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## Assessment of genetic variability, heritability and genetic components for yield traits in soybean (*Glycine max* (L.) Merrill)

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**Abstract**

The study revealed considerable genetic variability among the evaluated crosses for several important yield and yield-related traits. High heritability coupled with high genetic advance as percent of mean was recorded for plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant, indicating predominance of additive gene action and effectiveness of direct selection. Observations were recorded on twelve quantitative and quality traits including significant genetic variability among generations for all traits across the seven crosses. PCV and GCV (%) estimates indicated low genetic variation for days to 50% flowering, days to maturity, number of seeds per pod and 100-seed weight in most crosses, while moderate to high variation was observed for plant height, number of primary branches, number of pods per plant, number of seeds per plant and seed yield per plant. Quality traits (protein and oil content) exhibited generally low genetic variation.

**Keywords:** Genetic variability, PCV and GCV, heritability, GAM

**Introduction**

The soybean (*Glycine max* (L.) Merrill),  $2n = 40$ , belongs to the Leguminosae or Fabaceae family and the Papilionoideae subfamily. It is believed to have originated in Eastern Asia, particularly in North and Central China. Since 2006, soybean has maintained its prominent status as a leading oilseed crop in India, significantly contributing to the country's vegetable oil supply and bolstering the national economy through substantial foreign exchange earnings from soymeal exports. The United States of America is the world's largest soybean producer, accounting for 55% of global production and 45% of the soybean-growing area. It is also grown in Brazil, Argentina, China and India. Soybean is known as the "Golden Bean" and the "Miracle Crop" because of its dual properties of high protein and oil content, making it one of the most important crops of the 21st century. It contributes significantly to meeting the world's current and future protein and edible oil demands. Soybean seeds contain 37-42% high-quality protein, 6% ash, 29% carbohydrates and 17-24% oil (Kumari *et al.*, 2022) <sup>[7]</sup>.

**Materials and Methods**

The present experimental material comprised five generations i.e.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$  of each of the seven crosses, viz., NRC 127  $\times$  KDS 11-49, NRC 127  $\times$  RSC 10-46, NRC 127  $\times$  NRC 12, NRC 127  $\times$  RSC 10-52, NRC 127  $\times$  RSC 11-42, PS 1689  $\times$  RSC 10-46 and PS 1689  $\times$  RSC 11-42. The parental plants were grown and the crossing programme was carried out during *Kharif* 2022. Thereafter, the  $F_1$  seeds along with their parents were sown during Rabi 2022-23 and observations on the characterization of  $F_1$  and parental lines were recorded. During Rabi 2022-23,  $F_2$  seeds were produced. These  $F_2$  seeds, along with their parents, were sown during *Kharif* 2023. During Rabi 2023-24, the  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$  generations were grown and observations were recorded. The observations were taken from 12 yield attributing traits.

