**Investigation of Genetic Variability and Character Connotation for Yield Augmentation in Soybean (Glycine max [L.] Merrill)**

**Abstract**

*Glycine max* [L.] Merrill), widely recognized as the “Golden Bean,” is a universally significant legume crop appreciated for its high protein (~40%) and oil (~20%) content, accompanied by its comprehensive adaptableness athwart diverse agro-ecological zones. To address the increasing demand for yield augmentation and stress pliability, an inclusive investigation was steered during the *Kharif*, 2023 at the Department of Genetics & Plant Breeding, RVSKVV, Gwalior, Madhya Pradesh. Ninety-two diverse soybean genotypes were evaluated in a Randomized Block Design with two replications to assess genetic variability, heritability, genetic advance, and the interrelationships among chief agronomical characters. Substantial variability was investigated for traits for instance harvest index, biological yield, and plant height, that displayed high genotypic and phenotypic coefficients of variation, heritability, and genetic advance, signifying predominance of additive gene effects and appropriateness for enhancement through direct selection. Correlation analysis exposed sturdy positive connotations of seed yield per plant with 100-seed weight, harvest index, numbers of pods per plant, and seeds per pod. Moreover, path coefficient analysis identified 100-seed weight as exerting the highest positive direct effect on yield, tracked by biological yield and harvest index. These findings highlighted presence of considerable genetic diversity and recognized key traits for selection, offering treasured insights for the development of high-yielding, stress-resilient soybean cultivar (s). Furthermore, integration of molecular tools and multi-environmental trials are recommended for incorporation in future breeding strategies.

**Keywords**: Correlation coefficient analysis, Genetic variability, Genotypic coefficient of variation (GCV), Heritability, Path coefficient analysis, Phenotypic coefficient of variation (PCV), Soybean (*Glycine max*).

**Introduction**

Soybean (*Glycine max* [L.] Merrill), frequently denoted to as the “Golden Bean,” stands among the most nutritionally impenetrable and economically momentous leguminous crops grown universally (Mishra et al., 2020;). It is a critical component of the global food, feed and industrial sectors owing to its amusing seed composition, encompassing around 40% high-quality protein and 20% oil (Mishra et al., 2021a; Sharma et al., 2021; Mishra et al., 2024a; Jhariya et al., 2025a). Beyond its macronutrient significance, it is also an excellent source of bioactive compounds for instance isoflavones, essential amino acids, and vitamins, which enhance its value in functional foods and nutraceutical applications (Mishra et al., 2021b; Mishra et al., 2024b; Jhariya et al., 2025b; Mishra et al., 2025a).

The crop is broadly adapted to an array of agro-climatic zones and plays a crucial role in supportable agriculture through its symbiotic nitrogen fixation with *Bradyrhizobium* spp., thereby enhancing soil fertility and reducing reliance on synthetic nitrogen fertilizers (Upadhayay et al., 2020a; Nakei *et al.,* 2022; Hu *et al.,* 2023). In India, it is generally grown in *kharif* season, particularly in central and western states including Madhya Pradesh, Maharashtra and Rajasthan (Mishra et al., 2022). Madhya Pradesh, often dubbed the “Soybean Bowl of India,” alone accounts for over half of the national production (Upadhayay et al., 2020b). The crop subsidizes meaningfully to income generation, cropping system diversification, and livelihood security for millions of smallholder farmers (Mishra et al., 2021c; Sharma et al., 2023; Mishra et al., 2024c; Mishra et al., 2025b).

Contempt to remarkable advances in breeding and agronomic practices, accomplishing higher and stable soybean yields remnants inspiring owing to the polygenic nature of yield and its susceptibility to environmental variability (Mishra et al., 2021d; Vogel et al., 2021; Mishra et al., 2024c; Vargas-Almendra et al., 2024). Yield in soybean is a complex character predisposed by multiple interacting components and genotype × environment interactions, making direct selection for yield less effective, particularly in early generations (Mishra et al., 2021e; Tripathi et al., 2022). Thus, understanding the extent of genetic variability and the interrelationships among yield-contributing traits is essential for devising efficient breeding strategies (Saroj et al., 2021; Mishra et al., 2024d; Mitiku et al., 2025).

