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Genetic variability studies and morphological characterization in soybean (*Glycine max* L. Merril)

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Abstract

Soybean production and productivity is mainly depends on the improved cultivars. First step in any crop improvement is mining of diverse genotypes in yield and others beneficial agronomical traits from available germplasm. Twenty five soybean genotypes were evaluated for genetic variability among eight morphological characters using Randomized Block Design during *Kharif* season, 2022 with three replications at Research Farm, under Mandsaur University, Mandsaur (M.P.). ANOVA showed significant differences for all eight traits among the accessions. Significant variability was recorded in mean performance for traits under study, which indicates that the lines showed level of exploitable genetic variability to be use for further breeding of development of suitable cultivars. The PV value was more than the corresponding GV value of all eight traits. High GCV & PCV were noted for plant height (cm) (30.20 and 30.48) and pods per plants in number (23.82 and 23.97). Whereas, moderate, for number of primary branches/ plant (12.42 and 12.95), 100 seed weight (gm) (11.42 and 11.42) and days to 50% flowering (10.12 and 10.37). All the eight quantitative traits under investigation showed the high Heritability with range from 99.98 (100 seed weight) to 91.93 (number of primary branches/ plant). Heritability of 99.98% was maximum for 100 seed weight (gm) followed by number of pods per plants (98.76), plant height (cm) (98.16), days to 50% pod initiation (96.73), grain yield/plant (gm) (95.84), days taken to 50% flowering (95.29), days to maturity (94.30) and number of primary branches/ plant (91.93). High h^2 (heritability) along with high GA (genetic advance) was revealed by plant height (cm) followed by number of pods per plants, number of primary branches/ plant, 100 seed weight (gm) and days to 50% flowering. It is showing that these traits are governed by additive gene action and there is huge scope for genetic improvement by simple selection in soybean.

Keywords: Genotypes, genetic variability, soybean, characterization, heritability, genetic advance

Introduction

Soybean (*Glycine max* L.) is a major oilseed crop of *Fabaceae* family and also known as 'golden bean and miracle of the 21st century' (Bairagi *et al.* 2023; Mishra and Patidar 2023) [3, 34]. About thirty species (perennial) are reported in subgenus of *glycine* having valuable characters for breeder, with a center of diversity in Australia and found in different habitats viz. rocky outcrops, temperate etc. (Chung and Singh, 2008) [9]. Worldwide, among oilseeds, soybean is main oilseed crop due to its 25% share to the edible oil production at global level and abundant source of protein in formulated animals feeds. Every year, after processing, around 85% of the soybean in the world is used as soybean meal (by product of oil extraction) and oil. Maximum oil (95%) is used in eating purposes and remaining for industry purposes like in making of soaps and biodiesel (Verma and Chandrakar 2023) [50].

The USA, Argentina, China and Brazil are top countries in production of soya (Bairagi *et al.*, 2023) [3]. It has significant share in edible oil among diet of peoples of India and cultivated in Madhya Pradesh, Karnataka, Andhra Pradesh, Maharashtra, Rajasthan, and Chhattisgarh during *kharif* season (Bairagi *et al.*, 2023) [3]. Soybean is a one important crop for prosperity of farmers in India due to enhancement in income by export of its de-oiled cake (Dhurwey *et al.*, 2019) [13].

In India, Madhya Pradesh is known as soya state and has ranked first in production due to large area coverage. Low productivity and yield of it in relation may be due to unavailability of high yielding genotypes and use of their poor quality seeds, narrow genetic base of genotypes which are used for cultivation, lack of irrigation and poor management practices (Nair *et al.*, 2023) [35].

