



Genetic Variability and Correlation Studies in Advance Families of Groundnut (*Arachis hypogaea* L)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Genetic variability is a major component which helps in selecting better genotypes under different environmental conditions. Thus, this study was conducted to understand the genetic variability and its components and their trait associations of yield characters from the cross of GKVK-13 and KCG-2 that contribute to the F6 and F7 families. In an augmented block design with three checks, TMV-2, KCG-6, and KCG-2, the study was carried out at the University of Agricultural Sciences, Bangalore, in the 2017 summer and Kharif (rainy seasons). Highly significant differences between the families were found in the analysis of variance for all the characters studied in the F6 and F7 generations, indicating that there is enough variation. Furthermore, medium to high Phenotypic coefficient of variation and Genotypic coefficient of variation values coupled with high heritability and medium to high genetic advance as *per cent* mean observed in most of the traits showed that the majority of the attributes were controlled by additive gene activity and that there was adequate variability. In addition, phenotypic correlation coefficients depicted significant positive associations

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for most of the traits studied. The implications of the results are discussed. The study concludes that there was the presence of additive genes controlling most of the traits and early selection of these traits is possible for groundnut improvement in the breeding programme.

Keywords: *Genotypic coefficient of variation; phenotypic coefficient of variation; heritability; genetic advance; water use efficiency.*

1. INTRODUCTION

The annual herb known as groundnut (*Arachis hypogaea* L.), which has the chromosomal number $2n=40$, is a self-pollinating, cleistogamous member of the Leguminaceae family. In terms of acreage and productivity, it is the most significant oilseed crop in both India and the entire world. It is referred to informally as peanut, monkey nut, earthnut, and pigmy nut among other names. Two subspecies of cultivated groundnut, subs. fastigiata and subsp. hypogaea, are recognised. The var. vulgaris, var. fastigiata, var. peruviana, and var. aequatoriana are the four botanical varieties that make up the subsp. fastigiata. Two varieties, var. hypogaea and var. hirsuta, make up the subsp. hypogaea. According to Krapovickas and Gregory [1], each of the botanical types has distinctive plant, pod, and seed features. Low yield levels can be linked to a variety of factors, including scarcity or unavailability. Yield is a complex trait, controlled by many genes and there is ample evidence to show that selection directly for grain yield in plants is not easy. Since the groundnut's economic component is a pod that grows underground, predicting its performance using aerial morphological traits is nearly impossible [2]. Since groundnut pod yield is not only polygenically controlled but also influenced by its component characters, the gain under direct selection for pod yield is low and slow [3]. For the purpose of creating high yielding genotypes, it is crucial to understand the current variability, the strength of the link between pod yield and its contributing characters, and the relative contribution of each character to pod yield. Breeders can estimate the level of genetic variety in crops using tools like heritability and genetic progress. To determine the strength of the relationship between the characters, correlation analysis is helpful. The results revealed that high PCV and GCV was observed for harvest index and pod yield per hectare (q) respectively. High heritability accompanied with high genetic advance as *per cent* of mean was recorded for number of mature pods per plant, biological yield per plant (g), pod yield per plant (g), biological yield per hectare (q), pod yield per hectare (q),

harvest index, kernel yield per plant (g), kernel yield per hectare(q) 100 kernel weight (g) and oil yield per hectare (q) which indicated the preponderance of additive gene action which may be exploited through simple selection methods.

