Understanding the Genetic Architecture of Yield and Associated Traits in Soybean (*Glycine max* L.): Implications for Crop Improvement

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Original Research Article

ABSTRACT

The experiment consisting of 22 soybean cultivar/varieties were laid out in a Research farm (Genetics and Plant Breeding) AKS University Sherganj, Satna, Madhya Pradesh during Kharif, 2022. The 14 characters were studied viz. days to 50% germination, days to 50% flowering, plant height (cm), days to maturity, number of primary branches per plant, number of clusters per plant, number of pods per clusters, number of pods per plants, pod length (cm), number of seed per pods, 100 seed weight (g), biological yield (gm), harvest index (%) and seed yield per plant (g). The magnitude of GCV ranged from days to 50% flowering (5.989) to the number of clusters per plant (31.701) and the magnitude of PCV ranged from days to 50% flowering (6.782) to number of clusters per plants (31.956). In general, higher estimates (h^2b) >80% were observed for all the characters except days to 50% germination, harvest index, seed yield per plant (g) and days to

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50% flowering. The heritability value ranged from days to 50% germination (69.9%) to number of clusters per plant (98.4%). The expected genetic advance in percent of mean @ 5% ranged from days to 50% flowering (10.896%) to the number of clusters per plants (64.78%). High estimates of expected genetic advance were found for number of clusters per plants followed by number of pods per plant, pod length (cm), number of primary branches per plants, seed yield per plant (g), biological yield (gm) and number of seed per pods at 5% level. High heritability coupled with high genetic advance as a percent of mean at 5% observed for number of clusters per plant followed by a number of pods per plants, pod length (cm), number of seed /pods and biological yield (gm) indicating that these characters could be prominently governed by additive gene action.

1. INTRODUCTION

Soybean, scientifically known as *Glycine max*, is a remarkable crop with numerous attributes that make it highly valuable. This leguminous, self-pollinated annual plant originated in China and was introduced to India in 1968 from the United States. It belongs to the Fabales order, Leguminosae family, and Faboideae subfamily. Soybean is celebrated as a "wonder crop" due to its exceptional nutritional profile. It contains around 37-42% high-quality protein, 17-24% oil rich in unsaturated fatty acids, and essential fatty acids like linoleic and linolenic acid [1]. This nutritional composition, including its abundance in lysine and tryptophan, sets soybeans apart from conventional cereal grains. Additionally, it is a valuable source of vitamins, antioxidants like ascorbic acid and beta-carotene, and isoflavones such as daidzein and genistein. The biological value of soybean protein rivals that of meat and fish. Soybean is versatile in terms of cultivation, thriving in tropical, subtropical, and temperate climates. It exhibits resilience to extreme temperatures, although its growth rate varies with temperature fluctuations. One of the key ecological benefits of soybean is its ability to enhance soil fertility by fixing atmospheric nitrogen through root nodules and leaf decomposition. Furthermore, it aids in reducing soil erosion, weed suppression, and complements intercropping and sequential cropping patterns. Despite its low input requirements, soybean commands a high market price [2]. Soybean is the most important oilseed crop in the world in terms of acreage and production. Major soybean-cultivating countries are Brazil, the United States, Argentina, China, India, Paraguay, Canada, Ukraine, Russia, Bolivia, South Africa, Uruguay, Italy, Indonesia and others. This figure highlights the world's leading soybean development countries in 2022-23. Brazil was the top global producer of soybeans from in 2022-23. India ranks fourth in acreage and fifth in production in the world. Soybean productivity in India is very low compared to the rest of the dominant producers. Soybean production of India (2020) is estimated at 127.20 lakh tonnes as compared to 128.97 lakh tonnes in 2020-21, (Anonymous 2022). The major soybean-growing Indian states are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka, and Telangana accounting for about 95 percent of the country's total area and soybean production. In India, as of 17th September 2021 area under soybean during 2021-22 was 121.76 lakh hectares as against 121.20 lakh hectares during 2020-21. Among the states, Madhya Pradesh stood first with 55.84 lakh ha followed by Maharashtra (46.01 lakh ha), Rajasthan (10.62 lakh ha), Karnataka (3.82 lakh ha), Gujarat (2.24 lakh ha) and Telangana (1.51 lakh ha). The major constraints in production include the non-availability of adequate amounts of quality seed of improved varieties, poor adoption of improved production technology and the risks of crop cultivation in rain-fed conditions. Soybean seed is the least storable and is vulnerable to mechanical damage. Given the importance of soybean as a crop, understanding its genetic variability is crucial. While natural variation is limited in heavily self-pollinated crops like soybeans, studying genetic variations can provide insights into selecting suitable parent plants for breeding programs (Ram and Singh, 2005). Genetic parameters such as variability, heritability, and expected genetic advancement are essential for yield improvement. Character association analysis helps identify traits correlated with seed yield, aiding breeding efforts. In short, soybean's exceptional nutritional value, adaptability, and ecological benefits make it a significant crop globally. Enhancing its yield and quality through genetic variability studies and breeding efforts is vital for addressing protein-based malnutrition and increasing soybean productivity.

