

Original Research Article

Assessment of Genetic Variability of F₄ 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 includes evaluating 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 on identifying the superior F₄ progenies for selection for potential development of high-yielding groundnut varieties.

Key words: *Genetic variability, F₄ progenies, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Augmented design.*

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 and heritability (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 AND METHODS

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 F₄ progenies along with checks used for present study

Comment [SK1]: Not mentioned in the reference list

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 F₄ 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 <i>per cent</i> and SMK <i>per cent</i> .
KCG-6	2016	UAS, Bengaluru	TAG-24 × ICGV-92238	Matures in 110 to 115 days, high yielding with high oil content (47-48 <i>per cent</i>).

Plan and layout of the experiment

Experiment consisting of 71 F₄ progenies and five checks was laid out in augmented design. In total there were eight blocks with each block having nine F₄ progenies along with five check varieties which were replicated twice in each block (table. 3).

Blocks	Rows																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	C 5	T6 2	T3 9	C 2	C 2	T6 3	C 5	T4 7	T6 1	C 4	C 3	C 1	C 1	T2 8	C 4	T4 1	T 4	T1 7	C 3
2	C 2	C 3	T2 6	T5 8	T 9	T4 3	T4 4	C 3	C 5	C 5	C 1	T2 3	C 4	C 1	C 2	T3 8	C 4	T4 6	T2 1
3	T4 9	C 4	C 1	C 2	T 8	T2 5	T1 9	C 5	C 4	C 1	C 3	C 7	T 3	C 6	T6 7	T6 7	T1 5	C 0	T1 2
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	T1	C	T	C	C	T3	T1	C	T6	C	T3	T5	T5	C	T4	C	C	C	C
	5	3	5	2	4	1	1	4	8	3	7	2	3	1	5	5	5	1	2
6	C	C	T2	C	C	C	C	T	C	C	T3	T5	T5	T5	T	C	C	T1	
	5	3	2	2	4	4	5	6	1	1	2	5	4	6	7	2	3	2	6
7	C	C	T1	C	C	C	T3	T3	C	T7	C	C	C	C	T2	T6	T1	T1	T4
	3	2	2	4	2	4	6	5	5	0	1	5	1	3	4	0	4	3	8
8	C	T3	T5	C	C	C	T5	C	C	C	T5	T4	T3	C	T6	C	T2		
	3	3	0	2	5	1	5	1	3	4	2	9	0	0	4	9	1	9	

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 F₄ 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 F₄ population

To estimate variability parameters for the F₄ population, several genetic parameters were calculated. Genotypic variance (σ^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 (σ^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 $\frac{\sigma_p}{\bar{x}} \times 100$, with Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of

Comment [SK2]: Not mentioned in the reference list

Variation (GCV) calculated as $\frac{\sigma_p}{\bar{x}} \times 100$ and $\frac{\sigma_g}{\bar{x}} \times 100$ 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 $GAM = \frac{GA}{\bar{x}} \times 100$. Variability and heritability were classified into low, moderate, and high based on established thresholds.

Comment [SK3]: Check the spelling

RESULTS AND DISCUSSION

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 (F₄ progenies + checks)	75	5.99 **	4.47 **	0.63 **	43.68**	36.46 **	17.81 **	19.87 **	33.44 **
F₄ 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 **
F₄ 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 \pm SE	Range		Standardized range	Coefficient of variability		Broad-sense h^2 (%)	Expected GAM (%)
			Min	Max		PCV (%)	GCV (%)		
1	Days to 50% flowering	43.82 \pm 0.28	38	49	0.25	5.6	5.01	80.14	9.26
2	Plant height (cm)	38.57 \pm 0.24	32.06	46.91	0.38	4.9	4.24	74.89	7.57
3	Branches plant ⁻¹	5.45 \pm 0.08	3	7	0.73	12.49	9.15	53.72	13.84
4	Pods plant ⁻¹	25.14 \pm 0.78	9.5	48.1	1.53	26.15	23.26	79.14	42.69
5	Pod yield plant ⁻¹	18.65 \pm 0.69	5.2	38.9	1.8	31.64	27.43	75.16	49.06
6	Kernel yield plant ⁻¹	12.38 \pm 0.50	3.22	30	2.16	33.39	28.05	70.57	48.62
7	Shelling (%)	67.44 \pm 0.46	55.66	81.68	0.38	5.26	4.34	67.95	7.38
8	SMK (%)	82.15 \pm 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).

