Original Research Article

Assessment of Genetic Variability of F_4 Progenies for Enhanced Pod Yield and Component Traits in Groundnut

Abstract

The present study aimed to assess genetic variability among F4 progenies for pod yield and its components in groundnut. Conducted with 71 F4 progenies from three crosses—TMV-2 × ICGV-91114, TMV-2 × TG-69, and TMV-2 × ICGV-00350—alongside five check varieties, the investigation was carried out in an augmented design during Kharif 2019. The key objective includesevaluating genetic variability for pod yield and its components. Analysis of variance revealed significant genetic variability among the F4 progenies for all eight traits studied. The range of variability was highest for kernel yield plant-1, followed by pod yield plant-1 and pods plant-1, with minimal variation observed in days to 50 percent flowering. Genetic variability assessments showed high phenotypic and genotypic coefficients of variation for pods plant-1, pod yield plant-1, and kernel yield plant-1, while traits like days to 50 percent flowering and plant height exhibited lower variability. High heritability estimates, coupled with substantial genetic advances for pods plant-1, pod yield plant-1, and kernel yield plant-1, indicated potential for effective selection. Future work should focus onidentifying the superior F4 progenies for selection for potential development of high-yielding groundnut varieties.

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Key words: *Genetic variability, F_4 progenies,Phenotypic Coefficient of Variation (PCV),Genotypic Coefficient of Variation (GCV),Augmented design*.

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Introduction

Groundnut, also known as peanut, is an extensively cultivated oilseed crop recognized globally by various names, including earthnut, goober, and monkey nut. In India, it is referred to as moongphalee in Hindi and kadalekai in Kannada. Groundnut is a rich source of energy, highly valued for its edible oil content (43-55%), proteins (25-28%), and carbohydrates (20%) on a dry kernel basis (Savage and Keenan, 1994). The kernels also provide essential minerals like calcium, phosphorus, and iron, as well as vitamins such as vitamin-E, niacin, folacin, thiamine, and riboflavin. Groundnut haulm, used as fodder, contains significant amounts of protein (8-15%), lipids (1-3%), minerals (9-17%), and carbohydrates (38-45%), with a nutrient digestibility of around 53% and crude protein digestibility of 88% in animals. Groundnut, a self-pollinated allo-tetraploid crop, belongs to the Leguminosae or Fabaceae family, with a basic chromosome number of ten (2n=4x=40) and a genome size of 2800 Mb (Gautami et al., 2009). It is believed to have originated from a hybridization event between the diploid species *Arachis duranensis* (AA) and *Arachis ipaensis* (BB), followed by spontaneous chromosome duplication (Halward et al., 1991). These species are native to northwest Argentina and southeast Bolivia (Krapovickas and Gregory, 1994). Groundnut is now cultivated in over 108 countries, primarily in tropical, subtropical, and warm temperate regions (Vavilov, 1926).

India, the second-largest producer of groundnut after China, cultivates the crop on approximately 70 lakh hectares, with a production of 8.5 million metric tonnes and a productivity of 1465 kg/ha (Anon., 2018(b)). Major producing states include Gujarat, Rajasthan, Andhra Pradesh, Tamil Nadu, and Karnataka. Globally, groundnut ranks fourth in oilseed production, with 60% of the crop used for oil extraction and 40% for table consumption and seed purposes. The crop is predominantly rainfed, with the Kharif season accounting for 80% of total production. Groundnut is adaptable to a wide range of climatic conditions, making it suitable for both Kharif and Rabi seasons in southern India. Crop improvement in groundnut is essential to address challenges such as low genetic variability, a consequence of its polyploidy and single hybridization origin.Selection based on yield can be misleading due to the polygenic nature of pod yield, necessitating an understanding of genetic variability andheritability (Alam et al., 1985).

This study was conducted to investigate the genetic variability for pod yield and its associated traits in groundnut, focusing on the F4 generation. The primary objectives were to evaluate the F4 progenies of crosses TMV-2 × ICGV-91114, TMV-2 × TG-69, and TMV-2 × ICGV-00350—alongside five check varieties for the extent of genetic variability for pod yield and its component traits. By addressing these objectives, the study aims to enhance the understanding of the genetic factors influencing pod yield and to facilitate the selection of superior genotypes for breeding programs.

Material aAnd Methods

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The experiment was conducted during the Kharif season of 2019 at the AICRP on National Seed Project (Crops), University of Agricultural Sciences, GKVK, Bengaluru. The site is situated at an elevation of 930 meters above mean sea level (MSL) with geographical coordinates of 13°08' N latitude and 77°57' E longitude.

