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Estimation of Genetic Variability Parameters and Parent-offspring Correlation, Regression in 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 major component which helps in selecting better genotypes under different environmental conditions, with this aim an experiment was conducted to understand the genetic potential, heritability, genetic advance and traits association of yield contributing characters for F_6 and F_7 families derived from the cross GKVK-6 × KCG-2 at the University of Agricultural Sciences, Bangalore in an augmented block design along with three checks *viz*., TMV-2, KCG-6 and KCG-2 during summer and *Kharif* 2017. Results from analysis of variance (ANOVA) revealed that highly significant differences were observed for all the characters studied. High genetic variability was observed for major yield contributing characters like the number of pods per plant (g), pod yield (g),

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kernel yield per plant (g), SMK% (sound mature kernel *per cent*), SCMR (SPAD chlorophyll meter reading) and SLA (specific leaf area) (cm^2/g). Narrow difference between GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) was observed for pods per plant, pod yield, SCMR and SLA and high heritability coupled with moderate genetic advance *per cent* mean was recorded for pod yield, SCMR and SLA indicating the involvement of additive gene action in controlling these traits. Three superior families were noticed with more pods plant^{-1}, high pod yield plant^{-1}, high kernel yield^{-1}, high shelling (%), high SMK (%), high SCMR value, and low SLA value. Further, these superior families also revealed the presence of high parent offspring regression and intergeneration correlation, implying increased efficiency of selection for most of the traits considered and these were identified to be the important characters that could be used in selection for yield Keywords: GCV, PCV, Heritability, GAM, water use efficiency, Groundnut.

Keywords: GCV; PCV; heritability; GAM; water use efficiency; groundnut.

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a self-pollinated, cleistogamous annual herb belonging to the family Leguminaceae with a chromosome number of 2n=40. It is the most important oilseed crop of India and the world in terms of area and production. It is vernacularly known by different names as peanut, monkey nut, earthnut and pigmy nut. Cultivated groundnut is classified into two subspecies, subs. *fastigiate* and subsp. *hypogaea*. The subsp. *fastigiata* contains four botanical varieties, var. *vulgaris*, var. *fastigiata*, var. *peruviana*, and var. *aequatoriana*. The subsp. *hypogaea* contain two varieties, var. *hypogaea* and var. *hirsuta*. Each of those botanical types has the contrasting plant, pod and seed characteristics [1]. Yield is a complex trait, governed by many traits and there is ample evidence to show that selection directly for grain yield in plants is not easy. Since the economic a part of groundnut may be a pod that's developed under the soil, prediction of its performance supported aerial morphological characters is nearly difficult [2]. Gain under direct selection for pod yield in groundnut is low and slow as pod yield isn't only polygenically controlled but also influenced by its component characters [3]. The knowledge of existing variability and degree of association between pod yield and its contributing characters and their relative contribution to pod yield is important for developing high yielding genotypes. Heritability and genetic advance is a useful tool for breeders in determining the amount of genetic variation present in crops. Correlation analysis is useful to work out the magnitude of association among the characters and their relative contribution to pod yield. More than 70% of the groundnut growing area falls under arid and semi-arid regions, where groundnut frequently experiences drought stresses for various durations and intensities [4]. Yield losses attributable to drought are highly variable depending on timing, intensity and duration in addition to other location-specific environmental stress factors like high irradiation and temperature [5]. Losses in yield that are due to water stress can be tackled partially by developing varieties that are better adapted to water scares conditions [6].

