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Identification of Trait-specific and Multiple Traits-specific Soybean [*Glycine max* (L.) Merrill] Germplasm Accessions

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Abstract

Soybean is a self-pollinated pulse crop. To maintain and improve the crop productivity, exploring and utilizing the genetic variability present within the gene pool is a critical step. Current study is focused on analysing the genetic variability of yield attributing traits and identification of trait and multiple traits-specific accessions in 5000 soybean germplasm entries that were sourced from Indian Institute of Soybean Research, Indore, Madhya Pradesh. Present experiment was carried out during *kharif* 2023 at Zonal Agricultural Research Station (ZARS), UAS, GKVK, Bengaluru, Karnataka. The 5000 germplasm entries along with three standard checks (KBS 23, JS 335 and Karune) were sown in an augmented design. Observations on seven quantitative traits were recorded for all the 5000 accessions and statistical analysis was performed. A wide range of mean values were recorded for all the seven yield contributing traits. Genotypic coefficient of variation (GCV) estimates were slightly lower to phenotypic coefficient of variation (PCV) estimates depicting the narrow impact of external environment on the biometrical traits. High estimates of heritability along with high genetic advance as per cent of mean was recorded for the traits *viz*., plant height, days to 80 per cent maturity, number of pods plant^{-1}, days to 50 per cent flowering and hundred seed weight. Frequency distribution of seven quantitative traits was studied with the aid of skewness and kurtosis value of the character. Identification of superior performing germplasm entries was performed on the basis of trait mean values. The obtained experimental results are analysed in association with suitable strategies that could be adopted for soybean crop improvement programme to substantially increase the overall crop productivity.

Keywords : Soybean, PCV, GCV, Skewness, Kurtosis, Yield traits, Heritability

Soybean [*Glycine max* (L.) Merrill] is a globally important pulse crop, as the crop fulfils the protein demand of one-third of the world's population. Soybean is known as 'Miracle pulse' due to its valuable seed composition, multiple industrial end-uses and consistent genetic gain across the world. Persistent genetic gain in soybean has led to widespread adaptation. Soybean seed contains about 21 per cent oil, 41 per cent protein and 33 per cent carbohydrates (Isanga and Zhang, 2008). Genome size of soybean ranges from 1.0 to 1.4 GB with a somatic chromosome number of 40 (2n=40). The major amino acids that are essential for human diet are present in soybean *viz.,* histidine, lysine, methionine, isoleucine, threonine, leucine, valine and tryptophan. Seeds are also rich source of fibre, calcium, iron, B vitamins and zinc (Young *et al.*, 1979).

In the world, USA ranks first in both productivity and production with 3159 kg/ha and 96.60 million tonnes, respectively with the soybean growing area of 308.04 lakh hectares. India is the fifth largest producer of soybean covering an area of 114.5 lakh ha with a productivity of 850 kg/ha and production of 9.08 million tonnes (Anonymous, 2022). India's share in the global soybean production is only 4.8 per cent despite the area contribution of 10.6 per cent emphasizing the poor level productivity of soybean in India. Therefore, it invariably urges the broadening of narrow genetic base by means of increased utilization of diverse genetic resources *i.e.,* germplasm.

Assessment and quantification of variability is a critical step for any crop improvement programme. Multiple germplasm conservation centres have been created with the mandate of preserving the available genetic variability before the crop losses its genetic diversity due to monocropping and widespread use of improved modern cultivar (Schoen and Brown, 1991).

Advancement of any suitable selection strategy requires knowledge of existing variability in the crop and it can be assessed by estimating the Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability and Genetic advance as percentage of mean (GAM). The basic source of exploiting the superior potentiality of a genotype relies on the extent of heritable portion of variation of the concerned traits. PCV and GCV of a trait gives the magnitude of influence that the environment poses on the trait. Estimation of heritability helps in quantifying the heritable portion of quantitative traits. While, Genetic advance helps in formulation of best suited selection strategy. Identification of trait-specific and multiple traits-specific accessions based on mean performance aids in exploitation of natural genetic variability to meet immediate short-term objectives of crop improvement.