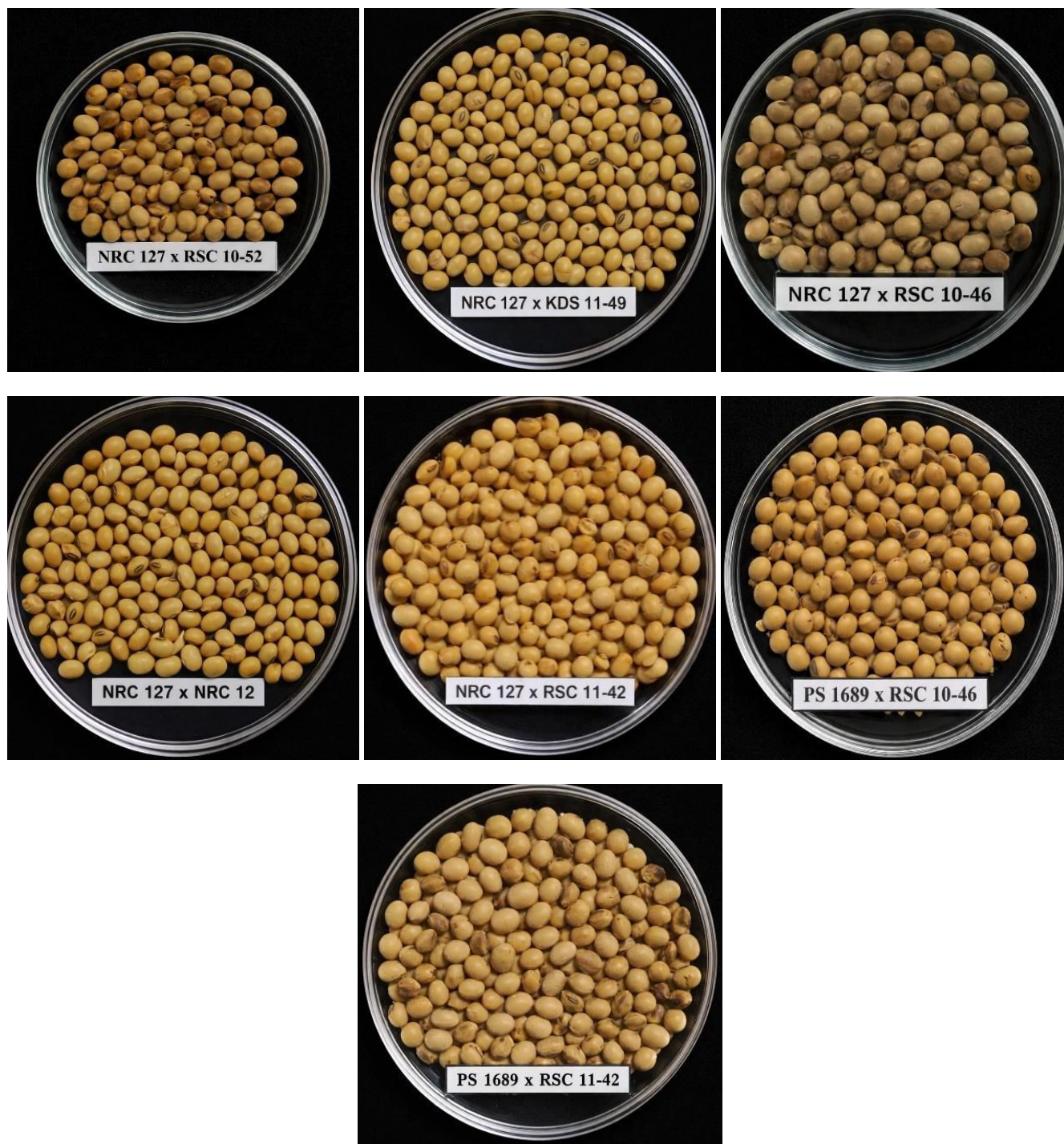


**Fig 1:** Seed morphology of seven crosses

## Results and Discussion

### Genotypic and phenotypic coefficient of variation

The estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicates the existence of significant variability among the genotypes studied for different traits. The GCV and PCV values are categorized as low (less than 10%), moderate (10-20%) and high (more than 20%), as suggested by Sivasubramanian and Madhavamenon (1973).

### Days to 50% flowering

In all seven crosses, the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV). The PCV and GCV percentages were observed to be below 10% (low) in all seven crosses. The maximum PCV (6.87%) and GCV (5.30%) were observed

in the cross NRC 127 × RSC 11-42. These findings are in accordance with the reports of Jain *et al.* (2017) <sup>[6]</sup>, Guleria *et al.* (2019) <sup>[4]</sup>, Sonkamble *et al.* (2020) <sup>[10]</sup> and Jandong *et al.* (2020) <sup>[5]</sup>.

### Days to maturity

Similarly, PCV and GCV percentages were observed to be low (less than 10%) in all seven crosses for days to maturity. The maximum PCV (6.45%) and GCV (6.11%) were observed in the cross NRC 127 × NRC 12. These findings are in accordance with the reports of Jandong *et al.* (2020) <sup>[5]</sup> and Bairagi *et al.* (2023) <sup>[2]</sup>.

### Plant height (cm)

Moderate to high (more than 20%) PCV and GCV percentages were observed among the seven crosses. The

crosses NRC 127 × KDS 11-49, NRC 127 × RSC 10-46, NRC 127 × NRC 12 and NRC 127 × RSC 10-52 showed high PCV and GCV values (more than 20%), while the remaining crosses exhibited moderate values. These findings are in accordance with the reports of Bairagi *et al.* (2023) <sup>[2]</sup>, Susanto *et al.* (2023) <sup>[11]</sup>, Singh *et al.* (2023) <sup>[12]</sup> and Paulos and Kindie (2025) <sup>[9]</sup>.

#### No. of primary branches per plant

All crosses showed high PCV and GCV percentages (*i.e.* more than 20%), except for the cross NRC 127 × RSC 10-46 which exhibited a moderate range of variation. These findings are in accordance with the reports of Sonkamble *et al.* (2020) <sup>[10]</sup>, Jandong *et al.* (2020) <sup>[5]</sup>, Bairagi *et al.* (2023) <sup>[2]</sup> and Susanto *et al.* (2023) <sup>[11]</sup>.

#### No. of Pods Per Plant

All crosses fell within the moderate range of PCV and GCV percentages (10-20%) except for the cross NRC 127 × RSC 11-42 which was categorized as high, with PCV (20.91%) and GCV (20.39%). These findings are in accordance with the reports of Sonkamble *et al.* (2020) <sup>[10]</sup>, Jandong *et al.* (2020) <sup>[5]</sup>, Bairagi *et al.* (2023) <sup>[2]</sup> and Susanto *et al.* (2023) <sup>[11]</sup>.

#### Pod bearing length (cm)

The only cross NRC 127 × RSC 10-52 showed high range of PCV and GCV % that is 22.12 and 21.73 respectively, remaining crosses fell in low to moderate category. These findings are in accordance with the work of Jandong *et al.* (2020) <sup>[5]</sup>, Bairagi *et al.* (2023) <sup>[2]</sup>, Susanto *et al.* (2023) <sup>[11]</sup> and Singh *et al.* (2023) <sup>[12]</sup>.

#### Number of seeds per pod

All crosses exhibited a low range of PCV and GCV %. These findings are in accordance with the reports of Jain *et al.* (2017) <sup>[6]</sup>, Bairagi *et al.* (2023) <sup>[2]</sup>, Susanto *et al.* (2023) <sup>[11]</sup> and Singh *et al.* (2023) <sup>[12]</sup>.

