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HH Maru
Ph.D. Scholar (Agriculture),
Department of Genetics and
Plant Breeding, College of
Agriculture, Junagadh
Agricultural University,
Junagadh Gujarat, India

Dr. RB Madariya
Professor and Head,
Department of Genetics and
Plant Breeding, College of
Agriculture, Mota Bhandariya,
Junagadh Agricultural
University, Junagadh,
Gujarat, India

Dr. GK Sapara
Assistant Research Scientist,
Main Oilseeds Research
Station, Junagadh Agricultural
University, Junagadh,
Gujarat, India

Dr. CJ Rajani
Assistant Research Scientist,
Main Oilseeds Research
Station, Junagadh Agricultural
University, Junagadh,
Gujarat, India

Corresponding Author:
HH Maru
Ph.D. Scholar (Agriculture),
Department of Genetics and
Plant Breeding, College of
Agriculture, Junagadh
Agricultural University,
Junagadh Gujarat, India

Estimation of Genetic Parameters and Selection Potential in Groundnut (*Arachis hypogaea* L.) Genotypes

HH Maru, RB Madariya, GK Sapara and CJ Rajani

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Abstract

A comprehensive genetic evaluation was conducted on seventy groundnut (*Arachis hypogaea* L.) genotypes, including eight control varieties, during the Summer-2026 season using a Randomized Complete Block Design (RCBD). Fourteen quantitative and qualitative traits were assessed to determine genetic variability, heritability and selection potential. Analysis of variance revealed highly significant genetic differences among genotypes for all traits except days to maturity, indicating substantial genetic diversity within the experimental material. High genotypic coefficient of variation (GCV) was recorded for harvest index (27.00%), with moderate GCV values for yield-contributing traits including biological yield per plant (19.05%), number of mature pods per plant (17.09%) and 100-kernel weight (16.36%). Phenotypic coefficient of variation (PCV) values was consistently higher than GCV values, with harvest index showing the highest PCV (27.77%), followed by kernel yield per plant (22.93%), number of mature pods per plant (22.06%) and biological yield per plant (24.56%), indicating good scope for effective selection. High broad-sense heritability estimates (>60%) were observed for nine traits, with harvest index showing the highest heritability (94.53%), followed by 100-kernel weight (86.05%) and sound mature kernel (82.74%). Notably, traits exhibiting both high heritability and high genetic advance as a percentage of mean—namely harvest index (54.09%), 100-kernel weight (31.27%), biological yield per plant (30.44%) and number of mature pods per plant (27.28%) demonstrated exceptional potential for phenotypic selection. These findings indicate the predominance of additive gene action and minimal environmental influence on these traits, suggesting that direct selection will be highly effective for improving groundnut productivity and its contributing attributes.

Keywords: Groundnut, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, pod yield

Introduction

Arachis hypogaea L. represents a significant economic oilseed crop on the international stage, positioning itself as the 13th most important food crop globally. The crop functions as humanity's fourth primary oil resource and third major supplier of plant-based proteins. From a botanical perspective, this species constitutes an annual herb within the Fabaceae (Leguminosae) family. The scientific nomenclature originates from Greek terminology, where *Arachis* signifies a pulse crop and *hypogaea* translates to "subterranean," highlighting the distinctive trait wherein pod maturation takes place underground. Chromosomally, groundnut exhibits an allotetraploid configuration ($2n = 4x = 40$) with a fundamental chromosome value of $x = 10$ (Stalker, 1991) [23]. The plant demonstrates cleistogamous pollination mechanisms, which results in predominantly self-fertilizing characteristics (Knauft and Wynne, 1995) [11].