MATERIAL AND METHODS

Current experiment consisted of 5000 soybean germplasm accessions sourced from Indian Institute of Soybean Research (IISR), Indore, Madhya Pradesh and three checks *viz.,* KBS 23, JS 335 and Karune. The germplasm entries along with the checks were raised in 49 blocks by following an augmented design (Federer, 1957) during *kharif* season of 2023 in the experimental plot of Zonal Agricultural Research Station (ZARS), University of Agricultural Sciences, GKVK, Bengaluru, Karnataka which is situated at 930m above the mean sea level, 77ºC 36' East longitude and 12ºC 59' North latitude. Fortyseven blocks consisted of 102 accessions each and two blocks each with 103 entries of germplasm and the three checks were sown in all the 49 blocks. The seeds of each accession were sown in a row length of 1.50 m with a spacing of 45×10 cm. All the recommended plant protection and cultural practices were performed timely to maintain the healthy crop stand.

Observations were recorded from the five randomly selected plants from each entry for seven biometrical characters *viz.,* days to 50 per cent flowering, plant height (cm), number of secondary branches plant^{-1}, days to 80 per cent maturity, number of pods plant^{-1}, hundred seed weight (g) and seed yield plant^{-1} (g). The mean of five selected plants were taken into account for all the statistical analysis *viz.,* range and mean (Chandrawat *et al*., 2015), genotypic and phenotypic coefficient of variation (Burton, 1952), genetic advance as per cent of mean and heritability (Johnson *et al*., 1955), Skewness and kurtosis (Kapur, 1981) were used to calculate the respective statistical estimates in the present investigation by using R software.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for 5000 germplasm lines of soybean for all the seven quantitative traits were presented in Table 1 as per the augmented design. The accessions, checks and total entries reported significant differences for all the seven quantitative traits studied. This indicates that sufficient variation was existed among the entries studied and there is a scope for selection of genotypes for the specific traits.

Mean and Range

Observed range and corresponding mean performance value of each quantitative trait for 5000 accessions is

TABLE 1

Analysis of variance (ANOVA) for seven quantitative traits in soybean germplasm

Source of variation	df	Mean sum of squares (MSS)						
		Days to 50% flowering	Plant height (cm)	Number of secondary branches plant^{-1}	Number of pods plant^{-1}	Days to 80% maturity	100 seed weight (g)	Seed yield plant^{-1} (g)
Blocks	48	796.98 **	879.00 **	2.56 **	665.79 **	1562.67 **	89.06 **	7678.23 **
Accessions + checks	5002	78.35 **	99.75 **	1.20 **	184.01 **	106.90 **	21.87 **	2784.01 **
Accessions	4999	85.43 **	96.90 **	1.03 **	179.55 **	154.00 **	19.09 **	1209.24 **
Checks	2	132.09 **	4509.52 **	8.92 **	25.07 **	1023.16 **	150.19 **	4321.02 **
Accessions vs Checks	1	1108.37 **	1543.56 **	7.65 **	3201.54 **	162.74 **	70.92 **	5376.77 **
Error	96	10.90	9.79	0.19	10.65	51.03	0.83	46.65

** significance at 1% level

represented in Table 2. Mean values of all the 5000 germplasm accessions exhibited a broad range of variations for all the seven quantitative traits *viz.,* days to 50 per cent flowering (33.00 - 68.00), plant height (30.00 - 78.00 cm), secondary branches plant^{-1} (3.00 - 13.00), number of pods plant^{-1} (12.00 - 84.00), days to 80 per cent maturity (87.00 - 114.00), hundred seed weight (10.00 - 20.58 g) and seed yield plant^{-1} (11.24 - 31.92 g). The obtained results give a clear indication of presence of sufficient variation among the germplasm accessions for the traits under study. This emphasizes the existence of greater opportunity for the improvement of these traits related to yield in soybean (Table 2). This broad range of variability reported for all the seven quantitative traits, can potentially serve as a basic requirement for formulating novel breeding programmes in soybean. Similarly broad range of variations for the mean value of the traits *viz.,* seed yield plant^{-1} (g), number of pods plant^{-1}, number of secondary branches plant^{-1} and days to 50 per cent flowering was observed by Kuswantoro (2017), Krisnawati and Adie (2019), Chawan *et al.*, (2023) and Bairagi *et al.* (2023) in soybean.