2. MATERIALS AND METHODS

The collections of twenty-two varieties/strains of soybean [*Glycine max* (L.) Merrill] germplasm comprising indigenous genotypes, constituted the experimental materials for this study. These genotypes exhibit a wide spectrum of variability for various agronomic and morphological characters. Genotypes were collected ten from JNKVV, Jabalpur, M. P. three from RVSKVV, Gwalior, M. P., six from KVK, Indore M. P. and three genotypes from KVK, Majhgawan, Satna, (M. P.). The field experiment was carried out throughout *Kharif* (2022) using a Randomised Block Design with three replications. Genotypes were raised in four rows of three metres each, with a row-row spacing of 40 cm and a plant-plant distance of 15 cm between them. Fourteen characters were recorded from 5 randomly selected plants in each: Days to 50% germination, Days to 50% flowering, Plant height (cm), Days to maturity, Number of primary branches per plants, Number of clusters per plants, Number of pods per clusters, Number of pods per plants, Pod length (cm), Number of seed per pods, 100 seed weight (g), Biological yield (gm), Harvest index (%) and Seed yield per plant (g). The analysis of variance was performed by [3] and the analysis of genotypic coefficient of variation and phenotypic coefficient of variation [4]. Heritability and genetic advance estimates were estimated using heritability formula given by Hanson et al. [5] and Johnson et al. [6], respectively.

3. RESULTS AND DISCUSSION

3.1 Mean Performance and Range

The grand means of 22 genotypes and range for 14 quantitative characters of soybean are presented in Table 1 and Table 2. Days to 50% germination ranged from JS-20-98 (4.97 days) to RVS 2001 4 (8.05 days). The genotype JS-20-98 (4.97 days) have taken a minimum of days to 50% germination followed by JS 20 69 (5.08 days), NRC 86 (5.20 days), HIMSO 1689 (5.20 days), RVS 76 (5.32 days), NRC 152 (5.34 days) and AMS MB 100 39 (5.40 days). The days to 50% flowering ranged from minimum JS 95 60 (35.33 days) to maximum JS 20 29 (45.55 days). The genotype JS 95 60 (35.33 days) have taken a minimum of days to 1st flowering followed by AMS MB 100 39 (36.52 days), JS 20 34 (36.67 days), NRC 152 (36.85 days), JS 21 72 (36.99 days), JS 20 69 (37.74 days), NRC 86 (38.07 days) and JS 20 116 (38.40 days). The

genotypes JS 20 29 (45.55 days) have taken maximum days to 50% flowering followed by RVS 2001 4 (43.22 days) JS-20-98 (43.11 days) NRC 94 (43.07 days) RVS 2011 35 (42.78 days) and RVS 18 (42.06 days). The maximum plant height (cm.) has been observed for NRC 152 (62.99 cm.) and the minimum for AMS MB 100 39 (35.66cm.). Minimum plant height (cm.) was observed for AMS MB 100 39 (35.66 cm.) followed by RVS 18 (38.14 cm.), JS 21 72 (38.81 cm.), NRC 94 (40.62 cm.), NRC 86 (41.15 cm.), RVS 76 (41.65 cm.) and JS-20-98 (42.81 cm.). The lowest and highest days to maturity ranged from 81.73 days to 108.34 days (JS 21 72 and HIMSO 1689), respectively. Minimum days to maturity were observed in JS 21 72 (81.73 days), followed by JS 95 60 (83.50 days), NRC 152 (85.10 days), AMS MB 100 39 (87.77 days), JS 20 34 (88.85 days) and NRC 150 (90.68 days). The varieties HIMSO 1689 (108.34 days) followed by JS 20 2 (108.07 days), NRC 94 (105.33 days), RVS 76 (101.89 days) and NRC 136 (99.53 days) have taken maximum days to maturity. The number of primary branches per plant ranged from minimum JS 95 60 (2.94) to maximum HIMSO 1689 (8.53). The highest number of primary branches per plant was observed in HIMSO 1689 (8.53) followed by JS 20 29 (6.06), RVS 76 (5.90), NRC 94 (5.70), NRC 157 (5.28), NRC 150 (5.12) and NRC 138 (5.00). The number of clusters per plant ranged from JS 95 60 (6.76) to RVS 76 (21.04). The highest number of clusters per plant was observed in RVS 76 (21.04) followed by JS 20 29 (20.26), NRC 94 (19.65), HIMSO 1689 (18.63), JS 20 69 (17.95), RVS 2001 4 (16.18) and RVS 18 (15.81). The highest number of pods per cluster was observed in genotype JS 20 29 (7.64) while the lowest number of pods per cluster was observed in JS 95 60 (4.10). The top best lines for number of pods per cluster are viz., JS 20 29 (7.64) followed by AMS MB 100 39 (7.11), RVS 76 (6.98), RVS 18 (6.80), NRC 150 (6.62), NRC 136 (6.49), NRC 86 (6.32) and JS 20 116 (6.00). The highest number of pods per plant was observed in genotype JS 20 69 (59.04) while the lowest number of pods per cluster was observed in AMS MB 100 39 (21.34). The top best lines for number of pods per plant are viz., JS 20 69 (59.04), RVS 2001 4 (48.77), NRC 157 (48.43), JS 20 116 (47.10), RVS 18 (45.69), NRC 86 (41.43) and NRC 150 (41.15). The longest and shortest pod length ranges observed in JS 20 94 and JS 20 69 (4.67 cm. and 2.15 cm.) respectively. The highest pod length was recorded in JS 20 94 (4.67 cm.) followed by NRC 138 (4.23 cm.), NRC 152 (4.34 cm.), RVS 18