#### No. of Seeds per Plant

The crosses exhibited moderate to high PCV and GCV percentages. The maximum values were observed in the cross NRC 127 × RSC 10-46 with PCV and GCV of 30.00% and 29.51%, respectively. These findings are in accordance with the reports of Jandong *et al.* (2020) <sup>[5]</sup>, Bairagi *et al.* (2023) <sup>[2]</sup>, Susanto *et al.* (2023) <sup>[11]</sup> and Singh *et al.* (2023) <sup>[12]</sup>.

#### 100 seed weight (g)

The PCV and GCV percentages in all crosses were low, except for the cross NRC 127 × NRC 12 which exhibited a moderate range of variation, with PCV and GCV values of 13.38% and 13.12% respectively. These findings are in accordance with the reports of Jain *et al.* (2017) <sup>[6]</sup>, Guleria *et al.* (2019) <sup>[4]</sup>, Susanto *et al.* (2023) <sup>[11]</sup> and Singh *et al.* (2023) <sup>[12]</sup>.

#### Protein content (%)

All crosses showed very low PCV and GCV percentages which fall under the low variability category. These findings are in accordance with the reports of Jain *et al.* (2017) <sup>[6]</sup> and Guleria *et al.* (2019) <sup>[4]</sup>.

#### Oil content (%)

Similar to protein content, oil content also exhibited a low category of PCV and GCV percentages (less than 10%). Among the crosses PS 1689 × RSC 11-42 and PS 1689 × RSC 10-46 exhibited the maximum values with PCV and GCV ranging from 5.24% to 4.18% and 4.87% to 4.72% respectively. These findings are in accordance with the reports of Bairagi *et al.* (2023) <sup>[2]</sup>, Susanto *et al.* (2023) <sup>[11]</sup>, Singh *et al.* (2023) <sup>[12]</sup> and Paulos and Kindie (2025) <sup>[9]</sup>.

#### Seed yield per plant (g)

The crosses exhibited moderate to high PCV and GCV percentages (10-20%) and above 20%). The maximum PCV and GCV values were observed in the cross NRC 127 × RSC 10-46 (PCV 31.00% and GCV 27.31%) followed by the cross PS 1689 × RSC 10-46 (25.83% and 25.27% respectively). These findings are in accordance with the reports of Jain *et al.* (2017) <sup>[6]</sup>, Guleria *et al.* (2019) <sup>[4]</sup>, Susanto *et al.* (2023) <sup>[11]</sup>, Singh *et al.* (2023) <sup>[12]</sup> and Paulos and Kindie (2025) <sup>[9]</sup>.

#### Heritability

Assessment of heritability is one of the most important genetic parameters used in breeding programmes. It is a statistical measure that indicates the proportion of total variation within a population that is attributable to genetic differences rather than environmental factors. Heritability values range from 0 (entirely environmental influence) to 1 (entirely genetic influence). It reflects how much of the observed variation in a trait is due to genetic differences, not how much of the trait itself is determined by genes.

Heritability values are categorized as low (<30%), moderate (30-60%) and high (>60%) as suggested by Johnson *et al.* (1955). Heritability is useful in the selection of elite genotypes from homozygous populations and can be estimated from parental and segregating generations based on total genetic variance.

#### Days to 50% flowering

A high heritability estimate (81.09%) was observed for the cross NRC 127 × KDS 11-49, whereas the lowest estimate (13.81%) was observed for the cross PS 1689 × RSC 10-46. Similar findings were reported by Sharmila *et al.* (2022) <sup>[7]</sup>, Saicharan *et al.* (2022) <sup>[13]</sup>, Tandekar *et al.* (2023) <sup>[15]</sup> and Kalamkhede *et al.* (2025) <sup>[8]</sup>.

#### Days to maturity

The highest heritability value (89.69%) was recorded in the cross NRC 127 × NRC 12 whereas the lowest value (19.02%) was recorded in the cross NRC 127 × RSC 10-52. Similar findings were reported by Sharmila *et al.* (2022) <sup>[7]</sup>, Saicharan *et al.* (2022) <sup>[13]</sup>, Tandekar *et al.* (2023) <sup>[15]</sup> and Kalamkhede *et al.* (2025) <sup>[8]</sup>.

#### Plant height

High heritability values were observed in the crosses PS 1689 × RSC 10-46 (98.87%), NRC 127 × RSC 10-52 (98.69%), PS 1689 × RSC 11-42 (94.33%) and NRC 127 × KDS 11-49 (97.15%). All the crosses exhibited high heritability values. Similar findings were reported by Sharmila *et al.* (2022) <sup>[7]</sup>, Saicharan *et al.* (2022) <sup>[13]</sup> and Kalamkhede *et al.* (2025) <sup>[8]</sup>.

**Number of primary branches/plants**

All the crosses showed high heritability values. Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**No. of pods/plant**

All crosses showed high heritability values. Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**Pod bearing length**

All crosses showed high heritability values, except for the cross PS 1689 × RSC 10-46 (52.34%). Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup> and Tandekar *et al.* (2023)<sup>[15]</sup>.

**Number of seeds per pod**

The crosses PS 1689 × RSC 10-46 (87.12%) and NRC 127 × KDS 11-49 (73.33%) exhibited high heritability estimates, whereas NRC 127 × RSC 10-52 (15.18%) showed the lowest heritability value. Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup> and Tandekar *et al.* (2023)<sup>[15]</sup>.