Genetic Variability

In the present investigation, phenotypic coefficient of variation estimates were slightly higher than the estimates of genotypic coefficient of variation for all the seven quantitative traits indicating the necessary involvement of environment on the trait expression.

Moderate values of GCV were observed for the traits *viz.,* hundred seed weight (18.20), plant height (18.03), secondary branches plant^{-1} (16.28) and number of pods plant^{-1} (13.23). The high estimates of GCV were observed for, seed yield plant^{-1} (34.36), days to 80 per cent maturity (22.57) and days to 50 per cent flowering (22.10). Moderate values of PCV were reported for the traits *viz.,* number of secondary branches plant^{-1} (19.50), plant height (19.39), hundred seed weight (18.96) and number of pods plant^{-1} (13.80). High estimates of PCV were observed for seed yield per plant (39.39), days to 50 per cent flowering (23.98) and days to 80 per cent maturity (22.96) (Table 3). Selection would be effective based

TABLE 2

Descriptive statistics for seven quantitative traits in soybean germplasm

Traits	Mean ± Std. Error	Range		Standardized range
		Min.	Max.	
Days to 50% flowering	41.38 ± 0.07	33.00	68.00	35.00
Plant height (cm)	41.56 ± 0.14	30.00	78.00	48.00
Secondary branches plant^{-1}	6.87 ± 0.03	3.00	13.00	10.00
Number of Pods plant^{-1}	42.18 ± 0.24	12.00	84.00	72.00
Days to 80% maturity	98.71 ± 0.05	87.00	114.00	27.00
100 seed weight (g)	14.02 ± 0.02	10.00	20.58	10.58
Seed yield plant^{-1} (g)	20.10 ± 0.08	11.24	31.92	20.68

TABLE 3

Parameters of variability for seven quantitative traits in soybean germplasm

Traits	Coefficient of variability		Broad sense heritability (%)	Expected Genetic Advance as per cent of mean
	GCV%	PCV%		
Days to 50% flowering	22.10	23.98	84.97	41.97
Plant height (cm)	18.03	19.39	85.74	26.76
Secondary branches plant^{-1}	16.28	19.50	65.70	17.01
Number of pods plant^{-1}	13.23	13.80	92.33	26.13
Days to 80% maturity	22.57	22.96	80.20	36.02
100 seed weight (g)	18.20	18.96	92.11	34.59
Seed yield plant^{-1} (g)	34.36	39.39	75.21	19.21

on the heritable nature of these biometrical traits. Similar results of high GCV and PCV for the traits secondary branches plant^{-1}, days to 80 per cent maturity and days to 50 per cent flowering was recorded by Sharma *et al*. (1983), Baraskar *et al.* (2014), Karnwal & Singh (2009) and Dutta *et al.* (2021).

PCV and GCV estimates the proportion of variation present in a particular trait. However, they will not measure the heritable proportion of total variation in a trait. Therefore, estimation of heritability which depicts the inheritable proportion of total variation existing in the trait is carried out (Baraskar *et al.*, 2014).

Heritability and Genetic Advance as per cent of Mean (GAM)

Broad sense heritability estimates for all the seven quantitative traits under study are mentioned in Table 3. The heritability estimate was varied from 59.70 to 92.33 per cent. The heritability was moderate for number of secondary branches plant^{-1} (59.70%) and high for number of pods plant^{-1} (92.33), 100 seed weight (92.11), plant height (85.74), days to 50 per cent flowering (84.97), days to 80% maturity (80.20) and seed yield per plant (75.21). Soybean is predominantly a self-pollinated crop. Hence, the accessions used in the study are a mixture of pure lines whose expressions predominantly determined by additive genetic effects and additive × additive type of epistasis. Consequently, broad-sense heritability is a reflection of narrow-sense heritability. Thus, the selection of desired accessions from highly heritable traits would be most effective in the present investigation. High heritability for the characters *viz*., number of pods plant^{-1}, hundred seed weight and single plant yield was reported by Bhandarkar (1999), Karnwal & Singh (2009), Dutta *et al*. (2021) and Thakur & Tandekar (2022) in soybean.