Genetic enhancement relies profoundly on the incidence of considerable genetic variability and the effectiveness of selection, which can be evaluated through genetic parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (Bankapur et al., 2018; Rai et al., 2020; Sharma et al., 2023; Jian et al., 2024a; Paliwal et al., 2024; Gautam et al., 2025). Traits exhibiting high heritability coupled with higher genetic advance are typically controlled by additive gene action (Jain et al., 2024b) and are ideal targets for direct selection. In addition, correlation (Miller et al., 1958) and path coefficient (Wright, 1921) analyses serve as critical tools in identifying traits with significant direct and indirect contributions to yield, enabling the development of effective selection indices (Khan & Dar, 2010; Mefsin et al., 2018; Shrivastav et al., 2023; Yadav et al., 2023; Jain et al., 2024b; Rajput et al., 2024; Puri et al.,2025). Given this circumstantial, the current investigation was undertaken to assess genetic variability, heritability, and genetic advance for key agronomic traits and to evaluate the relationships among yield and its component traits in a diverse set of soybean genotypes. The ultimate objective is to recognize promising traits and genotypes that can be efficiently employed in breeding programmes aimed to enhance productivity, stability, and adaptability under variable agro-ecological circumstances.

**2. Material & Methods**

**2.1 Experimental Site**

The present investigation was conducted during the Kharif season of 2023 at the Experimental Farm, Department of Genetics and Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, Madhya Pradesh, India. The experimental site is located in an agro-climatic zone characterized by a hot and arid environment, exhibiting significant seasonal variations in temperature. Peak temperatures are typically observed in June, reaching up to 48°C, while winter temperatures may drop as low as 4°C, with an annual temperature range spanning from 2°C to 50°C. The region receives an average annual precipitation of 750–800 mm, predominantly during the southwest monsoon period, which arises from late June through September, sporadically augmented by sporadic winter showers. During the crop growing period (July to October 2023), a total rainfall of 907.7 mm was recorded. However, the distribution of rainfall was erratic and uneven across the season. Despite these irregularities, the climatic conditions remained within the normal range for the region. The mean maximum and minimum temperatures during the cropping period were recorded at 35.2°C and 24.5°C, correspondingly, supporting the optimal growth and development of the experimental crop.

**2.2 Experimental Details**

The experimental trial was laid out in a Randomized Block Design (RBD) with two replications to evaluate the performance of ninety-two soybean genotypes. Each genotype was sown in a plot comprising three rows, with an inter-row spacing of 30 cm and intra-row spacing of 10 cm. The plot size was standardized at 3.0 meters in length and 1.20 meters in width. For the assessment of quantitative traits, data were recorded from five randomly selected plants per plot. Uniform agronomic practices were followed throughout the cropping period to ensure optimal crop management and reliable expression of the genetic potential of the genotypes.

**3. Results & Discussion**

**3.1 Genetic Variation, Heritability & Genetic Advance**

The analysis of genotypic and phenotypic coefficients of variation (GCV and PCV) for yield and its associated traits revealed substantial variability among the ninety-two soybean genotypes evaluated, as summarized in Table 1 and Fig.1. In general, the PCV values were slightly higher than their corresponding GCV values for all traits, indicating the influence of environmental factors on phenotypic expression. However, the relatively narrow differences between GCV and PCV suggest a predominant of genetic control for most of the traits (Chacko et al., 2023; BharathKumar et al., 2024). Among the traits, the harvest index (%) exhibited the highest GCV (45.33%) and PCV (46.37%), followed by biological yield (GCV: 40.58%, PCV: 41.61%) and plant height (GCV: 21.73%, PCV: 22.74%), signifying a high degree of genetic variability and thus, substantial scope for selection. Moderate levels of GCV and PCV were observed for numbers of pods per plant, numbers of seeds per pod, yield per plant, numbers of primary branches per plant, and 100-seed weight, whereas traits like days to 50% flowering (GCV: 8.10%, PCV: 9.26%) and days to maturity (GCV: 5.98%, PCV: 7.00%) displayed relatively low variability, possibly due to tighter genetic regulation or stronger environmental influence (Khan et al., 2020; Sharma et al., 2022).

