

GENETIC VARIABILITY AND CHARACTER ASSOCIATION AMONG YELLOW MOSAIC DISEASE RESISTANT DERIVATIVES OF SOYBEAN VARIETY JS 335

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ABSTRACT

Soybean is one of the important oilseed crops in the legume family. The success of the breeding program highly depends on the variation present in the material. The present experiment was conducted to assess the genetic variability and character association between grain yield and its component traits. 86 F_{2:7} and backcross derived genotypes from the cross of elite soybean variety JS 335 (S) and SL 525 (R) were evaluated in randomized complete block design with three replications at two locations (Ludhiana and Gurdaspur). The analysis of variance, heritability, genetic advance, correlation, and path coefficient analysis were carried out to validate the results. The analysis of variance revealed the presence of sufficient genetic variability in the population. High phenotypic coefficient of variation (PCV) values over genotypic coefficient of variation (GCV) values were observed for all traits indicating the influence of environmental effects on the expression of characters. High PCV and GCV values were recorded for grain yield per plant, number of pods per plant and 100-seed weight. High heritability coupled with high genetic advance was observed for grain yield per plant followed by 100-seed weight. The number of pods per plant and 100-seed weight showed a significant positive correlation with grain yield per plant. Path coefficient analysis also revealed that number of pods per plant and 100-seed weight showed high and positive direct effect on grain yield per plant. Thus, number of pods per plant and 100-seed weight were important determinants of grain yield in soybean.

Keywords: Correlation, Genetic variability, Heritability, Path coefficient analysis, Soybean

Soybean (*Glycine max* (L.) Merrill) is considered the most important legume crop in the world. Because of multiple uses, soybean is also called the 'Golden bean' or 'Miracle legume' of the 21st century. It 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. It provides the highest protein content (30-45%) among all food crops and contains a considerable oil content (15-24%) comprising high percent of unsaturated fatty acids (Akram *et al.*, 2011). Soybean seeds also contain other nutrient elements like calcium, iron, phosphorus, carotene and vitamin-B1, vitamin B2 and vitamin-C (Gopalan *et al.*, 1971).

In India, within a short period of time soybean has emerged as a major oilseed crop. In 1970, soybean was under cultivation in area of 0.03 m ha. It expanded at an unprecedented pace and touched the figure of 12.99 million hectares area with the production of 13.71 million tons and average productivity of 10.5 q/ha in 2021 (Indiastat, 2021). Mainly soybean production in India increased due to increase in area whereas its productivity is hovering around 1.0 t/ha since last four

decades. Because of assured irrigation facilities, Indo-Gangetic Plains are considered future potential area of soybean expansion. However, high yielding and yellow mosaic disease (YMD) resistant varieties that can make soybean a viable alternative to rice (the dominant crop of the area), are lacking. To diversify some area from rice to soybean, high yielding and YMD resistant genotypes are required for Northern India. For any crop improvement program, it is important to have a large amount of genetic variability in available material. The presence of variability in material indicates the scope for further improvement of crop (Baiget *et al.*, 2018). But in the case of highly self-pollinated crops like soybean, presence of natural variation is less, resulting in limited scope for selection opportunity (Jain *et al.*, 2018). Therefore, creation of desirable genetic variability is must to develop improved varieties through selection. Generally diverse and elite varieties are crossed to produce genetically variable base population, upon which selection is practiced. To synthesize potential breeding material of soybean for northern plain zone (NPZ), the cultivar JS 335 was crossed and backcrossed with another variety, SL 525. JS 335 is high yielding, widely adapted but susceptible to yellow mosaic disease (YMD) whereas SL 525 is recommended for cultivation in NPZ and is resistant to YMD. The F_{2:7} and backcrossed derived populations from cross of JS

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335 and SL 525 are expected to generate segregants combining high yield and YMD resistance. It is worth mentioning that the North-West part of the country is a hot spot for YMD.

Phenotypic and genotypic coefficient of variation, heritability, correlation and path coefficient analyses are the genetic parameters used to assess the genetic potential of any breeding population. Thus, the objectives of this study were to estimate the nature and magnitude of genetic variability in a group of YMD resistant derivatives of JS 335, estimate correlations and path coefficients as a guide for developing high yielding genotypes of soybean.

