

## Deciphering of genetic variability, heritability and genetic advance for yield enhancement in groundnut (*Arachis hypogaea* L.)

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### Abstract

A study was conducted with 33 genotypes of groundnut which includes 29 advanced breeding lines and four checks to evaluate genetic variability, heritability, and genetic advance for 15 yield and yield component traits. Analysis of variance revealed significant differences among genotypes for all traits, indicating substantial genetic variability. PCV, GCV, heritability (broad-sense) and GAM revealed that, highest variability recorded for number of secondary branches plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, number of matured pods plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>(g), pod yield plant<sup>-1</sup> (g) and plant height (cm) indicating a wide range of genetic variability and substantial scope for effective selection to improve these traits. High heritability coupled with high GAM (additive gene action) Observed for number of secondary branches plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, number of matured pods plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>, plant height(cm), pod yield plant<sup>-1</sup>(g), dry haulm yield plant<sup>-1</sup>(g) and harvest index(%) the preponderance of additive gene action implying that environmental influence is minimal, making these traits amenable to improvement through simple selection. These traits were identified as promising selection criteria for improving pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup> in future groundnut breeding programs.

**Keywords:** Groundnut, PCV (phenotypic coefficient of variation), GCV (genotypic coefficient of variation), heritability, GAM (genetic advance as percent of mean) and ANOVA (analysis of variance)

### Introduction

Groundnut (*Arachis hypogaea* L, 2n = 4x = 40), belonging to the family Fabaceae, which is highly self-pollinated legume crop native to the eastern foothills of the Andes in southern Bolivia and northern Argentina. It is widely recognized as “The King of Oilseeds” owing to its substantial contribution to global edible oil production. It ranks as the fifth most important oilseed crop in the world after oil palm, soybean, rapeseed, and sunflower. Besides being a rich source of high-quality edible oil (45–55%) and protein (22–30%), groundnut kernels also contain significant amounts of carbohydrates, vitamins (E, K, and B-complex), minerals and dietary fiber. The crop provides multiple benefits through kernels, oil, industrial by-products, and haulms, which are used as nutritious fodder and green manure.

Globally, groundnut is cultivated over an area of 37.3 million hectares with a production of 55.9 million tonnes and productivity of 1,656 kg/ha (Anonymous, 2024-25 a) <sup>[1]</sup>. China, India, Nigeria, and the USA are the major producing countries. In India, it occupies 5.4 million hectares with a production of 11.31 million tonnes and productivity of 2,097 kg/ha. The crop is particularly important in Andhra Pradesh, where it is grown over 0.35 million hectares, yielding 0.36 million tonnes with a productivity of 1,041 kg/ha, making it the second most important crop after paddy in the state.

Owing to its autogamous nature, groundnut possesses a narrow genetic base, which limits the scope for further improvement. The success of any crop breeding programme largely depends on the extent of genetic variability present

in the germplasm. Therefore, assessment of genetic variability using quantitative and qualitative traits is fundamental for effective selection. Genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance provide critical information on the nature of gene action and help identify traits amenable to selection.

The present study was undertaken to evaluate the extent of genetic variability, heritability, and genetic advance among groundnut genotypes for yield and its component traits, with the aim of identifying superior genotypes for future breeding programmes.

### Material and Methods

The experiment was carried out during *rabi*, 2025-26 at dry land farm, S.V. Agricultural College, Tirupati, Acharya N. G. Ranga Agricultural University, Andhra Pradesh situated in Southern Agro- climatic Zone of Andhra Pradesh, India located at an altitude of 182.9 m above from mean sea level, 13° N latitude and 79° E longitude. The experimental material comprised of 33 genotypes of groundnut which includes 29 advanced breeding lines and four checks obtained from ARS, Kadiri. The experimental material was evaluated by employing randomized block design with two replications. The crop was sown at a spacing of 30 cm x 10 cm. Standard agronomic practices recommended for groundnut cultivation were also followed to ensure optimal crop growth and development. The observations were recorded on for 15 yield and its contributing traits viz, Initial plant stand (No.), Final plant stand (No.), Days to 50% flowering, Days to maturity, Plant height (cm), Number of

primary branches plant<sup>-1</sup>, Number of secondary branches plant<sup>-1</sup>, Number of mature pods plant<sup>-1</sup>, Pod yield plant<sup>-1</sup> (g), Kernel yield plant<sup>-1</sup>(g), Dry haulm yield plant<sup>-1</sup>(g), Harvest index(%), Shelling(%), Sound mature kernel (%) and Hundred kernel weight (g). The statistical analytics was performed in R software (version 4.6.0), variability package (Singh, R.K. and Chaudhary, B.D, 1977).

