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Research Article

Genetic variability and association of yield contributing traits in advanced breeding lines of soybean

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Abstract
Characterization of genotypes for various traits is a basic and very essential criterion for crop varietal improvement programmes. Under the present investigation fifty seven advanced breeding lines along with three best checks (JS 20-98, JS 20-116 and JS 20-34) were evaluated to characterize 17 phenotypic and 11 yield attributing traits at JNKVV, Jabalpur. Morphological/phenotypic traits were described as per DUS guidelines. Yield attributing traits were utilized to work out various biometric parameters (Phenotypic Coefficient of Variation,(PCV), Genotypic Coefficient of Variation (GCV), heritability with genetic advance, correlation and path coefficient). Phenotypic characterization exhibited huge variability among advanced breeding genotypes for most of the descriptor traits. Semi-erect growth habit (100%), presence of peroxidase activity in ripe seed (100%), Semi-determinate growth type (95%), Yellow colour ripe seed testa (90%) and tawny colour pod hair (86.8%) were most common traits studied in genotypes. Significant variation was also obtained for yield attributing quantitative traits. PCV was higher in magnitude than GCV for all the traits and the highest for seed yield per plant (39.10 and 36.76, respectively). The highest heritability and genetic advance as per cent of mean were recorded for biological yield per plant and seed yield per plant, respectively. Seed yield per plant demonstrated a highly significant positive relation with biological yield (0.797**) followed by 100 seed weight (0.735**) and the number of pods per plant (0.620**). Whereas, it was negatively correlated with plant height (-0.303**). The genotypic path coefficient analysis also revealed that the highest positive direct effect on seed yield per plant was due to biological yield per plant followed by 100 seed weight.

Keywords: Heritability, Phenotypic traits, Correlation, Path Coefficient, soybean

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is considered to have the highest protein content (30-45%) with an outrageous gross output of plant based oil (15-24%) among all the cultivated crops in the world (Singh, 2010; Sharma *et al.,* 2014). Soybean oil provides a number of health benefits to the consumers because it contains omega-3 fatty acids as well as it is rich in unsaturated fatty acids. Soybean seeds also contain a good amount of other nutrients like calcium, phosphorus, iron and vitamins like Vit-B_1, Vit-B_2 and Vit-C (Gopalan *et al.,* 1971). Soybean is gaining enormous popularity among farmers because it offers multiple uses and various possibilities of growth under diverse cropping systems.

It is very important to develop cultivars with a broad genetic base and higher genetic yield potential for continuous growth and sustainable production of soybean in India. Improvement through selection is solely based on the amount of variability present in the genotypes. This variability is attributable to the different genetic constitutions of the genotypes and the variable environments of growth (Baraskar *et al*., 2014). The genotypic coefficient of variation measures the heritable genetic component of the total variation therefore it is considered as one of the most appropriate parameters to compare the variability of various traits. Assessment of genetic variability helps in selecting suitable parents for hybridization, exploitation of heterosis, identifying superior lines and above all for long term selection gain (Chauhan and Singh, 1982). Heritability is a measure of transmission of variability from one generation to another and the consistent performance of selection depends on it (Wysmierski and Velo, 2013). The GCV and heritability estimates together will give the best results expected for selection rather than heritability alone (Burton, 1952). Selection of genotypes should be done based on plant phenotypic performance as well as the relatedness and genetic parameters of the targeted character, (Kuswantoro, 2019). Therefore, the identification and selection of superior genotypes will be effective for enabling the plant breeders with the estimates of variability, heritability and genetic advance parameters (Baraskar *et al.,* 2014).

Simultaneously, multiple superior genotypes are to be handled in the seed production and varietal development programme at a time. There are several chances of duplication and mixing of genotypes. The government of India approved its own *sui generis* system under the Protection of Plant Varieties and Farmers Rights Act (PPV&FRA), 2001 which aims to provide protection to the plant varieties based on distinctiveness, uniformity and stability (DUS). Varieties/ genotypes are morphologically identified by using descriptors based on distinctiveness, uniformity and stability (DUS) in soybean and other crops (Ramteke and Muralidharan. 2012; Dhaliwal *et al*., 2020). Since the qualitative characters exhibit stability over varying environments and generations, it proves to be a reliable way to characterize genotypes. Looking to all these aspects, an investigation was carried out to characterize the recently developed advanced breeding lines of soybean on the basis of phenotype and to draw important selection indices by estimating genetic variability, heritability and genetic advance with respect to the different yield attributing traits.

