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GENETIC VARIABILITY AND HERITABILITY IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) FOR YIELD AND QUALITY TRAITS

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ABSTRACT

This research assessed the genetic variability among sixty-three genotypes of groundnut (*Arachis hypogaea* L.), including three standard checks, for twelve agronomic and biochemical traits using an augmented block design. Most traits exhibited significant genotypic variation, demonstrating the presence of substantial genetic diversity. High GCV and PCV values for number of branches/plant and 100-kernel weight suggest considerable genetic variability with limited environmental influence. Heritability estimates ranged from low to high, with protein content, 100-kernel weight and oil content showing strong genetic control. The integration of high heritability along with substantial genetic advance as a percent of the mean (GAM) for key traits suggested strong additive type of gene action and promising opportunities for selection. The observed findings provide a basis for identifying promising genotypes and enhancing groundnut improvement through trait-based selection.

Key words : Genetic variability, Heritability, Genetic advance, Groundnut.

Introduction

Groundnut (*Arachis hypogaea* L.) serves as a significant pulse crop of high economic importance, cultivated on a large scale in tropical and sub-tropical areas. It has been recognized as a yearly, soft-stemmed plant in the Fabaceae family. Its root system consists of a main tap root with side branches that enhance soil fertility through a partnership with nitrogen-fixing bacteria. After the plant's flowers are pollinated, a structure known as the peg grows and buries the developing seed pod beneath the soil, a unique process called geocarpy. It serves as an essential oilseed and food crop, contributing substantially to both the agricultural economy and human nutrition. Groundnut seeds provide substantial amounts of protein and oil, making them vital for nutrition and industrial utilization. Groundnut, extensively cultivated in tropical and subtropical regions, occupied 30.9 million hectares worldwide in 2023–24, yielding 54.27 million tonnes, with a mean productivity of 1755 kg per hectare. The leading producers were China,

India, and Nigeria (FAO, 2024). In India, groundnut remains the leading oilseed crop, producing 10.18 million tonnes from 4.7 million hectares with 2163 kg/ha productivity. Gujarat dominated national production, followed by Rajasthan, Madhya Pradesh, and Tamil Nadu, contributing nearly 85% of the total, with other states making smaller contributions (DA and FW, 2024). Despite its importance, groundnut productivity is often limited by restricted genetic diversity and vulnerability to various biotic and abiotic challenges. Consequently, augmenting genetic variability is imperative for breeding programs aimed at enhancing yield potential, stress resilience, and environmental adaptability.

Genetic variability refers to the diversity in genetic composition among individuals within a species. In groundnut, this variability arises through natural mutations, genetic recombination and targeted breeding efforts. It is expressed in key agronomic and physiological traits such as seed size, pod yield, oil and protein percentage, drought tolerance and resistance against pests and

pathogens. Systematic evaluation of these traits across a broad range of genotypes facilitates the identification of superior parental lines for hybridization.

Despite its importance, genetic improvement of groundnut is constrained by its narrow genetic base. The narrow spectrum of genetic diversity in cultivated groundnut results from emerging through a single hybridization between two diploid ancestors, and later resulting in chromosome doubling (Janila *et al.*, 2013). Most wild *Arachis* species are diploid, whereas the cultivated form is an allotetraploid, making the transfer of beneficial alleles from wild relatives more difficult. Furthermore, the underground development of pods contributes to yield instability and creates a considerable gap between potential and realized yields, particularly under rainfed conditions where crops are exposed to diverse biotic and abiotic stresses. Moreover, the utility of genetic variability is trait-specific; while some variants may confer adaptive advantages, others may be neutral or even deleterious. Notably, traits such as flowering time and root architecture can have profound effects on crop performance under diverse agro-climatic conditions.

Therefore, this study was undertaken to evaluate essential genetic parameters, which include variance, coefficient of variation, heritability and genetic advance, in groundnut genotypes to gain insights into their key genetic attributes.

Materials and Methods

The experimental set up was conducted under AICRP on Groundnut, Rajasthan Agricultural Research Institute, Durgapura, Jaipur, which falls under Semi-Arid Eastern Plain Zone (Zone IIIA) with location coordinates of 26°51' N, 75°47' E at an altitude of 390 meter above mean sea level. The experiment was sown on June 20, 2024 in rainfed conditions. The crop growing season standard and uniform agronomic practices were adopted. Timely plant protection measures were also taken as necessary for a healthy and uniform crop stand. A total of sixty-three genotypes were used in the experiment which included the following three standard check varieties: RG 638, RG 559-3 and RG 578. The experiment was set in an augmented block design. This experiment was divided into six blocks. In each block all check genotypes and a sub set of test genotypes are included. Phenotypic data were collected on twelve traits: days to 50% flowering, days to peg initiation, days to maturity, number of branches/plants, number of pods/plants, pod yield/plant, kernel yield/plant, shelling %, sound mature kernel (SMK%) and 100 kernel weight, protein content and oil content. Phenological characteristics such as days

to flowering, pegging, and maturity were scored at the plot level while the other characteristics were scored on five randomly selected plants within each genotype. The protein content of groundnut was determined according to the method outlined by Lowry *et al.* (1951), while the oil content of groundnut kernels was determined using the Soxhlet (1979) extraction process and average oil percentage calculated.