(3.84cm.), JS 20 116 (3.83 cm.), RVS 24 (3.59 cm.), NRC 150 (3.58 cm.) and NRC 157, JS 20 29 and JS 21 72 (3.54 cm.). The highest number of seeds per pod was observed in the case of JS 20 94 (4.66) and the lowest number of seeds per pod was recorded in AMS MB 100 39 (2.45). In the top cultivars for the higher number of seeds per pod recorded in JS 20 94 (4.66) followed by NRC 138 (4.30), NRC 152 (4.53), NRC 94 (3.82), RVS 2001 4 (3.75), RVS 2011 35 and JS 20 34 (3.64), JS 20 29 (3.59), JS 20 69 (3.57) and NRC 152 (4.53). 100 seed weight (Seed index) ranged from maximum NRC 86 (16.74 gm.) to minimum JS-20-98 (10.08 gm.). The top cultivars for high 100 seed weight (Seed index) are NRC 86 (16.74 gm.) followed by HIMSO 1689 (15.94 gm.), NRC 136 (15.93 gm.), RVS 24 (14.88 gm.), NRC 157 (14.82 gm.) and NRC 150 (14.55 gm.). The highest and lowest mean performance for biological yield per plant was observed in JS 20 29 (53.04 gm.) and JS 21 72 (18.51 gm.) respectively. Out of 22 varieties/genotypes best six lines for higher biological yield viz., JS 20 29 (53.04 gm.) followed by RVS 2001 4 (46.28 gm.), RVS 18 (44.15 gm.), NRC 136 (40.07 gm.), RVS 2011 35 (39.64 gm.) and JS 20 69 (39.23 gm.). The highest harvest index was exhibited by NRC 138 (47.33%) while NRC 152 (29.41%) showed the lowest harvest index. The best six varieties/ genotypes for this trait were NRC 138 (47.33%) followed by NRC 150 (43.47%), JS 20 116 (41.16%), RVS 2011 35 (41.03%), HIMSO 1689 (39.84%) and JS 20 69 (39.08%). The highest seed yield per plant (20.68gm.) was produced by JS 20 29 while, the lowest seed yield per plant (7.18 gm.) was recorded in JS 21 72. The most promising lines/varieties for this trait in order to merit were JS 20 29 (20.68 gm.) followed by RVS 2001 4 (17.42 gm.), RVS 18 (16.98 gm.), RVS 2011 35 (16.26 gm.), JS 20 69 (15.35 gm.), NRC 136 (14.43 gm.) and NRC 150 (14.36 gm.). The most desirable genotypes of soybean for 14 quantitative traits as per mean performance are identified (Table 2) for days to 50% germination JS-20-98, JS 20 69 and NRC 86, days to 50% flowering JS 95 60, AMS MB 100 39 and JS 20 34, plant height (cm) AMS MB 100 39, RVS 18 and JS 21 72, days to Maturity JS 21 72, JS 95 60 and NRC 152, number of primary branches/plants HIMSO 1689, JS 20 2 and RVS 76, number of clusters per plants RVS 76, JS 20 29, and NRC 94, number of pods per clusters JS 20 29, AMS MB 100 39 and RVS 76, number of pods per plants JS 20 69, RVS 2001 4 and NRC 157, pod length (cm) JS 20 94, NRC 138 and NRC 152, number of seed /pods JS 2094, NRC 138 and NRC 152, 100 seed weight (g) NRC 86,

HIMSO 1689 and NRC 136 biological yield/plant (gm) JS 2029, RVS 2001 4 and RVS 18, harvest index NRC 138, NRC 150 and JS 20 116, seed yield per plant (g) JS 20 29, RVS 2001 4, RVS 18, RVS 2011 35 and JS 20 69. These results are corroborating with earlier results of wide range of variation in soybean was reported by Jagdish et al. [7], Rajanna et al. [8], Dixit et al. [9], Chettri et al. [10], Bhairav et al. [11] and Gohil et al. [12] indicating the presence of sufficient variability among the evaluated genotype for the traits under consideration.

3.2 Analysis of Variance (ANOVA)

The analysis of variance for the design of the experiment involving 22 soybean strains/varieties were evaluated in Randomized Block Design with three replications for the fourteen quantitative characters. The design of the experiment indicated highly significant differences due to treatments for all the characters. The maximum variances due to replication were found for number of clusters per plants (185.83) and due to treatment for number of pods per plants (291.97). Non-significant differences due to replications were observed for all the characters (Table 3). This indicates that the present sufficient variability for most of the characters among different genotypes and thus suggested a substantial scope of selection Fig. 2. These results are corroborating with earlier results of wide range of variation in soybean was reported by Jandong et al. [13], Nayana and Fakrudin [14], Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17] and Ningwal et al. (2023 indicating the presence of sufficient variability among the evaluated genotype for the traits under consideration.