Genetic variability analyses in available genetic material or genotypes are a primary requirement for start any breeding programme of a crop and for decide selection strategy (Koraddi and Basavaraja, 2019) [29]. Both, h^2 and GA are known as valuable selection parameters (Singh and Narayanan, 1997) [44]. Heritability (h^2) may be dividing as broad sense (h^2_{bs}) and narrow sense (h^2_{ns}) heritability respectively (Holland *et al.*, 2003) [18]. Broad sense heritability (h^2_{bs}) gives information on the genetic variation in relation to total variation (genetic plus environment) in plant population taken for study of a particular trait (Holland *et al.*, 2003; Visscher *et al.*, 2008) [18, 51]. GA values show the mode of gene action of quantitative characters and assists in use of appropriate techniques for crop improvement (Singh and Narayanan, 1997) [44]. Thus, values of h^2 along with values of GA are more precise and fruitful in predicting the gain under selection than individual focus on the parameters for selection of different characters.

The present experiment of the genetic component responding yield and quality attributing traits included for evaluation of

different genotypes.

Materials and Methods

The present experiment was laid out with twenty five entries in three replications using randomized block design at Research Farm, under Mandsaur University, Mandsaur (M.P.) during the *Kharif* season of 2022-2023. The genotypes were planted each in three rows with spacing 45 cm (between two rows) 45 cm and 5 cm (between plants). Recommended package as well as practices were applied for healthy propagation of plants.

Experimental Material

Seed of twenty five diverse genotypes/varieties of soybean were procured from different geographical sources and collected from Indian Institute of Soybean research, Indore listed in Table 1. The data for all the characters were observed on the basis of "National Test Guidelines for the Conduct of DUS Testing of soybean under the PPV & FR Act of Article 15.3 (b).

Table 1: Name of 25 genotypes of Soybean used for study

S. No	Name of genotypes	Source	S.No	Name of genotypes	Source
1	TGX 86-24-2F	IISR, Indore	14	UPSL 742	IISR, Indore
2	SQL 113	IISR, Indore	15	NP 4	IISR, Indore
3	AGS 205	IISR, Indore	16	AURDC 508	IISR, Indore
4	AURDC 5	IISR, Indore	17	AGS 218	IISR, Indore
5	AMSS 44	IISR, Indore	18	JS 335	IISR, Indore
6	AMUS 542	IISR, Indore	19	JS 2034	IISR, Indore
7	SQL 110	IISR, Indore	20	JS 9560	IISR, Indore
8	NALIYAS	IISR, Indore	21	SL 432	IISR, Indore
9	UPSL 63	IISR, Indore	22	TGX 93-36E	IISR, Indore
10	TGX 860-11D	IISR, Indore	23	TGX 293-65E	IISR, Indore
11	B-327	IISR, Indore	24	SQL 97	IISR, Indore
12	AGS 25	IISR, Indore	25	AMUS 76	IISR, Indore
13	AGS 156	IISR, Indore			

Table 2: ANOVA table for Randomized Complete Block Design

Source of variation	d.f.	Sum of squares	Mean squares	F ratio	Expected mean squares
Replication	(r-1)	S.Sr	Mr	Mr/Me	-
Genotypes	(g-1)	S.Sg	Mg	Mg/Me	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	S.Se	Me		σ^2_e
Total	(rg-1)				

Where,

r = number of replications

g = number of genotypes

σ^2_e = error mean square

σ^2_g = genotypic mean square

Quantitative characters for recording observations

Randomly Five plants, from each replication in an accession were selected for observe data. The tagged selected individual plant observations were noted for the plant height (cm), pods per plant in number (at the time of maturity), numbers of branches per plant (at the time of maturity), date of maturity (when in a plot, 95% of the plants change the pod color from green to lemon yellow), grain yield per plant and 100 seeds weight characters except for days taken to 50 percent flowering after sowing and days to maturity. The data of character, days to 50% flowering was taken from sowing dates of seeds to the date of 50% blooming of the plants in a row. Days to beginning of 50% pod initiations were noted from number of days after sowing.

