and 100-seed weight indicating the predominance of additive gene action in controlling the trait. Number of branches /plant, number of seeds /pod, biological yield/plant and harvest index exhibited significantly positive correlation with seed yield /plant both at phenotypic and genotypic levels. Two traits *viz*., harvest index and biological yield /plant could be considered as direct selection indices for yield improvement in soybean.

Key words: Correlation, Genetic advance, Genetic variability, Heritability, Path coefficient analysis, Soybean.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is also called the 'Golden bean' or 'Miracle legume' of the twenty first century because of its multiple uses. Soybean is a self-pollinated crop (2n=4x=40) and belongs to family *Fabaceae*. Soybean could be regarded as an ideal food for the people of poor and developing countries as it contains high quality protein and a reasonable quantity of oil as a source of energy.

The crop is considered as an important oilseed in the globe due to its high oil content (20%) and protein (40%). Soybean can cater the nutritional requirements of the undernourished as it is a good source of protein, unsaturated fatty acids and minerals like calcium and phosphorus including vitamins A, B, C and D. In India, soybean has emerged as a major oilseed crop in a short period of time. Beginning with a meagre area of 0.03 million hectares under cultivation in 1970, the crop has expanded at an unprecedented pace and touched the figure of 11.40 million hectares area with the production of 11.50 million tons and average productivity of 10.1 q/ha in 2016 (Anonymous 2017).

The large amount of variability present in any genetic material indicates the scope for further improvement of the crop (Baig *et al*., 2018). 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 (Jain *et al.,* 2017). Similarly, information on the nature of associations between yield and its component characters and their direct and indirect contributions on seed yield is necessary for efficient selection. The present investigation was carried out to assess the nature and magnitude of genetic variability available and associations between seed yield and its component characters in soybean germplasm lines which would help in selection of efficient genotypes for further utilization in hybridization programme.

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MATERIALS AND METHODS

The experimental material consisted of 303 germplasm lines which also includes derivatives of local germplasm material from Indore, Jabalpur, Parbhani, New Delhi, Ludhiana and released varieties. All the genotypes were evaluated along with four checks *viz*., Hara Soya, Him Soya, Palam Soya and Palam Early Soya-1 in augmented randomized block design in four blocks with a spacing of 45cm between rows and 15cm between plants at the experimental farm area of

Department of Crop Improvement, CSKHPKV, Palampur (H.P.) during *kharif* 2014. Out of 303 lines, twenty seven promising lines were selected and evaluated along with same four checks in randomized block design with three replications with same inter-row and inter-plant spacing during *kharif* 2015 at CSKHPKV, Palampur (H.P.). Five plants per genotype per replication were randomly selected for recording the observations at appropriate stages of crop growth during both the seasons on characters *viz.* plant height, number of branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight and seed yield/plant. The observations on days to 50 per cent flowering and 75 per cent maturity were recorded on plot basis. The data were analyzed for augmented randomized block design (Federer, 1956) and randomized block design (Panse and Sukhatme, 1984). Genetic parameters such as genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance were statistically computed (Burton and De Vane, 1953 and Johnson *et al*.1955). The inter-relationships among yield and its components and their direct and indirect contributions towards seed yield and correlation coefficients were calculated (Al-Jibouri *et al.* 1958). Path coefficient analysis was done as per Dewey and Lu, 1959.

RESULTS AND DISCUSSION

Based upon the morphological characterization, 181 genotypes exhibited purple flower color whereas 126 genotypes exhibited white flower color. All the white and purple flowered genotypes could be grouped into thirteen and sixteen distinct groups based upon different characters, respectively. Analysis of variance for augmented randomized block design revealed that mean squares due to blocks ignoring the treatments were significant for days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight and seed yield/plant. When the analysis was done for both ignoring blocks and eliminating blocks, the mean sum of squares due to the treatments were significant for days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of seeds/pod, 100-seed weight and seed yield /plant. The mean sum of squares due to the genotypes were significant for all traits except for number of branches /plant and number of pods/ plant indicating the availability of sufficient genetic variation among the genotypes for all traits except for these two traits. The mean sum of squares due to genotypes vs. checks were significant for all traits except for number of pods/plant and number of seeds /pod indicating sufficient variability among the treatments for all traits except for these two characters. Earlier, similar results were reported by Bhartiya and Aditya (2016) for all the characters studied except for number of pods/plant in soybean. High PCV and moderate GCV were recorded for plant height and number of pods/plant. High heritability estimates coupled with high genetic advance were observed for plant height, 100-seed weight and seed yield/ plant. Similar results have been reported by Kumar *et al*. (2015) for plant height and 100-seed weight and Ekka and Gabrial (2016) for seed yield/plant in soybean.