3.3 Coefficient of Variation

The maximum genotypic coefficient variation was observed in number of clusters per plants followed by number of pods per plants, seed yield per plant (g), number of primary branches per plants, biological yield (gm), pod length (cm) and number of seed per pods. This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits. The high PCV were recorded for number of clusters per plants, seed yield per plant (g), number of pods per plants, biological yield (gm), number of primary branches per plants, pod length (cm) and number of seed /pods. The magnitude of GCV and ranged from days to 50% flowering (5.989)

to number of clusters per plants (31.701) and magnitude of PCV ranged from days to 50% flowering (6.782) to number of clusters per plants (31.956). The traits with high phenotypic coefficient of variation indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection programme because the environmental variations are unpredictable in nature and may mislead the results (Table 4). The PCV were higher than the GCV indication of lesser influence of environmental over these characters and effectiveness of selection based on phenotypic value for grain yield and yield contributing traits. Similar results were observed by Ningwal et al. (2023), Sahoo et al. [16], Saicharan et al. [17], Camelia et al. [18], Jandong et al. [13], Nayana and Fakrudin [14], Sonkamble et al. [19], Bhairav et al. [11], Jagdish et al. [7], Rajanna et al. [8], Archana et al. [20], Shrivastava [21], Praneetha and Thamburaj [22] reported that PCV were higher than the GCV for all the characters. Ningwal et al. (2023) documented high PCV and GCV for biological yield per plant, numbers of pods per plant and 100-seed weight. Sahoo et al. [16] recorded highest GCV and PCV (%) for seed yield per plant and dry matter weight per plant. Saicharan et al. [17] recorded high GCV and PCV for the number of pods per plant, the number of pods per cluster, seed yield per row, and seed yield per plant. Jandong et al. [13] observed high value of PCV and GCV for plant height, number of leaves, number of pods and seed yield. Nayana and Fakrudin [14], reported high GCV for number of clusters/plant, 100-seed weight, number of branches/plant, plant height, number of pods/cluster and seed size. Sonkamble et al. [19] observed high values of GCV and PCV for 100 seed weight, seed yield and harvest index.

3.4 Heritability

The major function of heritability estimates is to provide information on transmission of characters from parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effect in phenotypic variation and thus aid in selection. Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. Johnson et al. [6] have suggested heritability estimates in association with genetic advance are much useful for selection than heritability alone. Burton [4] suggested that the GCV along with heritability estimate could provide better

picture of the genetic advance to be expected by phenotypic selection. Heritability in broad sense includes both additive and non-additive gene effects [5]. Heritability in broad sense was estimated for all the 14 characters of soybean and has been presented in (Table 4). In general, higher estimates (h_2b) >80% were observed for all the characters except days to 50% germination (69.9%), harvest index (70.9%) seed yield per plant (g) (77.4%) and days to 50% flowering (78%). The heritability value ranged from days to 50% germination (69.9%) to number of clusters per plants (98.4%). High heritability estimates were found for number of clusters per plants (98.4%) followed by number of seed /pods (98.1%), 100 seed weight (g) (98%), number of pods per plants (96.9%), pod length (cm) (96.5%), number of primary branches per plants (87.8%), days to maturity (87.6%), number of pods per clusters (85.5%), plant height (cm) (84.1%) and biological yield (gm) (80.5%) suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transmit the gene to their progenies. However, moderate heritability (>40% to <80%) observed for days to 50% germination (69.9%), harvest index (70.9%) seed yield per plant (g) (77.4%) and days to 50% flowering (78%) and low Heritability (<40%) was not observed for any studied character. Conflicting results on high heritability for days to 50% flowering have been observed by Rahaman et al. [15], Sahoo et al. [16], Jandong et al. [13], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], Koraddi and Basavaraja [24], for plant height (cm) Ningwal et al. (2023), Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Jandong et al. [13], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], Koraddi and Basavaraja [24], for days to Maturity Ningwal et al. (2023), Sahoo et al. [16], Saicharan et al. [17], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], for number of primary branches per plants Ningwal et al. (2023), Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], for number of clusters per plants Nayana and Fakrudin [14], Guleria et al. [23], for number of pods per clusters Saicharan et al. [17], Nayana and Fakrudin [14], for number of pods per plants Ningwal et al. (2023), Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Sonkamble et al. [19], Guleria et al. [23], Koraddi and Basavaraja [24], for pod length (cm)

Rahaman et al. [15], Nayana and Fakrudin [14], Guleria et al. [23] for number of seed per pods Nayana and Fakrudin [14], Sonkamble et al. [19], Koraddi and Basavaraja [24], for 100 seed weight (g) Ningwal et al. (2023), Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], Koraddi and Basavaraja [24], for biological yield (gm) Ningwal et al. (2023), Koraddi and Basavaraja [24], for harvest index Ningwal et al. (2023), Sahoo et al. [16], Sonkamble et al. [19] for seed yield per plant (g) Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Sonkamble et al. [19], Guleria et al. [23], Koraddi and Basavaraja [24].