Comment [SK4]: Not mentioned in the reference

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.

References

ALAM, M. S., RAHMAN, A. R. M. S. AND KHAIR, A. B. M. A., 1985, Genetic variability and character association in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Agric. Res.*, **10**(4): 9-16.

ANAMIKA, R., LAL AHMED, M., AMARAVATHI, Y., VISWANATH, K., DAYAL, P. B. Y. AND SREEKANTH, B., 2018, Genetic variability, heritability and genetic advance of yield and yield attributes in groundnut (*Arachis hypogaea* L.). *The Andhra Agric. J.* **65**(1): 88-91.

ANONYMOUS, Indiastat, 2018 (a).

ANONYMOUS, USDA, 2018 (b).

ASHUTOSH, K. S. AND PRASHANT, K. R., 2014, Evaluation of groundnut genotypes for yield and quality traits. *Ann. Plant Soil Res.*, **16**(1): 41-44.

AZAD, M. A. K. AND HAMID, M. A., 2000, Genetic variability, character association and path analysis in groundnut (*Arachis hypogaea* L.). *Thai J. Agri. Sci.*, **33**: 153-157.

BENEDICT, C., OYIGA, MICHAEL, I. AND UGURU, 2011, Interrelationship among pod and seed yield traits in Bambara groundnut (*Vigna subterranean* L. Verdc) in Derived Savanna Agro-Ecology of South – Eastern Nigeria under Two Planting Dates. *Int. J. Plant Breed.*

BURTON, G. W. AND DEVANE, E. H., 1953, Estimating heritability in tall fescue (*Festua arundinaceae*) from replicated colonial material. *Agron. J.*, **45**: 478-481.

Comment [SK5]: Not mentioned in the text

Comment [SK6]: Not mentioned in the text

Comment [SK7]: Not mentioned in the text

Comment [SK8]: Not mentioned in the text

Comment [SK9]: Not mentioned in the text

Comment [SK10]: Not mentioned in the text

CHAVADHARI, R. M., KACHHADIA, V. H., VACHHANI, J. H. AND VIRANI, M. B., 2017, Genetic variability studies in groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.*, **8**(4): 1288-1292.

Comment [SK11]: Not mentioned in the text

DOLMA, T., REDDI SEKHAR, M. AND RAJA REDDY., 2010, Genetic variability, correlation and path analysis for yield, its components and late leaf spot resistance in groundnut (*Arachis hypogaea* L.). *Oilseeds Res. J.*, **27**(2): 154- 157.

Comment [SK12]: Not mentioned in the text

FEDERER, W. T., 1956, Augmented designs. *Hawaiian Planters Record*, **55**: 191-208.

Comment [SK13]: Not mentioned in the text

FISHER, R. A. AND YATES, F., 1963, Statistical tables for biological, agricultural and medical research, Oliver and Boyd, Edinburgh. *Heredity*, **63**: 73-81.

Comment [SK14]: Not mentioned in the text

GAUTAMI, B. K., RAVI, M. L., NARASU, D. A., HOISINGTON. AND VARSHNEY, R. K., 2009, Novel set of groundnut SSR markers for germplasm analysis and interspecific transferability. *Int. J. Integrative Biol.*, **7**(2): 100-106.

GOLAKIA, P. R., MAKNE, V. G. AND MONPARA, B. A., 2005, Heritable variation and association in Virginia runner and Spanish bunch group of groundnut. *Nat. J. Plant. Imprv.*, **7**(1): 50-53.

GONYANAYAK, P., VENKATAIAH, M., REVATHI, P. AND SRINIVAS, B., 2018, Correlation and genetic variability studies in groundnut (*Arachis hypogaea* L.) genotypes. *Int. J. Genet.*, **10**(2): 354-356.

Comment [SK15]: Not mentioned in the text

GOPINATH, J., VENKATARAVANA, P. AND RAO, M. R. G., 2008, Evaluation of water use efficient groundnut germplasm and identification of elite genotypes for Southern Karnataka. *Legume Res.*, **31**(2): 122-125.

