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Assessment of genetic variability parameters in f_2 segregating generation of groundnut (*Arachis hypogaea* L.)

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Abstract

The effectiveness of any crop improvement program relies on the variability and heritability of desirable traits. An investigation was conducted during the *Rabi*/summer 2023-24 at the University of Agricultural Sciences, Raichur to assess the extent of variability generated by hybridization and to estimate the heritability and genetic advance as per cent of mean for pod yield and its attributing traits in F_2 generation of the cross TMV-2 $\times$ R-8808. The segregating population thus obtained was evaluated for ten quantitative traits, revealing significant variability due to genetic segregation. The phenotypic co-efficient of variation (PCV) was slightly higher than the genotypic co-efficient (GCV), indicating minimal environmental influence. High GCV and PCV values coupled with high heritability and GAM values were observed for number of branches per plant, number of mature pods per plant, dry pod yield per plant, kernel weight per plant, biological yield per plant and harvest index suggesting that selection for the improvement of these traits is likely to be effective.

Keywords: Genetic variability, F_2 population, genetic co-efficient of variation, phenotypic co-efficient of variation, broad sense heritability and genetic advance

Introduction

Cultivated groundnut (*Arachis hypogaea* L.) is a key oil and protein-producing legume grown in tropical and sub-tropical regions. It belongs to the Fabaceae family and is divided into two subspecies, *hypogaea* and *fastigiata*, each with several botanical varieties. Groundnut thrives in semi-arid regions between 40° N and 40° S latitudes. The eastern foothills of the Andes (Southern Bolivia and Northern Argentina) are considered the crop's center of origin. In India, groundnut is mainly grown in rainfed conditions, making it a vital part of crop diversification. India leads globally in groundnut acreage, covering 8.5 million hectares, but ranks second in production, behind China, with 8.4 million tonnes. Indian groundnut productivity is relatively low, averaging 988 kg/ha, compared to 2,995 kg/ha in the USA and 2,688 kg/ha in China. Cultivation occurs across three seasons—*Kharif*, *Rabi* and summer—primarily in Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka and Maharashtra, contributing 80 per cent of the total area and production. Karnataka ranks fourth, producing 1.167 million tons annually from 1.22 million hectares (Anon. 2023) ^[1].

Genetic variability is the basic requirement for crop improvement as this provides a wider scope for selection ^[8]. Thus, the effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in materials and the extent to which it is heritable. Despite being developed and released in 1940, TMV-2 continues to dominate the market, even though there are other varieties with higher pod yields. Oil mills prefer TMV-2 for oil extraction due to its uniformly sized pods and attractive kernels. However, since the government has officially withdrawn TMV-2, it is no longer available through the official seed distribution system. There is a pressing need to create a new variety that surpasses TMV-2 in yield but retains its desirable pod and kernel characteristics. This is essential to bridge the productivity gap between groundnut cultivation in Karnataka and the national average. For crop improvement, it is crucial to have access to genetic variability, as this offers a broader selection

and heritability. Given that the existing variability has been maximized through selection, generating new variability in segregating populations by crossing top genotypes is necessary (Byadagi *et al.* 2018) ^[7].

In this study, we sought to assess the variation in key traits associated with pod yield and the factors influencing it. We also determined variability indices, including the genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), broad-sense heritability (h^2 bs) and genetic advance as a per cent of mean (GAM).

2. Materials and Methods

In the present investigation, F_2 population of cross TMV-2 $\times$ R-8808 consisting of 91 plants and seven checks namely R-8808, TMV-2, K-9, ICRC-1, Dh-256, Dh-257 and K-1812 belonging to both Virginia and Spanish habit groups were evaluated for genetic variability for pod yield and its attributing traits at All India Co-ordinated Research Project on groundnut research block, Main Agricultural Research Station (MARS), UAS, Raichur during *Rabi*/summer, 2023-24. The F_2 plants were planted in unreplicated block (Kempton and Gleeson 1997) ^[14] with 15 rows of F_2 population followed by two rows of each check planted with a spacing of 30 cm between rows and 10 cm between plants respectively. The crop was raised by following all the agronomic practices as per the package of practices recommended for groundnuts in the North-eastern dry zone of Karnataka (Zone 2).