For seven quantitative traits, the range of genetic advancement as a percentage of mean was 17.01 to 41.97. For five quantitative traits - days to 50 per cent flowering (41.97), days to 80 per cent maturity (36.02), hundred seed weight (34.59), plant height (26.76) and number of pods per plant (26.13), high genetic advance as a percentage of mean was recorded. Higher estimates of expected genetic advance which takes into account of variability and heritability are conformity evidence for scope and effectiveness of a selection of genotypes. For the number of secondary branches per plant (17.01) and seed yield per plant (19.21), moderate estimates of genetic advance expressed as a percentage of mean of was recorded (Table 3).

High heritability coupled with high genetic advance as per cent of mean was exhibited by the characters *viz.,* number of pods per plant (26.13 and 92.33), days to 50 per cent flowering (41.97 and 84.97), days to 80 per cent maturity (36.02 and 80.20), hundred seed weight (34.59 and 92.11) and plant height (26.76 and 85.74), respectively. High estimates of genetic advance as per cent of mean in association with high heritability suggested that the character was conditioned by low genotype environmental interaction. In such a situation, selection may be rewarding (Dutta *et al*., 2021).

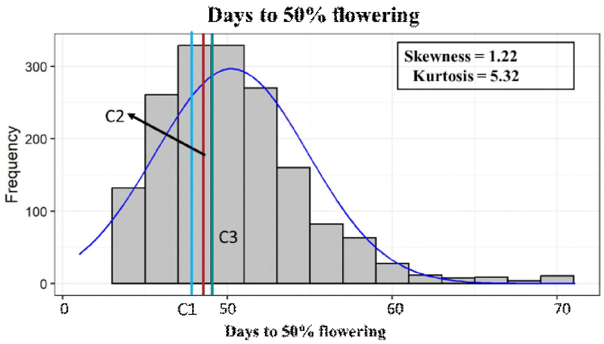
Moderate estimates of heritability along with moderate genetic advance as per cent of mean was exhibited by number of secondary branches per plant (17.01 and 59.70), respectively. High heritability coupled with moderate genetic advance as per cent of mean was exhibited by single plant yield (19.21 and 75.21) respectively. In such a situation, improvement in these traits through simple selection may not be effective. However, recombination breeding and recurrent selection is advocated for improvement of such traits. Similar results were obtained by Bhandarkar (1999) and Baraskar *et al*. (2014) in soybean.

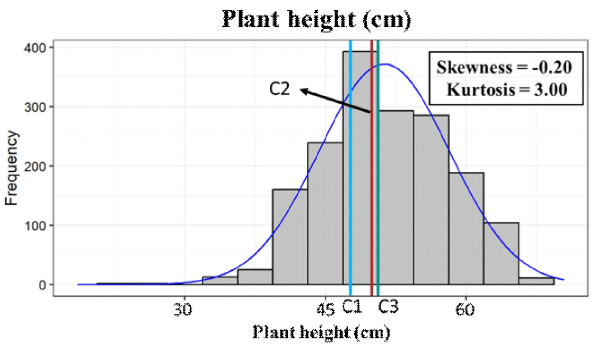
Frequency Distribution of Quantitative Traits

Skewness aids in measuring the level of asymmetry present in a distribution. Positive skewness indicates that the tail of the distribution is more pronounced on the right side than on the left. It implies that greater number of extreme values of the character are on the right side of the distribution. Whereas, negative skewness indicates that the tail of the distribution is more pronounced on the left side and extreme values of the trait are present on the left side of the distribution (Nayana and Fakrudin, 2020).

Kurtosis and skewness were estimated for seven quantitative traits. Skewness was positive for number of secondary branches plant^{-1} (0.16), days to 50 per cent flowering (1.22), hundred seed weight (0.30), number of pods plant^{-1} (2.00) and days to 80 per cent maturity (1.40) (Fig. 1). This implies that a greater number of germplasm accessions are below the mean than expected in the normal distribution for the traits with positive skewness and these traits can be improved rapidly with intensive selection (Nayana and Fakrudin, 2020).