Comment [SK16]: Not mentioned in the text

GOURANGA, S. M., ARPITA, D., DEBIKA, D., BHOLANATH, M., BIJOY, K. S., 2017, Genetic variability and character association studies in groundnut (*Arachis hypogaea* L.). *Scholars J. Agric. Vet. Sci.*, **4**(10): 424-433.

Comment [SK17]: Not mentioned in the text

HALWARD, T., STALKER, H. T., LARUE, E. AND KOCHERT, G., 1991, Genetic variation detectable with molecular markers among unadapted germplasm resources of cultivated peanut and related wild species. *Genome*, **34**: 1013-1020.

HUANG, L., HE, H., CHEN, W., REN, X., CHEN, Y., ZHOU, X., XIA, Y., WANG, X., JIANG, X., LIAO, B. AND JIANG, H., 2015, Quantitative trait locus analysis of agronomic and quality related traits in cultivated peanut (*Arachis hypogaea* L.). *Theor. Appl. Genet.*, **128**:1103-1115.

Comment [SK18]: Not mentioned in the text

INJETI, S. K., VENKATARAVANA, P. AND RAO, M. R., 2008, Evaluation of new germplasm and advanced breeding lines of groundnut (*Arachis hypogaea* L.) under late *kharif* situation. *Legume Res.*, **31**(4): 254-258.

Comment [SK19]: Not mentioned in the text

JAYALAKSHMI, V., RAJAREDDY, C. AND REDDY, G. L. K., 2001, Heterosis in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **23**(3): 155-158.

Comment [SK20]: Not mentioned in the text

JOHN, K., RAGHAVA REDDY, P., HARIPRASAD REDDY, P., SUDHAKAR, P. AND ESWAR REDDY, N. P., 2011, Genetic variability for morphological, physiological, yield and yield traits in F₂ population of groundnut (*Arachis hypogaea* L.). *Int. J. Appl. Biol. Pharma. Technol.*, **2**(4): 463-469.

Comment [SK21]: Not mentioned in the text

JOHN, K., VASANTHI, R. P., VENKATESWARLU, O., MURALIKRISHNA, T. AND HARINATH, N. P., 2008, Genetic analysis and regression studies for yield and yield attributes in F₂ segregating population of groundnut crosses. *Legume Res.*, **31**(1): 26-30.

JOHN, P. M., ALIYU, B., ADENIJI, T. O. AND BELLO, D., 2013, Seasonal variation and Pearson correlation in yield and yield components in Bambara groundnut (*Arachis hypogaea* L.). *World J. Agric. Sci.*, **8**(1): 26-32.

JOHNSON, R. C., MUEHLBAUER, F. J. AND SIMON, C. J., 1955, Genetic variation in water use efficiency and its relation to photosynthesis and productivity in lentil germplasm. *Crop Sci.*, **35**:457-463.

Comment [SK22]: Not mentioned in the text

KAMADI, S. R., PATIL SHANTI, R., KADU, P. R., BHASME SHUBHANGI, P. AND KOTHIKAR. R. B., 2017, Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.). College of Agriculture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Nagpur, Akola.

Comment [SK23]: Not mentioned in the text

KHOTE, A. C., PATIL, P. P., PATIL, S. P. AND WALKE, B. K., 2009, Genetic variability studies in groundnut (*Arachis hypogaea* L.). *Int. J. Plant Sci.*, **4**(1): 141-149

Comment [SK24]: Not mentioned in the text

KORAT, PITHIA, V. P., SAVALIYA, M. P., PANSURIYA, J. AND SODAVADIYA, P. R., 2009, Studies on genetic variability in different genotypes of groundnut (*Arachis hypogaea* L.). *Legume Res.*, **32**(3): 224-226.

Comment [SK25]: Not mentioned in the text

KORAT, V. P., PITHIA, M. S., SAVALIYA. J. J., PANSURIYA, A. G. AND SODAVADIYA, P. R., 2010, Studies on characters association and path analysis for seed yield and its components in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **33**(3): 211-216.

Comment [SK26]: Not mentioned in the text

KRAPOVICKAS, A. AND GREGORY, W. C., 1994, Taxonomy of genera *Arachis* (*Leguminosae*). *Bonplandia*, **8**:1-186.

KUMAR, C. V. S. AND RAJAMANI, S., 2004, Genetic variability and heritability in groundnut (*Arachis hypogaea* L.). *Progressive Agric.*, **4**(1): 69-70.