Statistical analysis

Analysis of variance

The mean performance selected plants were statistically analyzed for variability. To test the significance of differences among the genotypes, the ANOVA was according to Bairagi *et al.* (2023) [3] and by methods of Panse and Sukhatme (1967) [38].

Parameters of genetic variability

Mean: Mean is estimated by using below formula.

$$\bar{X} = \frac{\sum X_i}{N}$$

Where, \bar{X} = Mean of character X, $\sum X_i$ = Sum of all the observations of i^{th} traits and N is total number of observations

Range

Range is recorded as minimum and maximum value for characters.

Genotypic and phenotypic coefficient of variation (%)

Both were analysed according to Bairagi *et al.* (2023)^[3].

GCV % (Genotypic coefficient of variation)

$$\text{GCV\%} = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

$$\sigma_g = \sqrt{\sigma_g^2}$$

PCV % (Phenotypic coefficient of variation)

Since,

$$\text{PCV} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

$$\sigma_p = \sqrt{\sigma_p^2}$$

Where, σ_p^2 is phenotypic variance, σ_p is phenotypic standard deviation, σ_g^2 is genotypic variance, σ_g is genotypic standard deviation and \bar{X} is General Mean of the character respectively.

The estimates of high (> 20 percent), moderate (10-20 percent) and low (< 10 percent) PCV and GCV were noticed as suggested by Sivasubramanian and Menon (1973)^[45].

Heritability and expected genetic advance

The heritability in broad sense and expected genetic advance was analysed as described by Bairagi *et al.* (2023)^[3].

The broad sense heritability estimates were measured as low

(<50%), moderate (50 to 70%) and high (> 70%) suggested by Robinson (1949).

Genetic advance as percentage of mean

It was calculated by the formula.

$$\text{GA as percentage of mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA is Genetic Advance and (\bar{X}) is Mean of the character.

The GA is categorized as high (> 20%), moderate (10-20%) and low (<10) respectively.

Morphological traits

Leaf shape, flower color (at the time of 50% flowering), seed color (after fully maturity of seed) and pubescence appearance were observed visually in a group of plants.

Results and Discussion

Parameters of variability

Analysis of variance: Results showed significant mean sums of square in almost all the genotypes (Table 3a and 3 b), which indicated that there was abundant genetic variability exists amongst genotypes. Maximum and highly significant (729.43**), mean sum of square was observed by number of pods per plants and minimum (0.696**) by number of primary branches per plant.

The magnitude of variability was in decreasing sequence for remaining traits *viz.*, number of pods per plants, plant height (cm), days to 50% flowering, days to 50% pod initiation, days to maturity, grain yield/plant (gm), 100 seed weight(gm) and number of primary branches/plant. These findings are supported by Jain *et al.*, (2017)^[20]; Broyles *et al.*, (2014)^[6]; Khan *et al.*, (2022)^[27] and Gilles *et al.*, (2022)^[16]. Mean performance that having significant variability for all the eight traits shows that the genotypes have enough exploitable level of genetic variability to be utilized for further breeding of suitable cultivars or pre-breeding lines (James *et al.*, 2015; Zhang and Boahen, 2010)^[22, 52]. These variations in mean values of genotypes might come from variations either in genetic or environmental factor under (Roth *et al.*, 2020)^[41].

Table 3 (a): Analysis of variances for yield & yield attributing traits of soybean genotypes

Source of variation	df	Days to 50% Flowering	Days to 50% pod initiation	Plant height (cm)	Number of pods per plants
Repl	2	9.854	5.494	3.720	6.840
Treat	24	79.269**	76.664**	442.174**	729.430**
Error	48	1.284	0.854	2.748	3.048
Total	74	26.808	25.567	145.291	238.734

Table 3 (b): Analysis of variances for yield & yield attributing traits of soybean genotypes

Source of variation	df	No of primary branches/ plant	Days to maturity	100 Seed Weight (gm)	Grain Yield/plant (gm)
Repl	2	0.012	0.494	0.0010	0.152
Treat	24	0.696**	32.009**	2.8822**	4.037**
Error	48	0.020	0.632	0.0002	0.058
Total	74	0.239	10.805	0.9349	1.351