Diverse geographical regions assign different terminologies to this legume. North American regions favour the "peanut," though numerous alternative appellations exist including African nut, Chinese nut, Manila nut, Kipper nut, Hawk's nut, Jar nut, Earth chestnut, Monkey nut, Goober pea, Ground pea and Ground bean (Johnson, 1964). Within India, the crop receives the traditional name mungphali. Its substantial commercial importance has earned it the prestige title "King of Oilseeds." This legume thrives across tropical, subtropical and warm temperate zones between approximately 40° N and 40° S latitude

bands. Historical evidence from phylogenetic and geographic analyses indicates the species originated in southern Bolivia along with northern Argentina (Kochert *et al.* 1996) ^[12]. The genus *Arachis* demonstrates its highest genetic variation across South America, particularly throughout western Brazil, Bolivia, Paraguay and northern Argentina, where wild relatives and ancestral variants are naturally distributed. The country's low groundnut production is mostly attributable to a lack of adoption of better varieties and uneven performance in a variety of locations, notably rainfed situations. Therefore, the creation of high-yielding cultivars with wide adaptability, fertilizer responsiveness and resistance to biotic and abiotic challenges, together with short seed dormancy, is crucial to increase output. It also has many health benefits including weight gain control (Petersen *et al.*, 2022) ^[14]., prevention of cardiovascular diseases (Feldman, 2002) ^[7]., protection against Alzheimer's disease (Vaishnavi *et al.*, 2023) ^[25], and cancer inhibition (Wang *et al.*, 2021) ^[26]. Groundnuts contain 21 - 36.4% protein, 18% carbohydrates, 36-54% fat and 100-120 grams of fibre per kg of kernels (Bonku and Yu, 2020) ^[3]. Genetic variability parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) developed by Burton and De Vane (1953) ^[4]., broad-sense heritability (h^2 bs) and genetic advance expressed as percentage of mean (GAM) formulated by Johnson *et al.* (1955) ^[10]., are essential statistical measures in plant breeding to assess genetic variation and predict selection effectiveness. The classification criteria for these parameters, established by Sivasubramanian and Menon (1973) for GCV and PCV, and Johnson *et al.* (1955) ^[10]., for heritability and GAM, enable breeders to identify traits amenable to direct phenotypic selection. Traits exhibiting high values for all four parameters indicate substantial, stable, and heritable variation suitable for improvement through conventional breeding. Understanding these genetic variability parameters is essential for developing evidence based breeding strategies and identifying priority traits for improvement in crop improvement programs, particularly in oilseed crops such as groundnut where yield and oil percent enhancement is a major breeding objective.

Materials and Methods

The research utilized 70 peanut accessions sourced from the Main Oilseed Research Station at Junagadh Agricultural University, Junagadh procured during the Summer-2026. A Randomized Block Design framework incorporating three replications formed the basis of this experimental setup. Individual genotypes were sown in solitary rows measuring 2.0 m in length with 30 cm intervals between rows and 10 cm spacing between individual plants. Standard agronomic protocols and protective measures against pests and diseases were implemented throughout the cultivation period. Data collection focused on pod yield per plant alongside various associated parameters including days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of mature pods per plant, 100-pod weight (g), kernel yield per plant (g), 100-kernel weight (g), shelling percentage (%), sound mature kernel (%), biological yield per plant (g), harvest index (%), oil content (%) and subsequent correlation analysis along with path coefficient investigation. Oil content was determined using Nuclear Magnetic Resonance methodology. Five plants from each genotype per

replication were assessed for trait evaluation, with the exception of days to 50% flowering and days to maturity which were measured at the plot level rather than individual plant basis.

$$\text{Shelling percentage (\%)} = \frac{\text{Weight of kernels (g)}}{\text{Weight of pod samples (g)}} \times 100$$

$$\text{Sound mature kernel (SMK \%)} = \frac{\text{Number of well mature kernels}}{\text{Total number of kernels}} \times 100$$

$$\text{Harvest index (\%)} = \frac{\text{Pod yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

Variance analysis following the randomized complete block design (RCBD) framework was performed for each trait utilizing the statistical approach detailed by Panse and Sukhatme (1995) ^[13]. Genotypic, phenotypic and environmental variances were estimated from the analysis of variance table following Johnson *et al.* (1955) ^[10], and genotypic and phenotypic coefficients of variation (GCV and PCV) were computed and classified according to Sivasubramanian and Menon (1973) into low (<10%), medium (10-20%) and high (>20%) categories. Broad-sense heritability (h^2 bs) was estimated following Johnson *et al.* (1955) ^[10], and classified as low (0-30%), medium (30-60%) and high ($\geq 60\%$), while genetic advance expressed as percentage of mean (GAM) was calculated using Johnson *et al.* (1955) ^[10], with categories of low (0-10%), medium (10-20%) and high ($\geq 20\%$). All statistical computations were performed utilizing R-Studio statistical software.