**No. of seeds/plant**

All crosses exhibited high heritability values. The cross NRC 127 × NRC 12 showed the maximum value (97.26%). Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**100 seed weight (g)**

All crosses exhibited high heritability values. The cross NRC 127 × NRC 12 showed the maximum value (96.15%). Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**Protein content (%)**

The crosses NRC 127 × RSC 10-46 (78.79%) and PS 1689 × RSC 11-42 (67.68%) exhibited high heritability, whereas the remaining crosses showed low to moderate heritability. Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup> and Tandekar *et al.* (2023)<sup>[15]</sup>.

**Oil content (%)**

A high heritability estimate was observed for the cross PS 1689 × RSC 10-46 (94.11%), whereas the lowest value (7.02%) was observed for the cross NRC 127 × RSC 10-46. Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**Seed yield/plant (g)**

All crosses exhibited high heritability estimates except for the cross NRC 127 × RSC 11-42 (26.32%). Similar findings were reported by Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup> and Kalamkhede *et al.* (2025)<sup>[8]</sup>.

**Genetic advance as % of mean**

Genetic advance as a percentage of the mean (GAM) in plant breeding measures the expected genetic improvement of a new selection compared to the original population mean, expressed as a percentage. It helps predict the

effectiveness of selection for specific traits, with high values (>20%) indicating the predominance of additive gene action and high selection efficiency.

Johnson *et al.* (1955) classified GAM into three levels: Low: 0 to 10%, Moderate: 10 to 20%, High: > 20%.

**Days to 50% flowering**

The observations recorded for this trait in all seven crosses exhibited low genetic advance as a percentage of the mean. High heritability coupled with low GAM was recorded only in the crosses NRC 127 × KDS 11-49 and NRC 127 × RSC 10-46. This suggests that non-additive gene action or epistasis governs the trait in these two crosses. Similar findings were also reported by Sidramappa *et al.* (2019)<sup>[14]</sup>, Bhuvu and Babariya (2020)<sup>[11]</sup>.

**Days to maturity**

Similar to days to 50% flowering low GAM was observed in all seven crosses, except for the cross NRC 127 × NRC 12, where it was moderate. High heritability coupled with low GAM was observed in the crosses NRC 127 × RSC 10-46, NRC 127 × RSC 11-42 and PS 1689 × RSC 11-42. In contrast the cross NRC 127 × NRC 12 exhibited high heritability coupled with moderate GAM. Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup>, Kalamkhede *et al.* (2025)<sup>[8]</sup> and Fufa and Nepir (2025)<sup>[3]</sup>.

**Plant height (cm)**

This trait showed high GAM in all seven crosses. High heritability coupled with high GAM was observed in all crosses, indicating the role of additive gene action in controlling the trait. Sharmila *et al.* (2022)<sup>[7]</sup>, Saicharan *et al.* (2022)<sup>[13]</sup>, Tandekar *et al.* (2023)<sup>[15]</sup>, Kalamkhede *et al.* (2025)<sup>[8]</sup> and Fufa and Nepir (2025)<sup>[3]</sup>.

**Number of primary branches per plant**

High genetic advance as a percentage of the mean was observed in all seven crosses. In all crosses, high heritability coupled with high GAM was observed, indicating the role of additive gene action in controlling the trait. Tandekar *et al.* (2023)<sup>[15]</sup>, Kalamkhede *et al.* (2025)<sup>[8]</sup> and Fufa and Nepir (2025)<sup>[3]</sup>.

**Number of pods per plant**

Similar to the number of primary branches per plant, high GAM values were recorded for this trait in all seven crosses, except for the cross NRC 127 × NRC 12. High heritability coupled with high GAM was also observed in all crosses except NRC 127 × NRC 12, indicating the influence of additive gene action in controlling the trait. Similar findings were reported by Tandekar *et al.* (2023)<sup>[15]</sup>, Kalamkhede *et al.* (2025)<sup>[8]</sup> and Fufa and Nepir (2025)<sup>[3]</sup>.

**Pod bearing length (cm)**

Moderate to high GAM values were observed among the crosses. The crosses NRC 127 × RSC 10-46, NRC 127 × NRC 12, NRC 127 × RSC 10-52 and NRC 127 × RSC 11-42 exhibited high GAM values, whereas the remaining crosses showed moderate GAM values. In the crosses NRC 127 × NRC 12, NRC 127 × RSC 10-46, NRC 127 × RSC 10-52 and NRC 127 × RSC 11-42, high heritability coupled with high GAM indicated that the trait is predominantly controlled by additive gene action. Similar findings were reported by Kalamkhede *et al.* (2025)<sup>[8]</sup> and Fufa and Nepir (2025)<sup>[3]</sup>.

**Number of seeds per pod**

Low GAM values were observed in six crosses, whereas the cross PS 1689 × RSC 10-46 exhibited a moderate GAM value. High heritability coupled with low GAM was observed in the crosses NRC 127 × KDS 11-49 and PS 1689 × RSC 11-42, indicating that the trait in these crosses is governed by non-additive gene action. In contrast, the cross PS 1689 × RSC 10-46 exhibited high heritability coupled with moderate GAM. Similar findings were reported by Tandekar *et al.* (2023) <sup>[15]</sup>, Kalamkhede *et al.* (2025) <sup>[8]</sup> and Fufa and Nepir (2025) <sup>[3]</sup>.