“The quantity of water used in transpiration to create dry matter during a certain growth cycle is known as water usage efficiency (WUE). One of these traits that will boost productivity when faced with drought stress is WUE. Many easily measurable traits with a strong correlation to WUE are referred to as surrogate traits. Specific leaf area (SLA) and chlorophyll content, which are often assessed using a SoilPlant Analysis Development (SPAD) chlorophyll metre, are characteristics that have practical benefits for WUE” [4]. It has been suggested that SLA can be used as a surrogate characteristic to evaluate WUE in groundnut by Nageswara Rao et al. [5] and Sheshashayee et al. [6] who found “a direct association between SLA and carbon isotope discrimination and an indirect correlation with WUE in groundnut”. “The SPAD chlorophyll meter (SCMR) has been used effectively to determine leaf nitrogen content non-destructively in several crops including groundnut” [5]. “They reported significant and high negative inter-relationship among SLA and SCMR. The genotypes PI 502120 and AU-NPL 17 were recognised by Zhang et al. [7] as water spender genotypes because they demonstrated high yield, 13C, photosynthesis, and stomatal conductance during drought”. Upadhyaya [8] reported “a negative connection between SCMR and SLA and employed SCMR and SLA as surrogate characteristics for measuring WUE in the groundnut micro core germplasm collection. Heritability and genetic advance are important selection parameters”. “The ratio of GCV to the PCV or total variance (broad sense) or the ratio of genotypic variance to the phenotypic variance (narrow sense) is known as heritability, which indicates the heritable portion of phenotypic variance and a good index of the transmission of characters from parents to offspring. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under

selection than heritability estimate alone, it is not necessary that a character showing high heritability will also exhibit high genetic advance” [9].

Heritability value alone cannot provide information on the amount of genetic progress that would result from selection of best individuals. Johnson et al. [9] reported that heritability estimates along with genetic gain would be more useful in predicting the effectiveness of selecting the best individuals. Thus, the objective of this study was to assess the genetic variability and correlations amongst traits in groundnuts under water stress conditions to identify superior families for varietal development.

2. MATERIALS AND METHODS

2.1 Plant Matter and the Experiment's Location

The current study was carried out at the experimental field, GKVK, of the University of Agricultural Sciences, Bangalore, during the summer and Kharif of 2017. The 36 F6 and 24 F7 families of the cross GKVK-13 KCG-2 as well as the checks KCG-6, KCG-2, and TMV-2 made up the experimental material for this investigation. By mating parents who differed in terms of SLA, SCMR, pod yield per plant, kernel yield per plant, and pods per plant, populations were created. The F5 generation of the cross's chosen families were passed on to the F6 generation, and the process was repeated to raise the F7 generation.

2.2 Analysis of the F6 Generation

“During the summer of 2017, the F6 plants of the cross, along with their respective parents and checks (KCG-2, KCG-6, and TMV-2), were raised using the plant to progeny row method in an augmented design with 5 m rows and 30 cm and 10 cm of inter and intra row spacing, respectively” [4].

2.3 Analysis of the F7 Generation

“Individual F6 progenies were chosen and sown in a plant to progeny row for F7 evaluation of the traits SPAD chlorophyll metre reading (SCMR), pod yield, kernel yield, shelling percentage, and sound mature kernel (SMK) per cent. These progenies had mean values higher than the families grand mean and mean more than the

checks and the parents for the traits. They also had low mean values for specific leaf area (SLA)” [4].

2.4 Motif Information

“Ten morphological characteristics were recorded, including the days to 50% flowering (days to first flowering), plant height (cm), primary branches per plant, pods per plant, pod yield per plant (g), kernel yield per plant (g), shelling percentage, sound mature kernel (SKM) percentage, specific leaf area (SLA), and SPAD chlorophyll metre reading (SCMR)” [4]. The following formulas were used to obtain the shelling percentage. The following formulas were used to calculate the sound mature kernel (SMK) percentage and kernel weight (g)/pod weight (g) 100. Number of fully formed kernels divided by the total number of kernels is 100.

2.5 Water-Saving Characteristics

Specific leaf area (SLA): At 65 days following seeding, the second or third fully grown leaf of the main axis was harvested in butter paper coverings. A leaf area metre was used to calculate the leaf area. The leaves were then stored for three days at 70°C in an oven. A delicate balance was used to precisely measure the leaf's dry weight. Using the formula below, SLA was calculated and expressed as cm²/g.

SCMR for the SPAD Chlorophyll Metre: Chlorophyll content in leaves is typically influenced by nitrogen levels. The Minolta firm in New Jersey, USA, has created a device called the SPAD-502 that detects the light attenuation at wavelengths of 430 nm (the peak wavelength for chlorophyll a and chlorophyll b) and 750 nm.