* & ** indicate level of significant at 5% and 1%, respectively

Mean performance and range of different characters

Table 4

Days to fifty percent flowering ranged from 35.00 to 59.000 with overall mean of 50.39. The maximum days to fifty percent flowering were observed in genotype AGS-25 (59.00)

and it was minimum in JS-9560 (35.00). Days to 50% pod initiation ranged from 43.33 to 65.00 with a grand mean performance of 57.69. The days to first flower opening (maximum) was observed in AGS-25 (65.00) and minimum in JS-9560 (43.33). Plant height (cm) range was 21.33 to

66.00 with an overall mean (40.08). The plant height (cm) of JS-335 (66.00) was maximum and minimum in SQL-113 (21.33). Number of pods per plants differed from 39.67 to 93.00 with agr and mean of 65.32. The number of pods per plants was maximum in AGS-25 (93.00) and minimum in SQL-97 (39.67). Number of primary branches per plant varied from 03.33 to 04.70 with an overall mean performance of 03.82. The maximum number of primary branches per plant was found in AURDC-5 (4.70) and minimum in AGS-156, AGS-218 and TGX-93-36E (3.33). Days to maturity differed from 84.00 to 98.00 with a grand mean of 90.29. The maximum (98.00) days to maturity was observed in genotype JS-335 and minimum (84.00) in AMUS-76. Hundred seed weight (gm) ranged from 06.52 gm to 10.72 gm with an overall mean performance of 08.58 gm. The hundred seed weight (gm) was maximum in genotype UPSL-63 (10.72 gm) and minimum in AGS-25 (6.52 gm). Grain yield/plant (gm) ranged from 11.87 gm to 15.87 gm with an overall mean performance of 13.36 gm. The grain yield/plant (gm) was maximum of AURDC-5 (15.87 gm) and minimum of B-327 (11.87 gm).

Table 4: Genetic parameters of variability for yield and yield attributing traits of soybean genotypes

Traits	Mean	Range	
		Min.	Max.
Days to 50% Flowering	50.39	35.00	59.00
Days to 50% pod initiation	57.69	43.33	65.00
Plant height (cm)	40.08	21.33	66.00
Number of pods per plants	65.32	39.67	93.00
No of primary branches/ plant	03.82	03.33	04.70
Days to maturity	90.29	84.00	98.00
100 Seed Weight (gm)	08.58	06.52	10.72
Grain Yield/plant (gm)	13.36	11.87	15.87

Genotypic (GCV%) and phenotypic coefficient of variation (PCV%): Results of yield and related characters for GCV & PCV in Table 5 reported that the values of PCV were more than the values of GCV, which showing that GCV and PCV could express variability among genotypes. Similar results were found by Neelima *et al.*, 2018^[36]; Shilpashree *et al.*, 2021^[42] and Bairagi *et al.*, 2023^[3].

The high genotypic and phenotypic coefficient of variation was observed for plant height (cm) (30.20 and 30.48), followed by traits number of pods per plants (23.82 and 23.97), number of primary branches/plant (12.42 and 12.95), 100 seed weight (gm) (11.42 and 11.42), days to 50% flowering (10.12 and 10.37), days to 50% pod initiation (8.71 and 8.86), grain yield/plant (gm) (8.62 and 8.81) and days to maturity (3.58 and 3.69) respectively. The above results indicated the presence of substantial amount of genetic variability for the traits, which exhibited less influence of environment on the expression of these traits. Similar results for different characters have also been reported by Drabo *et al.*, (2013)^[14]; Machado *et al.*, (2017)^[31]; Kasper *et al.*, (2019)^[25]; Zida *et al.*, (2021)^[53] and Bairagi *et al.*, 2023^[3]. However, high GCV & PCV were recorded for plant height (cm) (30.20 and 30.48) and number of pods per plants (23.82 and 23.97). Whereas, moderate GCV & PCV were recorded for number of primary branches/ plant (12.42 and 12.95), 100 seed weight (gm) (11.42 and 11.42) and days to 50% flowering (10.12 and 10.37). Low GCV & PCV were recorded for days to 50% pod initiation (8.71 and 8.86), grain