Results and Discussion

Analysis of variance

During the Summer-2026 season, a comprehensive evaluation of seventy groundnut genotypes including eight control varieties was executed using a Randomized Complete Block Design (RCBD). Analysis of variance (ANOVA) was performed across all fourteen quantitative and qualitative traits to assess the significance of variation among the genotypes, as detailed in Table 1. Excluding days to maturity, the mean sum of squares attributed to genotypes was highly significant for all evaluated parameters, indicating the presence of extensive genetic diversity within the experimental material across the studied traits. This substantial variability offers significant scope for developing superior, high yielding breeding lines through targeted selection for key agronomic and economic attributes.

Genotypic coefficient of variation

The genotypic coefficients of variation (GCV) for different characters are presented in Table 2. A high GCV was recorded for harvest index (27.00%). Moderate GCV values were observed for biological yield per plant (19.05%), number of mature pods per plant (17.09%), 100-kernel weight (16.36%), kernel yield per plant (16.17%), 100-pod weight (13.58%) and pod yield per plant (13.20%). In contrast, number of primary branches per plant (9.94%), plant height (8.09%), sound mature kernel (7.31%), days to 50% flowering (6.39%), shelling percentage (5.60%), oil content (2.55%) and days to maturity (1.70%) exhibited low GCV values. The classification of characters based on genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), following the criteria proposed by Sivasubramanian and Menon (1973), is presented in Table 3 and Figure 1.

Table 1: Analysis of variance (mean sum of square) for fourteen characters under study in groundnut

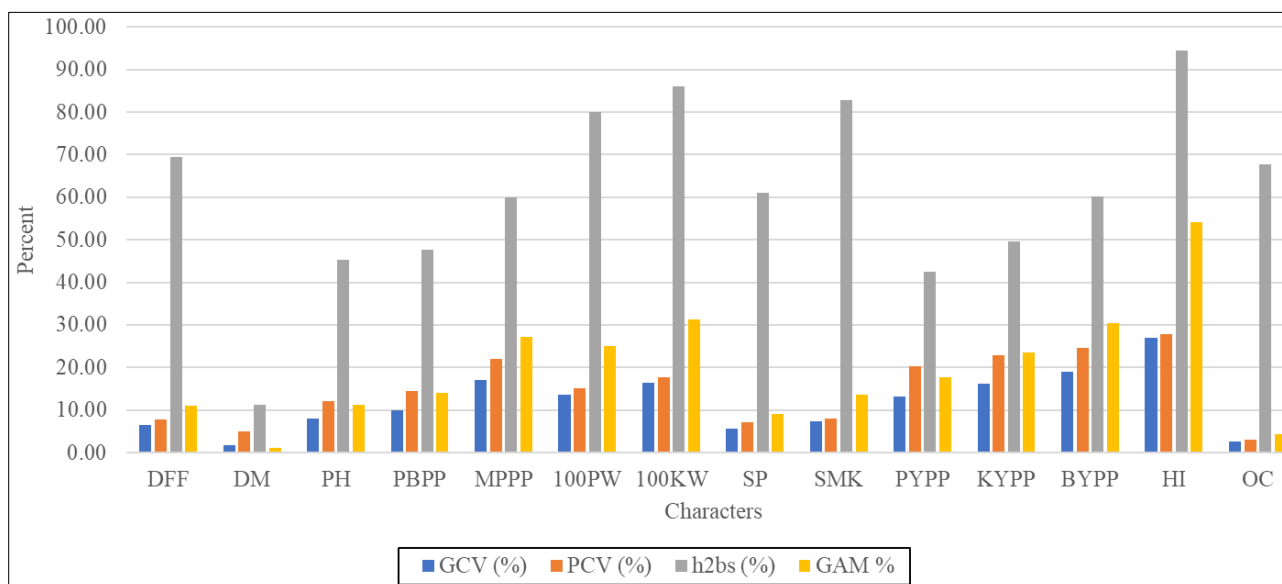
Source of Variation	d.f.	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of Primary Branches per Plant	Number of Mature Pods per Plant	100-Pod Weight (g)	100-Kernel Weight (g)
Replications	2	27.46**	137.84*	20.86**	11.13**	45.50**	1240.42**	45.93**
Genotypes	69	20.88**	43.37	11.04**	1.80**	36.84**	489.32**	95.88**
Error	138	2.67	31.41	3.16	0.48	6.69	37.79	4.91