3.5 Genetic advance

Genetic advance is a measure of genetic gain under selection which depends upon main factors viz., genetic variability, heritability, and selection index Allard RW (1960). The expected genetic advance in percent of mean @ 5% ranged from days to 50% flowering (10.896%) to number of clusters per plants (64.78%). High estimate of expected genetic advance were found for number of clusters per plants (64.78%) followed by number of pods per plants (55.016%), pod length (cm) (48.012%), number of primary branches per plants (47.631%), seed yield per plant (g) (45.243%), biological yield (gm) (44.856%) and number of seed /pods (42.937%) at 5% level. Low estimate of expected genetic advance as percent of mean were found for days to 50% flowering (10.896%) followed by harvest index (13.587%), days to maturity (13.548%), days to 50% germination (20.74%) and plant height (cm) (26.865%) at 5% level. High genetic advance at (5%) was observed for number of pods per plants (19.702%) followed by biological yield (gm) (14.755%), days to maturity (12.938%) and plant height (cm) (12.364%). Low estimates of expected genetic advance at (5%) were found for days to 50% germination (1.279%) followed by number of seed /pods (1.405%), pod length (cm) (1.519%), number of pods per clusters (1.705%) and number of primary branches per plants (2.188%) while moderate expected genetic advance as percent of mean were found for number of pods per clusters (30.079%), 100 seed weight (g) (28.605%) and plant height (cm) (26.865%). High heritability coupled with high genetic advance as

percent of mean at 5% observed for number of clusters per plants followed by number of pods per plants, pod length (cm), number of seed /pods and biological yield (gm) indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. Low heritability coupled with low genetic advance indicates that the trait is highly influenced by environmental effect and selection would be not effective. Heritability estimates alone do not provide reliable information about the gene action governing the expression of a particular character and also this does not provide the information of the amount of genetic progress resulting from the selection of the best individuals. Johanson et al. (1955) had pointed out that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection. The early reports on high genetic advance as a per cent of mean was recorded for days to 50% flowering Rahaman et al. [15], Sonkamble et al. [19], Koraddi and Basavaraja [24], for plant height (cm) Ningwal et al. (2023), Rahaman et al. [15], Saicharan et al. [17], Nayana and Fakrudin [14], Sonkamble et al. [19], Koraddi and Basavaraja [24], Prajapati et al. [27], for days to maturity Sonkamble et al. [19], for number of primary branches per plants Ningwal et al. (2023), Rahaman et al. [15], Jandong et al. [13], Nayana and Fakrudin [14], Sonkamble et al. [19], Guleria et al. [23], for number of clusters per plants Nayana and Fakrudin [14], for number of pods per clusters Nayana and Fakrudin [14], for number of pods per plants Ningwal et al. (2023), Sahoo et al. [16], Saicharan et al. [17], Tandekar et al. [25], Koraddi and Basavaraja [24], Dhopre et al. [28] for pod length (cm) Nayana and Fakrudin [14], Guleria et al. [23], for number of seed per pods Ningwal et al. (2023), Nayana and Fakrudin [14], Koraddi and Basavaraja [24], for 100 seed weight (g) Ningwal et al. (2023), Rahaman et al. [15], Nayana and Fakrudin [14], Sonkamble et al. [19], Koraddi and Basavaraja [24], for biological yield (gm) Ningwal et al. (2023), Tandekar et al. [25], Koraddi and Basavaraja [24], for harvest index Ningwal et al. (2023), Tandekar et al. [25], Prajapati et al. [26] Sonkamble et al. [19] and for seed yield per plant (g) Rahaman et al. [15], Sahoo et al. [16], Saicharan et al. [17], Tandekar et al. [25], Sonkamble et al. [19], Koraddi and Basavaraja [24].