Mean performance of the 31 genotypes revealed that only one genotype Himso-14-19 (18.65 g) was significantly superior to the best check Palam Soya (15.07 g) for seed yield. The genotypes such as Himso-14-1 (48.33 days), Himso-14-52 (48.33 days) and PS-1347 (48.67 days) were found to be significantly earlier in flowering. However, none of the genotype was significantly early in maturity than the best check Palam Early Soya. The genotypes such as Himso-14-14A (19.72%), Himso-14-145 (19.50%), Himso-14-19 (19.40%), Himso-14-39 (19.18%) and Himso-14-157 (19.03%) were higher in oil content than best check, Hara Soya (18.84%). The analysis of variance for twenty seven promising genotypes revealed that the mean squares due to genotypes were significant for all characters studied which indicated the existence of sufficient genetic variability in the material. High PCV coupled with moderate GCV values were observed for harvest index followed by biological yield /plant (Table 1). Similar results were observed by Aditya *et al.* (2011) and Sureshrao *et al.* (2014). Moderate PCV and GCV were recorded for the number of branches/plant, number of pods/plant, seed yield/plant, 100-seed weight, plant height and days to 50 per cent flowering. Present results were in accordance with the findings of Ganesamurty and

Table 1: Estimates of parameters of variability for different traits in soybean during *kharif*-2015.

Traits	Mean ± S.E	Range	PCV (%)	GCV (%)	ECV (%)	h^2_{bs} (%)	GA (% of mean)
Days to 50% flowering	54.56 ± 0.50	48.33-65.67	10.22	10.10	1.59	98	20.55
Days to 75% maturity	116.15 ± 0.53	108.33-127.00	5.35	5.30	0.79	98	10.79
Plant height (cm)	68.07 ± 3.73	54.06-90.27	16.51	13.51	9.49	67	22.79
No. of branches/ plant	5.21 ± 0.49	3.24-7.51	24.86	18.63	16.46	56	28.75
No. of pods/plant	51.63 ± 3.27	36.63-80.04	21.69	18.70	10.98	74	33.24
No. of seeds/pod	2.27 ± 0.09	2.06-2.67	8.15	4.59	6.74	32	5.32
100-seed weight (g)	13.01 ± 0.38	8.89-17.43	17.34	16.59	5.05	92	32.70
Seed yield/ plant (g)	12.59 ± 0.55	8.46-18.65	19.45	17.90	7.62	85	33.92
Biological yield / plant (g)	38.40 ± 2.63	23.50-70.74	25.80	22.91	11.84	79	41.93
Harvest index (%)	34.22 ± 2.50	21.19-62.79	26.50	23.29	12.64	77	42.17

Seshadri (2004), Karnwal and Singh (2009), Bhat and Basavaraja (2011) and Datt *et al.* (2011). Low PCV and GCV values were observed for days to 75 per cent maturity and number of seeds/pod. As GCV represents only the extent of genetic variability present for a character, therefore, it should be considered in combination with heritability and genetic advance to assess the effect of phenotypic selection. In the present study, high heritability (>70%) coupled with high genetic advance (>30%) were observed for harvest index followed by biological yield/plant, seed yield /plant, number of pods/plant and 100-seed weight indicating the predominance of additive gene action in the inheritance of these characters. Similar results were observed by Patil *et al.* (2011), Reni and Rao (2013), Chavan *et al.* (2014) Chandrawat *et al.* (2017) and Jain *et al*. (2018). While studying the correlation coefficients, it was observed that the genotypic correlation coefficients were higher than their corresponding phenotypic ones for most of the traits studied indicating an inherent association among the various characters under study (Table 2). At both genotypic and phenotypic levels, seed yield/plant was significantly and positively correlated with number of branches/plant, number of seeds/pod, biological yield/plant and harvest index. Similar findings have been reported by Ngalamu *et al.* (2012), Chandal *et al.* (2014) and Jain *et al.* (2014).