The characters were scored and data for twelve characters across sixty-three genotypes were statistically analyzed as per the method given by Panse and Sukhatme (1985) to study variability between the genotypes. The complete ANOVA table showing all sources of variation, degrees of freedom, sums of squares, and mean square expectations. Estimates of genetic variability parameters including genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation GCV and PCV were obtained as per burton 1952. Broad heritability is defined as the proportion of genotypic variance in relation to phenotypic variance. It was estimated using the equation proposed by Burton and Devane (1953). The expected genetic advance under selection for the different characters reflects the movement of the population mean toward superior side. This was estimated according to the formula proposed by Johnson *et al.* (1955). The formula given by Johnson *et al.* (1955) was used to compute the genetic advance as percent of means for each character.

Results and Discussion

ANOVA revealed most of the traits showed pronounced and statistically significant genotypic variation, including days to 50% flowering, number of branches/plants, number of pods/plants, dry pod yield/plant, kernel yield/plant, sound mature kernels, shelling percentage, 100-kernel weight, protein content and oil content, therefore reflecting the existence of considerable genetic variation. In contrast, traits such as days to initiation of pegging and days to maturity were non-significant, suggesting limited genetic differentiation for these characters (Table 1).

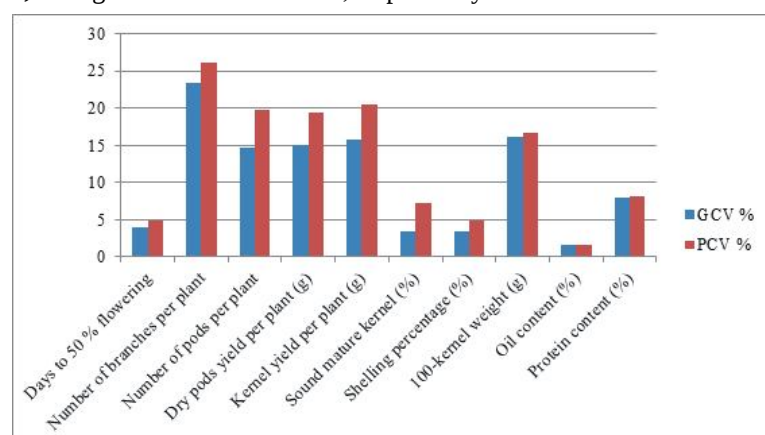
Similar patterns have been documented in earlier studies by Chavadhari *et al.* (2017), Gali *et al.* (2021), Mitra *et al.* (2021), Dharvesh *et al.* (2024), Kumar *et al.* (2024), Poojitha *et al.* (2024), Sravanti *et al.* (2024), Susmitha *et al.* (2024) and Yami and Abtew (2025). These findings confirm that substantial genetic variation was observed among the evaluated genotypes, which provides strong foundation for selection and breeding efforts.

Coefficients of variation at both the genotypic and phenotypic levels (GCV and PCV) serve as reliable

Table 1 : Analysis of variance (ANOVA) for dry pod yield and its contributing characters.

S. no.	Character	Block	Treatment	Check	Germplasm	Check v/s Genotype	Error
		[5]	[62]	[2]	[59]	[1]	[10]
1.	Days to 50 per cent flowering	0.19	1.75**	2.89**	1.74**	0.08	0.62
2.	Days to initiation of pegging	0.32	0.54	1.06	0.53	0.04	0.66
3.	Number of branches per plant	0.51	5.80**	8.28**	5.63**	10.91**	1.14
4.	Days to maturity	1.52	1.38	2.06	1.37	0.59	1.59
5.	Number of pods per plant	4.97	13.53**	19.65*	13.11**	26.37*	5.84
6.	Dry pods yield per plant (g)	6.05	20.56**	47.16**	19.71**	17.04	7.75
7.	Kernel yield per plant (g)	4.57	11.92**	35.09**	10.94**	23.35*	4.47
8.	Sound mature kernel (%)	38.03	44.20*	175.01**	39.49	60.86	30.97
9.	Shelling percentage (%)	4.53	12.52**	16.00	11.64**	57.26**	5.88
10.	100-kernel weight (g)	2.94	123.39**	946.32**	93.84**	221.14**	6.25
11.	Oil content (%)	0.15	0.67**	0.10	0.68**	1.06**	0.06
12.	Protein content (%)	0.11	6.12**	55.97**	4.50**	1.82**	0.05