2.6 Statistical Analysis

The mean data was analyzed using WINDOSTAT *version* 8.5 for augmented design and Statistical Packages for Social Sciences (SPSS) *version*..... was used for descriptive statistics. Phenotypic and genotypic coefficients were worked out as suggested by Burton [10].

Phenotypic coefficient of variance (PCV (%)) = $\frac{\sqrt{\text{Phenotypic variance}}}{\text{General mean}} \times 100$

$$\text{Genotypic coefficient of variance (GCV (\%))} = \frac{\sqrt{\text{Genotypic variance}}}{\text{General mean}} \times 100$$

Heritability in broad sense was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage, Lush [11].

$$\text{Heritability in Broad sense } h_{bs}^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$$h_{bs}^2 = \text{Heritability per cent (Broad sense)}$$

$$\sigma_g^2 = \text{Genotypic variance}$$

$$\sigma_p^2 = \text{Phenotypic variance}$$

The extent of genetic advance expected through selection for each character was estimated by using the following formula of Johnson et al. [9].

$$GA = h^2 \times K \times \sigma_p$$

Where,

GA= Genetic Advance
 h^2 = heritability estimate
 K = selection differential which is equal to 2.06 at 5 per cent intensity of selection.
 σ_p = phenotypic standard deviation

3. RESULTS AND DISCUSSION

Groundnut F6 and F7 generations were used in the analysis of variance for features associated to water usage efficiency, pod yield, and its component characters.

The results of the analysis of variance for growth, water use efficiency traits, yield, and its component characters in the F6 and F7 generations of the groundnut cross GKVK-13 KCG-2 are shown in Table 2 and Fig. 1. For all of the features, the mean sum of squares of families showed a highly significant difference. With the exception of SMK percent in the F6 generation, which was not significant, similar results were seen in the checks versus families. As a result, selection for additional breeding could be based on the variations seen in the types.

3.1 Estimates of Genetic Variability, Characteristics, and Pod Yield Parameters

The genetic variability parameters were analyzed and presented in the Table 3. From our study the

presence of wider range of variation was observed for plant height (25 to 35 cm with the mean of 30.22), SCMR (26.29 to 42.91 with the mean of 35.99), pods per plant (13 to 41.14 with the mean of 25.18), pod yield per plant (8.35 to 32.64 with the mean yield of 20.13) kernel yield per plant (3.82 to 19.51 with the mean of 11.45), SMK *per cent* (24.88 to 89.36 with the mean of 61.61) and shelling *per cent* (35.70 to 80.86 with the mean of 60.76) in F₆ generation, similarly wider range of variation was observed for plant height (11.50 to 46.45 cm with the mean of 30.17), SCMR (33.56 to 50.78 with the mean of 41.36), pods per plant (9 to 52 with the mean of 27.70), pod yield per plant (6.28 to 43.25 with the mean yield of 23.17) kernel yield per plant (3.60 to 27.20 with the mean of 13.74), SMK *per cent* (26.37 to 94.01 with the mean of 61.90) and shelling *per cent* (50.48 to 69.84 with the mean of 61.30) in F₇ generation, suggest that there is presence of wider range of phenotypes hence selection can be practiced.

With regard to plant height, pods per plant, pod yield per plant, kernel yield per plant, and SMK percent in F6 and F7 generation, there is a high GCV and high PCV in addition to a small gap between GCV and PCV. The presence of some degree of variation in the aforementioned qualities is indicated by the medium to high estimations of GCV and PCV. As a result, these qualities can be practised in individual plant selection. In the BC1F1, BC1F2, and BC1F3 populations, Chauhan et al. [12] showed high GCV, PCV for shelling%, kernel yield per plant, and pod yield per plant. Meta and Monpara [13], Makhan et al. [14], Golakia et al. [15], John et al. [16], Rao et al. [17], and Vishnuvardhan et al. [18] all reported similar findings. Sridevi et al. [19] in groundnut. Lower GCV and PCV were recorded for days to first flowering and SCMR in F₆ and F₇ generation, SLA (F₆) and shelling % (F₇). This indicates the lower magnitude of variability for these traits in relation to their generations. Narrow difference between GCV and PCV observed generally indicated that the environmental influence was less and the variability present was mostly controlled by additive genes and thus early selection using these traits could be possible. These results are in agreement with Makhan Lal et al. [14]; Nandini et al. [20] John et al. [21];. Khote et al. [22]; Vishnuvardhan et al. [18] and Maurya et al. [23].