## Results and Discussion

Analysis of variance (Panse and Sukhatme) was performed for 33 genotypes of groundnut which includes 29 advanced breeding lines and four checks for 15 yield and its component traits. ANOVA revealed that the mean sum of squares was significant for all the traits indicates high degree of genetic variability was present among the genotypes (Table 1).

**Table 1:** ANOVA for 15 traits among 33 groundnut genotypes during rabi 2025-26

| S. No | Source of variation                              | Mean sum of squares  |                     |                 |
|-------|--------------------------------------------------|----------------------|---------------------|-----------------|
|       |                                                  | Replication (df = 1) | Treatment (df = 32) | Error (df = 32) |
| 1     | Initial plant stand (No.)                        | 23.05                | 23.65**             | 8.01            |
| 2     | Final plant stand (No.)                          | 23.05                | 25.63**             | 7.01            |
| 3     | Days to 50% flowering*                           | 0.55                 | 8.42**              | 1.36            |
| 4     | Days to maturity *                               | 5.47                 | 88.66**             | 5.22            |
| 5     | Plant height (cm)                                | 16.10                | 70.11**             | 4.14            |
| 6     | Number of primary branches plant <sup>-1</sup>   | 0.53                 | 3.81**              | 0.19            |
| 7     | Number of secondary branches plant <sup>-1</sup> | 0.07                 | 1.41**              | 0.06            |
| 8     | Number of matured pods plant <sup>-1</sup>       | 3.14                 | 59.63**             | 4.16            |
| 9     | Pod yield plant <sup>-1</sup> (g)                | 13.96                | 47.37**             | 7.65            |
| 10    | Dry haulm yield plant <sup>-1</sup> (g)          | 0.36                 | 57.22**             | 8.29            |
| 11    | Harvest index (%)                                | 3.26                 | 50.13**             | 1.073           |
| 12    | Shelling (%)                                     | 5.70                 | 26.22**             | 11.31           |
| 13    | Kernel yield plant <sup>-1</sup> (g)             | 10.81                | 26.47**             | 3.33            |
| 14    | Sound mature Kernel (%)                          | 17.40                | 23.86**             | 4.24            |
| 15    | Hundred Kernel weight (g)                        | 23.68                | 44.77**             | 11.46           |

df = Degrees of freedom; \* Significance at 5%; \*\* Significance at 1%

The analysis on genetic variability (Table 2) revealed that PCV estimates were higher than the corresponding GCV values for all the traits which indicates that influence of environment on trait expression (Table 2). High PCV and GCV estimates (>20%) were recorded for number of secondary branches plant<sup>-1</sup> (29.52 and 28.19) with the less differences between PCV and GCV estimates indicating a preponderance of additive gene action and low environmental influence and scope for direct selection for improvement of this trait. These results agreed with Sridevi *et al.* (2022) <sup>[14]</sup>.

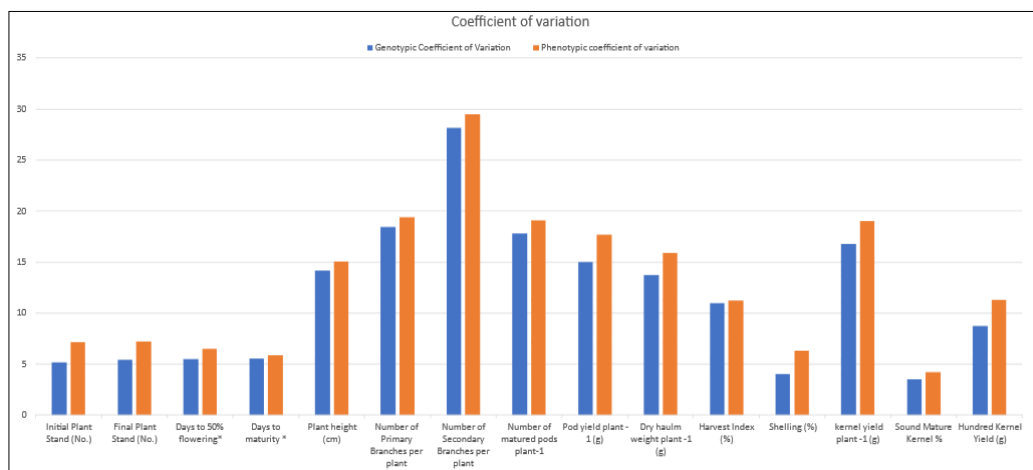
The moderate PCV and GCV were exhibited by the traits viz, number of primary branches plant<sup>-1</sup>(19.41 and 18.47), number of mature pods plant<sup>-1</sup> (19.11 and 17.82), pod yield plant<sup>-1</sup> (17.68 and 15.02), kernel yield plant<sup>-1</sup> (16.78 and 14.90), plant height (15.07 and 14.20), dry haulm yield plant<sup>-1</sup> (15.89 and 13.73) and harvest index (11.23 and 10.99) indicates there is substantial potential for improvement of these traits through direction selection processes as the existence of both additive and non-additive gene action. Similar findings are reported by Poojitha *et al.* (2024) <sup>[11]</sup>, Sanjeev Sharma *et al.* (2025) <sup>[12]</sup> and Yami *et al.* (2025) <sup>[15]</sup> for the traits hundred kernel weight, number of mature pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup>(Table 2).