Table 1 List of F_4 progenies along with checks used for present study

F4 Progenies					
P1-L-7-3-1	P1-L-5-6-2	P2-L-9-8-1	P2-L-10-14-2	P2-L-6-3-1	P3-L-5-9-2
P1-L-7-3-2	P1-L-5-6-3	P2-L-9-8-2	P2-L-10-14-3	P2-L-6-3-2	P3-L-6-13-1
P1-L-2-12-1	P1-L-16-8-1	P2-L-9-8-3	P2-L-10-14-4	P2-L-6-3-3	P3-L-6-13-2
P1-L-2-12-2	P1-L-16-8-2	P2-L-7-12-1	P2-L-10-14-5	P2-L-5-3-4	P3-L-5-10-1
P1-L-2-12-3	P1-L-16-8-3	P2-L-7-12-2	P2-L-12-3-1	P3-L-10-16-1	P3-L-5-10-2
P1-L-2-12-4	P1-L-16-8-4	P2-L-7-12-3	P2-L-12-3-2	P3-L-10-16-2	P3-L-14-8-1
P1-L-3-8-1	P1-L-4-8-1	P2-L-7-12-4	P2-L-17-5-1	P3-L-9-13-1	P3-L-14-8-2
P1-L-3-8-2	P1-L-4-8-2	P2-L-7-12-5	P2-L-5-2-1	P3-L-9-13-2	P3-L-1-8-1
P1-L-3-8-3	P1-L-1-4-1	P2-L-7-6-1	P2-L-5-2-2	P3-L-9-13-3	P3-L-1-8-2
P1-L-6-10-1	P1-L-1-4-2	P2-L-10-13-1	P2-L-5-3-1	P3-L-4-12-1	P3-L-8-12-1
P1-L-6-10-2	P1-L-1-4-3	P2-L-10-13-2	P2-L-5-3-2	P3-L-4-12-2	P3-L-8-12-2
P1-L-5-6-1	P2-L-1-4-4	P2-L-10-14-1	P2-L-5-3-3	P3-L-5-9-1	
Checks					
GKVK-5	TMV-2	KCG-6	ICGV-9114	TG-69	

The experimental material comprised 71 F4 progenies derived from F3 generations of three distinct crosses. The breakdown of the F4 progenies from each cross is as follows:

1. TMV-2 × ICGV-91114: 23 progenies

2. TMV-2 × TG-69: 29 progenies

3. TMV-2 × ICGV-00350: 19 progenies

In this study, TMV-2 served as the common female parent, which was crossed with three high-yielding varieties: ICGV-91114, TG-69, and ICGV-00350. Additionally, five check varieties were included: GKVK-5, TMV-2, ICGV-91114, KCG-6, and K-6. Tables 1 and 2 provide the list of the 71 F4 progenies and a brief description of the parents used in the crosses, along with their salient features.

Evaluation of F_4 progenies

The superior F3 plants were selected and advanced to the F4 generation, which was evaluated on a plant-to-row progeny basis in an augmented design with checks (GKVK-5, KCG-6, TMV-2, ICGV-91114, and K-6) during Kharif 2019. The plants were spaced 30 cm apart between rows and 10 cm within rows at the National Seed Project, UAS, GKVK, Bengaluru. All recommended practices were followed to ensure a healthy crop.

Table 2 Salient features of groundnut varieties used as parents in the crosses and checks

Varieties	Year of release	Source	Parentage	Special features
TMV-2	1940	TNAU, Coimbatore	Selection from Gudiyatham bunch	Old variety, wider adaptability, desirable pod and kernel shape & size, kernels small with salmon colour testa, susceptible to drought and foliar diseases.
ICGV-91114	2007	ICRISAT, Hyderabad	ICGV-86055 ×ICGV-86353 Bulk pedigree method	Early maturing, moderate yielding, bold seeded, tolerant to drought & LLS, good seed size, better digestibility and palatability of haulms
ICGV-00350	2012	ICRISAT, Hyderabad	ICGV-87290× ICGV-87846 Bulk pedigree method	High yield and high oil content, resistant to LLS, rust and tolerant to drought and stem rot.
TG-69	2011	BARC, Trombay, Mumbai	Mutant variety	High harvesting index, shelling *per cent* and SMK *per cent.*
KCG-6	2016	UAS, Bengaluru	TAG-24× ICGV-92238	Matures in 110 to 115 days, high yielding with high oil content (47-48 *per cent*).

Plan and layout of the experiment

Experiment consisting of 71 F_4 progenies and five checks was laid out in augmented design. In total there were eight blocks with each block having nine F_4 progenies along with five check varieties which were replicated twice in each block (table. 3).