Source of Variation	d.f.	Shelling Percentage (%)	Sound Mature Kernel (SMK) (%)	Pod Yield per Plant (g)	Kernel Yield per Plant (g)	Biological Yield per Plant (g)	Harvest Index (%)	Oil Content (%)
Replications	2	36.40**	13.92	97.04**	33.06**	424.05**	23.88	5.74**
Genotypes	69	45.07**	96.02**	20.71**	11.37**	160.86**	555.32**	6.01**
Error	138	7.91	6.24	6.44	2.86	29.08	10.50	0.82

*, ** Significant at 5% and 1% levels, respectively

Table 2: Variability parameters for pod yield and its contributing traits in groundnut

Characters	Range of variation		Grand Mean	Coefficient of range (%)	GCV (%)	PCV (%)	Heritability in broad sense (h^2_{bs}) (%)	Genetic Advance	Genetic Advance (% Mean)
	Min.	Max.							
Days to 50% flowering	31.33	43.67	38.54	16.44	6.39	7.67	69.38	4.23	10.97
Days to maturity	109.33	123.67	117.14	6.15	1.70	5.08	11.27	1.38	1.18
Plant height (cm)	15.02	25.17	20.04	25.25	8.09	12.00	45.39	2.25	11.22
Number of primary branches per plant	4.73	8.67	6.68	29.35	9.94	14.40	47.65	0.94	14.13
Number of mature pods per plant	11.40	27.87	18.54	41.93	17.09	22.06	60.03	5.06	27.28
100-pod weight (g)	64.05	124.10	90.31	31.91	13.58	15.19	79.93	22.59	25.02
100-kernel weight (g)	24.47	52.21	33.65	36.17	16.36	17.64	86.05	10.52	31.27
Shelling percentage (%)	53.46	70.77	62.89	13.92	5.60	7.16	61.01	5.66	9.00
Sound mature kernel (SMK %)	57.21	88.05	74.80	21.23	7.31	8.04	82.74	10.25	13.70
Pod yield per plant (g)	8.46	25.13	16.52	49.60	13.20	20.26	42.48	2.93	17.73
Kernel yield per plant (g)	5.33	16.83	10.41	51.87	16.17	22.93	49.69	2.44	23.48
Biological yield per plant (g)	20.86	54.30	34.78	44.48	19.05	24.56	60.17	10.59	30.44
Harvest index (%)	22.11	85.90	49.90	59.04	27.00	27.77	94.53	26.99	54.09
Oil content (%)	48.45	54.42	51.66	5.79	2.55	3.09	67.81	2.23	4.32

**Fig 1:** Comparative percent values of various variability parameters of 14 characters under study

[GCV = Genotypic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; h^2_{bs} = Heritability in broad sense; GAM = Genetic Advance (% Mean) DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); BPPP: Number of primary branches per plant; MPPP: Number of mature pods per plant; (g); 100PW: 100-

pod weight (g); 100KW: 100-kernel weight (g); KYPP: Kernel yield per plant (g); SP: Shelling percentage (%); SMK: Sound mature kernel (%); BYPP: Biological yield per plant (g); HI: Harvest index (%); OC: Oil content (%); PYPY: Pod yield per plant (g)]