MATERIALS AND METHODS

The experiment was carried out on fifty seven advanced lines along with three best check varieties (JS 20-98, JS 20-116 and JS 20-34) of soybean at the research field of AICRP Soybean, Seed Breeding Farm, Department of Plant Breeding and Genetics, J.N.K.V.V., Jabalpur during *kharif,*2020. All these 57 genotypes evolved from the crosses of recently developed/identified superior genotypes at JNKVV, Jabalpur. The list of genotypes studied is given in **Table 1**. The experiment was laid out in a randomized complete block design with three replications. The entries were sown in three rows each of 3 m in length with a plant to plant spacing of 7 cm and row to row spacing of 30 cm. The experimental site had uniform topography, medium black soil with7.5 pH and free from water logged conditions. Plant to plant distance was maintained by uprooting of extra plant at 10 days after sowing. All the recommended packages and practices were followed for caring and nourishing of plants throughout the growth period.

The observations for yield associated traits were recorded from five randomly selected competitive plants from each replication for each genotype. The observations were taken from 11 yield attributing traits *viz*., the number of primary branches per plant, the number of pods per plant, the number of seeds per plant, 100 seed weight (g), biological yield per plant (g), harvest index (%), seed yield per plant (g), days to flowering, days to 50% flowering and days to maturity. The mean and standard error were calculated as per standard methods of estimation of genetic variability. The heritability and genetic advance as a percentage of mean (GA %) were estimated by the formula suggested by Allard (1960). The genotypic (GCV) and phenotypic coefficients of variation (PCV) were estimated according to the formula suggested by Burton (1952) and Singh and Chaudhary (1985). The observations on morphological traits were recorded from the individual plant as well as a net plot basis for 17 morphological traits as per the DUS guidelines of Soybean (Ramteke and Muralidharan, 2012).

RESULTS AND DISCUSSION

Phenotypic characterization as per DUS guidelines and frequency distribution of their specific descriptors revealed that there was huge variation in genotypes for different class of descriptors (**Table 2 and Fig. 1**). Semi-erect growth habits and the presence of peroxidase activity in ripe seeds were common traits in all genotypes. Semi-determinate growth type (95%), Yellow colour ripe seed testa (90%) and tawny pod hair colour (86.8%) were also most common in genotypes studied (**Table 2 and Fig. 1**). Hypocotyls color (anthocyanin pigmentation), which is considered as a distinct trait because of monogenic controlled and was present in 29 genotypes and absent in 31. It was also observed that the trait hypocotyl color was closely associated to the trait flower color as all the pigmented genotypes had violet flowers and white flowers were seen in genotypes having non pigmented hypocotyls. Out of 60 genotypes, determinate type growth was observed in three (JS 23-04, JS 23-01 and JS 20-34) and the rest were semi determinate (**Table 3**). Four kinds of leaf shapes were observed i.e. Rounded ovate (11), pointed ovate (33), lanceolate (15) and triangular (1, JS 22-39). Among the pointed ovate genotypes, JS 22-38 was distinct with the presence of light green color leaves. The pods of 38 genotypes were pubescent (33-tawny hair and 5- grey hair), (**Fig.2**). Thirteen genotypes exhibited dark brown pod colour. Seeds of two genotypes (JS 22-24 and JS 22-17) were distinct with an elongated shape and other genotypes with elongated flattened (11), spherical (18) and spherical flattened (29) in shape, **(Fig.2).**