Negative skewness was exhibited by the characters *viz*., seed yield per plant (-0.23) and plant height (-0.20) (Table 4) implying that a greater number of germplasm accessions are above the mean value than





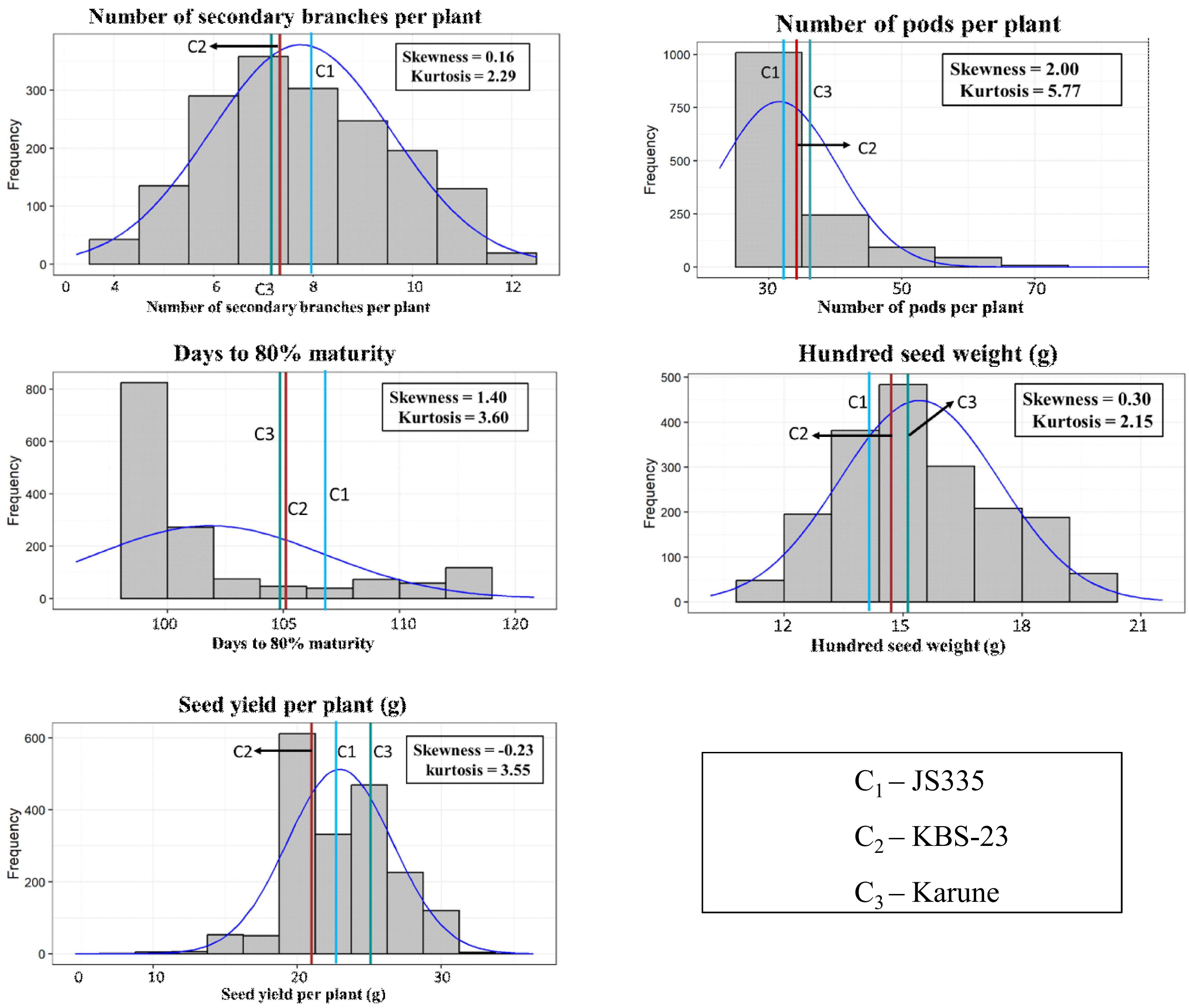


Fig. 1 : Frequency distribution of the seven quantitative traits

TABLE 4

Skewness and kurtosis of seven quantitative traits

Traits	Skewness	Kurtosis
Days to 50 per cent flowering	1.22 **	5.32 **
Plant height (cm)	-0.20 **	3.00 **
Secondary branches plant^{-1}	0.16 **	2.29 **
Number of pods plant^{-1}	2.00 **	5.77 **
Days to 80% maturity	1.40 **	3.60 **
100 seed weight (g)	0.30 **	2.15 **
Seed yield plant^{-1}(g)	-0.23 **	2.55 **

**significance at 1% level

expected in the normal distribution for the above mentioned traits. Adoption of mild selection would result in faster gain for these traits (Neelima *et al.*, 2018).

All the traits showed leptokurtic nature *viz*., days to 50 per cent flowering (5.32), plant height (3.00), seed yield plant^{-1} (2.55), Secondary branches plant^{-1} (2.29), hundred seed weight (2.15), number of pods plant^{-1} (5.77) and days to 80 per cent maturity (3.60) (Table 4) (Fig.1). Neelima *et al.* (2018) and Aditya *et al.* (2011) reported leptokurtic distribution for single plant yield and plant height in soybean. Leptokurtic nature of a curve indicates fatter tails with higher

TABLE 5

Superior performing trait-specific accessions selected from the germplasm collection

Traits	Selection criteria	Range	Number of germplasm accessions
Days to 50 % flowering	Earliness (Mean-1SD) ≤ 36.25	33.00 - 36.25	346
Plant height (cm)	Dwarf (Mean-1SD) ≤ 32.4	30.00 - 32.4	358
Number of secondary branches plant^{-1}	High (Mean+2SD) ≥ 10.93	10.93 - 13.00	305
Number of pods plant^{-1}	High (Mean+2SD) ≥ 76.74	76.74 - 84.00	243
Days to 80% maturity	Earliness (Mean-1SD) ≤ 95.01	87.00 - 95.01	391
Hundred seed weight (g)	High (Mean+2SD) ≥ 16.54	16.54 - 20.58	287
Single plant yield (g)	High (Mean+2SD) ≥ 30.06	30.06 - 31.92	295