Table 3: Classification of characters based on the GCV and PCV values according to Sivasubramanian and Menon (1973)

Value	Class	Classification of characters based on GCV values	Classification of characters based on PCV values
0-10	Low	Number of primary branches per plant, plant height, sound mature kernel, days to 50% flowering, shelling percentage, oil content and days to maturity	Sound mature kernel, days to 50% flowering, shelling percentage, days to maturity and oil content -
10-20	Medium	Biological yield per plant, number of mature pods per plant, 100 kernel weight, kernel yield per plant, 100 pod weight, pod yield per plant	100 kernel weight, 100 pod weight, number of primary branches per plant, plant height
20 and above	High	Harvest index	Harvest index, biological yield per plant, kernel yield per plant, number of mature pods per plant and pod yield per plant

Phenotypic coefficient of variation

The phenotypic coefficients of variation (PCV) for all characteristics are shown in Table 2. The harvest index had the greatest PCV (27.77%), followed by the number of mature pods per plant (22.06%), biological yield per plant (24.56%), kernel yield per plant (22.93%) and pod yield per plant (20.26%). Plant height (12.00%), number of primary branches per plant (14.40%), 100-kernel weight (17.64%) and 100-pod weight (15.19%) all had moderate PCV levels. Days to 50% flowering (7.67%), shelling percentage (7.16%), oil content (3.09%), days to maturity (5.08%) and sound mature kernel (8.04%) all had lower PCV values.

The high estimates of both GCV and PCV for harvest index, biological yield per plant, kernel yield per plant, number of mature pods per plant and pod yield per plant indicate the presence of substantial genetic variability and good scope for effective selection. Similar findings were reported by Chavadhari *et al.* (2017) [5], Gali *et al.* (2021) [8], Shrotri *et al.* (2021) [20], Ragiri *et al.* (2023) [16], and Yami and Abteu (2025) [28], who also observed high GCV and PCV for these traits in groundnut.

Heritability (h^2_{bs})

Broad-sense heritability is defined as the proportion of total

phenotypic variance that is attributable to genetic variance and is generally expressed as a percentage. It represents the extent to which phenotypic variation is governed by genetic factors and therefore, reflects the likelihood of transmitting a trait from parents to their offspring. High estimates of broad-sense heritability indicate that phenotypic performance is a reliable measure of genetic potential, thereby enhancing the effectiveness of selection for quantitative traits. The broad-sense heritability estimates for the different characters in the present study are presented in Table 4.2. Highest heritability estimate was recorded for harvest index (94.53%) followed by 100 kernel weight (86.05%), sound mature kernel (82.74%), 100 pod weight (79.93%), days to 50 % flowering (69.38%), oil content (67.81%), shelling percentage (61.01%), biological yield per plant (60.17%) and mature pod per plant (60.03%). The findings were akin to Solanki *et al.* (2019) [21], Sridevi *et al.* (2022) [22], Ragiri *et al.* (2023) [16], Reddy *et al.* (2023) [18], Vaishali *et al.* (2023) [24], Yadav *et al.* (2023) [27], Poojitha *et al.* (2024) [15], Rajput *et al.* (2024) [17], for high heritability in 100 kernel weight. High heritability for oil content was reported by Devarakonda *et al.* (2024) [6], and Yami and Abteu (2025).

Table 4: Classification of characters based on heritability (broad sense) according to Johnson *et al.* (1955) [10].