Table 1. List of genotypes used in the present study

S. No.	Genotypes	Pedigree
1	JS 22-10	JS 20-30 × JS 95-60
2	JS 22-12	JS 20-53 × JS 20-34
3	JS 22-13	JS 20-71 × JS 20-22
4	JS 22-14	JS 20-53 × JS 20-34
5	JS 22-15	JS 20-71 × JS 20-22
6	JS 22-16	JS 20-88 × JS 20-34
7	JS 22-17	SL 738 × JS 95-60
8	JS 22-18	JS 20-53 × JS 20-34
9	JS 22-19	JS 20-89 × JS 20-34
10	JS 22-20	JS 20-29 × JSM 275
11	JS 22-21	JS 20-63 × JS 20-35
12	JS 22-22	JS 20-75 × JS 20-14
13	JS 22-23	JS 20-79 × JS 335
14	JS 22-24	JS 20-53 × JS 20-34
15	JS 22-25	JS 20-63 × JS 20-35
16	JS 22-26	JS 20-09 × PS 1475
17	JS 22-27	JS 20-82 × JS 95-60
18	JS 22-28	JS 20-29 × JS 20-22
19	JS 22-29	JS 20-63 × JS 95-60
20	JS 22-30	JS 20-29 × JS 20-22
21	JS 22-31	NRC-86 × JS 20-34
22	JS 22-32	JS 20-71 × JS 20-22
23	JS 22-33	JS 20-63 × JS 20-35
24	JS 22-34	JS 20-29 × JS 93-05
25	JS 22-36	JS 20-29 × JS 93-05
26	JS 22-37	JS 20-82 × JS 95-60
27	JS 22-38	JS 20-74 × JS 20-22
28	JS 22-39	JS 20-88 × JSM 196
29	JS 22-40	JS 20-63 × JS 95-60
30	JS 22-41	JS 20-53 × JS 20-34
31	JS 22-42	JS 20-89 × JS 20-34
32	JS 22-43	JS 20-53 × JS 20-34
33	JS 22-44	JS 20-29 × JSM 275
34	JS 22-45	JSM 226 × JS 20-34
35	JS 22-46	JS 97-52 × JS (15) 90-5-12-1
36	JS 22-47	JS 20-29 × JS 93-05
37	JS 22-48	SL 738 × JS 95-60
38	JS 22-49	JS 20-69 × JS 335
39	JS 22-50	JS 20-88 × JSM 196
40	JS 22-51	JS 20-53 × JS 20-34
41	JS 22-52	JS 20-79 × JS 335
42	JS 22-53	JS 20-71 × JS 20-22
43	JS 22-54	JS 20-29 × JS 20-22
44	JS 22-55	JS 20-09 × JSM 258
45	JS 22-56	Selection from AGS-31
46	JS 22-57	Selection from AGS-48
47	JS 23-01	JS 20-53 × JS 20-34
48	JS 23-02	JS 20-89 × JS 20-34
49	JS 23-03	JS 20-53 × JS 20-34
50	JS 23-04	JS 20-63 × JS 20-35
51	JS 23-05	JS 20-63 × JS 20-35
52	JS 23-06	JS 22-21-20-63 × JS 20-35
53	JS 23-07	JS 22-22-20-75 × JS 20-14
54	JS 23-08	JS 20-29 × JS 93-05
55	JS 23-09	JS 20-88 × JSM 196
56	JS 23-10	JS 20-63 × JS 95-60
57	JS 23-13	JS 20-71 × JS 20-22
58	JS 20-98 (c)	JS 97-52 × SL 710
59	JS 20-116 (c)	JS 97-52 × JSM 120 A
60	JS 20-34 (c)	JS 98-63 × PK 768

Table 2. Morphological descriptor classes and their distribution in genotypes

S.No.	Descriptor	Class of descriptor	Frequency	Percent distribution
1.	Hypocotyl Coloration	Present	29	48.3
		Absent	31	51.6
2.	Growth Type	Semi-determinate	57	95.0
		Determinate	3	5.0
3.	Growth Habit	Semi Erect	60	100.0
4.	Flower Colour	Violet	29	48.3
		White	31	51.6
5.	Leaf Size of Lateral Leaflet	Small	4	6.66
		Medium	35	58.3
		Large	21	35.0
6.	Leaf Shape of Lateral Leaflet	Pointed ovate	33	55.0
		Round ovate	11	18.3
		Lanceolate	15	25.0
		Triangular	1	1.6
7.	Leaf Intensity of Green Colour	Light green	1	1.6
		Green	45	75.0
		Dark Green	14	23.3
8.	Pod Hairiness	Pubescence	38	63.3
		Glabrous	22	36.6
9.	Pod: colour of hair	Tawny	33	86.8
		Grey	5	13.1
10.	Pod: Intensity of brown colour	Light	24	40.0
		Medium	23	38.3
		Dark	13	21.6
11.	Seed: Ripe seed shape	Spherical	18	30.0
		Spherical flattened	29	48.3
		Elongated	2	3.33
		Elongate Flattened	11	18.3
12.	Seed : Ripe seed size	Small (<10g)	17	28.3
		Medium (10-13g)	29	48.3
		Bold/ large (>13g)	14	23.3
13.	Ripe seed: Ground color of testa	Yellow	54	90.0
		Yellow-green	5	8.33
		Green	2	3.33
14.	Ripe seed: seed coat lustre	Shiny	4	6.66
		Intermediate	47	78.3
		Dull	11	18.33
15.	Ripe seed: peroxidase activity	Present	60	100.0
		Absent	0	
16.	Ripe seed: Hilum Colour	Brown	18	30.0
		Imperfect Black	6	10.0
		Black	35	58.3
17.	Ripe seed: Color of Hilum Funicle	Same as testa	58	96.6
		Different from testa	2	3.33