Table 1. Mean performance of 14 quantitative characters of soybean genotypes

Genotypes	DTFG	DTFF	PH	DTM	NPBPP	NCPP	NPPC	NPPP	PL	NSPP	100-SW	BYPP	HI	SYPP
RVS 2011 35	7.19	42.78	43.73	95.88	3.76	8.02	5.48	25.41	2.5	3.64	13.4	39.64	41.03	16.3
AMS MB 100 39	5.4	36.52	35.66	87.77	3.41	12.37	7.11	21.34	3.43	2.45	14.48	26.88	37.73	10.1
JS-20-98	4.97	43.11	42.81	96.88	3.76	9.9	4.69	38.83	2.28	2.48	10.08	37.45	37.48	14.1
JS 21 72	5.48	36.99	38.81	81.73	4.43	11.44	4.7	23.46	3.54	2.68	14.48	18.51	38.95	7.18
JS 20 116	7.1	38.4	43.86	94.47	4.14	9.52	6	47.1	3.83	3.41	12.88	30.58	41.16	12.6
HIMSO 1689	5.2	39.55	46.7	108.34	8.53	18.63	4.69	27.65	2.51	2.61	15.94	29.78	39.84	11.9
JS 95 60	7.07	35.33	43.9	83.5	2.94	6.76	4.1	28.72	3.33	2.75	13.76	27.82	36.89	10.3
RVS 2001 4	8.05	43.22	56.51	98.68	4.44	16.18	4.58	48.77	2.42	3.75	12.27	46.28	37.64	17.4
NRC 86	5.2	38.07	41.15	95.77	3.27	12.33	6.32	41.43	2.29	2.7	16.74	22.38	38.75	8.67
RVS 76	5.32	40.85	41.65	101.89	5.9	21.04	6.98	35.9	2.43	3.47	13.9	32.83	38.74	12.7
JS 20 29	6.59	45.55	53.53	108.07	6.06	20.26	7.64	25.34	3.54	3.59	12.79	53.04	38.77	20.7
NRC 138	5.69	39.75	45.93	95.91	5	14.21	5.1	33.95	4.23	4.3	11.62	26.53	47.33	12.7
NRC 152	5.34	36.85	62.99	85.1	3.82	11.18	5.68	36.8	4.34	4.53	10.32	35.29	29.41	10.4
RVS 24	6.59	40.27	43.07	95.54	4.16	9.55	5.45	35.22	3.59	2.52	14.88	34.76	38.57	13.5
RVS 18	6.45	42.06	38.14	93.77	3.84	15.81	6.8	45.69	3.84	3.5	10.83	44.15	38.5	17
JS 20 69	5.08	37.74	48.06	96.62	4.55	17.95	5.96	59.04	2.15	3.57	10.94	39.23	39.08	15.4
NRC 94	6.37	43.07	40.62	105.33	5.7	19.65	4.92	29.91	2.63	3.82	12.97	19.19	37.67	7.27
NRC 157	7.23	39.07	50.57	98.42	5.28	12.69	5.03	48.43	3.54	2.65	14.82	29.41	31.96	9
JS 20 94	6.41	40.02	44.48	98.22	4.64	11.51	4.87	37.74	4.67	4.66	11.52	35.61	37.75	13.5
NRC 150	5.43	39.06	45.1	90.68	5.12	12.86	6.62	41.15	3.58	2.71	14.55	33.33	43.47	14.4
NRC 136	6.43	41.85	61.91	99.53	4.24	10.11	6.49	31.18	2.55	2.57	15.93	40.07	35.3	14.4
JS 20 34	7.1	36.67	43.27	88.85	4.09	8.29	5.54	24.79	2.43	3.64	12.74	20.92	35.88	7.51

Table 2. Analysis of variance (mean sum of squares) for 14 quantitative characters in soybean

Traits	df	DTFG	DTFF	PH	DTM	NPBPP	NCPP	NPPC	NPPP	PL	NSPP	100-SW	BYPP	HI	SYPP
Replication	2	0.83	34.07	11.07	25.8	51.38	185.83	48.43	27.91	0.10	0.99	5.51	70.07	4.09	15.26
Genotypes	16	2.36**	21.91**	152.85**	154.15**	4.39**	53.32**	2.81**	291.97**	1.75**	1.44**	10.60**	237.77**	38.04**	38.31**
Error	32	0.71	4.82	24.33	19.09	0.54	0.85	0.41	8.92	0.06	0.03	0.22	46.47	11.08	8.67

Table 3. Most desirable genotypes of soybean identified for 14 quantitative traits as per mean performance

Traits	Genotypes
DTFG	JS- 20- 98, JS -20 -69, NRC- 86, HIMSO -1689 and RVS- 76
DTFF	JS -95- 60, AMS- MB -100- 39, JS- 20- 34, NRC- 152 and JS -21- 72
PH	AMS -MB -100 -39, RVS -18, JS -21 -72, NRC- 94 and NRC- 86
DTM	JS -21 -72, JS -95 -60, NRC- 152, AMS- MB- 100- 39 and JS -20- 34
NPBPP	HIMSO- 1689, JS -20 -29, RVS- 76, NRC- 94 and NRC- 157
NCPP	RVS- 76, JS -20 -29, NRC- 94, HIMSO- 1689 and JS- 20- 69
NPPC	JS- 20 -29, AMS-MB- 100- 39, RVS -76, RVS- 18 and NRC- 150
NPPP	JS -20 -69, RVS- 2001 -4, NRC- 157, JS -20- 116 and RVS -18
PL	JS -20- 94, NRC- 138, NRC -152, RVS -18 and JS -20 -116
NSPP	JS -2094, NRC -138, NRC- 152, NRC -94 and RVS -2001- 4
TSW	NRC 86, HIMSO 1689, NRC 136, RVS 24 and NRC 157
BYPP	JS -2029, RVS- 2001- 4, RVS -18, NRC -136 and RVS -2011 -35
HI	NRC -138, NRC -150, JS- 20 -116, RVS -2011 -35 and HIMSO- 1689
SYPP	JS -20 -29, RVS -2001- 4, RVS -18, RVS- 2011 -35 and JS- 20- 69

Table 4. Genotypic, Phenotypic, environmental variances and coefficient of variation for 14 quantitative characters in soybean