	Rows																		
Blocks	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	C5	T62	T39	C2	C2	T63	C5	T47	T61	C4	C3	C1	C1	T28	C4	T41	T4	T17	C3
2	C2	C3	T26	T58	T9	T43	T44	C3	C5	C5	C1	T23	C4	C1	C2	T38	C4	T46	T21
3	T49	C4	C1	C2	T8	T25	T19	C5	C4	C1	C3	T7	C3	T66	T67	T1	C5	T10	C2
4	C	T2	C	T3	T4	T6	T6	T7	C	T	C	T1	C	C	C	C	C	T2	C

	3	0	3	4	2	4	5	1	4	3	1	8	5	4	1	2	5	7	2
5	T15	C3	T5	C2	C4	T31	T11	C4	T68	C3	T37	T52	T53	C1	T45	C5	C5	C1	C2
6	C5	C3	T22	C2	C4	C4	C5	T6	C1	C1	T32	T55	T54	T56	T57	T2	C3	C2	T16
7	C3	C2	T12	C4	C2	C4	T36	T35	C5	T70	C1	C5	C1	C3	T24	T60	T14	T13	T48
8	C3	T33	T50	C2	C5	C1	C5	T51	C3	C4	C2	T59	T40	T30	C4	T69	C1	T29	

Table .3 Layout of experimental plot

Data collection

Data were recorded on 20 randomly selected competitive plants from each progeny row and checks for several traits. Days to 50 percent flowering was noted as the number of days from sowing until 50 percent of plants flowered. Plant height was measured from the base to the apical leaflet at 80 days after sowing. The number of primary branches and pods per plant was recorded at 80 days, and total pod and kernel yields per plant were measured after harvesting and drying. Shelling percentage was calculated as the ratio of kernel weight to pod weight, while Sound Mature Kernel (SMK) percentage was determined by sorting kernels into well-developed and shrivelled types and expressing the ratio of well-developed kernels as a percentage.

Statistical analysis

Statistical analysis of the mean data was done by using *metan* package in R software for the Augmented Design of F_4 generation data. The details of statistical methods used for analysing the data are presented below.

Descriptive statistics for the F4 generation were computed following Sunder Raj et al. (1972). The mean was calculated as the average of all observations, while range, both absolute and standardized, was determined by the difference between the highest and lowest values. Standard error was estimated by dividing the standard deviation by the square root of the number of observations.

Estimation of variability parameters for F_4 population

To estimate variability parameters for the F4 population, several genetic parameters were calculated. Genotypic variance $(\sigma^2\ g)$ was derived from the difference between the mean sum of squares due to progenies and error, divided by the number of blocks, while phenotypic variance ($\sigma^2 p$) was obtained by adding the genotypic variance to the mean sum of squares due to error. The coefficient of variation (CV%) was computed using the formula $\frac{\sigma_p}{X^-} \times 100$, with Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) calculated as $\frac{\sigma_P}{X} \times 100$ and $\frac{\sigma_g}{X^-} \times 100$ respectively. Heritability in broad sense (h^2 _BS) was estimated as the ratio of genotypic variance to phenotypic variance, expressed as a percentage. Genetic Advance (GA) was calculated using GA $= h^2 \times K \times \sigma_P$, with Expected Genetic Advance as a Percentage of Mean (GAM) given by GAM $= \frac{GA}{X^-} \times 100$. Variability and heritability were classified into low, moderate, and high based r^-stablished thresholds.

Results aAnd Discussion

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The results obtained from the present investigation on various aspects in F_4 generation are presented and discussed in this chapter.

Exploiting natural genetic variability provides a short-term solution to address the immediate needs of farmers, consumers, and end-users, as historical selection by farmers and plant breeders has markedly improved crop productivity. However, for medium- and long-term improvements, it is crucial to generate variation through strategic crosses among genotypes with desired traits. Analysis of variance (ANOVA) serves as a fundamental diagnostic tool for detecting genetic variability in the experimental material. In this study, ANOVA revealed significant mean sum of squares for all traits due to progenies, indicating considerable variability among them (Table 4). Additionally, significant mean sum of squares due to checks were observed for all traits except days to 50 percent flowering, highlighting variability among the checks. The significant mean sum of squares for the comparison of 'F4 progenies vs checks' indicated substantial differences between F4 progenies and checks for all traits, except plant height, pods per plant, and sound mature kernels (SMK) percent (Table 4).