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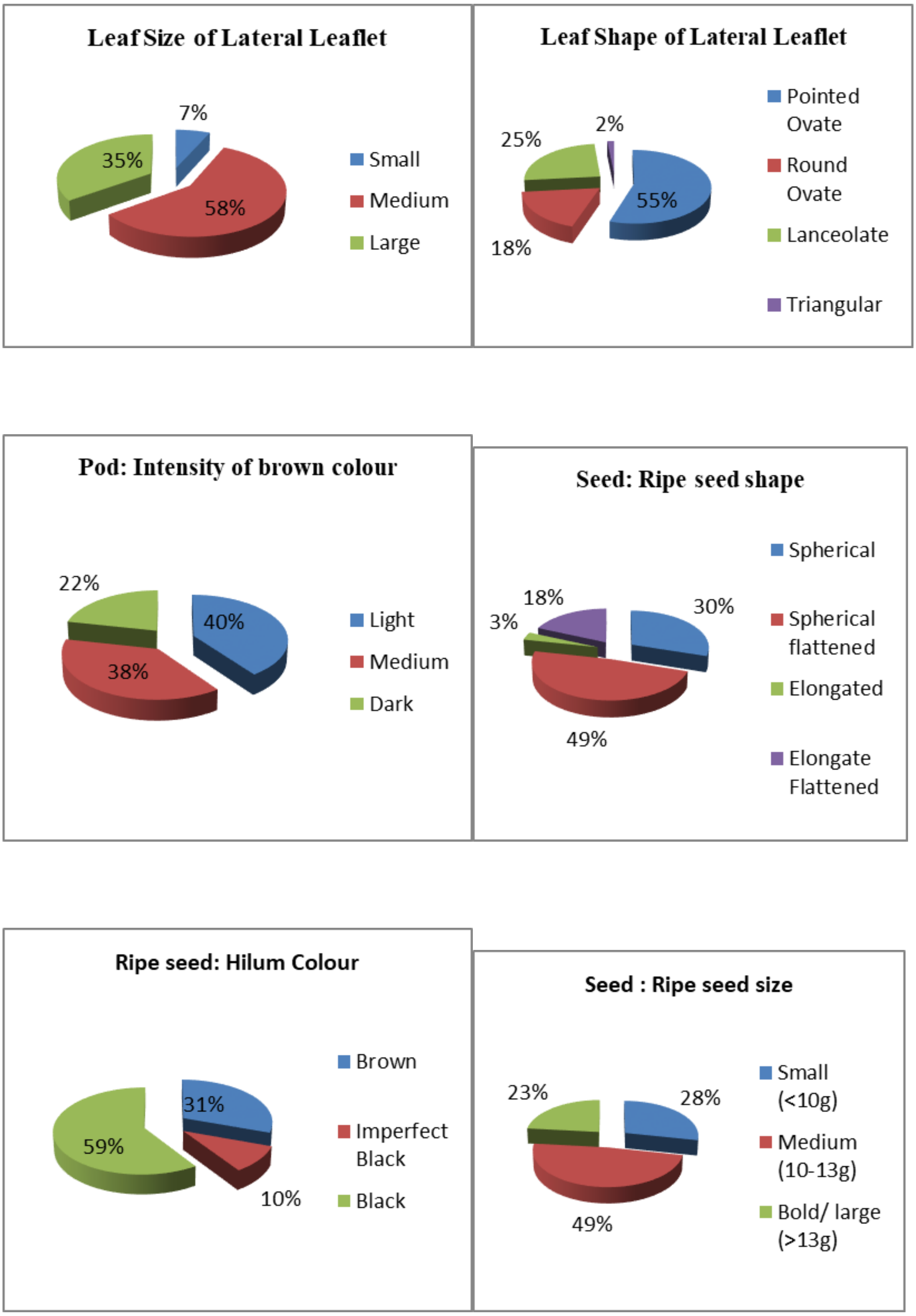