The low estimates of PCV and GCV were recorded by hundred kernel weight (11.32 and 8.72), days to maturity (5.89 and 5.55), days to 50% flowering (6.49 and 5.51), final plant stand (7.20 and 5.44), initial plant stand (7.14 and 5.17) and shelling percent (4.22 and 3.53) (Table 2). This

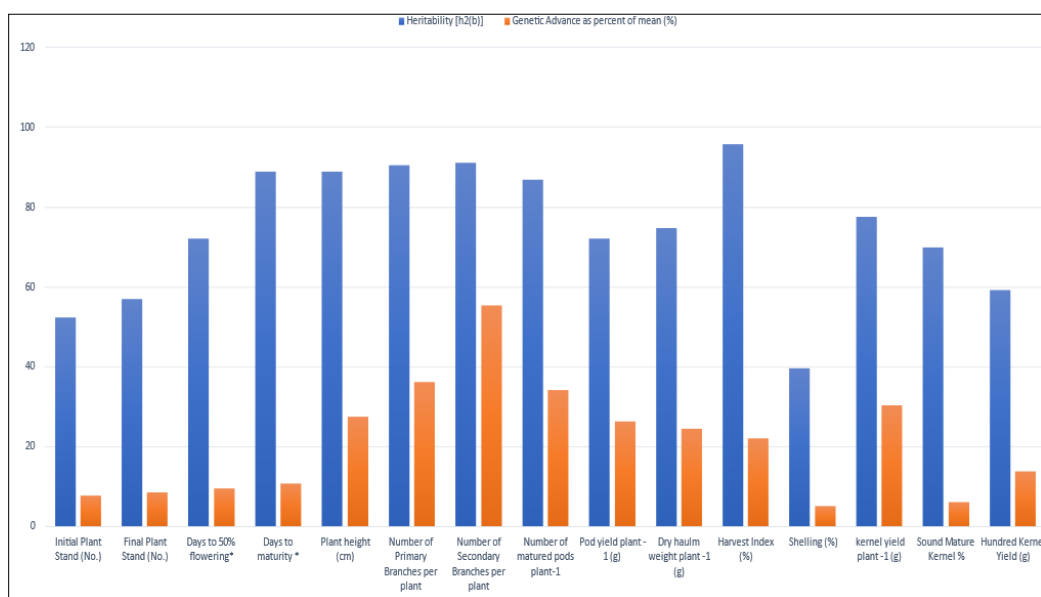
implies the presence of non-additive gene action and hybridization followed by selection in the advanced generations is fruitful for improvement of these traits. These results are in accordance with Poojitha *et al.* (2024) <sup>[11]</sup> and Yami *et al.* (2025) <sup>[15]</sup>.

The genotypic coefficient of variation (GCV) by itself does not provide a reliable estimate of the potential genetic gain achievable through phenotypic-based selection unless the heritability of the trait is known (Burton G.W.). Heritability measures the proportion of total phenotypic variation that is attributable to genetic factors, which is crucial for predicting the effectiveness of selection. Additionally, genetic advance expressed as a percentage of the mean (GAM) quantifies the expected improvement in the trait after selection. Together, heritability and GAM serve as key parameters for guiding crop improvement programs by identifying traits that can respond well to selection under given environmental conditions.

In the present research, heritability estimates for the traits evaluated was ranged from 39.73% to 95.81%, while GAM ranged from 5.19% to 55.46% (Figure 2). High heritability was shown by the traits viz, days to 50% flowering (72.22%), days to maturity (88.89%), plant height (88.85%), number of primary branches plant<sup>-1</sup> (90.54%), number of secondary branches plant<sup>-1</sup> (91.21%), number of mature pods plant<sup>-1</sup> (86.95%), dry haulm yield plant<sup>-1</sup> (74.67%), harvest index (95.81%), kernel yield plant<sup>-1</sup> (77.62%), sound mature kernel (69.82%) and pod yield plant<sup>-1</sup> (72.19%)(Table 2).