Among the other component characters, days to 50 per cent flowering showed significant and positive correlation with days to 75 per cent maturity (0.392), plant height (0.536), number of branches/plant (0.528), number of pods/plant (0.304), number of seeds/pod (0.218) and harvest Index (0.229). Days to 75 per cent maturity had significant and positive correlation with plant height (0.251), number of branches/plant (0.424) and number of seeds /pod (0.222). Plant height had significant and positive correlation with number of branches/plant (0.445), number of pods/plant (0.421) and harvest Index (0.167). Number of branches/plant showed significant and positive correlation with number of pods/plant (0.398) and number of seeds/pod (0.414). A significantly positive correlation of number of pods/plant was observed with number of seeds/pod (0.253) while it was significant and negatively correlated with 100-seed weight (-0.303). Number of seeds /pod exhibited significant and positive correlation with biological yield/plant (0.214) but, it was significantly and negatively associated with 100-seed weight and harvest Index. A significant and positive correlation of biological yield/plant was observed with seed yield/plant. Similar results were recorded by Iqbal *et al.* (2010) and Kumari (2011) in soybean. Seed yield is a complex character which is highly influenced by interaction of various component traits and the environment. Compartmentalization of correlation coefficients into direct and indirect effects revealed the true nature of associations observed among various characters (Table 3, Fig 1). The path coefficient analysis using phenotypic correlation coefficients among pair of characters depicting direct and indirect effects on seed yield showed that harvest index and

Table 2: Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits of soybean.

Traits		Days to 75% maturity	Plant height(cm)	No. of branches/plant	No. of pods/plant	No. of seeds/pod	100-seed weight (g)	Biological yield/plant(g)	Harvest Index (%)	Seedyield/ plant (g)
Days to 50 % flowering	P	**0.392***	**0.536***	**0.528***	**0.304***	**0.218***	**-0.283***	**-0.066**	**0.229***	0.155
	G	0.404	0.657	0.689	0.367	0.386	-0.304	-0.071	0.271	0.170
Days to 75% maturity	P		**0.251***	**0.424***	**0.040**	**0.222***	**-0.198**	**-0.244***	**0.144**	-0.028
	G		0.318	0.572	0.041	0.387	-0.215	-0.300	0.186	-0.041
Plant height (cm)	P			**0.445***	**0.421***	**0.078**	**-0.338***	**-0.163**	**0.167**	0.017
	G			0.661	0.512	0.067	-0.441	-0.247	0.232	-0.030
No. of branches/plant	P				**0.398***	**0.414***	**-0.475***	**0.143**	**0.062**	**0.258***
	G				0.393	0.672	-0.650	0.080	0.147	0.252
No. of pods/plant	P					**0.253***	**-0.303***	**0.114**	**0.013**	0.141
	G					0.470	-0.378	0.044	0.095	0.151
No. of seeds/pod	P						**-0.110**	**0.214**	**-0.045**	**0.235***
	G						-0.212	*0.406	-0.206	0.241
100 - seed weight (g)	P							**0.047**	**-0.106**	-0.059
	G							0.055	-0.116	-0.067
Biological yield/plant(g)	P								**-0.640***	**0.345***
	G								-0.608	0.350
Harvest Index (%)	P									**0.427***
	G									0.469

P: Phenotypic level, G: Genotypic level, *Significant at P≤0.05.

Table 3: Estimates of direct and indirect effects of different traits on seed yield in soybean.