Fig. 1. Graphical Distribution of Phenotypic Traits showing Variability

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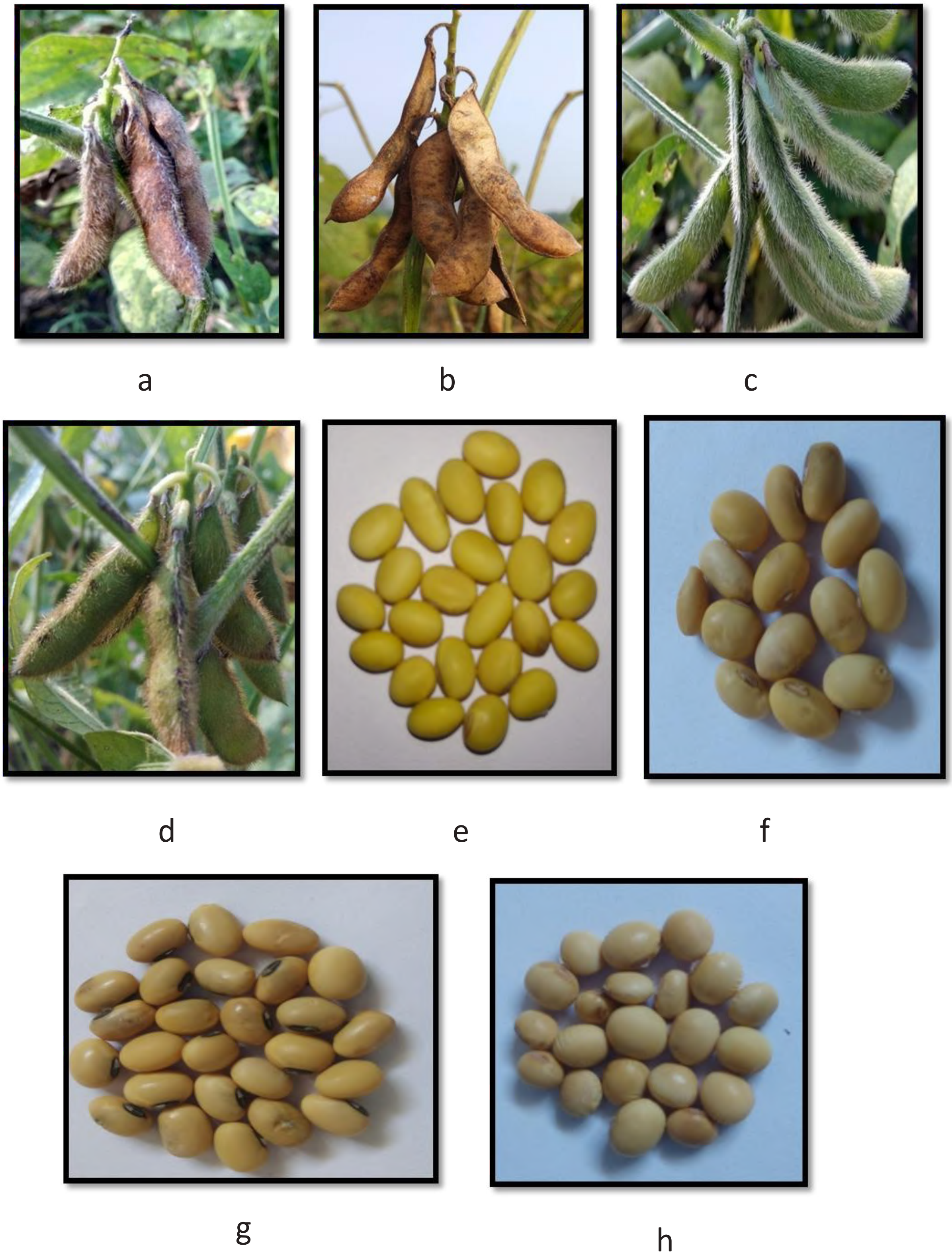
Table 3. Unique genotypes found under distinct descriptor classes

S.No.	Descriptor	Class of descriptor	Genotypes
1.	Growth Type	Determinate	JS 23-04, JS 23-01, JS 20-34
2.	Leaf Size of Lateral Leaflet	Small	JS 22-10, JS 22-55, JS 22-21, JS 23-06,
3.	Leaf Shape of Lateral Leaflet	Round Ovate	JS 22-23, JS 22-24, JS 22-26, JS 22-27, JS 22-28, JS 23-13, JS 22-40, JS 22-48, JS 22-49, JS 22-52, JS 20-34
		Lanceolate	JS 22-25, JS 22-33, JS 22-34, JS 22-36, JS 22-37, JS 22-45, JS 22-46, JS 22-47, JS 22-50, JS 22-10, JS 22-21, JS 23-06, JS 23-04, JS 23-08, JS 23-09
		Triangular	JS 22-39
4.	Leaf intensity of Green colour	Dark Green	JS 22-25, JS 22-26, JS 22-27, JS 22-28, JS 22-29, JS 22-40, JS 22-45, JS 22-47, JS 22-50, JS 22-52, JS 22-10, JS 23-08, JS 20-116, JS 20-34
5.	Pod Colour of Hair	Grey	JS 22-26, JS 22-27, JS 22-28, JS 22-37, JS 22-46,
6.	Pod :Intensity of brown colour	Dark Brown	JS 22-23, JS 22-27, JS 22-29, JS 22-34, JS 22-37, JS 22-46, JS 22-49, JS 22-50, JS 22-52, JS 22-22, JS 23-08, JS 23-10, JS 23-07
7.	Seed: Ripe seed shape	Elongated	JS 22-24, JS 22-17,
		Elongated Flattened	JS 22-28, JS 22-30, JS 22-31, JS 22-32, JS 22-38, JS 22-40, JS 22-48, JS 22-52, JS 22-54, JS 22-15, JS 23-10
8.	Seed: Ripe seed size	Large	JS 22-24, JS 22-31, JS 23-13, JS 22-37, JS 22-38, JS 22-41, JS 22-43, JS 22-48, JS 22-53, JS 22-54, JS 22-12, JS 22-17, JS 22-13, JS 22-15
9.	Ripe seed: Ground colour of testa	Yellow- Green	JS 22-28, JS 22-56, JS 22-41, JS 22-52, JS 22-22,
		Green	JS 22-39, JS 22-57
10.	Ripe seed: Colour of Hilum	Imperfect Black	JS 22-39, JS 22-45, JS 22-57, JS 22-19, JS 22-16, JS 23-10
11.	Ripe seed : Colour of Hilum Funicle	Different from testa	JS 22-39, JS 22-57