yield/plant (gm) (8.62 and 8.81) and days to maturity (3.58 and 3.69). King and Purcell, (2001)^[28]; Aditya *et al.*, (2011)^[1]; Baraskar *et al.*, (2014)^[4]; Thai *et al.*, (2019)^[48] and Bairagi *et al.* (2023)^[3] also reported similar result.

Heritability (%) in broad sense

The concept of heritability is valuable to know, whether phenotypic variations noticed among various plants of genotypes are cause of genetic changes or environment. According to Lush (1940)^[30] heritability may be grouped in broad sense and narrow sense. The estimation of heritability in broad sense reported that all eight traits depicted the high heritability (Table 5). It varied from 99.98 (100 seed weight) to 91.93 (primary branches/ plant). The character, 100 seed weight (gm) revealed maximum (99.98%) heritability followed by number of pods per plants (98.76), plant height (cm) (98.16), days to 50% pod initiation (96.73), grain yield/plant (gm) (95.84), days taken to 50% flowering (95.29), days to maturity (94.30) and number of primary branches/ plant (91.93). Visscher *et al.*, 2008^[51]; Aditya *et al.*, (2011)^[1]; Shilpashree *et al.*, (2021)^[42] and Bairagi *et al.* (2023)^[3] found in support with our finding. High heritability indicated that expression of character namely 100 seed weight, number of pods per plants, plant height, days to 50% pod initiation, seed yield/plant (gm), days taken to 50% flowering, days taken to maturity and number of primary branches per plant was least influenced by the environment. But, according to Singh and Narayanan, 1997^[44], selection may not be effective for these character due to dependency of h^2 (bs), on total genetic variance [fixable (additive) and non-fixable (dominance and epistatic)] variances.

Genetic advance as percent of mean

GA as percentage of mean was analysed to know the genetic gain and presented in Table 5. The highest GA as percentage of mean was noticed for plant height (cm) (61.63), followed by number of pods per plants (48.77), number of primary branches/ plant (24.53), 100 seed weight (gm) (23.53) and days to 50% flowering (20.35). Pimentel *et al.*, 2005^[39] found in support with our finding. Medium GA as percentage of mean were expressed by days to 50% pod initiation (17.65) and grain yield/plant (gm) (17.39) whereas, low GA as percentage of mean were expressed by days to maturity (7.16).

Heritability and GA as percentage of mean

Heritability and GA are crucial genetic parameters for selection. The analysis of heritability may be used for the prediction of genetic gain, which shows the genetic improvement that would results from the selection of best individual. GA is the improvement in the mean genetic value of selected plants over the parental population.

Values of heritability for traits are valid for only one generation, GA vary from generation to generation. Data of heritability in broad sense and GA as percentage of mean of every character should always be considered and interpreted simultaneously to know the role of additive gene action (Holland *et al.*, 2003 and Visscher *et al.*, 2008)^[18, 51].

Heritability and GA was high for plant height (cm) followed by number of pods per plants, number of primary branches/ plant, 100 seed weight (gm) and days taken to 50% flowering. Jalata *et al.*, 2010^[21]; Pimentel *et al.*, 2005^[39]; Aditya *et al.*, (2011)^[1] for number of pods per plant; Shilpashree *et al.*,

(2021) [42] for plant height and number of pods per plant, Bairagi *et al.*, (2023) [3] for number of pods per plants, plant height and primary branches per plant in number found in support with our finding.