**Fig 1:** Genotypic and phenotypic coefficient of variation for yield and its component traits among advanced breeding lines of groundnut



**Fig 2:** Heritability and Genetic Advance as Percent of Mean (GAM) for Yield and Its Component Traits among Advanced Breeding Lines of Groundnut

However, high genetic advance as per cent of mean were reported by plant height (27.58%), number of primary branches plant<sup>-1</sup> (36.20%), number of secondary branches plant<sup>-1</sup> (55.46%), number of mature pods plant<sup>-1</sup> (34.23%), dry haulm yield plant<sup>-1</sup> (24.44%), harvest index (22.17%), kernel yield plant<sup>-1</sup> (30.44%) and pod yield plant<sup>-1</sup> (26.29%) (Table 2).

The combined estimates of heritability and genetic advance provide a more accurate assessment of the potential genetic gain through selection (Johnson *et al.*, 1955) [6]. High heritability coupled with high genetic advance as a percentage of the mean (GAM) was observed for plant height (88.85% and 27.58%), number of primary branches plant<sup>-1</sup> (90.54% and 36.20%), number of secondary branches plant<sup>-1</sup> (91.21% and 55.46%), number of mature pods plant<sup>-1</sup> (86.95% and 34.23%), dry haulm yield plant<sup>-1</sup> (74.67 % and 24.44%), harvest index (95.81% and 22.17%), kernel yield plant<sup>-1</sup> (77.62% and 30.44%) and pod yield plant<sup>-1</sup> (72.19% and 26.29%) which indicates that these traits are governed by additive gene effects and can response to selection effectively. Similar findings were reported by Poojitha *et al.* (2024) [11], Yami *et al.* (2025) [15] and Bindhu *et al.* (2026) [8]. Prioritizing the selection of these traits

would be beneficial for rapid improvement of pod yield in groundnut.

Higher estimates of heritability with moderate GAM values were recorded for the trait days to maturity (88.89% and 10.78) which indicates the influence of both additive and non-additive genes effects in their inheritance. These results are earlier reported by Poojitha *et al.* (2024) [11] and Yami *et al.* (2025) [15].

Meanwhile, moderate to high heritability coupled with low GAM was exhibited by the hundred kernel weight (59.25% and 6.08%) and moderate to high heritability coupled with low GAM were exhibited by the traits such as, initial plant stand (52.39% and 7.70%), final plant stand (57.03% and 8.46%), days to 50 % flowering (72.22% and 9.65%), shelling percent (39.73% and 5.19%) and sound mature kernel (69.82% and 6.07%)(Table 2). Similar results are reported by Kulheri *et al.* (2022) [9] and Kannappan *et al.* (2022) [7]. Conversely, traits showing high heritability but low genetic advance suggest a major role of non-additive gene action and environmental influence in their inheritance. To harness this non-additive genetic variance effectively, for improvement of such traits may exploited from hybridization followed by selection in advanced generations.