Green seed coat was recorded in two genotypes (JS 22-39 and JS 22-57) and yellowish- green seed coat in five (22-28, JS 22-56, JS 22-41, JS 22-52, JS 22-22). Whereas, most of the genotypes (90%) have showed yellow seed coat colour. Among these, six genotypes were distinct, in which imperfect black hilum colour was noticed. Since qualitative traits provide stability over changing environments and generations, they prove to be good morphological markers for differentiating species and varieties. Characterization of soybean genotypes was also done by previous researchers and they noticed similar kinds of phenotypic variations in their findings (Verma *et al.,* 2015; Painkra *et al.,* 2019; Ramteke and Muralidharan, 2012).

The Analysis of variance exhibited that the mean sum of squares due to genotypes was highly significant for all the eleven yield attributing traits under study (**Table 4**). This clearly indicated that genotypes which were developed through hybridization had a sufficient amount of exploitable level of genetic variability. In the present investigation, phenotypic coefficient of variation (PCV) was higher in magnitude than the genotypic coefficient of variation (GCV) for all the 11 yield contributing traits (**Table 5**). The phenotypic and genotypic coefficient of variation were categorized as low (<10%), moderate (10-20%) and high (>20%). The highest PCV and GCV were observed for seed yield per plant (39.10 and 36.76) followed by biological yield per plant (33.56 and 31.84), the number of pods per plant (29.73 ad 28.15), 100 seed weight (g) (29.51 and 27.82), the number of primary branches per plant (26.12and 22.30), harvest index (22.49 and 18.32) and the number of seeds per plant (22.43 and 21.04). Moderate values of PCV and GCV were recorded for plant height (13.81 and 10.32). Whereas, lower values of PCV and GCV were observed for days to flower initiation (5.98 and 5.47), days to 50% flowering (5.65 and 4.94) and days to maturity (4.33 and 3.85). These results indicated the expression of characters was highly influenced by genetic components and least affected by environmental factors. Significant differences for yield associated traits were also observed by previous workers in soybean Upadhyay *et al.* (2020). The highest PCV and GCV were also obtained by several researchers such as Berhanu *et al.* (2019) for primary branches per plant, seed yield per plant and biological yield per plant,



a b c

d e f

g h

Fig. 2. a – Pod Pubescence b – Glabrous; c – Grey Pubescence; d – Tawny Pubescence; e - Seed-Elongated Flattened; f - Elongated; g – Spherical Flattened; h – Spherical

Table 4. Analysis of variance for yield attributing traits

Source of Variation	d.f	Days to flower initiation	Days to 50% flowering	Days to Maturity	Number of pods per plant	Number of seeds per plant	Number of primary branches per plant	Plant height	Biological yield per plant	Hundred deed weight	Harvest index	Seed yield per plant
Replications	2	3.35	5.50	5.17	8.38	80.58	0.047	4.36	12.63	1.16	65.21	0.77
Treatments	59	14.12**	15.022**	44.676**	326.7**	672.38**	2.81**	170.11**	89.39**	28.57**	239.43**	23.77**
Error	118	0.86	1.38	3.67	12.15	29.26	0.30	35.39	3.17	1.13	34.56	0.99

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

Table 5. Parameters of genetic variability for quantitative traits

S. No.	Character	Mean	Range		PCV (%)	GCV (%)	h^2b (%)	GA as % of mean
			Minimum	Maximum				5%
1	Days to flower initiation	38.43	34.66	46.33	5.98	5.47	83.7	10.30
2	Days to 50% flowering	43.10	38.00	51.66	5.65	4.94	76.6	8.91
3	Days to maturity	96.02	87.66	107.66	4.33	3.85	78.8	7.04
4	Number of pods per plant	36.37	14.13	78.10	29.73	28.15	89.6	54.90
5	Number of seeds per plant	69.57	39.10	139.50	22.43	21.04	88.0	40.66
6	Number of primary branches per plant	4.09	2.76	7.93	26.12	22.30	72.9	39.25
7	Plant height (cm)	64.88	46.68	81.53	13.81	10.32	55.9	15.91
8	Biological yield per plant (g)	16.83	9.40	36.10	33.56	31.84	90.1	62.26
9	100 seed weight (g)	10.86	5.24	18.21	29.51	27.82	88.9	54.06
10	Harvest index (%)	45.08	23.19	64.64	22.49	18.32	66.4	30.76
11	Seed yield per plant (g)	7.49	3.50	20.20	39.10	36.76	88.4	71.22

Mehra *et al*. (2020) for the number of pods/plant and the number of seed/plant. Moderate values of PCV and GCV observed for plant height was in accordance with the results of Dubey. (2015). The lowest PCV and GCV values for days to maturity and days to 50% flowering were similar to the findings of Mehra *et al*. (2020).