Observations were recorded for ten quantitative characters viz. days to flowering, days to maturity, number of branches per plant, number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), shelling percentage (%), sound mature kernel (%), biological yield per plant (g) and harvest index (%). Observations on yield and yield-associated traits were recorded from individual plants since the F_2 population exhibits significant variability due to the segregation of genes at each locus where the parents differed. The mean and range were calculated as per Sunderaraj *et al.* (1972) ^[26], while genotypic co-efficient of variance (GCV) and phenotypic co-efficient of variance (PCV) were computed for the F_2 population for each

character as per the method suggested by Burton and Devane (1953) ^[6]. Heritability (%) in the broad sense was determined according to Lush's (1949) method, while genetic advance as a per cent of mean was estimated by using the formula of Johnson *et al.* (1955) ^[13].

3. Results and Discussion

3.1 Genotypic and phenotypic co-efficient of variance

The studies on the co-efficient of variation use a percentage of the mean to represent variance. The findings related to phenotypic co-efficient of variance (PCV), genotypic co-efficient of variance (GCV), heritability and genetic advance expressed as a per cent of mean are detailed by trait in Table 1. The outcomes of PCV and GCV are depicted in fig. 1, further heritability and GAM in Fig. 2. These statistical values offer insights into the existing variability, gene action and the potential for enhancing these traits through selective breeding or other genetic strategies. The phenotypic co-efficient of variation ranged from 3.68 per cent for days to maturity to 54.08 per cent for dry pod yield per plant. Similarly, the genotypic co-efficient of variation (GCV) ranged from 3.47 per cent for days to maturity to 48.98 per cent for dry pod yield per plant.

A higher magnitude of GCV and PCV values were recorded for dry pod yield per plant (g) followed by kernel weight per plant (g), biological yield per plant (g), number of mature pods per plant, number of branches per plant and harvest index (%). These results reveals that the traits mentioned above exhibit significant genetic variability indicating the potential for genetic improvement through a selection of these traits.

The results were on par with the studies of Yadlapalli (2014) ^[30] for number of branches per plant; Arunakumari *et al.* (2019) ^[3] for number of matured pods per plant; Blummel *et al.* (2012) ^[5] for dry pod yield per plant (g); Parameshwarappa *et al.* (2005) ^[22] for kernel weight per plant (g); Shinde *et al.* (2010) ^[24] for biological yield per plant (g) and Golakia *et al.* (2005) ^[10] for harvest index, who similarly reported that high PCV and GCV values are indicative of traits with a strong genetic basis and reduced environmental variability.

Table 1: Estimates of genetic variability parameters for yield and its attributing traits in F_2 generation of cross TMV-2 $\times$ R-8808

Sl. No.	Characters	Co-efficient of variation		h^2 Broad sense (%)	GAM (%)
		PCV (%)	GCV (%)		
1	Days to flowering	14.43	14.10	95.45	28.37
2	Days to maturity	3.68	3.47	89.01	6.744
3	No of branches per plant	30.32	27.30	81.01	50.60
4	No. of mature pods per plant	38.89	38.57	98.37	78.80
5	Dry pod yield per plant (g)	54.08	48.98	82.03	91.39
6	Kernel weight per plant (g)	52.81	48.52	84.39	91.81
7	Shelling (%)	6.60	5.73	75.40	10.24
8	Sound matured kernels (%)	4.47	3.73	69.89	6.43
9	Biological yield per plant (g)	45.78	45.75	99.87	94.20
10	Harvest index (%)	27.88	26.84	92.66	53.23

PCV (%): Phenotypic co-efficient of variation

GCV (%): Genotypic co-efficient of variation

GAM: Genetic advance as a per cent of mean

h^2 bs: Broad sense Heritability

The minimal difference between the GCV and PCV values for all ten quantitative traits suggests that the phenotypic variation in a trait is largely due to genetic factors, rather than environmental influences. The selection based on the phenotype is likely to be effective because the traits being selected for are strongly genetically controlled.