S. No.	Traits	Grand mean	Range		GCV	PCV	Heritability (h²b %)	Gen. Adv. as 5% of Mean
			Min	Max				
1	DTFG	6.17	4.97	8.05	12.05	14.41	69.90	20.74
2	DTFF	39.85	35.33	45.55	5.99	6.78	78.00	10.90
3	PH	46.02	35.66	62.99	14.22	15.51	84.10	26.87
4	DTM	95.50	81.73	108.34	7.03	7.51	87.60	13.55
5	NPBPP	4.59	2.94	8.53	24.68	26.35	87.80	47.63
6	NCPP	13.19	6.76	21.04	31.70	31.96	98.40	64.78
7	NPPC	5.67	4.10	7.64	15.79	17.08	85.50	30.08
8	NPPP	35.81	21.34	59.04	27.12	27.55	96.90	55.02
9	PL	3.16	2.15	4.67	23.73	24.16	96.50	48.01
10	NSPP	3.27	2.45	4.66	21.04	21.24	98.10	42.94
11	HSW	13.26	10.08	16.74	14.03	14.17	98.00	28.61
12	BYPP	32.89	18.51	53.04	24.28	27.06	80.50	44.86
13	HI	38.27	29.41	47.33	7.83	9.31	70.90	13.59
14	SYPP	12.59	7.18	20.68	24.97	28.39	77.40	45.24

DTFG: Days to 50% germination, DTFF: Days to 50% flowering, PH: Plant height (cm), DTM: Days to Maturity, NPBPP: Number of primary branches/plants, NCPP: Number of clusters per plants, NPPC: Number of pods per clusters, NPPP: Number of pods per plants, PL: Pod length (cm), NSPP: Number of Seed /pods, TSW: 100 seed weight (g), BYPP: Biological yield/plant (gm), HI: Harvest index and SYPP: Seed yield per plant (g)
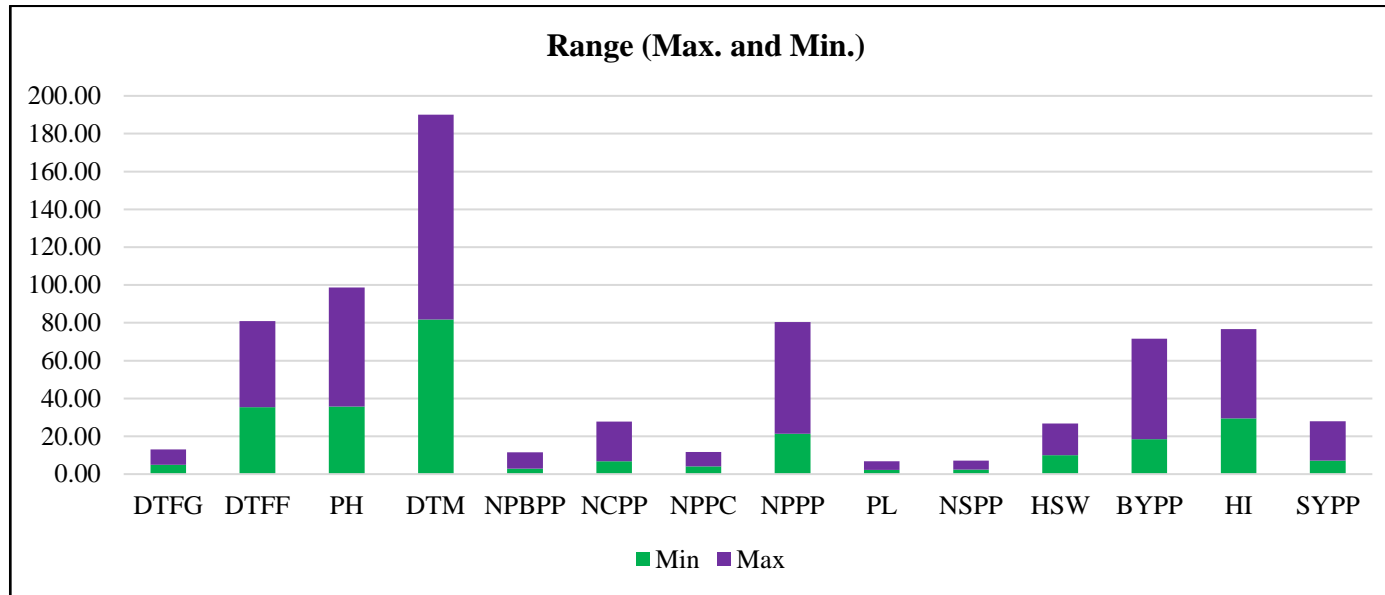
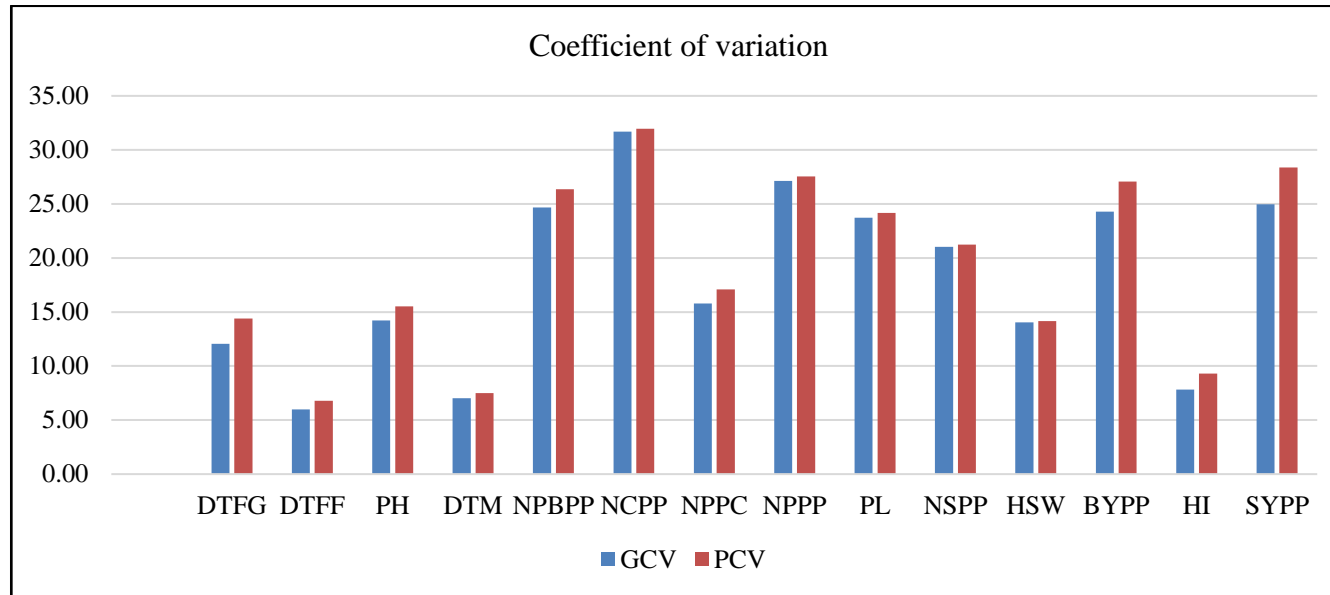**Fig. 1. Range of different traits of accessions**