Important selection criteria include heritability and genetic progress. Heritability, which denotes the heritable portion of phenotypic variance and is a

reliable indicator of the transmission of traits from parents to offspring, is measured as the ratio of GCV to PCV, or total variance (in the broad sense), or as the ratio of additive genetic variance to the phenotypic variance (in the narrow sense). It is not always the case that a character exhibiting high heritability will also exhibit strong genetic advance [9]. Heritability estimates combined with genetic advance are typically more helpful in predicting the gain under selection than heritability estimate alone.

Heritability value alone cannot provide information on the amount of genetic progress that would result from selection of best individuals. Johnson et al. [9] reported that heritability estimates along with genetic gain would be more useful in predicting the effectiveness of selecting the best individuals. High heritability coupled with medium to high genetic advance over mean was recorded for all

the traits except days to flower (F_6) and SCMR (F_6) (Table 3). The results indicated that these characters were under the influence of additive genetic control and selection will be effective in contributing to yield. Similar results of High heritability coupled with high genetic advance over mean were reported by Nath et al. [24] and Golakia et al. [15] for plant height, pods per plant and pod yield per plant Rao et al. [17] for pods per plant, Padmaja et al. [25] for pod yield per plant, Zaman et al. [26] and Rao et al. [17] for kernel yield per plant, Reddi et al. 1991; Venkataravana et al. 2001 for SMK *per cent*. High heritability accompanied with low genetic advance as *per cent* of mean was noticed for traits like days to first flowering and SCMR in the F_{6-7} generation. This indicates the presence of non-additive gene action and narrow range of variation for these traits suggesting limited scope for further improvement of these characters. Similar results were reported by Makhan et al. [14] in groundnut.