Traits		Days to 50 % flowering	Days to 75% maturity	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	No. of seeds/ pod	100 -seed weight (g)	Biological yield/ plant (g)	Harvest index (%)	Correlation with Seed yield/ plant (g)
Days to 50%	P	**-0.099**	0.033	0.014	0.019	0.001	0.010	-0.009	-0.070	0.257	0.155
flowering	G	**-0.122**	0.029	-0.091	0.161	0.040	-0.039	-0.028	-0.071	0.291	0.170
Days to 75%	P	-0.039	**0.084**	0.007	0.015	0.000	0.010	-0.006	-0.260	0.161	-0.028
maturity	G	-0.049	**0.072**	-0.044	0.134	0.005	-0.039	-0.020	-0.298	0.200	-0.041
Plant height	P	-0.053	0.021	**0.026**	0.016	0.001	0.004	-0.010	-0.174	0.187	0.017
(cm)	G	-0.080	0.023	**-0.138**	0.154	0.056	-0.007	-0.041	-0.246	0.248	-0.030
No. of branches /	P	-0.052	0.036	0.012	**0.035**	0.001	0.019	-0.014	0.152	0.070	0.258*
plant	G	-0.084	0.041	-0.091	**0.234**	0.043	-0.068	-0.061	0.080	0.158	0.252*
No. of pods/	P	-0.030	0.003	0.011	0.014	**0.003**	0.012	-0.009	0.122	0.015	0.141
plant	G	-0.045	0.003	-0.071	0.092	**0.109**	-0.047	-0.035	0.044	0.102	0.151
No. of seeds/	P	-0.022	0.019	0.002	0.015	0.001	**0.046**	-0.003	0.229	-0.051	0.235*
pod	G	-0.047	0.028	-0.009	0.157	0.051	**-0.101**	-0.020	0.404	-0.221	0.241*
100 - seed	P	0.028	-0.017	-0.009	-0.017	-0.001	-0.005	**0.030**	0.050	-0.119	-0.059
weight (g)	G	0.037	-0.015	0.061	-0.153	-0.041	0.021	**0.092**	0.055	-0.124	-0.067
Biological yield/	P	0.007	-0.021	-0.004	0.005	0.000	0.010	0.001	**1.064**	-0.717	0.345*
plant(g)	G	0.009	-0.022	0.034	0.019	0.005	-0.041	0.005	**0.993**	-0.652	0.350*
Harvest index	P	-0.023	0.012	0.004	0.002	0.000	-0.002	-0.003	-0.682	**1.118**	0.427*
(%)	G	-0.033	0.013	-0.032	0.035	0.010	0.021	-0.011	-0.604	**1.071**	0.469*

Residual effects (P) = 0.3916; (G) = 0.3525; P = Phenotypic level and G = Genotypic level.

*Significant at P≤0.05, Bold diagonal values denote the direct effects.

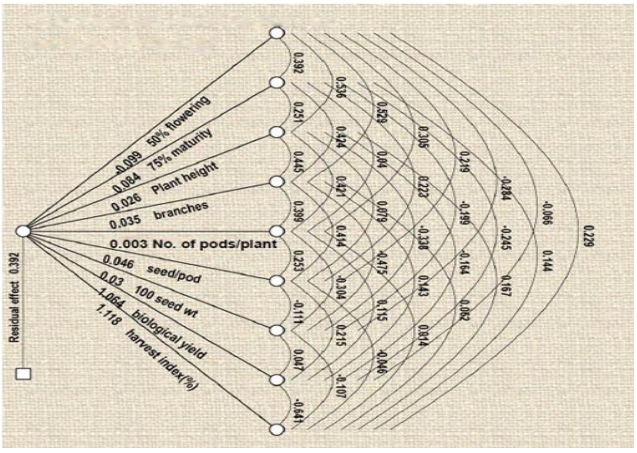


Fig 1: Phenotypical path diagram for seed yield/plant in soybean.

biological yield/plant had high and positive direct effects on seed yield which suggests them as most important component characters contributing to yield. However, days to 75 per cent maturity, number of seeds/pod, number of branches/plant, 100-seed weight, plant height and number of pods/plant had low positive and direct effects on seed yield/plant. Low residual effects at phenotypic and genotypic levels indicated that most of the variation found in the dependent traits was well explained by the contributed traits studied.

CONCLUSION

It is concluded that sufficient genetic variability existed for agro morphological, seed yield and its related traits in the present material. On the basis of mean performance, Himso-14-19 was found to be superior for seed yield/plant. Himso-14-1, Himso-14-52 and PS-1347 showed early flowering. Genotypes Himso-14-14A, Himso-14-145, Himso-14-19, Himso-14-39 and Himso-14-157 exhibited high oil content. Correlation studies revealed that number of branches/plant, number of seeds/pod, biological yield/plant and harvest index exhibited significant and positive correlation with seed yield/plant both at phenotypic and genotypic levels. Path coefficient analysis revealed that harvest index and biological yield/plant could be considered as the direct selection indices for yield improvement in soybean.

As Indian soybean varieties are either introductions or are a result of hybridization between the germplasm introduced. Therefore, there is a need to broaden the genetic base of soybean cultivars. The wealth of genetic diversity from exotic germplasm has not been utilized fully. These germplasm lines based on the mean performance having excellent source of genetic variability, could be exploited to broaden the genetic base of soybean.

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