Fig. 2. Coefficient of variation of of different traits of accessions
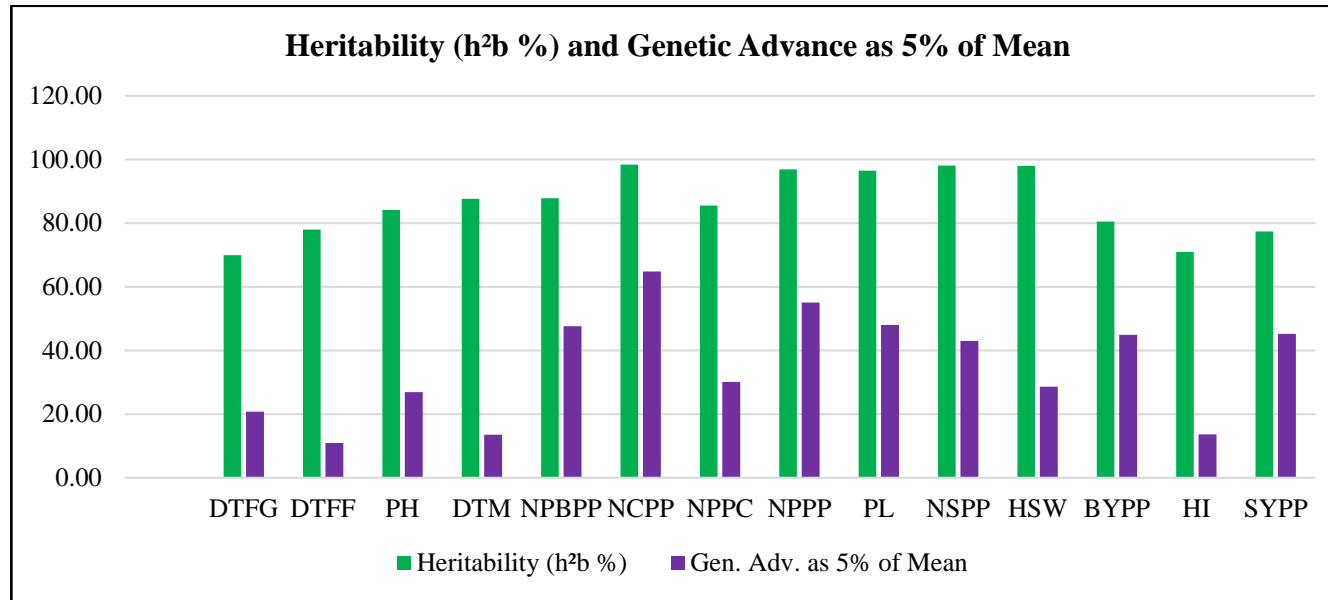
Fig. 3. Heritability (h²b %) and Gen. Advance as 5% of mean of different traits of accessions

4. CONCLUSION

The analysis of variance intended for all of the traits included in this investigation was found to be significant, demonstrating that each trait has access to enough genetic diversity. High heritability coupled with high genetic advance as percent of mean at 5% observed for number of clusters per plants followed by number of pods per plants, pod length (cm), number of seed /pods and biological yield (gm) indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. Low heritability combined with low genetic progress suggests that the trait is heavily impacted by environmental effects and therefore selection would be ineffective. The selection of high yielding breeding traits to increase the crop's genetic yield potential could be based on qualities discovered to have more heritability as well as high genetic advance as a % of mean. A systematic hybridization program might be constructed by taking into account traits with higher heritability and strong genetic progress as a percentage of mean for the selection of transgressive segregants in segregating generations. Along with improved breeding value, the segregants will be critical to increasing the output and productivity of the greengram in the future.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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