Mass selection or pure line selection would be effective for a limited extent for days to 50% pod initiation and grain yield/plant (gm) because showing high heritability and moderate genetic advance (Aditya *et al.*, 2011; Barcchiya *et*

al., 2018; Jandong *et al.*, 2020) [1, 5, 23]. Both traits indicated the presence of intermediate expression for both additive and dominance gene effect. Whereas, high heritability with low GA as percentage of mean were expressed by days to maturity. Similar results were also found by Kavera, (2008) [26] in groundnut and Malik *et al.*, (2006) [32] in soybean respectively.

Table 5: Genetic parameters of variability for yield & yield attributing traits of soybean genotypes

Genotypes	Heritability (%)	GA	GA as % of mean	GCV (%)	PCV (%)
Days to 50% Flowering	95.29	10.25	20.35	10.12	10.37
Days to 50% pod initiation	96.73	10.18	17.65	8.71	8.86
Plant height (cm)	98.16	24.70	61.63	30.20	30.48
Number of pods per plants	98.76	31.85	48.77	23.82	23.97
No of primary branches/ plant	91.93	0.94	24.53	12.42	12.95
Days to maturity	94.30	6.47	7.16	3.58	3.69
100 Seed Weight (gm)	99.98	2.02	23.53	11.42	11.42
Grain Yield/plant (gm)	95.84	2.32	17.39	8.62	8.81

Morphological characterization of the qualitative characters

Overall 25 genotypes were used for morphological characterization. Four morphological traits namely leaf shape, flower colour, seed colour and pod pubescence on five randomly selected plants of each genotype per replication were recorded and characterized as per UPOV guideline (Table 6 and 7).

Table 6: Essential characters along with descriptor and their scale

S.N	Characteristics	Observations (Scale)			
		Lanceolate (1)	Pointed ovate (2)	Rounded ovate (3)	-
1	Leaf: Shape	Lanceolate (1)	Pointed ovate (2)	Rounded ovate (3)	-
2	Flower Colour	White (1)	Purple (2)	-	-
3	Seed: colour	Yellow (1)	Yellow green (2)	Green (3)	Black (4)
4	Pod: Pubescence	Absent (1)	Present (9)	-	-

Table 7: Characterization of 25 lines as per note number given in DUS Guideline

S. No.	Germplasm	4-Leaf: Shape	7-Flower Colour	09- Pod: Pubescence	16-Seed Colour
1	TGX-86-24-2F	2	2	9	1
2	SQL-113	3	1	9	4
3	AGS-205	2	2	9	1
4	AURDC-5	2	2	9	1
5	AMSS-44	3	2	9	1
6	AMUS-542	2	2	9	1
7	SQL-110	2	2	9	1
8	NALIYAS	2	2	9	4
9	UPSL-63	2	2	9	4
10	TGX-860-11D	2	2	9	1
11	B-327	1	1	9	1
12	AGS-25	2	2	9	1
13	AGS-156	2	2	9	4
14	UPSL-742	2	2	9	4
15	NP-4	2	2	9	1
16	AURDC-508	2	2	9	1

Note: 1 to 9 alphabets are used here to tabulate the observations (Scale) as per note number given in DUS guideline.

All three leaf shapes *viz.*, lanceolate, pointed ovate and rounded ovate were noticed in all 25 germplasms, which show

much variation (Table 7), two lanceolate type *viz.*, B-327 and JS-9560, similarly nineteen pointed ovate type genotypes namely TGX-86-24-2F, AGS-205, AURDC-5, AMUS-542, SQL-110, NALIYAS, UPSL-63, TGX-860-11D, AGS-25, AGS-156, UPSL-742, NP-4, AURDC-508, AGS-218, SL-432, TGX-93-36E, SQL-97 and AMUS-76 whereas, rounded ovate type leaf shape reported in five genotypes *viz.*, SQL-113, MSS-44, JS-335, JS-2034 and TGX-293-65E. Like to it Mehra *et al.*, (2020) [33] and Chavan *et al.*, (2016) [8] found 7 lanceolate type and 12 pointed ovate type genotypes only.