**Number of seeds per plant**

The important yield-contributing trait, i.e. number of seeds per plant, exhibited both high GAM and high heritability estimates in all seven crosses, indicating the effective role of additive gene action in controlling this trait. This trait can be selected from all crosses for further improvement in the breeding programme. Kalamkhede *et al.* (2025) <sup>[8]</sup> and Fufa and Nepir (2025) <sup>[3]</sup>.

**100 seed weight (g)**

The 100-seed weight is another important trait influencing yield. The results revealed that only two crosses, namely NRC 127 × NRC 12 and NRC 127 × RSC 12, exhibited high GAM values. In both these crosses, high heritability was coupled with high GAM, indicating the important role of additive gene action in controlling the trait. Similar findings were reported by Kalamkhede *et al.* (2025) <sup>[8]</sup> and Fufa and Nepir (2025) <sup>[3]</sup>.

**Protein content (%)**

The results for this quality trait revealed that very low GAM values were observed in all seven crosses, indicating that there is little scope for improvement in progenies over the population mean. The cross NRC 127 × RSC 10-46 showed the involvement of non-additive gene action in controlling this trait, as high heritability was coupled with low GAM. Similar findings were reported by Kalamkhede *et al.* (2025) <sup>[8]</sup> and Fufa and Nepir (2025) <sup>[3]</sup>.

**Oil content (%)**

Observations of this trait revealed low GAM values in all seven crosses, whereas non-additive gene action was found in the crosses PS 1689 × RSC 10-46, PS 1689 × RSC 11-42, NRC 127 × NRC 12 and NRC 127 × KDS 11-49. Similar findings were reported by Kalamkhede *et al.* (2025) <sup>[8]</sup> and Fufa and Nepir (2025) <sup>[3]</sup>.

**Seed yield per plant (%)**

Seed yield per plant one of the most important economic traits revealed that high GAM values were observed in six crosses. In these crosses, high heritability was coupled with high GAM, indicating the important role of additive gene action in controlling this trait. Only the cross NRC 127 × RSC 11-42 exhibited low GAM and low heritability. Similar findings were reported by Sidramappa *et al.* (2019) <sup>[14]</sup>, Bhuvu and Babariya (2020) <sup>[1]</sup>, Sharmila *et al.* (2022) <sup>[7]</sup>, Saicharan *et al.* (2022) <sup>[13]</sup>, Tandekar *et al.* (2023) <sup>[15]</sup>.

**Table 1:** Genetic variability parameters for yield and yield attributing traits in soybean

| Crosses                                  | Mean  | Min.  | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
|------------------------------------------|-------|-------|--------|---------|---------|-----------------------|---------------------------|
| <b>Days to 50% flowering</b>             |       |       |        |         |         |                       |                           |
| NRC 127 x KDS 11-49                      | 39.86 | 38.40 | 41.90  | 4.75    | 4.28    | 81.09                 | 7.93                      |
| NRC 127 x RSC 10-46                      | 40.96 | 39.10 | 43.40  | 5.58    | 4.34    | 60.57                 | 6.96                      |
| NRC 127 x NRC 12                         | 40.86 | 38.40 | 42.70  | 5.69    | 4.25    | 55.83                 | 6.54                      |
| NRC 127 x RSC 10-52                      | 40.41 | 39.10 | 41.53  | 3.97    | 2.90    | 53.40                 | 4.37                      |
| NRC 127 x RSC 11-42                      | 41.24 | 38.80 | 44.10  | 6.87    | 5.30    | 59.58                 | 8.43                      |
| PS 1689 x RSC 10-46                      | 40.84 | 39.90 | 41.50  | 4.08    | 2.52    | 13.81                 | 1.16                      |
| PS 1689 x RSC 11-42                      | 40.42 | 38.50 | 42.10  | 5.59    | 4.01    | 51.51                 | 2.40                      |
| Crosses                                  | Mean  | Min.  | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance % mean    |
| <b>Days to maturity</b>                  |       |       |        |         |         |                       |                           |
| NRC 127 x KDS 11-49                      | 94.64 | 92.20 | 99.10  | 4.31    | 2.32    | 28.87                 | 2.57                      |
| NRC 127 x RSC 10-46                      | 93.22 | 87.70 | 97.60  | 5.29    | 4.52    | 72.87                 | 7.95                      |
| NRC 127 x NRC 12                         | 94.42 | 89.40 | 101.00 | 6.45    | 6.11    | 89.69                 | 11.92                     |
| NRC 127 x RSC 10-52                      | 92.94 | 91.50 | 95.00  | 2.19    | 0.95    | 19.02                 | 0.86                      |
| NRC 127 x RSC 11-42                      | 92.46 | 89.60 | 94.60  | 3.07    | 2.51    | 66.90                 | 4.24                      |
| PS 1689 x RSC 10-46                      | 89.81 | 86.20 | 93.36  | 5.26    | 2.95    | 31.41                 | 3.40                      |
| PS 1689 x RSC 11-42                      | 94.58 | 90.50 | 101.20 | 5.69    | 4.64    | 66.65                 | 7.81                      |
| Crosses                                  | Mean  | Min.  | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
| <b>Plant height (cm)</b>                 |       |       |        |         |         |                       |                           |
| NRC 127 x KDS 11-49                      | 44.54 | 31.50 | 51.00  | 24.44   | 24.09   | 97.15                 | 48.91                     |
| NRC 127 x RSC 10-46                      | 42.68 | 29.80 | 55.60  | 32.33   | 31.00   | 91.94                 | 61.24                     |
| NRC 127 x NRC 12                         | 42.34 | 31.20 | 53.80  | 24.42   | 23.03   | 88.87                 | 44.71                     |
| NRC 127 x RSC 10-52                      | 42.26 | 31.30 | 59.40  | 30.87   | 30.67   | 98.69                 | 62.75                     |
| NRC 127 x RSC 11-42                      | 41.72 | 34.80 | 47.90  | 18.94   | 18.20   | 92.37                 | 36.04                     |
| PS 1689 x RSC 10-46                      | 44.02 | 36.80 | 52.00  | 18.59   | 18.48   | 98.87                 | 37.86                     |
| PS 1689 x RSC 11-42                      | 45.58 | 37.90 | 53.50  | 18.55   | 18.01   | 94.33                 | 36.14                     |
| Crosses                                  | Mean  | Min.  | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
| <b>No. of primary branches per plant</b> |       |       |        |         |         |                       |                           |
| NRC 127 x KDS 11-49                      | 3.42  | 2.40  | 4.40   | 29.37   | 27.32   | 86.51                 | 52.34                     |
| NRC 127 x RSC 10-46                      | 3.22  | 2.75  | 3.60   | 12.87   | 12.15   | 89.08                 | 23.62                     |
| NRC 127 x NRC 12                         | 2.95  | 1.95  | 4.20   | 35.94   | 35.12   | 95.51                 | 70.71                     |
| NRC 127 x RSC 10-52                      | 3.80  | 2.30  | 5.10   | 36.80   | 35.83   | 94.79                 | 71.86                     |
| NRC 127 x RSC 11-42                      | 3.66  | 2.50  | 5.25   | 35.50   | 34.99   | 97.14                 | 71.04                     |
| PS 1689 x RSC 10-46                      | 3.42  | 2.28  | 5.30   | 43.89   | 42.84   | 95.26                 | 86.14                     |
| PS 1689 x RSC 11-42                      | 3.63  | 2.80  | 4.70   | 25.56   | 24.68   | 93.26                 | 49.10                     |