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

**Fig. 1 :** Chart representation of genotypic coefficient of variation and phenotypic coefficient of variation.

indicators of the magnitude of genetic and total variability, respectively. High Values of GCV and PCV estimated for traits such as number of branches/plant (23.39% and 26.20%) and 100-kernel weight (16.09% and 16.66%) revealed marked genetic diversity with limited environmental effects. Conversely, relatively low GCV corresponding to days to 50% flowering (3.90%) and oil percentage (1.57%) reflected restricted genetic variability (Table 2). The narrow differences between GCV and PCV for most traits further indicated that environmental influence was generally limited, though it was more pronounced for kernel yield and sound mature kernel percentage (Fig. 1). Substantially high GCV and PCV values were observed for number of branches and kernel yield corroborate earlier findings by Chavadhari *et al.* (2017), Kumari and Sasidharan (2020), Krishna *et al.* (2024), and Yami and Abteu (2025). Together, these results highlight that while most traits are primarily governed by genetic factors, a few traits remain sensitive

to environmental variation.

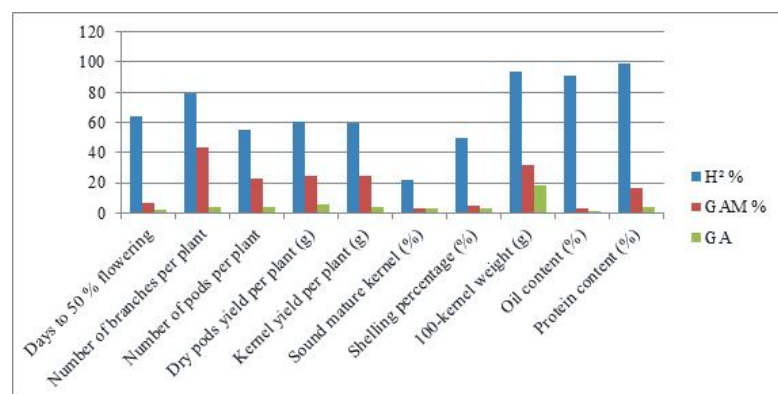
Moderate extent of genotypic variation (GCV) was recorded for number of pods/plants, pod yield/plant, kernel yield/plant and 100-kernel weight, which are in accordance with reports by Mitra *et al.* (2021), Kulheri *et al.* (2022) and Susmitha *et al.* (2024). In contrast, traits such as protein content, oil content, shelling percentage, and sound mature kernel percentage exhibited low GCV, supporting earlier observations by Chavadhari *et al.* (2017), Sravanti *et al.* (2024), and Poojitha *et al.* (2024). This suggests that yield-contributing traits tend to display greater variability than quality-related traits, offering more opportunities for genetic improvement through

selection.

The evaluated traits exhibited heritability estimates ranging from low to high. High heritability was recorded for protein content (98.81%), 100-kernel weight (93.34%), and oil content (90.61%), indicating strong genetic control. Moderate heritability was observed for attributes such as days to 50 per cent flowering (64.34%) and pod yield/plant (60.71%), whereas sound mature kernel percentage showed low heritability (21.57%), suggesting a greater environmental influence. Notably, when characters demonstrate high heritability in association with high GAM - such as number of branches (43.01%) and 100-kernel weight (32.03%), this indicates the predominance of additive gene action and suggests considerable scope for direct selection (Fig. 2). Similarly, traits with moderate GAM, including kernel yield (25.01%) and pod yield (24.29%), also demonstrate potential for genetic enhancement. In contrast, low GAM estimates for traits

Table 2 : Genetic variability parameters for dry pod yield and its contributing characters.

Characters	Mean	GCV %	PCV %	H ² %	GA	GAM %
Days to 50 % flowering	27.12	3.90	4.87	64.34	1.75	6.45
Number of branches per plant	9.26	23.39	26.20	79.69	3.90	43.01
Number of pods per plant	18.71	14.66	19.69	55.42	4.13	22.48
Dry pods yield per plant (g)	23.12	15.13	19.42	60.71	5.55	24.29
Kernel yield per plant (g)	16.42	15.78	20.52	59.15	4.03	25.01
Sound mature kernel (%)	85.74	3.38	7.29	21.57	2.79	3.24
Shelling percentage (%)	70.92	3.41	4.84	49.49	3.48	4.94
100-kernel weight (g)	59.07	16.09	16.66	93.34	18.63	32.03
Oil content (%)	50.25	1.57	1.65	90.61	1.54	3.07
Protein content (%)	26.16	8.04	8.09	98.81	4.32	16.46

**Fig. 2 :** Chart representation of heritability, genetic advance and genetic advance as per cent of mean.

such as shelling percentage (4.94%) and sound mature kernels (3.24%) indicate limited expected response to selection despite moderate heritability (Table 2). These findings are in conformity with the results obtained by Mitra *et al.* (2021), Kulheri *et al.* (2022), Kumar *et al.* (2024), Sravanti *et al.* (2024), Susmitha *et al.* (2024), Yami and Abteew (2025), thereby reinforcing the reliability of the observed trends. In summary, traits characterized by high heritability and GAM are promising for breeding, whereas those with low GAM may require alternative improvement methods like hybridization or marker-assisted approaches.

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