The investigation recorded a moderate GCV as well as PCV values for days to flowering which was in accordance with the results of Aparna *et al.* (2018) ^[2] and Padmaja *et al.* (2013) ^[21].

A lower GCV and PCV values were observed for days to maturity, sound matured kernels and shelling percentage suggesting minimal genetic variability within these traits for

selection. The results were on par with the studies of Zaman *et al.* (2011) [31] and Kumar and Sasidharan (2020) [15] for days to maturity, Mohapatra and Khan (2020) [16] and Meta and Monpara (2010) for sound matured kernels and shelling percentage.

3.2 Heritability and genetic advance

Broad-sense heritability ranged from 69.89 per cent for shelling percentage to 99.87 per cent for biological yield per plant. The genetic advance as a per cent of mean varied from 6.43 per cent for shelling percentage to 94.20 per cent for biological yield per plant.

Estimates of higher broad sense heritability coupled with high genetic advance as per cent of mean (GAM) were observed for days to flowering, number of branches per plant, number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), biological yield per plant (g) and harvest index (%) indicating that these traits are governed by additive gene action and direct selection for the higher phenotypic value of this trait will be effective.

This findings were in accordance with the results of earlier workers Vijayabharathi (2020) [29] for days to flowering; Nandini

et al. (2011) [19] for number of branches per plant; Veeramani *et al.* (2005) [28] for number of matured pods per plant; Hamasselbe *et al.* (2011) [11] for dry pod yield per plant (g); Sumathi *et al.* (2009) [25] for kernel weight per plant (g); Chavadhari *et al.* (2017) [32] for biological yield per plant (g); Bhargavi *et al.* (2016) [4] for harvest index (%), who observed that traits with high heritability and genetic advance are primarily governed by additive genetic effects, making them highly amenable to selection.

Days to maturity and sound matured kernels (%) exhibited high broad sense heritability but a low GAM value while shelling percentage recorded a moderate GAM value revealing the prevalence of both additive and non-additive gene actions. Improvement of these traits could be achieved through simple selection, progeny selection or modified selection methods that focus on fixing additive gene effects rather than solely relying on selection. High heritability and low genetic advance as a per cent of mean were on par with the findings of Gali *et al.* (2021) [9] and Savaliya *et al.* (2009) for days to maturity and Narasimhulu *et al.* (2012) [20] and John *et al.* (2005) [12] for sound matured kernel. Prabhu *et al.* (2015) [23] and Suthar *et al.* (2023) [27] had a similar result for shelling percentage.