MATERIALS AND METHODS

This experiment was conducted during kharif at two locations i.e., Pulse Research area of Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana and Regional Research Station, Gurdaspur. The experimental material comprised of 86 genotypes belonging to 4 populations ($F_{2.7}$, BC_1F_6 , BC_2F_5 and BC_3F_4) from the cross JS335xSL525 and backcross with JS335. The 86 soybean genotypes comprised of 27 genotypes derived from $F_{2.7}$ generation, 24 genotypes from BC_1F_6 , 18 genotypes from BC_2F_5 and 15 genotypes from BC_3F_4 generation and two parents viz SL 525 and JS 335. The experimental design was randomized complete block design with three replications at two locations. The genotypes were sown in a row length of 5-meter, paired rows per entry and spacing between the rows was 45 cm with a plant-to-plant distance of 5 cm at Ludhiana and Gurdaspur locations. The crop was raised by following the recommended agronomic practices and fertilizer dose. Five plants were randomly taken from each genotype per replication at each location and phenotypic observations were recorded for seven agronomic traits viz. days to 50% flowering, days to maturity, plant height at maturity (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g) and grain yield per plant (g). Ludhiana is known as natural hotspot location for YMV disease therefore YMD score was recorded only for Ludhiana

location. Responses of the genotypes to YMV disease was scored using 0-9 scale proposed by Lal *et al.* 2005 (Table 1). Genetic parameters such as genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance were statistically computed (Burton and De Vane, 1953). Genotypic and phenotypic correlation coefficients and path coefficients were determined by applying method given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance for randomized complete block design based on pooled data of Ludhiana and Gurdaspur locations revealed that genotypes had significant variation for all the traits except number of seeds per pod (Table 2); thus, indicating the availability of sufficient genetic variation among the genotypes for all traits except for number of seeds per pod. In a recent study significant genetic variation for days to 50% flowering, plant height, number of pods per plant and grain yield per plant has also been reported in a set of genotypes (Kumar *et al.*, 2020).

Mean performance of 86 genotypes revealed that one genotype SLJSB-3-9 (23.5 g), which was derived from BC_3F_4 generation was significantly superior among all genotypes for grain yield per plant and also had resistance to YMD. Another genotypes SLJSF-1 (derived from $F_{2.7}$) and SLJSB-1-11 (derived from BC_1F_6) were found to be high yielding and resistant to yellow mosaic. Genotypes such as SLJSB-3-3 (46.0 days), SLJSB-2-18 (46.2 days), SLJSB-1-24 and SLJSB-2-10 (46.3 days) were early in flowering besides resistant to YMD. Genotypes SLJSF-1 (125.5 days), SLJSF-9 (125.5 days), SLJSF-8 (125.7 days) SLJSB-3-14 (126.5 days) and SLJSB-3-15 (126.5 days) were early in maturity and were found to have moderate to high resistance. A higher number of pods per plant was observed in genotype SLJSB-1-19 (82) which was highly resistant to YMD. Genotypes like SLJSF-7 (2.5) and SLJSF-18 (2.5) were observed to have a greater number of seeds per pod and resistance to YMV. The genotypes like SLJSF-17 (10.2), SLJSB-1-15(10.2)

Table 1. Rating scale for YMV (Lal *et al.*, 2005)

Grade	Description	Reaction
0	No visible symptoms or yellow minute specks covering 1-5 % leaf area	Resistant (R)
3	Mottling of leaves and covering 5-15 % leaf area	Moderately Resistant (MR)
5	Yellow mottling and discoloration of 15-30 % leaf area	Moderately Susceptible (MS)
7	Yellow mottling and discoloration of leaves and pods, plants covering 30-75 % of foliage	Susceptible (S)
9	Severe yellow discoloration of leaves, covering 75-100 % of foliage, stunting of plants	Highly susceptible (HS)

Table 2. Mean squares for different characters in soybean based on pooled data over locations

Source of variation	df	Days to 50% flowering	Plant height at maturity (cm)	Days to maturity	No of pods per plant	No of seeds per pod	100-seed weight (g)	Grain yield per plant
Replication	2	0.01	768.13	5.67	29.16	1.23	0.36	2.14
Treatment	85	1.46**	132.92**	6.39**	223.59**	0.02	2.98**	15.22**
Error	170	0.40	26.38	1.17	53.78	0.02	0.33	1.29

* Significant at 5% ** Significant at 1%

were ranked at the top for 100-seed weight.

The significance of mean squares for genotypes for different traits indicates quantum of genetic variation present in the material. To quantify phenotypic and genotypic variation present in material, phenotypic (PCV) and genotypic (GCV) coefficients of variation were estimated. High PCV values over GCV values were observed for all traits indicating high influence of environmental effects on expression of characters (Table 3). High PCV and high GCV values were observed for grain yield per plant. Slightly high PCV values were observed for the number of pods per plant than grain yield per plant. Moderate PCV and GCV values were observed for plant height at maturity and 100-seed weight. Results of present study were supported by findings of Kumar *et al.*, 2020. Low PCV and GCV values are observed for days to 50% flowering, days to maturity and number of seeds per 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 (>20%) was observed for grain yield per plant followed by 100-seed weight and pods per plant indicating the predominance of additive gene action in the inheritance of these characters. Present results were in accordance with the findings of Patil *et al.* (2011), Reni and Rao (2013), Chavan *et al.* (2014), Chandrawat *et al.* (2017) and Jain *et al.* (2018).