Comment [SK27]: Not mentioned in the text

- LUSH, J. L., 1945, Heritability of quantitative characters in farm animals. *Proc. 8th Cong. Genet. Heriditas.*, **35**: 356-375. Comment [SK28]: Not mentioned in the text
- MAHALAKSHMI, P., MANIVANNAN, N. AND MURALIDHARAN, V., 2005, Variability and correlation studies in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **28**(3): 194-197. Comment [SK29]: Not mentioned in the text
- MAHESH, R. H., HASANKHAN, B.V., TEMBURNE, J. P. AND AMAREGOUDA, A., 2018, Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *J. Pharmacogn. Phytochem.*, **7**(1): 870-874. Comment [SK30]: Not mentioned in the text
- MAKHANLAL, R. D. AND OJHA, O. P., 2003, Genetic variability and selection response for root and other characters in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **26**(2): 128-130. Comment [SK31]: Not mentioned in the text
- MAKINDE, S. C. O. AND ARIYO, O. J., 2013, Genetic divergence, character correlations and heritability study in 22 accessions of Groundnut (*Arachis hypogaea* L.). *J. Plant Studies*, **2**(1): 7-17. Comment [SK32]: Not mentioned in the text
- MALLIKARJUN, K. AND SAVITHRAMMA, D. L., 2017, Genetic variability, heritability, correlation and regression in F₃ and F₄ segregating generation for traits related to WUE and yield in the cross NRCG 12274 × ICG 12370 of groundnut (*Arachis hypogaea* L.). *Int. J. Curr. Microbiol. Appl. Sci.*, **6**(11): 3912-3921. Comment [SK33]: Not mentioned in the text
- MOHAN, K., VISHNUVARDHAN, R. P., VASANTHI, K., HARIPRASAD R. AND BHASKAR REDDY, B. V., 2012, Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). *Int. J. Appl. Biol. Pharma. Technol.*, **3**(1): 390-394.
- MONISHA, M., SAIKAT, G. AND RAJIB, K., 2019, Genetic variability, character association and genetic divergence in groundnut (*Arachis hypogaea* L.). *Legume Res.* Comment [SK34]: Not mentioned in the text
- MUKESH, B. AND LAL, G. M., 2017, Estimation of genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.). *germplasm. Chem. Sci. Rev. Lett.*, **6**(22): 1107-1112. Comment [SK35]: Not mentioned in the text
- NAAZER, A., MALIK, S.N., KHURRM, B. AND MIRZA, M. Y., 2000, Genetic variability, heritability and correlation studies in groundnut. *Sarhad J. Agric.*, **16**: 533-36. Comment [SK36]: Not mentioned in the text
- NAGAVENI, K. AND HASAN, KHAN., 2019, Genetic variability studies in terminal drought tolerant groundnut (*Arachis hypogaea* L.). *J. Pharmacogn. Phytochem.*, **8**(2): 747-750. Comment [SK37]: Not mentioned in the text