Table 4 Analysis of variance of groundnut F_4 progenies for quantitative trait

Sources of variation	Degrees of freedom	Mean sum of squares							
		Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Pods plant^{-1}	Pod yield plant^{-1}	Kernel yield plant^{-1}	Shelling %	SMK %
Blocks	7	0.90	0.65	0.15	14.69	12.68	7.44	5.71	5.60 *

Entries (F_4 progenies + checks)	75	5.99 **	4.47 **	0.63 **	43.68**	36.46 **	17.81 **	19.87 **	33.44 **
F_4 progenies	70	6.02 **	4.36 **	0.57 *	43.23 **	34.81 **	17.10 **	12.61 **	33.00 **
Checks	4	2.54	7.52 **	1.17 **	59.96 **	65.48 **	25.11 **	27.97 **	48.98 **
F_4 progenies *vs*. checks	1	17.67**	0.41	2.42 **	10.00	36.14	38.20 *	495.89**	2.37
Error	28	0.26	1.19	5.03	9.02	1.09	8.65	4.04	2.24

*Significant @ P=0.05 level; **Significant @ P=0.01 level

Mean Performance of F4 Progenies of Groundnut

The evaluation of the 71 F4 progenies of groundnut revealed a wide range of variation in several traits. The plant height varied from 32.06 to 46.91 cm, with a mean of 38.57 cm. The number of branches per plant ranged from 3 to 7, averaging 5.45. For days to 50 percent flowering, the mean was 43.82 days, with a range of 38 to 49 days. The number of pods per plant showed a significant range from 9.50 to 48.10, with a mean of 25.14. Pod yield per plant ranged from 5.20 g to 38.90 g, averaging 18.65 g, while kernel yield per plant ranged from 3.22 to 30.00 g, with a mean of 12.38 g. The shelling percentage ranged from 55.66 to 81.68 percent, with a mean value of 67.44 percent. The sound mature kernel (SMK) percentage ranged from 50.82 to 93.94 percent, with an average of 82.15 percent. These results indicate significant variability among the F4 lines for all traits studied (Table 5).

Among the lines, the maximum plant height was observed in P1-L-2-12-4 (46.91 cm), while the minimum was noted in P3-L-14-8-2 (32.06 cm). Line P1-L-6-10-1 had the highest days to 50 percent flowering (49 days), while P2-L-5-3-2 had the earliest flowering at 38 days. The maximum number of branches per plant (7) was recorded in P2-L-7-12-4, and the minimum (3) was seen in P1-L-5-6-3. The highest number of pods per plant (48.10) was recorded in P1-L-5-6-2, with the lowest (9.50) in P3-L-14-8-1. The maximum pod yield (38.90 g) was also in P1-L-5-6-2, whereas the minimum yield (5.20 g) was in P3-L-14-8-1. For kernel yield, the highest (30.00 g) was again in P1-L-5-6-2, while the lowest (3.22 g) was recorded in P3-L-14-8-1. Line P1-L-1-4-1 showed the maximum shelling percentage (81.68), and P2-L-7-12-5 had the minimum (55.66). The maximum SMK percentage (93.94) was noted in P3-L-14-8-1, with the minimum (50.82) in P3-L-6-13-1 (Appendix I).

Standardized Range Studies

The highest standardized range was observed for kernel yield per plant (2.16), followed by pod yield per plant (1.80), number of pods per plant (1.53), primary branches per plant (0.73), sound mature kernel (SMK) percentage (0.52), shelling percentage (0.38), and plant height (0.38). The least standardized range was for days to 50 percent flowering (0.25). These findings highlight a significant amount of variability across the traits, offering extensive opportunities for selection to improve productivity (Table 5).

Table 5 Descriptive statistics for eight quantitative traits in groundnut

Sl. No.	Traits	Mean ± SE	Range		Standardized range	Coefficient of variability		Broad-sense h^2 (%)	Expected GAM (%)
			Min	Max		PCV (%)	GCV (%)		
1	Days to50% flowering	43.82 ± 0.28	38	49	0.25	5.6	5.01	80.14	9.26
2	Plant height (cm)	38.57 ±0.24	32.06	46.91	0.38	4.9	4.24	74.89	7.57
3	Branches $plant^{-1}$	5.45 ± 0.08	3	7	0.73	12.49	9.15	53.72	13.84
4	Pods $plant^{-1}$	25.14 ±0.78	9.5	48.1	1.53	26.15	23.26	79.14	42.69
5	Pod yield $plant^{-1}$	18.65 ±0.69	5.2	38.9	1.8	31.64	27.43	75.16	49.06
6	Kernel yield $plant^{-1}$	12.38 ±0.50	3.22	30	2.16	33.39	28.05	70.57	48.62
7	Shelling (%)	67.44 ±0.46	55.66	81.68	0.38	5.26	4.34	67.95	7.38
8	SMK (%)	82.15 ±0.66	50.82	93.94	0.52	6.99	6.75	93.21	13.45

SE-Standard Error, PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, GAM- Genetic advance as % of mean

Genetic Variability Among F4 Progenies

The success of crop improvement programs relies on the presence of genetic variability within the breeding material. Significant variation is crucial for effective selection by breeders. The genetic variability parameters for eight traits in the F4 progenies were analyzed, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and heritability (broad sense), as detailed in Table 5.