| Crosses                        | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
|--------------------------------|-------|-------|-------|---------|---------|-----------------------|---------------------------|
| <b>No. of pods per plant</b>   |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49            | 79.82 | 66.00 | 90.20 | 18.56   | 17.67   | 90.62                 | 34.65                     |
| NRC 127 x RSC 10-46            | 77.96 | 68.90 | 92.50 | 16.24   | 15.82   | 94.87                 | 31.74                     |
| NRC 127 x NRC 12               | 83.25 | 75.30 | 90.00 | 9.14    | 7.47    | 66.88                 | 12.59                     |
| NRC 127 x RSC 10-52            | 76.90 | 62.90 | 93.20 | 18.76   | 16.63   | 78.51                 | 30.34                     |
| NRC 127 x RSC 11-42            | 78.90 | 63.80 | 98.40 | 20.91   | 20.39   | 95.09                 | 40.95                     |
| PS 1689 x RSC 10-46            | 83.59 | 69.70 | 96.80 | 16.37   | 14.69   | 80.43                 | 27.13                     |
| PS 1689 x RSC 11-42            | 81.50 | 66.80 | 99.20 | 18.65   | 16.64   | 79.66                 | 30.60                     |
| Crosses                        | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> (%)    | Genetic advance as % mean |
| <b>Pod bearing length (cm)</b> |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49            | 40.90 | 37.70 | 45.90 | 11.04   | 9.21    | 69.49                 | 15.81                     |
| NRC 127 x RSC 10-46            | 43.43 | 36.00 | 50.40 | 17.17   | 16.57   | 93.19                 | 32.96                     |
| NRC 127 x NRC 12               | 42.70 | 34.90 | 50.10 | 15.87   | 15.79   | 98.91                 | 32.34                     |
| NRC 127 x RSC 10-52            | 43.82 | 35.70 | 53.70 | 22.12   | 21.73   | 96.47                 | 43.97                     |
| NRC 127 x RSC 11-42            | 43.30 | 37.60 | 50.60 | 14.98   | 12.44   | 68.98                 | 21.29                     |
| PS 1689 x RSC 10-46            | 41.68 | 36.10 | 46.70 | 12.76   | 9.23    | 52.34                 | 13.76                     |
| PS 1689 x RSC 11-42            | 40.24 | 35.00 | 47.70 | 15.63   | 12.26   | 61.50                 | 19.80                     |