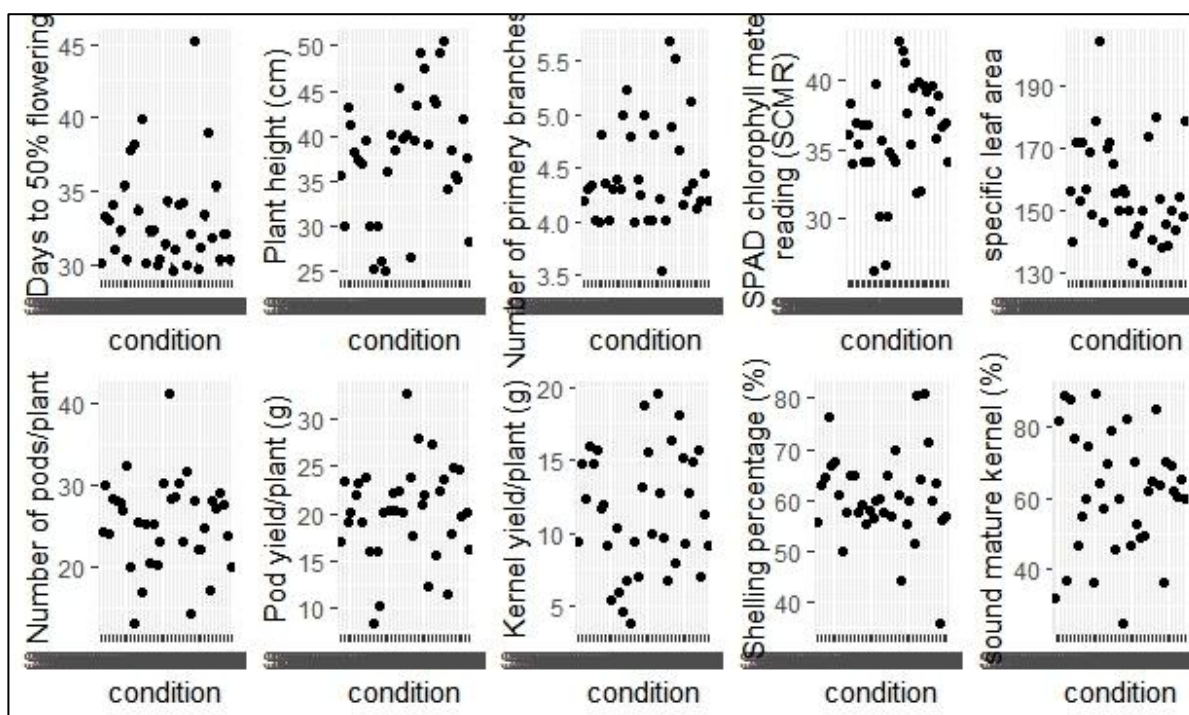


Fig. 1. Box plots depicting variation in studied traits of groundnut

Table 1. Important characteristics of parents and checks

Genotypes	SCMR	SLA (cm ² /g)	Pods/plant	Pod yield (g/plant)	SMK (%)
GKVK-13	42.44	140.17	27.32	25.00	87.00
*KCG-2	34.25	160.20	22.00	20.29	71.00
*KCG-6	45.39	142.00	30.14	29.28	65.12
*TMV-2	35.38	152.15	18.00	15.00	60.75

Table 2. Analysis of variance for water use efficiency, pod yield and its component characters in F₆ and F₇ generation

SV	Generations	df	DFF	Plant height (cm)	Primary Branches plant ⁻¹	SCMR	SLA(cm ² /g)	Pods Plant ⁻¹	Pod yield plant ⁻¹ (g)	Kernel yield plant ⁻¹ (g)	Shelling (%)	SMK (%)
Blocks	F ₆	5.00	17.95	58.97**	0.64	13.47	134.06	21.51	16.86	15.51	34.35	128.73
	F ₇	3.00	12.75	43.95*	0.23	28.42	131.41	78.19	15.48	14.76	32.84	258.34*
Checks	F ₆	2.00	12.88	20.86	0.24	25.83	156.16	90.84*	17.25	27.07	36.33	372.23**
	F ₇	2.00	12.23	25.49	1.007	34.42	126.58	25.88	18.95	36.87	18.34	109.08
Families	F ₆	35.00	30.14**	47.15**	10.15**	194.82**	248.65**	129.85**	104.57**	87.42**	77.95**	280.86**
	F ₇	23.00	20.82**	171.53**	10.53**	221.56**	244.56**	116.39**	95.49**	100.11**	89.02**	256.33**
Checks vs. Families	F ₆	70.00	59.25**	183.04**	33.96**	311.98**	370.93**	553.97**	138.76**	116.81**	125.54**	89.56
	F ₇	46.00	25.68*	152.10**	20.15**	322.55**	300.12**	655.16**	122.05**	133.60**	129.84**	337.43*
Error	F ₆	20.00	2.08	7.21	0.14	5.99	17.80	12.73	11.01	9.11	13.15	25.54
	F ₇	12.00	2.66	6.48	0.04	6.64	13.25	14.33	13.81	6.57	15.16	28.35

Note: * Significant at 0.05 probability level, ** Significant at 0.01 probability level.

SV- Source of variation, df: Degrees of freedom, DFF: Days to first flowering, SCMR: SPAD chlorophyll meter reading, SLA: Specific leaf area, SMK: Sound mature kernels

Table 3. Genetic variability parameters for water use efficiency, pod yield and its component characters in F₆ and F₇ generation