Heritability values (%)	Classification	Characters
0-30	Low	Days to maturity
30-60	Medium	Kernel yield per plant, number of primary branches per plant, plant height and pod yield per plant
60 and above	High	harvest index, 100 kernel weight, sound mature kernel, 100 pod weight, days to 50 % flowering, oil content, shelling percentage, biological yield per plant and number mature pod per plant

The genotypic coefficient of variation (GCV) alone cannot reveal how much of the observed variation is inherited genetically. Therefore, estimating heritability is essential to determine the likely effectiveness of selection and the expected genetic improvement in quantitative traits. When GCV is considered together with heritability, it provides a clearer understanding of the genetic potential of a trait and its probable response to selection. Burton (1952) [1], emphasized that the combined evaluation of GCV and heritability offers a more reliable basis for identifying traits that can be effectively improved through selection in plant breeding programmes. $H^2_{(bs)}$ estimates were recorded for nine characters: oil content, shelling percentage, biological yield per plant, harvest index, 100-kernel weight, sound mature kernel, 100-pod weight, days to 50% flowering and number of mature pods per plant. High broad-sense heritability suggests that a significant amount of the

observed variance is genetically determined and that these qualities are less affected by environmental influences. These findings imply that the attributes have significant genetic variability and may react well to selection in groundnut breeding programs since the current study calculated broad-sense heritability, which encompasses both additive and non-additive gene effects.

Genetic advance expressed as per cent of mean (gam)

Genetic advance expressed as a per cent of mean for different characters is presented in Table 2. Harvest index (54.09%) had the largest genetic progress as a percentage of the mean, followed by 100-kernel weight (31.27%), biological yield per plant (30.44%), number of ripe pods per plant (27.28%), 100-pod weight (25.02%) and kernel yield per plant (23.48%). The significant genetic diversity that may be exploited is shown by the high genetic progress seen

for these qualities, which implies that selection-based improvement would be successful. The current results are supported by similar findings for high genetic progress,

especially for harvest index, which were also reported by Abubakar et al. (2024)^[2], and Yami and Abtew (2025)^[28].

Table 5: Classification of characters based on genetic advance as per cent of mean given by Johnson *et al.* (1955)^[10].

GA as per cent of mean	Classification	Characters
0-10	Low	Shelling percentage, oil content and days to maturity
10-20	Medium	Pod yield per plant, number of primary branches per plant, sound mature kernel, plant height and days to 50% percent flowering
20 or above	High	harvest index, 100 kernel weight, biological yield per plant, number of mature pods per plant, 100 pod weight and kernel yield per plant

Genetic advance as a per cent of mean shows the accumulation of advantageous alleles in subsequent generations and indicates the anticipated increase in a population's mean performance after selection. According to Johnson *et al.* (1955)^[10], evaluating heritability and genetic advancement together yields a more accurate prediction of the anticipated response to selection than evaluating heredity alone. Therefore, these characteristics are helpful in identifying features that may be effectively increased through breeding. For harvest index, 100-kernel weight, biological yield per plant and number of ripe pods per plant, the current study found significant broad-sense heritability combined with high genetic progress as a percentage of the mean. This combination reveals that environmental influences have less of an impact on these qualities and shows the prevalence of additive gene action. According to Panse (1957), direct phenotypic selection for these variables is thus anticipated to be successful in enhancing groundnut production and its contributing attributes.

Conclusion

The study revealed extensive genetic diversity in seventy groundnut genotypes with significant heritable variation suitable for crop improvement. Five traits—harvest index, biological yield per plant, kernel yield per plant, number of mature pods per plant and pod yield per plant exhibited high GCV and PCV values with favourable selection potential. Harvest index emerged as the most promising trait, combining the highest heritability (94.53%) and genetic advance (54.09%). Nine traits displayed high broad-sense heritability (>60%), indicating predominance of additive gene action and minimal environmental influence. Harvest index, 100-kernel weight, biological yield per plant and number of mature pods per plant are reliable targets for direct phenotypic selection and rapid genetic gain. Traits with low GCV and heritability (days to maturity, oil content, shelling percentage) require alternative breeding strategies such as hybridization or molecular approaches. The identified genetic diversity provides excellent opportunity for groundnut improvement through phenotypic selection. Multi-location evaluation and correlation analysis are recommended for future studies.

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Conflict of Interest: None

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