| Crosses                        | Mean   | Min.   | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
|--------------------------------|--------|--------|--------|---------|---------|-----------------------|---------------------------|
| <b>Number of seeds per pod</b> |        |        |        |         |         |                       |                           |
| NRC 127 x KDS 11-49            | 2.59   | 2.47   | 2.77   | 5.54    | 4.74    | 73.33                 | 8.37                      |
| NRC 127 x RSC 10-46            | 2.57   | 2.40   | 2.80   | 8.46    | 6.09    | 51.72                 | 9.02                      |
| NRC 127 x NRC 12               | 2.63   | 2.61   | 2.68   | 5.09    | 3.19    | 39.37                 | 4.13                      |
| NRC 127 x RSC 10-52            | 2.71   | 2.60   | 2.82   | 4.68    | 1.82    | 15.18                 | 1.46                      |
| NRC 127 x RSC 11-42            | 2.61   | 2.48   | 2.66   | 4.15    | 2.52    | 36.90                 | 3.15                      |
| PS 1689 x RSC 10-46            | 2.67   | 2.55   | 2.90   | 6.39    | 5.96    | 87.12                 | 11.46                     |
| PS 1689 x RSC 11-42            | 2.65   | 2.42   | 2.78   | 7.29    | 5.77    | 62.54                 | 9.39                      |
| Crosses                        | Mean   | Min.   | Max.   | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
| <b>No. of Seeds per Plant</b>  |        |        |        |         |         |                       |                           |
| NRC 127 x KDS 11-49            | 157.06 | 125.80 | 189.90 | 23.56   | 21.79   | 85.57                 | 41.52                     |
| NRC 127 x RSC 10-46            | 164.98 | 114.70 | 211.50 | 30.00   | 29.51   | 96.79                 | 59.81                     |
| NRC 127 x NRC 12               | 169.34 | 142.50 | 197.70 | 18.86   | 18.60   | 97.26                 | 37.79                     |
| NRC 127 x RSC 10-52            | 164.52 | 134.30 | 204.50 | 23.91   | 22.76   | 90.63                 | 44.64                     |
| NRC 127 x RSC 11-42            | 165.14 | 138.00 | 204.50 | 23.23   | 21.36   | 84.54                 | 40.45                     |
| PS 1689 x RSC 10-46            | 168.33 | 137.30 | 200.10 | 21.51   | 18.17   | 71.35                 | 31.61                     |
| PS 1689 x RSC 11-42            | 171.34 | 135.10 | 203.40 | 22.79   | 21.95   | 92.73                 | 43.53                     |

| Crosses                    | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
|----------------------------|-------|-------|-------|---------|---------|-----------------------|---------------------------|
| <b>100 seed weight (g)</b> |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49        | 10.39 | 9.43  | 11.19 | 9.14    | 7.56    | 68.45                 | 12.89                     |
| NRC 127 x RSC 10-46        | 10.64 | 9.60  | 11.80 | 10.60   | 9.20    | 75.37                 | 16.45                     |
| NRC 127 x NRC 12           | 10.64 | 9.38  | 12.50 | 13.38   | 13.12   | 96.15                 | 26.49                     |
| NRC 127 x RSC 10-52        | 10.83 | 9.40  | 11.61 | 10.24   | 9.24    | 81.39                 | 17.16                     |
| NRC 127 x RSC 11-42        | 10.39 | 9.20  | 11.30 | 12.46   | 12.19   | 95.79                 | 24.58                     |
| PS 1689 x RSC 10-46        | 10.37 | 9.80  | 11.20 | 6.71    | 5.66    | 71.11                 | 9.83                      |
| PS 1689 x RSC 11-42        | 10.62 | 9.61  | 11.40 | 8.37    | 7.52    | 80.75                 | 13.93                     |
| Crosses                    | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
| <b>Protein content (%)</b> |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49        | 39.75 | 39.47 | 40.06 | 1.00    | 0.14    | 1.95                  | 0.04                      |
| NRC 127 x RSC 10-46        | 39.75 | 38.91 | 40.20 | 1.60    | 1.42    | 78.79                 | 2.60                      |
| NRC 127 x NRC 12           | 39.86 | 39.50 | 40.60 | 1.61    | 0.99    | 38.00                 | 1.26                      |
| NRC 127 x RSC 10-52        | 39.60 | 38.95 | 40.40 | 2.29    | 1.67    | 52.98                 | 2.50                      |
| NRC 127 x RSC 11-42        | 39.95 | 39.60 | 40.10 | 0.83    | 0.41    | 24.46                 | 0.42                      |
| PS 1689 x RSC 10-46        | 40.26 | 39.70 | 40.70 | 1.55    | 0.40    | 6.57                  | 0.21                      |
| PS 1689 x RSC 11-42        | 39.94 | 39.40 | 40.70 | 1.93    | 1.59    | 67.68                 | 2.70                      |

| Crosses                         | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
|---------------------------------|-------|-------|-------|---------|---------|-----------------------|---------------------------|
| <b>Oil content (%)</b>          |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49             | 18.29 | 17.85 | 18.55 | 2.05    | 1.65    | 64.92                 | 2.74                      |
| NRC 127 x RSC 10-46             | 18.50 | 18.23 | 18.70 | 2.02    | 0.54    | 7.02                  | 0.29                      |
| NRC 127 x NRC 12                | 18.83 | 17.91 | 19.45 | 4.29    | 3.57    | 69.47                 | 6.14                      |
| NRC 127 x RSC 10-52             | 18.78 | 18.30 | 19.50 | 3.29    | 2.43    | 54.64                 | 3.70                      |
| NRC 127 x RSC 11-42             | 18.78 | 18.55 | 19.20 | 2.11    | 0.91    | 18.47                 | 0.80                      |
| PS 1689 x RSC 10-46             | 18.89 | 18.15 | 20.10 | 4.87    | 4.72    | 94.11                 | 9.43                      |
| PS 1689 x RSC 11-42             | 19.02 | 17.93 | 19.80 | 5.24    | 4.18    | 63.55                 | 6.86                      |
| Crosses                         | Mean  | Min.  | Max.  | PCV (%) | GCV (%) | h <sup>2</sup> bs (%) | Genetic advance as % mean |
| <b>Seed yield per plant (g)</b> |       |       |       |         |         |                       |                           |
| NRC 127 x KDS 11-49             | 17.62 | 12.00 | 20.67 | 23.33   | 22.39   | 92.16                 | 44.28                     |
| NRC 127 x RSC 10-46             | 17.09 | 11.70 | 22.20 | 31.00   | 27.31   | 77.63                 | 49.57                     |
| NRC 127 x NRC 12                | 19.04 | 13.50 | 22.40 | 22.73   | 20.29   | 79.66                 | 37.30                     |
| NRC 127 x RSC 10-52             | 19.44 | 17.30 | 21.80 | 10.88   | 9.64    | 78.49                 | 17.60                     |
| NRC 127 x RSC 11-42             | 18.80 | 17.80 | 20.30 | 7.86    | 4.03    | 26.32                 | 4.26                      |
| PS 1689 x RSC 10-46             | 17.48 | 11.20 | 19.90 | 25.83   | 25.27   | 95.75                 | 50.94                     |
| PS 1689 x RSC 11-42             | 17.80 | 12.80 | 19.70 | 20.13   | 18.85   | 87.72                 | 36.38                     |