The knowledge of heritability is necessary to predict genetic advances for any yield attributing quantitative trait. The values for heritability estimates were different for different traits and classified as high (>70%), moderate (50-70%) and low (<50%) (**Table 5**). The highest heritability (90.1%) was obtained for biological yield per plant followed by the number of pods per plant (89.6%) and 100 seed weight (88.9%). Whereas, the lowest heritability was seen in plant height (55.9%). Similarly the highest genetic advance as percentage of mean (at 5% selection intensity) was recorded for seed yield per plant (71.22%) followed by biological yield per plant (62.26%) and the number of pods per plant (54.9%). Whereas, the lowest was observed in days to maturity (7.04%). Heritability and genetic advance are considered to be two very important tools for effective and précised selection of desirable traits for further improvement. In the present study, it was observed that high/moderate heritability coupled with high/moderate genetic advance was recorded for traits *viz*., the number of pods per plant, the number of seeds per plant, the number of primary branches per plant, biological yield per plant, 100 seed weight, seed yield per plant, days to flower initiation and plant height. High/moderate heritability coupled with high/moderate genetic advance indicates additive gene action. Previous study recorded the highest heritability and genetic advance as per cent of mean for the number of seeds per plant and seed yield per plant, (Upadhyay *et al.,* 2020) and for plant height and days to flower initiation (Satpute *et al.,* 2016) and for biological yield per plant and the number of primary branches per plant (Chandel *et al.,* 2017).

Correlations indicate the linear association present between a pair of traits. Generally a positive correlation between traits is preferred by a plant breeder since it helps in the improvement of both the associated traits. In the present investigation, genotypic correlation was higher than the phenotypic correlation indicates the role of genetic factors in the association between traits **(Table 6).** Seed yield per plant showed the highest positive significant correlation with Biological yield per

Table 6. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient

Characters	Days to flower initiation	Days to 50% flowering	Days to maturity	Number of pods per plant	Number of seeds per plant	Primary branches per plant	Plant height	Biological yield per plant	Hundred seed weight	Harvest index	Seed yield per plant
Days to flower initiation	**1.000**	0.798**	0.155*	0.348**	0.264**	0.273**	0.206**	0.395**	-0.101	-0.373**	0.112
Days to 50% flowering	0.775**	**1.000**	-0.018	0.201**	0.070	0.073	0.203**	0.364**	0.024	-0.381**	0.093
Days to maturity	0.182*	0.018	**1.000**	0.018	-0.027	-0.021	0.358**	-0.041	-0.029	-0.007	-0.083
Number of pods per plant	0.302**	0.180*	0.026	**1.000**	0.802**	0.748**	0.012	0.643**	0.089	-0.001	0.620**
Number of seeds per plant	0.234**	0.057	-0.007	0.793**	**1.000**	0.596**	0.003	0.629**	-0.080	-0.022	0.607**
Primary branches per plant	0.213**	0.064	-0.020	0.743**	0.604**	**1.000**	-0.077	0.499**	0.173**	0.096	0.559**
Plant height	0.151*	0.160*	0.237**	0.018	0.003	-0.043	**1.000**	-0.167*	-0.356**	-0.167*	-0.303**
Biological yield per plant	0.340**	0.293**	-0.042	0.608**	0.587**	0.468**	-0.140	**1.000**	0.452**	-0.204**	0.797**
Hundred seed weight	-0.079	0.029	-0.009	0.095	-0.058	0.171*	-0.253**	0.435**	**1.000**	0.559**	0.735**
Harvest index	-0.269**	-0.260**	0.038	0.046	0.067	0.135	-0.092	-0.230**	0.535**	**1.000**	0.438**
Seed yield per plant	0.106	0.084	-0.054	0.612**	0.607**	0.549**	-0.212**	0.753**	0.740**	0.438**	**1.000**