The correlation analysis was conducted for all possible combinations of characters. While studying the

correlation coefficients, it was observed that genotypic correlation coefficients were higher than their respective phenotypic correlation coefficients for all characters under the study indicating the major associations between traits due to genetic causes. This also indicates that phenotypic expression is reduced by the environmental effects. Similar results were observed by Chandel *et al.*, 2014. At both genotypic and phenotypic levels, grain yield per plant was significantly and positively correlated with days to maturity, number of pods per plant and 100-seed weight (Table 4 & Fig. 1). At genotypic level grain yield was positively correlated with number of pods per plant and number of seeds per pod. Similar results were reported by Mahbub *et al.* (2015) for days to maturity, number of pods per plant and 100-seed weight. Akram *et al.* (2011) reported similar results for days to maturity and number of pods per plant whereas for 100-seed weight, they reported negative correlation. Alakhder *et al.* (2015), Chavan *et al.* (2016) and Guleria *et al.* (2019) reported similar results for number of pods per plant and 100-seed weight. Grain yield observed to have negative correlation with days to 50% flowering. Similar results were found by Arshad *et al.* (2006).

Among the other component characters days to 50% flowering showed significantly and positive correlation with 100-seed weight (0.18) and negative correlation with days to maturity (-0.43). Plant height at maturity was significantly and positively correlated with days to maturity (0.14), number of pods per plant (0.16) and number of seeds per pod (0.14). Days to maturity had significant and positive correlation with number of pods per plant (0.18). The number of pods per plant

Table 3. Estimates of genetic parameters

Traits	Mean	h ² (bs) %	GA	GA (% of mean)	PCV (%)	GCV (%)
Days to 50% flowering	47.48	46.47	0.83	1.75	1.83	1.25
Plant height at maturity (cm)	65.78	57.38	9.30	14.14	11.96	9.06
Days to maturity	128.64	59.78	2.10	1.63	1.33	1.03
No of pods per plant	60.07	51.28	11.10	18.48	17.49	12.52
No of seeds per pod	2.30	7.14	0.02	0.88	6.00	1.60
Grain yield	13.96	78.20	3.93	28.11	17.45	15.43
100-seed weight (g)	7.64	72.93	1.66	21.67	14.42	12.32

Table 4. Correlation coefficients for all possible pairs of characters

S. No	Character	r	Plant height at maturity (cm)	Days to maturity	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Grain Yield (g)
1	Days to 50% flowering	$P_r G_r$	0.06 0.29	-0.43** 0.07	-0.08 -0.05	-0.05 0.21	0.18** 0.34	-0.01 -0.02
2	Plant height at maturity (cm)	$P_r G_r$	-	0.14* 0.23	0.16** 0.27	0.14* 0.40	0.05 0.10	0.02 -0.01
3	Days to maturity	$P_r G_r$		-	0.18** 0.28	0.04 0.07	-0.09 -0.14	0.13* 0.18
4	Number of pods per plant	$P_r G_r$			-	0.19** 0.12	-0.03 -0.11	0.54** 0.64
5	Number of seeds per pod	$P_r G_r$				-	0.08 0.23	0.09 0.38
6	100-seed weight (g)	$P_r G_r$					-	0.44** 0.45

* Significant at 5% level **Significant at 1% level

showed significant and positive correlation with number of seeds per pod (0.19). Similar results were reported by Kumar *et al.* (2020).

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 reveals the true nature of associations observed among various characters. The path coefficient analysis using phenotypic correlation coefficients showed direct and indirect effects of different traits on grain yield per plant. It was observed that number of pods per plant followed by 100-seed weight had high and positive direct effect on grain yield (Fig. 2) which suggests that selection

of these characters will help-- in improvement of crop yield. Similar results were reported by Patil *et al.* (2011) and Haghi *et al.* (2012) for number of pods per plant, and Arshad *et al.* (2006), Bhartiya and Aditya (2016) and Baig *et al.* (2017) for 100-seed weight. Days to maturity showed low positive direct effect on grain yield per plant. Characters like days to 50% flowering, plant height at maturity and number of seeds per pod showed negative direct effect on grain yield.