Purple flower colour were present in 20 lines namely TGX-86-24-2F, AGS-205, AURDC-5, AMSS-44, AMUS-542, SQL-110, NALIYAS, UPSL-63, TGX-860-11D, AGS-25, AGS-156, UPSL-742, NP-4, AURDC-508, AGS-218, JS-335, JS-9560, SL-432, TGX-93-36E and TGX-293-65E but other five lines found white colouration *viz.*, SQL-113, B-327, JS-2034, SQL-97 and AMUS-76. It is a satisfying suggestion that during evolution, purple pigmentation of various crop plants had been lost, so, this type of evolution had been also in soybean germplasms (Desissa and Gemechu, 2018) [12].

Yellow seed colouration found in 19 lines namely TGX-86-24-2F, AGS-205, AURDC-5, AMSS-44, AMUS-542, SQL-110, TGX-860-11D, B-327, AGS-25, NP-4, AURDC-508, AGS-218, JS-335, JS-2034, JS-9560, SL-432, TGX-293-65E, SQL-97 and AMUS-76 whereas, black seed colour found for 6 genotypes namely SQL-113, NALIYAS, UPSL-63, AGS-156, UPSL-742 and TGX-93-36E.

Pod pubescence found present in all 25 lines in which 22 lines had brown coloured and rest of three lines had grey coloured pod pubescence.

In soybean, flower color primarily control primary controlled by six genes (*W1, W2, W3, W4, Wm* and *Wp*) whereas pubescence color is controlled by two genes, *T* and *Td* (Palmer *et al.*, 2004; Takahashi *et al.*, 2008; Takahashi *et al.*, 2010) [37, 46, 47]. The coloration of flower, seed coats, and pubescence of soybeans is due to the hydroxylation pattern of B-ring in flavonoids.

Two key enzymes [flavonoid 3'-hydroxylase (F3'H) and flavonoid 3'5'-hydroxylase (F3'5'H)] involved and the B-ring of flavonoids can be hydroxylated at either the 3' position (to produce cyanidin-based pigments) or at both the 3' and 5' positions (produce delphinidin-based pigments). Both these enzymes are microsomal cytochrome P450 dependent

monoxygenases that require NADPH as a co-factor (Forkmann, 1991) [15].

Different experiments of chromatographic showed that the formation of flavonoids with 3', 4' and 3', 4', 5' B-ring hydroxylation patterns is due to gene *T* and *W1* loci (Buttery and Buzzell, 1973 & 1982 and Iwashina *et al.*, 2006) [19]. Hence, *T* and *W1* are known to encode F3'H and F3'5'H (Toda *et al.*, 2002) [49].

The gene, *W1* effect to both flower and hypocotyl color. The flavonoids in flower petals of soybean have been estimated for pubescence color (Iwashina *et al.*, 2006) [19]. Recessive genes *w1* and *w4* did not produce anthocyanin whereas, the amount of flavones and dihydroflavonols in genotypes studied by Takahashi *et al.*, 2010 [46] for *w1* or *w4* was largely equal to the lines with purple flowers concluded that *W1* and *W4* affect only anthocyanin biosynthesis.

Conclusion

Significant genetic variability in mean performance of all the traits under studied material indicates that genotypes have significant amount of genetic variability which may be used for further breeding program in variety development of soybean. High heritability and high genetic advance for plant height, number of primary branches/plant, 100 seed weight (gm), and days taken to 50% flowering indicated the presence of additive gene action and less effect of environment in governing of these characters. So, simple selection (mass or pure line) would be effective for these traits for soybean improvement. The hundred seed weight (gm) and grain yield per plant (gm) was maximum for UPSL-63 (10.72 gm) and AURDC (15.87 gm) respectively, which indicated that these genotypes should be considered during development of high yielding varieties in soybean.

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