Traits	Crosses	Mean	Range		Standardized range	GCV (%)	PCV (%)	h ² _(bs) %	GAM%
			Min.	Max.					
DFF	F ₆	30.22	25.00	35.00	0.33	05.30	06.79	78.14	09.54
	F ₇	32.13	30.00	35.00	0.16	03.43	03.87	88.64	27.86
Plant height (cm)	F ₆	37.86	25.12	50.60	0.67	12.75	15.92	80.15	26.29
	F ₇	30.17	11.50	46.45	01.18	21.39	24.37	87.81	44.09
Primary branches plant⁻¹	F ₆	04.18	03.00	05.00	0.48	08.30	12.29	67.61	27.24
	F ₇	05.03	04.05	06.13	0.41	12.85	14.60	88.06	26.49
SCMR	F ₆	35.99	26.29	42.91	0.46	08.82	10.42	84.69	03.15
	F ₇	41.36	33.56	50.78	0.41	08.23	10.08	81.73	12.81
SLA(cm²/g)	F ₆	156.22	131.00	204.80	0.47	07.14	9.67	73.90	14.76
	F ₇	127.50	90.00	189.00	0.78	12.09	13.48	89.70	16.02
Pods plant⁻¹	F ₆	25.18	13.00	41.14	01.12	17.84	19.94	89.51	20.33
	F ₇	27.70	09.00	52.00	01.54	27.27	35.18	77.54	41.69
Pod yield plant⁻¹(g)	F ₆	20.13	08.35	32.64	01.21	17.54	22.70	77.28	22.11
	F ₇	23.17	06.28	43.25	01.61	34.23	39.46	86.75	54.25
Kernel yield plant⁻¹(g)	F ₆	11.45	03.82	19.51	01.37	30.56	33.99	89.92	27.96
	F ₇	13.74	03.60	27.20	01.81	37.04	43.16	85.84	31.87

Traits	Crosses	Mean	Range		Standardized range	GCV (%)	PCV (%)	$h^2_{(bs)}\%$	GAM%
			Min.	Max.					
Shelling (%)	F ₆	60.76	35.70	80.86	0.74	10.74	14.41	74.57	19.36
	F ₇	61.30	50.48	69.84	0.32	06.13	07.37	83.29	20.50
SMK (%)	F ₆	61.61	24.88	89.36	01.05	20.76	23.61	87.93	42.77
	F ₇	61.90	26.37	94.01	01.20	20.44	23.98	85.25	42.11

Note: GCV - Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, $h^2_{(bs)}\%$ - Heritability in broad sense, GAM %- Genetic advance as per cent of mean.

Table 4. Phenotypic correlation studies for growth, traits related to water use efficiency, pod yield and its component traits

Traits	Generations	Plant height (cm)	Primary branches plant ⁻¹	SCMR	SLA (cm ² /g)	Pods Plant ⁻¹	Pod yield plant ⁻¹ (g)	Kernel yield plant ⁻¹ (g)	Shelling (%)	SMK (%)
DFF	F ₆	0.25*	0.36**	0.32*	0.24*	-0.33*	0.11	0.45**	-0.22*	0.24*
	F ₇	0.30**	0.50**	0.29*	0.15	-0.46**	0.17	0.29*	-0.27*	0.31**
Plant height(cm)	F ₆	1.00	-0.25*	0.34*	-0.29*	0.36**	0.44**	0.37**	0.36**	0.11
	F ₇	1.00	-0.17*	0.22*	-0.12	0.22*	0.31**	0.33**	0.22*	0.25*
Primary branches plant ⁻¹	F ₆		1.00	0.19*	-0.05	-0.19*	0.30**	0.24*	-0.15	0.22**
	F ₇		1.00	0.32**	-0.08	-0.12*	0.25*	0.33**	-0.18	0.28**
SCMR	F ₆			1.00	-0.34*	0.64**	0.57**	0.75**	0.27*	0.53*
	F ₇			1.00	-0.55**	0.77**	0.69*	0.64**	0.22*	0.65**
SLA(cm ² /g)	F ₆				1.00	-0.38*	-0.58**	-0.57**	-0.23*	-0.20*
	F ₇				1.00	-0.45**	-0.61	-0.49**	-0.35**	-0.32**
Pods plant ⁻¹	F ₆					1.00	0.77**	0.53**	0.52**	-0.33**
	F ₇					1.00	0.85**	0.74**	0.40*	-0.41**
Pod yield plant ⁻¹ (g)	F ₆						1.00	0.83*	-0.58*	0.85**
	F ₇						1.00	0.91**	-0.49*	0.55*
Kernel yield plant ⁻¹ (g)	F ₆							1.00	0.68**	0.73**
	F ₇							1.00	0.55**	0.61*
Shelling (%)	F ₆								1.00	0.40**
	F ₇								1.00	0.56**
SMK (%)	F ₆									1.00
	F ₇									1.00