Broad-sense heritability estimates arrayed between 83.13% to 97.75%, with harvest index (97.75%), biological yield (97.54%), plant height (95.55%), and yield per plant (94.43%) exhibited the highest values, suggesting that a large proportion of the observed variation is due to genetic origin and can be effectively exploited through selection (Chaithanya et al., 2019; Gudeta et al., 2025). Furthermore, the estimation of genetic advance as a percentage of mean supported these findings. Harvest index (95.36%), biological yield (85.61%), and plant height (46.81%) showed the highest expected genetic gain. Traits such as numbers of seeds per pod, yield per plant, and numbers of pods per plant also demonstrated higher genetic advance, indicating the presence of additive gene action and promising opportunities for genetic improvement (Ramakrishnan et al., 2018; Salman et al., 2021). While moderate genetic advance was evident for 100-seed weight and numbers of primary branches per plant, whereas days to 50% flowering (18.41%) and days to maturity (14.32%) demonstrated low genetic advance despite high heritability, demonstrating possible non-additive gene effects or environmental influence that could limit the response to selection. As earlier demonstrated by Nayak et al. (2024) and Gnanasekaran et al. (2024).

The overall pattern of variability, heritability and genetic advance advised that traits like harvest index, biological yield, and plant height are governed primarily by additive genes and may be ideal candidates for improvement through direct phenotypic selection. High heritability coupled with higher genetic advance in these traits emphasizes their reliability as selection criteria in soybean breeding programmes (Jain et al., 2017; Emmadishetty & Gurjar, 2022; Patil et al., 2023). Conversely, characters like days to flowering and maturity, despite having high heritability, demonstrated low genetic advance, reflecting the complexity of their genetic control and indicating the need for alternative breeding approaches such as recurrent selection or marker-assisted selection (Bello et al., 2012; Saxena et al., 2021). Overall, the investigation highlights the presence of substantial genetic variability among the soybean genotypes evaluated and identified key traits that can be strategically targeted in future crop improvement programmes aimed to improve productivity and adaptation.

**Table 1: Genetic parameters of variability for yield and its component traits in soybean genotypes**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Trait** | **GCV (%)** | **PCV (%)** | **Heritability (%)** | **GA as % of Mean** |
| Days to 50% flowering | 8.10 | 9.26 | 87.43 | 18.41 |
| Days to maturity | 5.98 | 7.00 | 85.38 | 14.32 |
| Plant height (cm) | 21.73 | 22.74 | 95.55 | 46.81 |
| Numbers of primary branches per plant | 15.64 | 18.82 | 83.13 | 30.32 |
| Numbers of pods per plant | 18.42 | 20.37 | 90.44 | 38.15 |
| Numbers of seeds per pod | 18.11 | 20.11 | 90.06 | 41.43 |
| 100- seed weight (g) | 14.67 | 15.67 | 93.61 | 32.27 |
| Biological yield (g) | 40.58 | 41.61 | 97.54 | 85.61 |
| Harvest index (%) | 45.33 | 46.37 | 97.75 | 95.36 |
| Yield per plant (g) | 17.67 | 18.71 | 94.43 | 38.37 |

**Fig.1: Diagrammatic representation of variation, heritability and genetic advance**

**3.2 Correlation Coefficient Analysis**

Correlation coefficient analysis at both genotypic and phenotypic levels provides valuable insights into the interrelationships among yield and its attributing traits in soybean ( Table 2 & Table 3). Yield per plant exhibited a strong and highly significant positive correlation with 100-seed weight (genotypic: 0.9539; phenotypic: 0.9517), tracked by harvest index (0.3886 and 0.3887), numbers of pods per plant (0.2493 and 0.2481), and numbers of seeds per pod (0.2123 and 0.2214), underscoring their significant role in determining yield potential. Positive but non-significant associations were also observed between yield and traits such as biological yield and numbers of primary branches per plant, while negative and non-significant correlations were recorded with days to maturity and plant height. Among yield-contributing traits, plant height displayed a significant positive correlation with the numbers of primary branches, biological yield, and numbers of pods per plant, while a significant negative correlation with harvest index. Similarly, the numbers of primary branches exhibited significant positive correlations with plant height, biological yield, numbers of pods per plant, and seeds per pod, and a significant negative correlation with harvest index. The numbers of pods per plant showed strong positive associations with numbers of primary branches, plant height, biological yield, and yield per plant, while negatively and significantly correlated with harvest index. Biological yield was significantly and positively correlated with plant height, numbers of primary branches, and numbers of pods per plant, whereas it demonstrated a strong negative correlation with harvest index (genotypic: -0.7849; phenotypic: -0.7843), indicating a possible inverse relationship between biomass accumulation and reproductive efficiency. Previously Baraskar et al. (2014) and Srivastava et al. (2018) found similar results. The 100-seed weight was not only strongly associated with yield but also with harvest index, suggesting its dual role in enhancing both seed size and resource allocation efficiency (Dianatmanesh et al., 2022; Raina & Khan, 2023). Overall, 100-seed weight and harvest index emerged as key determinants for deciding yield performance, while the antagonistic relationships of plant height and biological yield with harvest index highlighted the importance of a judicious selection strategy in soybean improvement programmes (Mimi et al., 2017; Lekota et al., 2021; Patil et al., 2024).