**Table 2:** Magnitude of Variability, Heritability and Genetic Advance for 15 traits among 33 genotypes of groundnut

| S. No | Trait                                            | Range  |        | Mean   | Variance  |            | Coefficient of variation (%) |            | Heritability [h <sup>2</sup> (b)] (%) | Genetic advance (GA) | Genetic advance as per cent of mean (%) |
|-------|--------------------------------------------------|--------|--------|--------|-----------|------------|------------------------------|------------|---------------------------------------|----------------------|-----------------------------------------|
|       |                                                  | Min.   | Max.   |        | Genotypic | Phenotypic | Genotypic                    | Phenotypic |                                       |                      |                                         |
| 1.    | Initial plant stand (No.)                        | 46.50  | 64.00  | 57.47  | 8.82      | 16.83      | 5.17                         | 7.14       | 52.39                                 | 4.42                 | 7.70                                    |
| 2.    | Final plant stand (No.)                          | 45.00  | 62.50  | 56.14  | 9.31      | 16.32      | 5.44                         | 7.20       | 57.03                                 | 4.75                 | 8.46                                    |
| 3.    | Days to 50% flowering*                           | 31.00  | 37.50  | 34.09  | 3.53      | 4.89       | 5.51                         | 6.49       | 72.22                                 | 3.29                 | 9.65                                    |
| 4.    | Days to maturity *                               | 105.00 | 127.50 | 116.38 | 41.72     | 46.94      | 5.55                         | 5.89       | 88.89                                 | 12.54                | 10.78                                   |
| 5.    | Plant height (cm)                                | 29.20  | 54.50  | 40.44  | 32.96     | 37.12      | 14.20                        | 15.07      | 88.85                                 | 11.15                | 27.58                                   |
| 6.    | Number of primary branches plant <sup>-1</sup>   | 5.40   | 10.85  | 7.28   | 1.81      | 1.99       | 18.47                        | 19.41      | 90.54                                 | 2.64                 | 36.20                                   |
| 7.    | Number of secondary branches plant <sup>-1</sup> | 1.70   | 4.90   | 2.91   | 0.67      | 0.73       | 28.19                        | 29.52      | 91.21                                 | 1.61                 | 55.46                                   |
| 8.    | Number of matured pods plant <sup>-1</sup>       | 21.10  | 44.70  | 29.59  | 27.37     | 31.90      | 17.82                        | 19.11      | 86.95                                 | 10.12                | 34.23                                   |
| 9.    | Pod yield plant <sup>-1</sup> (g)                | 21.80  | 41.15  | 30.24  | 19.86     | 27.51      | 15.02                        | 17.68      | 72.19                                 | 7.80                 | 26.29                                   |
| 10.   | Dry haulm yield plant <sup>-1</sup> (g)          | 17.03  | 44.95  | 36.02  | 24.46     | 32.76      | 13.73                        | 15.89      | 74.67                                 | 8.80                 | 24.44                                   |
| 11.   | Harvest index (%)                                | 36.52  | 56.22  | 45.04  | 24.53     | 25.60      | 10.99                        | 11.23      | 95.81                                 | 9.99                 | 22.17                                   |
| 12.   | Shelling (%)                                     | 59.11  | 73.67  | 68.36  | 7.46      | 18.77      | 3.99                         | 6.33       | 39.73                                 | 3.55                 | 5.19                                    |
| 13.   | Kernel yield plant <sup>-1</sup> (g)             | 14.88  | 29.75  | 20.51  | 11.57     | 14.90      | 16.78                        | 19.04      | 77.62                                 | 6.17                 | 30.44                                   |
| 14.   | Sound mature Kernel (%)                          | 82.04  | 95.21  | 88.80  | 9.81      | 14.05      | 3.53                         | 4.22       | 69.82                                 | 5.40                 | 6.07                                    |
| 15.   | Hundred Kernel weight (g)                        | 38.51  | 54.98  | 46.82  | 16.66     | 28.11      | 8.72                         | 11.32      | 59.25                                 | 6.47                 | 13.82                                   |

In brief, the PCV, GCV, heritability (broad-sense) and GAM revealed that, highest variability recorded for number of secondary branches plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, number of matured pods plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>(g), pod yield plant<sup>-1</sup> (g) and plant height (cm) indicating a wide range of genetic variability and substantial scope for effective selection to improve these traits. High heritability coupled with high GAM (additive gene action) was observed for number of secondary branches plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, number of matured pods plant<sup>-1</sup>, kernel yield plant<sup>-1</sup> (g), plant height (cm), pod yield plant<sup>-1</sup>(g), dry haulm yield plant<sup>-1</sup> (g) and harvest index(%) the preponderance of additive gene action

implying that environmental influence is minimal, making these traits amenable to improvement through simple selection (Table 3).

High heritability with moderate GAM was recorded for days to maturity, indicating the influence of both additive and non-additive gene action. Moderate-to-high heritability with low GAM was reported for days to 50% flowering, hundred kernel weight (g), sound mature kernel (g) and shelling percent representing the major role of non-additive gene action and environmental influence (Table 3). To harness this non-additive genetic variance effectively, these traits may benefit from hybridization followed by selection in advanced generations

**Table 3:**

| Genetic parameter                                               | Traits                                                                                                                                                                                                                                                  | Breeding strategy                                           |
|-----------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|
| High h <sup>2</sup> + High GAM<br>(additive gene action)        | Secondary branches plant <sup>-1</sup> , primary branches plant <sup>-1</sup> , matured pods plant <sup>-1</sup> , kernel yield plant <sup>-1</sup> , plant height, pod yield plant <sup>-1</sup> , dry haulm yield plant <sup>-1</sup> , harvest index | Direct / simple selection                                   |
| High h <sup>2</sup> + Moderate/Low GAM<br>(both / non-additive) | Days to maturity, days to 50% flowering, hundred kernel weight, sound mature kernel, shelling %                                                                                                                                                         | Hybridization followed by selection in advanced generations |
| Moderate h <sup>2</sup> + Low GAM<br>(non-additive)             | Initial plant stand, final plant stand                                                                                                                                                                                                                  | Limited gain; selection less effective                      |

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