Our study found that desirable genetic variability was generated for grain yield and its related traits in lines derived from direct cross of SL 525 and JS 335 and backcross derivatives using JS 335 as recurrent parent. Based on mean performance, genotype SLJSB-3-9

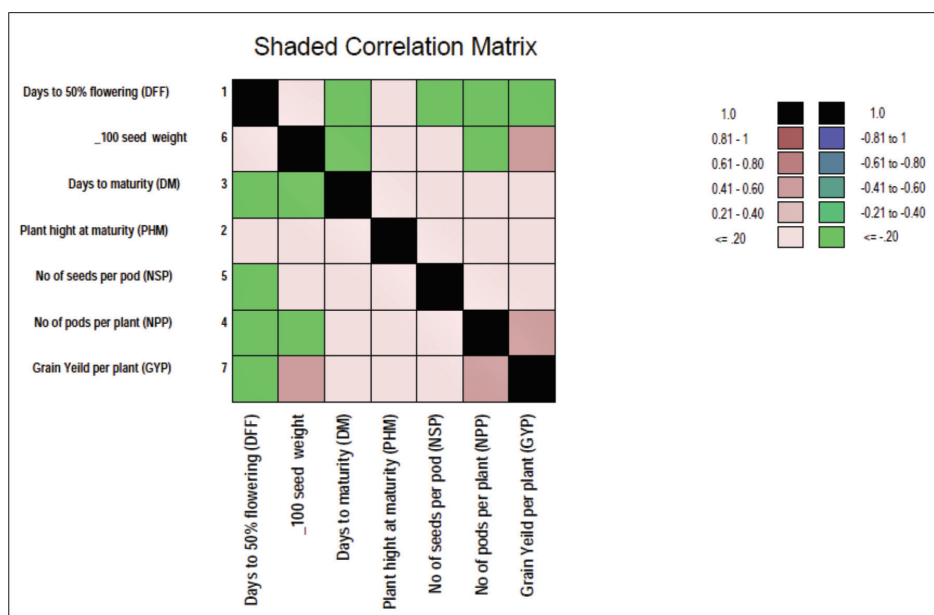


Fig. 1. Correlogram showing the correlation between grain yield and component characters of soybean genotypes

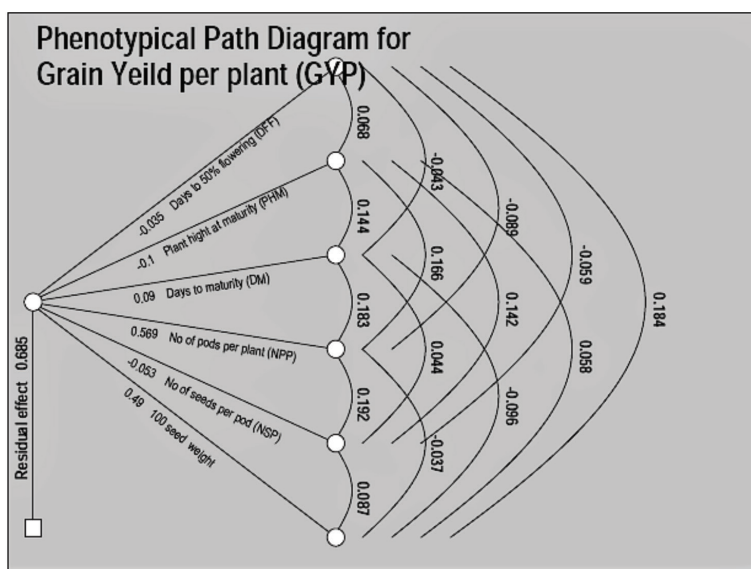


Fig. 2. Phenotypical path diagram indicating direct and indirect effect of various traits on grain yield of soybean genotypes

(derived from BC_3F_4) was found to be superior for grain yield per plant with YMD resistance. A higher number of pods per plant was observed in genotype SLJSB-1-19 which was also highly resistant to YMD. High 100-seed weight was found in genotypes SLJSF-17, SLJSB-1-15. Correlation studies revealed that number of pods per plant and 100-seed weight exhibited positive significant correlation with grain yield per plant at both phenotypic and genotypic levels. Path coefficient analysis showed that the number of pods per plant and 100-seed weight had high and positive direct effect on grain yield. This study concludes that high yielding and YMD resistant versions of a very popular soybean variety, JS 335 were identified that can be recommended for cultivation in Northern Plain Zone and Central Zone (Hub of soybean cultivation in the country) after thorough testing.

Authors' contribution

Conceptualization and designing of the research work (BSG, SKD); Execution of field/lab experiments and data collection (KVK, BSG, AK, AS); Analysis of data and interpretation (KVK, AK); Preparation of manuscript (KVK, MDP)

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