- NAGDA, A. K., DASHORA, A. AND JAIN, D. K., 2001, Character association in parents and hybrids of groundnut (*Arachis hypogaea* L.). *Crop Res.*, **22**(3): 463-468. Comment [SK38]: Not mentioned in the text
- NANDINI, C., SAVITHRAMMA, D. L. AND BABU, N. N., 2011, Genetic variability analysis for water use efficiency in F₈ recombinant inbred lines of groundnut (*Arachis hypogaea* L.). *Curr. Biotica.*, **5**(3): 282-288. Comment [SK39]: Not mentioned in the text
- NARASIMHULU, R., KENCHANAGOUDAR, P. V. AND GOWDA, M. V. C., 2012, Study of genetic variability and correlations in selected groundnut genotypes. *Int. J. Appl. Biol. Pharma. Technol.*, **3**(1): 355-358. Comment [SK40]: Not mentioned in the text
- NATH, U. K. AND ALAM, M. S., 2002, Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea* L.). *Online J. Biol. Sci.*, **2**(11): 762-764.
- OLUSANYA, C. A. AND MONINUOLA, A. A. V., 2016, Genotypic variation and correlations between yield system traits and yield components in African landraces of bambara groundnut. *S. Afr. J. Plant and Soil*, **34**(2): 125-137. Comment [SK41]: Not mentioned in the text
- OMIMA, B. H., AHMED, H. A. A., ADEL, M. F. AND AMIN, A. A., 2018, Variability, heritability and genetic advance of some groundnut genotypes (*Arachis hypogaea* L.) under saline sodic soil. *Ann. Rev. Res.*, **1**(1): ARR.MS.ID.555554. Comment [SK42]: Not mentioned in the text
- PADMAJA, D. S., ESHWARI, K. B., BRAHMESWARA R. M. V. AND MADHUSUDHAN, R., 2013, Genetic variability parameters for yield components and late leaf spot tolerance in BC₁F₂ population of groundnut (*Arachis hypogaea* L.). *Int. J. Innovative Res. Dev.*, **2**(8): 348-354.
- PADMAJA, D., ESWARI, K. B., BRAHMESWARA, R. M. V. AND SHIVAPRASAD, G., 2015, Genetic variability studies in F₂ population of groundnut (*Arachis hypogaea* L.). *Helix*, **2**: 668-672. Comment [SK43]: Not mentioned in the text
- PARAMESHWARAPPA, K. G., SHOBHAKRUPARANJI, K., MOHAN, G. AND BENTUR, 2005, Genetic Variability and character association in large seeded groundnut genotypes. *Karnataka J. Agric. Sci.*, **18**(2): 329-333. Comment [SK44]: Not mentioned in the text
- PRABHU, R., MANIVANNAN, N., MOTHILAL, A. AND IBRAHIM, S. M., 2017, Variability analysis for yield, yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). *Int. J. Pure Appl. Biosci.*, **5**(2): 206-214. Comment [SK45]:
- PRAKASH, B. G., KHANURE, S. K. AND SAJJANAVAR, G. M., 2000, Variability studies in spreading groundnut. *Karnataka J. Agric. Sci.*, **13**: 988-990.
- RAMAKRISHNAN, P., MANIVANNAN, N., MOTHILAL, A. AND MAHALINGAM, L., 2017, Correlation studies in back cross derived population for foliar disease Comment [SK46]: Not mentioned in the text

resistance in groundnut (*Arachis hypogaea* L.). *Int. J. Curr. Microbiol. Appl. Sci.*, **6**(5): 266-272.

RAO, V. T., VENKANNA, V., BHADRU, D. AND BHARATHI, D., 2014, Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *Int.J. Pure App. Biosci.*, **2**(2): 194-197.

Comment [SK47]: Not mentioned in the text

ROBINSON, H. F., COMSTOCK, R. E. AND HARVEY, P., 1949, Estimation of heritability and degree of dominance in corn. *Agron. J.*, **41**: 353-359.

Comment [SK48]: Not mentioned in the text

SAVAGE, G. P. AND KEENAN, J. I., 1994, The composition and nutritive value of groundnut kernels. In: *The Groundnut Crop: A Scientific Basis for Improvement*. (Eds.) Smart, J., Chapman and Hall London. 173-213.

SHASHIKUMARA, P., SANJEEV, B. G. AND VENKATARAVANA, P., 2016, Assessment of genetic variability and identification of transgressive segregants for pod yield and its component traits in F₂ segregating generation of groundnut (*Arachis hypogaea* L.). *Int. J. Farm Sci.*, **6**(4): 53-60.

SHINDE, P. P., KHANPARA, M. D., VACHHANI, J. H., JIVANI, L. L. AND KACHHADIA, V. H., 2010, Genetic variability in Virginia bunch groundnut (*Arachis hypogaea* L.). *Plant Archives*, **10**(2): 703-706.

SHOBHA, D., MANIVANNAN, N. AND VINDHIYAVARMAN, P., 2010, Gene effects of pod yield and its components in three crosses of groundnut (*Arachis hypogaea* L.). *Elec J. Plant Breed.*, **1**(6):1415-1419.

Comment [SK49]: Not mentioned in the text

SHRIDEVI, J. A., 2014, Genotypic variability for yield, its component traits and rust resistance in recombinants of groundnut (*Arachis hypogaea* L.). *Karnataka J. Agric. Sci.*, **27**(1): 71-73.