Plant Height (cm)

Plant height exhibited a higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV), with values of 4.9% and 4.24%, respectively. This indicates limited variability in the population and a minimal environmental effect on this trait. The trait showed high heritability at 74.89%, reflecting a strong influence of additive genetic factors, consistent with previous studies (Vange and Maga, 2014; Vasanthi et al., 2015).

Primary Branches Plant-1

For primary branches plant-1, moderate PCV of 12.49% and low GCV of 9.15% were recorded, with a moderate heritability of 53.72%. These findings suggest that environmental factors have some effect, but phenotypic selection remains feasible (John et al., 2008; Sumathi et al., 2009).

Days to 50 Percent Flowering

Days to 50 percent flowering showed low PCV and GCV values (5.60% and 5.01%, respectively). The trait demonstrated high heritability (80.14%), indicating it is predominantly controlled by additive genes, making selection for this trait effective (Prakash et al., 2000; John et al., 2013).

Pods Plant-1

Pods plant-1 exhibited high variability with PCV and GCV values of 26.15% and 23.26%, respectively, and high heritability at 79.14%. This indicates a strong genetic control, making selection for this trait advantageous (Padmaja et al., 2013; Yadlapalli, 2014).

Pod Yield Plant-1

Pod yield plant-1 had high PCV and GCV of 31.64% and 27.43%, respectively, coupled with high heritability (75.16%). This suggests significant genetic control and the potential for effective selection (Golakia et al., 2005; Nath and Alam, 2002).

Kernel Yield Plant-1

Kernel yield plant-1 also showed high PCV (33.39%) and GCV (28.05%) with high heritability (70.57%). This indicates that additive genetic effects are strong, and selection for this trait should be productive (Gouranga et al., 2017; Shashikumara et al., 2016).

Shelling Percent

Shelling percent had low PCV (5.26%) and GCV (4.34%), with high heritability of 67.95%. This reflects a strong genetic influence with limited environmental impact (Mohan et al., 2012; Shashikumara et al., 2016).

SMK Percent

SMK percent recorded low PCV (6.99%) and GCV (6.75%) but very high heritability (93.21%). This indicates that the trait is highly influenced by additive genes, and direct selection can be very effective (Ashutosh and Prashant, 2014; Zekeria et al., 2017).

Genetic Advance

The expected genetic advance as a percentage of the mean (GAM) varied from 7.38% to 49.06%. Traits like pod yield plant-1 (49.06%), kernel yield plant-1 (48.62%), and pods plant-1 (42.69%) showed high GAM, suggesting effective selection potential. In contrast, days to 50 percent flowering, plant height, and shelling percent had lower GAM, indicating less scope for improvement through selection (Table 5).

~~Summary and~~ Conclusion

The success of any breeding program is heavily dependent on the genetic variability present in the base population. Greater genetic variation in the material increases the likelihood of selecting promising types, making it crucial to understand the extent of this variability. Genetic variability, derived from phenotypic observations, reflects the interaction between genotype and environment. Effective selection is only possible when sufficient genetic variability exists within the population. Therefore, assessing the magnitude of genetic variability is essential for initiating a successful breeding program.

The study utilized 71 F4 progenies from three crosses—TMV-2 × ICGV-91114, TMV-2 × TG-69, and TMV-2 × ICGV-00350—along with five check varieties, evaluated in an augmented design during Kharif 2019 at UAS, GKVK, Bengaluru. Data on eight quantitative traits were collected from 20 randomly selected plants per progeny. Statistical analyses estimated mean traits, ranges, genetic coefficients (PCV and GCV), heritability, and expected genetic advance (GAM)Significant differences were found among F4 progenies, indicating substantial genetic variability. High variability was observed in kernel yield, pod yield, and pods per plant, with low variation in days to 50% flowering. The study revealed high heritability for most traits, with particularly high heritability and GAM for pods per plant, pod yield, and kernel yield.

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