• Significance @ 0.05%, ** significance @0.01%

• Note: *Significant at 0.05 probability level. ** Significant at 0.01 probability level

3.2 Association Studies Traits Related to Water Use Efficiency, Pod Yield and its Component Characters in F₆ and F₇ Generations of Groundnut

Correlation coefficient is an essential tool. Correlation studies between yield and its component traits would help plant breeders to enhance crop growth and yield of crop. In the present study phenotypic correlation between pod yield per plant with component characters and also with physiological traits were studied in both F₆ and F₇ generations.

Phenotypic correlation coefficients for traits related to water use efficiency, pod yield and yield and its component traits are presented in Table 4. Phenotypic correlation coefficient (0.01% and 0.05%) revealed that pod yield per plant had significant positive correlation with SCMR (0.85, 0.55), pods per plant (0.77, 0.85), kernel yield per plant (0.83, 0.91), DFF (0.11, 0.17) and plant height (0.44, 0.31), however, Pod yield per plant had significant negative correlation with SLA (-0.38, -0.45), SMK *per cent* (-0.58, -0.49) and shelling *per cent* (-0.58, -0.49) in F₆ and F₇ generation. This indicated that improvement in SCMR, pods per plant, kernel yield per plant and plant height will lead to improvement in yield. These results are in accordance with the reports of Sridevi et al. [19], Mukhtar et al. [27], Shoba et al. [28], Koolachart et al. [29] and Thakur et al. [30]. This indicates that selection of traits for low SLA leads to improvement in yield.

Shelling percentage showed significant positive correlation with kernel yield per plant (0.68, 0.55) in F₆ and F₇ generation indicated the shelling *per cent* could be improved by selecting more number of pod per plant with bold kernels. Similar result was noticed by Nandini et al. [20]. SLA exhibited significant negative correlation with SCMR (-0.34, -0.55), pods per plant (-0.38, -0.45), pod yield per plant (-0.58, -0.61) and kernel yield per plant (-0.57, -0.49) in F₆ and F₇ generation, suggesting the improvement of yield and water use efficiency could be done by selecting families that show low SLA. Rekha [31] and Reddy et al. [32] also reported similar kind of outcomes. SCMR exhibited highly significant positive association with pods per plant (0.64, 0.77), pod yield per plant (0.57, 0.69), kernel yield per plant (0.75, 0.64) and SMK *per cent* (0.54, 0.65). Furthermore, SCMR showed negative correlation with SLA (-0.34, -0.55) in F₆ and F₇ generation. Therefore, selection of genotypes with high SCMR offers the scope for simultaneous

improvement of yield and water use efficiency in groundnut as higher SCMR indicate high photosynthetic efficient genotypes. The results are in agreement with the reports of Songsri et al. [33] and Rekha [31]. John et al. [16] for SCMR. This shows that selection of families with SCMR values higher than the checks indirectly could lead to improvement of yield in groundnut since high SCMR indicates high photosynthetic efficient genotypes with high water use efficiency. The reports of Nageshwar Rao et al. (2001), Talwar et al. [34], Rekha [31], John et al. [16] and Krishnamurthy et al. [35] also confirmed the same association in groundnut [36-39].

4. CONCLUSIONS

Analysis of variance for all the characters studied in both F₆ and F₇ generations revealed highly significant differences among the families suggesting the presence of sufficient amount of variability. Thus, the breeding programme can take advantage and utilize these varieties for further crop improvement. Furthermore, medium to high PCV and GCV values coupled with high heritability and medium to high genetic advance as *per cent* mean observed in most of the traits indicated the presence of sufficient variability and involvement of additive gene action in both F₆ and F₇ generations for these traits and early selection for breeding of these traits in groundnuts is possible. Phenotypic correlation coefficient depicted significant positive associations for most of the traits and these traits could be considered in the selection for high yielding groundnut varieties.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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