Comment [SK50]: Not mentioned in the text

SIRISHA, P. AND VASANTHI, R. P., 2005, Genetic studies in F₃ and F₄ generations of five crosses in groundnut (*Arachis hypogaea* L.). *M. Sc. (Agri.) Thesis*, Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Comment [SK51]: Not mentioned in the text

STALKER, H. T. AND DALMACIO, R. D., 1986, Karyotype analysis and relationships among varieties of *Arachis hypogaea* L. *Cytologia*, **58**:617-629.

Comment [SK52]: Not mentioned in the text

STALKER, H. T., 1992, Utilization *Arachis* germplasm resources. In S. N. Nigam (ed.) *Groundnut-A Global Perspective. Proc. Int. Workshop, ICRISAT*, 281-295.

Comment [SK53]: Not mentioned in the text

SUDHA, J. D., VASANTHI, R. P., RAJA R. K. AND SUDHAKAR, P., 2012, Variability, heritability and genetic advances in F₂ generation of 15 crosses involving bold-

Comment [SK54]: Not mentioned in the text

seeded genotypes in groundnut (*Arachis hypogaea* L.). *Int. J. Appl. Biol. Pharma. Technol.*, **3**(1): 368-372.

SUMATHI, P., AMALABALU, P. AND MURALIDHARAN, V., 2009, Genetic variability for pod characters in large seeded genotypes of groundnut (*Arachis hypogaea* L.). *Adv. Plant Sci.*, **22**(1): 281-283.

SUNDARA **RAJ**, N., NAGARAJU, S., VENKATARAMU, M. N. AND JAGANNATH, M. K., 1972, Design and analysis of field experiments. Directorate of research, Univ. Agric. Sci., Bangalore, India. Pp. 419.

TIRKEY, S. K., EKHLAQUE, A. AND MAHTO, C. S., 2018, Genetic variability and character association for yield and related attributes in groundnut (*Arachis hypogaea* L.). *J. Pharmacogn. Phytochem.*, **1**: 2487-2489.

TOPROPE, V. N., SYED, A. A. J., PATIL, D. K. AND GITE, V. K., 2013, Genetic variability and character association in groundnut. *J. Agric. Res. and Tech.*, **38**(3): 393-397.

UMA, R. B., VENKATARAVANA, P. AND PRIYADARSHINI, S. K., 2018, Genetic variability studies in F₂ and F₃ population of three crosses of groundnut (*Arachis hypogaea* L.). *J. Pharmacogn. Phytochem.*, **7**(5): 3139-3143.

VANGE, T. AND MAGA, T. J., 2014, Genetic characteristics and path coefficient analysis in ten groundnut varieties (*Arachis hypogaea* L.). evaluated in the Guinea Savannah agro-ecological zone. *African J. Agri. Res.*, **9**(25): 1932-1937.

VASANTHI, R. P., SUNEETHA, N. AND SUDHAKAR, P., 2015, Genetic variability and correlation studies for morphological, yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **38**(1): 9-15.

VAVILOV, N. I., 1926, Studies on the origin of cultivated plants. *Inst. Appl. Bot. Plant Breed.*, Leningrad.

VINITHASHRI, G., MANIVANNAN, N., VISWANATHAN, P. L. AND SELVAKUMAR, T., 2019, Genetic variability, heritability and genetic advance of yield and related traits in F₃ generation of groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.*, **10**(3): 1292-1297.

WEBER, C. R. AND MURTHY, B. R., 1952, Heritable and non-heritable relationships and variability for oil content and agronomic characters in the F₂ generation of soybean crosses. *Agron. J.*, **44**: 202-209.

YADLAPALLI, S., 2014, Genetic variability and character association studies in groundnut (*Arachis hypogaea* L.). *Int. J. Plant Animal Environ. Sci.*, **4**(4): 298-300.

Comment [SK55]: Not mentioned in the text

Comment [SK56]: Not mentioned in the text

Comment [SK57]: Not mentioned in the text

Comment [SK58]: Not mentioned in the text

Comment [SK59]: Not mentioned in the text

Comment [SK60]: Not mentioned in the text

ZEKERIA, Y., HABTAMU, Z., WASSU, M., SHIMELIS, H. AND ARNO, H., 2017,
Estimate of genetic variability parameters among groundnut (*Arachis hypogaea* L.).
genotypes in Ethiopia. *Int. J. Plant Breed. Crop Sci.*, **4**(2): 225-230.

UNDER PEER REVIEW