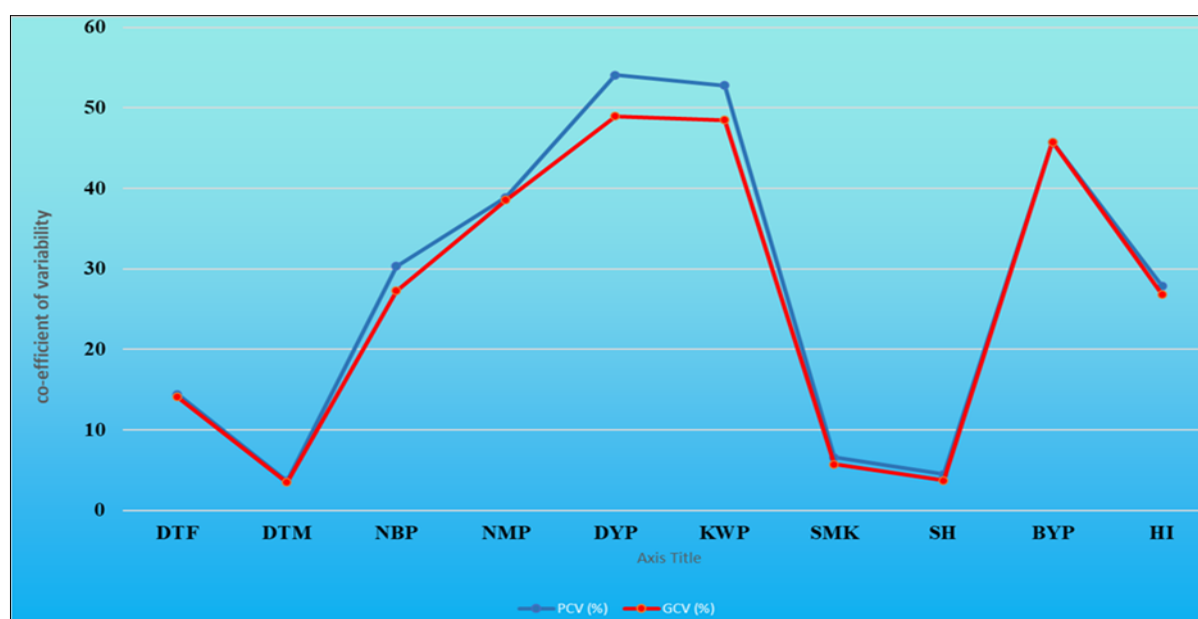


Fig 1: Phenotypic coefficient of variation (PCV) and Genotypic coefficient variation (GCV) for yield and yield attributing traits in F_2 population of cross TMV-2 $\times$ R-8808

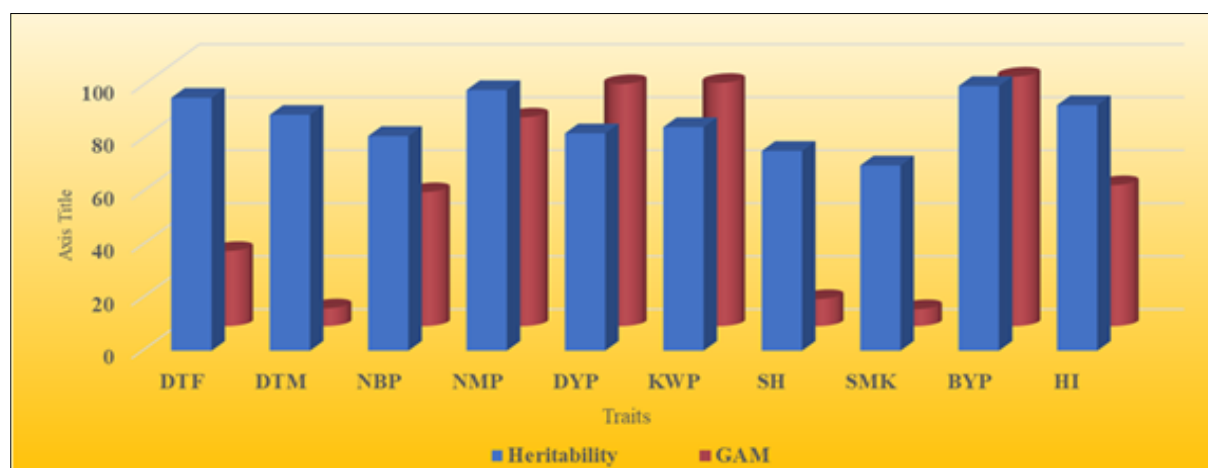


Fig 2: Broad sense heritability (h^2_{bs}) and genetic advance as per cent of mean (GAM) for yield and yield attributing traits in F_2 population of cross TMV-2 $\times$ R-8808.

4. Conclusion

The overall findings indicated a satisfactory level of variability among the studied genotypes. This variation can be effectively harnessed through suitable breeding methods and programmes to create enhanced varieties. Most traits exhibited high genotypic and phenotypic co-efficients of variation, suggesting significant variability among the genotypes, which is essential for selection. Additionally, many traits showed high heritability and genetic advance estimates, indicating the dominance of additive gene action, allowing for direct selection to improve yield.

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