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ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION AMONG YIELD-ATTRIBUTING TRAITS IN SOYBEAN (*Glycine max* L. Merrill) GENOTYPES

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ABSTRACT

A comprehensive study was conducted to assess genetic variability, heritability and genetic advance among nineteen soybean [*Glycine max* (L.) Merrill] genotypes for yield and yield-attributing traits. The experiment was laid out in a randomized complete block design with three replications. The mean sum of squares due to genotypes were highly significant for all of the traits under study, including days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, 100 seed weight, biological yield per plant, harvest Index (%) and Seed yield/plant. Analysis of variance revealed highly significant differences among genotypes for all eleven traits studied, indicating substantial genetic variation available for selection. Number of pods per plant exhibited the highest heritability (93.08%) and genetic advance (33.97%), indicating strong genetic control and substantial response to selection. Hundred seed weight, clusters per plant, and seed yield per plant showed high heritability values (65-90.95%) and genetic advances, suggesting their suitability for effective selection. The high heritability values combined with strong genetic gains make number of pods per plant, biological yield per plant, and number of clusters per plant excellent indices for improving yield in soybean breeding programs. These findings provide valuable information for designing effective breeding strategies in soybean improvement initiatives.

Key words: Soybean, Genetic variability, Heritability, Genetic advance, Correlation analysis

Introduction

Soybean [*Glycine max* (L.) Merrill] is one of the most important legume crops cultivated worldwide, serving as a primary source of plant protein and oil for human consumption and livestock feed (Kumar *et al.*, 2021). The cultivated soybean *Glycine max* and the annual wild soybean *Glycine soja* both belong to the subgenus *Soja* with chromosomal number of $2n = 40$. In global agriculture, soybean production is second only to cereals in terms of economic importance, with production exceeding 370 million tonnes annually (FAO, 2023). Despite its significance, soybean yields in many developing countries remain substantially below potential yields, primarily due to inadequate variety development and use of low-yielding traditional cultivars. Improvement of

soybean yield through selective breeding is a fundamental objective in crop improvement programs. However, the success of any breeding program depends on the availability of genetic variability within the germplasm (Saxena *et al.*, 2019). Genetic variability provides the raw material necessary for selection of superior genotypes, while understanding character associations helps in identifying and selecting for traits that significantly contribute to yield. Quantitative traits such as yield and its components are controlled by multiple genes and are influenced by environmental factors, making their improvement complex. Parameters such as heritability and genetic advance are critical indices for assessing the potential of traits for improvement through selection (Desai *et al.*, 2020). High heritability estimates combined with

high genetic advance indicate substantial genetic control and promise for effective selection. Conversely, high heritability with low genetic advance suggests that most variation is due to dominance or epistatic effects, with limited response to selection. The present investigation was undertaken to quantify the magnitude of genetic variability present in the soybean germplasm, determine phenotypic and genotypic correlations among various traits.

Materials and Methods

The experiment was conducted during the 2023-2024 *kharif* season at the crop research centre-I, sithouli campus, ITM University Gwalior. Nineteen soybean genotypes were used for the study. These genotypes were selected based on their genetic diversity, agronomic performance, and availability. The experiment was laid out in a randomized block design (RBD) with three replications at Crop Research Center-I, Sithouli Campus, ITM University, Gwalior, Madhya Pradesh. Each genotype was grown in individual plots of 4×3 meters, with a spacing of 60 cm between rows and 20 cm between plants within a row. Data were recorded on eleven quantitative traits from five randomly selected plants in each plot. The data were analyzed using standard statistical methods. Analysis of variance (ANOVA) was performed to test the significance of differences among genotypes for all traits using the general linear model. Genetic parameters including phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated as the ratio of phenotypic and genotypic standard deviation to the population mean multiplied by 100. Broad-sense heritability (h^2) was estimated as the ratio of genotypic variance to phenotypic variance. Genetic advance (GA) was calculated as $h^2 \times I_p$, where I_p is the selection intensity assumed to be 5%. Genetic advance as percentage of mean (GA%) was calculated as $(GA/\text{Mean}) \times 100$.

Results

The mean sum of squares for the genotypes was highly significant ($p < 0.01$ or < 0.05) for all eleven traits studied. This suggests that there is a significant amount of variation between the genotypes of all the traits, offering good scope for selection and improvement by breeding. Except for a few of the traits, the error mean squares were relatively small in comparison to the treatment mean square, suggesting reasonably good experimental design and homogeneity of experimental conditions between the replications. Days to 50% flowering showed a mean of 38 days with a range of 32 to 46 days. The range from 100 to 114 days with an

average of 105 days to maturity. The height of the plants ranged from 62.00 to 93.60 cm with an average of 79.13 cm. The number of primary branches per plant ranged from 1.70 to 5.10 with an average of 3.07. There was a wide range of the number of clusters per plant from 8.52 to 19.50, and the average was 13.65. The greatest variability was found in the number of pods per plant (42.00 to 167.00), and the average was 88.26. The range of number of pods per cluster was from 2.42 to 5.00 and the average was 3.54. Hundred seed weight ranged from 10.38 to 14.48 g with a mean of 12.13 g. biological yield per plant ranged from 19.60 to 53.00 g with a mean of 32.39 g. Harvest index ranged from 27.60 to 59.70% with a mean of 44.88%. Seed yield per plant varied from 6.06 to 23.55 g with a mean of 14.57 g, which is a good amount of variation for an economically important trait. Genotypic coefficient of variation (GCV) was greater than environmental coefficient of variation (ECV) for all traits, which signified that variation in the traits was observed more due to the genetic factors than environmental factors. The traits were categorized as high ($>20\%$), moderate (10-20%) and low ($<10\%$) GCV. The high GCV values for number of primary branches per plant (20.34%), number of pods per plant (32.14%), biological yield per plant (20.67%) and seed yield per plant (24.02%) showed that there was significant variation in these traits among the germplasm evaluated. Medium level of GCV values were obtained for days to maturity (10.26%), number of pods per cluster (13.47%) and harvest index (17.31%). The days to flowering (6.23 %), plant height (8.06 %) and hundred seed weight (7.77 %) showed low GCV value. All traits had a consistently larger phenotypic coefficient of variation than genotypic coefficient of variation, suggesting that environmental factors have an effect on the expression of the traits.

The observed variance for most traits was genetically determined as revealed by high heritability in broad sense ($h^2 > 70\%$). The heritability of the number of pods per plant was 93.08% the highest followed by that of seed yield per plant (90.95%) and biological yield per plant (89.55%). The heritability of number of clusters per plant was 84.34% and that of plant height was 82.28%. The heritability values of harvest index (80.32%) and number of pods per cluster (79.28%) were also high. Hundred seed weight and plant height had heritability values in the high to moderate range (65.00% and 82.28%, respectively). Days to maturity had moderate heritability (69.9%) and days to flowering was in moderate range (59.20%) but has the lowest heritability among all the traits. The percentage of genetic advance in the above characters in the present investigation were in the order

et al., (2019), who reported similar patterns in soybean germplasm evaluation studies.

Conclusion

The present study demonstrates that there is substantial genetic variation in the soybean genotypes for yield and yield-related traits. The high genetic variability and heritability estimates combined with high genetic advances for number of pods per plant, biological yield per plant, number of clusters per plant, and seed yield per plant indicate that these traits would respond effectively to selection. The most promising genotypes identified in this study can be utilized in future selection programs for developing superior varieties with higher seed yields.

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