chances of having extreme values in a particular trait. While, Platykurtic distribution have thinner tail values compared to normal distribution and have fewer extreme values.

Trait-specific Accessions

Utilization of naturally occurring genetic variability aims to satisfy the immediate needs of the consumers, farmers and end-users. Long-term plant breeding programmes require continuous availability of variability created through planned crosses among the genotypes having the desired traits. Evaluating the germplasm accessions will give the sufficient knowledge about the trait-specific accessions that can be utilized in future breeding programmes. In the current study, few of the germplasm entries showed superior performance for seven quantitative traits (Table 5). These accessions can be isolated and potentially used for improving the particular trait after carrying out multilocation trials.

TABLE 6

Superior soybean germplasm accessions for multiple traits

Accessions	Days to 50% flowering	Pods plant^{-1}	Seed yield plant^{-1}
IC0501865	34.00	84.00	31.92
IC0243571	36.00	82.00	31.33
EC291398	35.00	80.00	31.00
IC810278	36.00	79.00	28.93
EC0251396	33.00	76.00	27.85

Among 5000 germplasm entries, some accessions reported superiority for multiple traits and outperformed all the three check varieties (JS 335, Karune and KBS 23). Among the superior performing entries for multiple traits, top five are indicated in Table 6.

The germplasm accessions with high mean for yield and yield attributable traits can be utilized by the breeders for developing the high performing soybean varieties. In the current study, selection of accessions could be performed on the basis of the traits which shows high heritability along with high genetic advance viz., hundred seed weight, number of pods plant -1 , days to 50 per cent flowering, plant height and days to 80% maturity. Hence, during selection, due emphasis to be paid for these traits for improved productivity.

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