## Conclusion

The study revealed considerable genetic variability among the evaluated crosses for several important yield and yield-related traits. The phenotypic coefficient of variation (PCV) was generally slightly higher than the genotypic coefficient of variation (GCV), indicating minimal environmental influence and a predominant role of genetic factors in trait expression. Moderate to high genetic variation was observed for plant height, number of primary branches per plant, number of pods per plant, pod bearing length, number of seeds per plant, 100-seed weight, and seed yield per plant in most crosses. However, traits such as days to 50% flowering, days to maturity, number of seeds per pod, protein content and oil content exhibited low to moderate variability, reflecting limited genetic diversity. High heritability coupled with high genetic advance as a percentage of mean was recorded for major yield-contributing traits, suggesting the predominance of additive gene action and the effectiveness of direct selection. Therefore, these traits can be reliably improved through selection to develop high-yielding and genetically superior genotypes.

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## References

1. Bhuvra RB, Babariya CA. Genetic variability, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill). *Inter J Agric Plant Sci.* 2020;4(2):14-18.
2. Bairagi V, Mishra S, Sen R, Dixit S, Tyagi DB. Assessment of genetic variability in soybean (*Glycine max* (L.) Merrill). *Biol Forum-An Int J.* 2023;15(5):258-263.
3. Fufa WG, Nepir G. Assessment of genetic variability, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill) genotypes at Assosa, Western Ethiopia. *Asian J Biol Sci.* 2025;18(1):83-92.
4. Guleria H, Kumar P, Jyoti B, Kumar A, Paliwal A, Paliwal A. Genetic variability and correlation analysis in soybean (*Glycine max* (L.) Merrill) genotypes. *Int J Chem Stud.* 2019;7(1):1928-1932.
5. Jandong EA, Uguru MI, Okechukwu EC. Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). *Afr J Biotechnol.* 2020;19(4):201-206.
6. Jain RK, Joshi A, Chaudhary HR, Dashora A, Khatik CL. Study on genetic variability, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill). *Legume Res.* 2017;1-6.
7. Kumari S, Meena BL, Sharma SC, Koli NR, Tak Y, Fozdar P. Study on genetic variability parameters in soybean (*Glycine max* (L.) Merrill) genotypes. *J Agric Ecol.* 2022;14(2):72-76.
8. Kalamkhede P, Rathod MK, Gawali K, Sapkal D, Gangasagar P, Kharche KA. Estimation of genetic variability, heritability, and genetic advance in soybean (*Glycine max* (L.) Merrill) genotypes. *Int J Res Agron.* 2025;8(8):679-682.
9. Paulos M, Kindie B. Agro-morphological trait characterization of selected soybean (*Glycine max* (L.) Merrill) accessions at Dabus. *Indian J Adv Bot.* 2025;5(1):2582-9475.
10. Sonkamble P, Nandanwar RS, Sakhare SB, Jadhav PV, Varghese PV. Genetic variability for yield and its component traits in grain and vegetable type soybean. *Int J Chem Stud.* 2020;8(6):2287-2290.
11. Susanto GWA, Harnowo D, Soehendi R, Prayogo Y, Purwantoro MJ, Karyawati AS. Genetic parameters estimation of high yielding and large seed size of soybean (*Glycine max* (L.) Merrill) genotypes. *Legume Res.* 2023;46(5):562-567.
12. Singh M, Nag SK, Yadav RK. Determination of gene effects and inheritance of genes for various generations of soybean crosses (*Glycine max* (L.) Merrill). *Biol Forum-An Int J.* 2023;15(4):243-245.
13. Saicharan G, Dhuppe MV, Rathod ST, Sargar PR, Rao MV. Studies on genetic variability, heritability, and genetic advance for yield and yield contributing traits in soybean (*Glycine max* (L.) Merrill). *Pharm Innov J.* 2022;11(12):3131-3133.
14. Sidramappa, Konda CR, Shobharani M. Genetic variability studies in soybean. *Int J Curr Microbiol Appl Sci.* 2019;8(12):2991-2994.
15. Tandekar K, Nag SK, Shrivastava R, Gupta P, Thakur K. Studies on genetic variability of metric traits in germplasm of soybean (*Glycine max* L. Merrill). *Biol Forum-An Int J.* 2023;15(8):159-164.