**3.3 Path Coefficient Analysis**

Path coefficient analysis at both genotypic and phenotypic levels (Table 4 & Table 5, Fig. 2 & Fig. 3) elucidated the direct and indirect contributions of various yield-attributing traits towards seed yield per plant in soybean. At the genotypic level, 100-seed weight exhibited the highest positive direct effect on yield (0.8792), tracked by biological yield (0.1817), harvest index (0.1787), days to 50% flowering (0.0441), numbers of pods per plant (0.0270), and numbers of seeds per pod (0.0022). While negative direct effects were investigated for numbers of primary branches per plant (-0.0202), days to maturity (-0.0093), and plant height (-0.0034). Similarly, at the phenotypic level, 100-seed weight (0.8762) had the highest positive direct effect, followed by biological yield (0.1820), harvest index (0.1807), and days to 50% flowering (0.0421), while negative direct effects were recorded for numbers of primary branches (-0.0126), days to maturity (-0.0091), and plant height (-0.0068).

**Table 2: Genotypic correlation coefficient analysis for yield and its contributing traits in soybean genotypes**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Numbers of primary branches per Plant** | **Numbers of pods per plant** | **Numbers of seeds per pod** | **100- seed weight (g)** | **Biological Yield (g)** | **Harvest index (%)** | **Yield per plant (g)** |
| **Days to 50% flowering** | 1.0000 | 0.0923 | 0.0494 | 0.1078 | 0.0112 | 0.1363 | -0.0490 | 0.0917 | -0.1230 | -0.0068 |
| **Days to maturity** |   | 1.0000 | 0.1529 | 0.0821 | -0.0748 | 0.0438 | -0.0668 | 0.1735 | -0.1768 | -0.0682 |
| **Plant height (cm)** |   |   | 1.0000 | 0.58\*\* | 0.2952\*\* | 0.2388\* | -0.0296 | 0.4986\*\* | -0.4210\*\* | -0.0166 |
| **Numbers of primary branches per plant** |   |   |   | 1.0000 | 0.4410\*\* | 0.2934\*\* | -0.0137 | 0.4392\*\* | -0.3158\*\* | 0.0057 |
| **Numbers of pods per plant** |   |   |   |   | 1.0000 | 0.1325 | 0.0144 | 0.3116\*\* | -0.2157\* | 0.2493\* |
| **Numbers of seeds per pod** |   |   |   |   |   | 1.0000 | 0.0285 | 0.0082 | -0.0561 | 0.2123\* |
| **100-seed weight (g)** |   |   |   |   |   |   | 1.0000 | 0.0185 | 0.4031\*\* | 0.9539\*\* |
| **Biological yield (g)** |   |   |   |   |   |   |   | 1.0000 | -0.7849\*\* | 0.0580 |
| **Harvest index (%)** |   |   |   |   |   |   |   |   | 1.0000 | 0.3886\*\* |
| **Yield per plant (g)** |   |   |   |   |   |   |   |   |   | 1.0000 |