plant (0.797**) followed by 100 seed weight (0.740**), the number of pods per plant (0.620**), the number of seeds per plant (0.607**), the number of primary branches per plant (0.559**) and harvest index (0.438**). Whereas, seed yield per plant showed a negative significant correlation with plant height (-0.303**) (**Table 6).** This indicates improvement in these positively correlated characters will lead to yield enhancement whereas taller plants will have a negative impact on seed yield. Similarly the number of pods per plant is highly significantly correlated to the number of seeds per plant (0.802**), the number of primary branches per plant (0.748**) and biological yield per plant. Significant positive associations of seed yield per plant with other yield traits were also obtained by many researchers such as Upadhyay *et al*. (2020) for the number of pods per plant, Verma *et al.* (2021) with respect to the number of pods per plant and 100 seed weight, Uikey *et al.* (2021); Ekka and Lal. (2016) for the number of seeds per plant. Machado *et al.* (2017) for the number of pods per plant, Sileshi *et al.* (2019) for 100 seed weight and harvest index, Mehra *et al.* (2020) and Kumar *et al.* (2020) for biological yield per plant and harvest index.

Path analysis was carried out keeping the seed yield per plant as the dependent variable to know the direct and indirect effects of various yield attributing traits on seed yield. The genotypic path coefficient analysis revealed that the highest positive direct effect was due to biological yield per plant (0.488), followed by 100 seed weight (0.314), the number of seeds per plant (0.295) and harvest index (0.293) (**Table 7**). Whereas, the negative direct effect was due to days to flower initiation and plant height**.** Similarly, biological yield per plant exhibited an indirect effect on seed yield per plant via traits like the number of seeds per plant, 100 seed weight, primary branches per plant, days to 50% flowering, as well as the negative indirect effect was recorded due to traits such as days to flower initiation and harvest index. These results were in accordance with the findings of Jain *et al.* (2015) for biological yield per plant and 100 seed weight, Upadhyay *et al*. (2020) for biological yield per plant and harvest index, Uikey *et al.* (2021) and Amogne *et al.* (2020) for the number of seeds per plant and Mehra *et al.* (2020) for the number of pods per plant and the number of seeds per plant.

In the present study, it was seen that all the traits exhibited a sufficient amount of genetic variability, high heritability coupled with genetic advances were observed in traits like the number of pods per plant, the number of seeds per plant, the number of primary branches per plant, biological yield per plant, 100 seed weight and seed yield per plant which suggests that these traits should be selected to increase genetic advance in the population. These mentioned traits along with the harvest index prove to be effective for the improvement of seed yield. The DUS characterization of these genotypes was found to be very beneficial for the identification of these breeding lines during the breeding programme to avoid contamination,

Table 7. Path coefficient analysis for yield attributing traits

Characters	Days to flower initiation	Days to 50% flowering	Days to maturity	Number of pods per plant	Number of seeds per plant	Primary branches per plant	Plant height	Biological yield per plant	Hundred seed weight	Harvest index
Days to flower initiation	**-0.0591**	0.0669	-0.0001	0.0036	0.0784	0.0136	-0.0071	0.1368	-0.0318	-0.0888
Days to 50% flowering	-0.0472	**0.0838**	0.0000	0.0021	0.0207	0.0036	-0.0069	0.1174	0.0075	-0.0885
Days to maturity	-0.0092	-0.0015	**-0.0006**	0.0002	-0.0080	-0.0010	-0.0144	-0.0549	-0.0091	0.0156
Number of pods per plant	-0.0206	0.0169	0.0000	**0.0104**	0.2374	0.0372	-0.0015	0.3089	0.0278	0.0039
Number of seeds per plant	-0.0157	0.0059	0.0000	0.0083	**0.2958**	0.0296	-0.0014	0.3100	-0.0253	-0.0068
Primary branches per plant	-0.0161	0.0061	0.0000	0.0077	0.1761	**0.0498**	0.0003	0.2576	0.0543	0.0229
Plant height	-0.0113	0.0156	-0.0002	0.0004	0.0109	-0.0004	**-0.0371**	-0.1267	-0.1183	-0.0219
Biological yield per plant	-0.0166	0.0201	0.0001	0.0066	0.1877	0.0262	0.0096	**0.4885**	0.1617	-0.0349
Hundred seed weight	0.0060	0.0020	0.0000	0.0009	-0.0238	0.0086	0.0140	0.2515	**0.3140**	0.1622
Harvest index	0.0179	-0.0253	0.0000	0.0001	-0.0068	0.0039	0.0028	-0.0581	0.1736	**0.2935**
Seed yield per plant	0.112	0.093	-0.083	0.620	0.601	0.559	-0.303	0.797	0.735	0.406

R^2= 0.9873 ; RESIDUAL EFFECT = 0.1128

duplication etc. Based on these results we can conclude that these genotypes had a broad genetic base which can be used as donors to develop cultivars as well as these genotypes can also be a good source to create variation and develop desirable traits in future varieties.

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