\*Significant at 5%, \*\*Significant at 1% probability level

**Table 3: Phenotypic correlation coefficient analysis for yield and its contributing traits in soybean genotypes**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Numbers of primary branches Per Plant** | **Numbers of pods per plant** | **Numbers of seeds per pod** | **100- seed weight (g)** | **Biological yield (g)** | **Harvest index (%)** | **Yield per plant (g)** |
| **Days to 50% flowering** | **1.0000** | 0.0910 | 0.0482 | 0.0937 | 0.0141 | 0.1339 | -0.048 | 0.0908 | -0.1207 | -0.0070 |
| **Days to maturity** |   | **1.0000** | 0.1524\* | 0.0687 | -0.0668 | 0.0438 | -0.0667 | 0.1724\* | -0.1763\* | -0.0676 |
| **Plant height (cm)** |   |   | **1.0000** | 0.5144\*\* | 0.2814\*\* | 0.2387\*\* | -0.0295 | 0.498\*\* | -0.4205\*\* | -0.0166 |
| **Numbers of primary branches per plant** |   |   |   | **1.0000** | 0.3528\*\* | 0.2594\*\* | -0.0131 | 0.3857\*\* | -0.2762\*\* | 0.0050 |
| **Numbers of pods per plant** |   |   |   |   | **1.0000** | 0.1265 | 0.0134 | 0.2972\*\* | -0.2041\*\* | 0.2481\*\* |
| **Numbers of seeds per pod** |   |   |   |   |   | **1.0000** | 0.0282 | 0.0083 | -0.0561 | 0.2214\*\* |
| **100- seed weight (g)** |   |   |   |   |   |   | **1.0000** | 0.0186 | 0.4027\*\* | 0.9517\*\* |
| **Biological yield (g)** |   |   |   |   |   |   |   | **1.0000** | -0.7843\*\* | 0.0577 |
| **Harvest index (%)** |   |   |   |   |   |   |   |   | **1.0000** | 0.3887\*\* |
| **Yield per plant (g)** |   |   |   |   |   |   |   |   |   | **1.0000** |

\* Significant at 5%, \*\* Significant at 1% probability level

**Fig. 2: Genotypic path diagram for 10 characters of soybean genotypes**

Indirect effects varied among traits, with biological yield, 100-seed weight and harvest index consistently contributing to yield indirectly through other traits. Remarkably, harvest index and biological yield displayed antagonistic relationships, with biological yield exerting strong negative indirect effects *via* harvest index at both levels (genotypic: -0.1403; phenotypic: -0.1418). Harvest index also showed substantial positive indirect contributions through 100-seed weight (genotypic: 0.3544; phenotypic: 0.3529), highlighting their mutual influence on yield determination (Paliwal et al., 2024; Ragade et al., 2025). Residual effects were estimated to be 0.0530 and 0.0690 at genotypic and phenotypic levels, respectively, indicated that the majority of variation in yield could be explained by the traits under investigation (Veeramani et al., 2023; Nasir et al., 2023). Overall, 100-seed weight, harvest index and biological yield emerged as major determinants of yield, either directly or through strong indirect effects, suggesting their potential utility as selection criteria in soybean improvement programmes (Obua et al., 2024; Mishra et al., 2025b).

**Fig. 3: Phenotypic path diagram for 10 characters of soybean genotypes**

**Table 4: Genotypic path coefficient analysis for yield and its component characters in soybean genotypes**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Numbers of primary branches per plant** | **Numbers of pods per plant** | **Numbers of seeds per pod** | **100- seed weight (g)** | **Biological yield (g)** | **Harvest index (%)** | **Yield per plant (g)** |
| **Days to 50% flowering** | **0.0441** | -0.0009 | -0.0002 | -0.0022 | 0.0003 | 0.0003 | -0.0430 | 0.0167 | -0.0220 | -0.0068 |
| **Days to maturity** | 0.0041 | **-0.0093** | -0.0005 | -0.0017 | -0.0020 | 0.0001 | -0.0588 | 0.0315 | -0.0316 | -0.0682 |
| **Plant height (cm)** | 0.0022 | -0.0014 | **-0.0034** | -0.0117 | 0.0080 | 0.0005 | -0.0260 | 0.0906 | -0.0752 | -0.0166 |
| **Numbers of primary branches per plant** | 0.0048 | -0.0008 | -0.0020 | **-0.0202** | 0.0119 | 0.0007 | -0.0120 | 0.0798 | -0.0564 | 0.0057 |
| **Numbers of pods per plant** | 0.0005 | 0.0007 | -0.0010 | -0.0089 | **0.0270** | 0.0003 | 0.0127 | 0.0566 | -0.0386 | 0.2493 |
| **Numbers of seeds per pod** | 0.0060 | -0.0004 | -0.0008 | -0.0059 | 0.0036 | **0.0022** | 0.0250 | 0.0015 | -0.0100 | 0.2123 |
| **100- seed weight (g)** | -0.0022 | 0.0006 | 0.0001 | 0.0003 | 0.0004 | 0.0001 | **0.8792** | 0.0034 | 0.0720 | 0.9539 |
| **Biological yield (g)** | 0.0040 | -0.0016 | -0.0017 | -0.0089 | 0.0084 | 0.0001 | 0.0163 | **0.1817** | -0.1403 | 0.0580 |
| **Harvest index (%)** | -0.0054 | 0.0016 | 0.0015 | 0.0064 | -0.0058 | -0.0001 | 0.3544 | -0.1426 | **0.1787** | 0.3886 |

**Residual effect: 0.0530**

**Table 5: Phenotypic path coefficient analysis for yield and its component characters in soybean genotypes**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Numbers of primary branches per plant** | **Numbers of pods per plant** | **Numbers of seeds per pod** | **100- seed weight (g)** | **Biological yield (g)** | **Harvest index (%)** | **Yield per plant (g)** |
| **Days to 50% flowering** | **0.0421** | -0.0008 | -0.0003 | -0.0012 | 0.0003 | 0.0003 | -0.0421 | 0.0165 | -0.0218 | -0.0070 |
| **Days to maturity** | 0.0038 | **-0.0091** | -0.0010 | -0.0009 | -0.0016 | 0.0001 | -0.0584 | 0.0314 | -0.0319 | -0.0676 |
| **Plant height (cm)** | 0.0020 | -0.0014 | **-0.0068** | -0.0065 | 0.0068 | 0.0005 | -0.0258 | 0.0906 | -0.0760 | -0.0166 |
| **Numbers of primary branches per plant** | 0.0039 | -0.0006 | -0.0035 | **-0.0126** | 0.0085 | 0.0005 | -0.0115 | 0.0702 | -0.0499 | 0.0050 |
| **Number of pods per plant** | 0.0006 | 0.0006 | -0.0019 | -0.0045 | **0.0241** | 0.0002 | 0.0117 | 0.0541 | -0.0369 | 0.2481 |
| **Numbers of seeds per pod** | 0.0056 | -0.0004 | -0.0016 | -0.0033 | 0.0030 | **0.0019** | 0.0247 | 0.0015 | -0.0101 | 0.2214 |
| **100 -seed weight (g)** | -0.0020 | 0.0006 | 0.0002 | 0.0002 | 0.0003 | 0.0001 | **0.8762** | 0.0034 | 0.0728 | 0.9517 |
| **Biological yield (g)** | 0.0038 | -0.0016 | -0.0034 | -0.0049 | 0.0072 | 0.0000 | 0.0163 | **0.1820** | -0.1418 | 0.0577 |
| **Harvest index (%)** | -0.0051 | 0.0016 | 0.0028 | 0.0035 | -0.0049 | -0.0001 | 0.3528 | -0.1427 | **0.1807** | 0.3887 |

**Residual effect: 0.0690**

**Conclusion**

The present investigation demonstrated existence of significant genetic variability among 92 soybean genotypes evaluated under field conditions, affirming the potential for genetic improvement through targeted selection. Traits such as harvest index, biological yield, and plant height exhibited high genotypic and phenotypic coefficients of variation, heritability, and substantial genetic advance, indicating the predominance of additive gene action and their suitability for direct selection. Moderate variability in traits like numbers of pods per plant, numbers of seeds per pod, and 100-seed weight further highlights their relevance in yield improvement schemes. In contrast, low genetic advance in characters like days to 50% flowering and maturity, despite high heritability, suggests the influence of non-additive gene action or environmental effects, necessitating alternative breeding strategies. Correlation and path coefficient analysis revealed that 100-seed weight, harvest index, numbers of pods per plant, and numbers of seeds per pod had strong positive associations with seed yield, 100-seed weight and harvest index showing the highest direct effects. The low residual effects observed confirmed that most of the yield variation was explained by the traits investigated, reinforcing their reliability as selection criteria. Overall, the study identified that 100-seed weight, harvest index, and biological yield played as key traits for strategic selection to enhance soybean productivity. These findings offer a robust foundation for future breeding programmes focused on yield enhancement and resource-use efficiency. Validation across diverse environments and integration of molecular tools could further strengthen breeding efficiency and accelerate genetic gains in soybean improvement.

**Disclaimer (Artificial intelligence)**

Author (s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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