Water use efficiency is defined as the amount of water utilized in transpiration to produce dry matter during a specific growth period. Water Use Efficiency (WUE) is one such trait which will contribute to productivity under drought. There are numerous easily measurable traits having a high correlation with WUE that are identified as surrogate traits. Traits that have practical advantages for WUE are specific leaf area (SLA) and soil-plant analysis development and SPAD chlorophyll meter reading (SCMR). Nageswara Rao et al. [7] and Sheshashayee et al. [8] reported a direct correlation between SLA and carbon isotope discrimination, and a indirect correlation with WUE in groundnut, suggesting that SLA can be used as a surrogate trait to measure WUE in groundnut. SCMR has been used effectively to determine leaf nitrogen content non-destructively in several crops including groundnut [7] reported significant and high negative inter-relationship among SLA and SCMR. Upadhyaya [9] used SCMR and SLA as surrogate traits for assessing WUE in groundnut mini core germplasm collection and reported a negative correlation between SCMR and SLA. There are many reasons which are attributed to low yield levels *viz.,* lack or non-availability of improved high yielding cultivars, cultivation under shallow soils of low fertility, uneven rainfall distribution, continuous cropping without rotation of crop, low plant population and incidence of foliar diseases and pests are cited as the major limiting factors in most of the groundnut growing regions. Keeping all the above points in view, an effort has been made to study the genetic variability, an association of traits related to WUE with pod yield and its component traits, and to identify superior families performing better under drought stress conditions in F_6 and F_7 generation.

2. MATERIALS AND METHODS

2.1 Plant Material and Experimental Site

The present study was conducted during summer and *Kharif* 2017 at the experimental field, GKVK, University of Agricultural Sciences, Bangalore. The experimental material for the present study comprised of 12 F_6 and F_7 families along with three checks KCG-6, KCG-2 and TMV-2. The populations were developed by crossing the parents which were contrasting for the traits, SLA, SCMR, pod yield per plant, kernel yield per plant and pods per plant. The selected families from the F_5 generation of the cross were forwarded to the F_6 generation and the same procedure was repeated to rise F_7 generation. Statistical analysis of the mean data was analyzed in WINDOSTAT *version* 8.5 for augmented design and SPSS for descriptive statistics.

2.2 Evaluation of Plant Material

The F_6 plants of the cross, their respective parents and checks (KCG-2, KCG-6 and TMV-2) were raised in a plant to progeny row method in an augmented design during summer 2017 with 5 m row length and 30 cm and 10 cm inter and intra row spacing respectively. Individual F_6 progenies which had mean values higher than the families grand mean and mean more than the checks and the parents for the traits *viz.,* SPAD chlorophyll meter reading (SCMR), pod yield, kernel yield, shelling *per cent* and sound mature kernel (SMK) *per cent* and the low mean values for specific leaf area (SLA) were selected and sown in a plant to progeny row for F_7 evaluation of yield and water use efficiency-related traits as the salient features of parents and checks were given in (Table 1).

2.3 Data Recording

The data on ten morphological characters namely 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) *per cent*, specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) were recorded. Shelling percentage: was calculated by using the following formulae. Kernel weight (g)/Pod weight (g) ×100, Sound mature kernel (SMK) *per cent:* was calculated by using the following formulae. Number of well-developed kernels/Total number of kernels ×100.

2.4 Water use Efficient Traits

Specific leaf area (SLA): The second or third fully expanded leaf of the main axis was collected in butter paper covers at 65 days after sowing. The leaf area was measured using a leaf area meter. Then the leaves were kept in an oven at 70 ˚C for 3 days. The dry weight of the leaf was accurately measured using a sensitive balance. SLA was computed using the formula given below and expressed as cm^2/g.

SPAD Chlorophyll Meter Reading (SCMR): Leaf nitrogen content normally influences the leaf chlorophyll content. A device has been developed by Minolta company, New Jersey USA (SPAD-502) which measures the light attenuation at 430 nm (the peak wavelength for chlorophyll a and chlorophyll b) and 750 nm (near-infrared) with no transmittance. The unit less value measured by the chlorophyll meter is termed as SCMR (SPAD chlorophyll meter reading), which provides information on the relative amount of leaf chlorophyll. The SPAD meter (soil-plant analytical development) is a simple handheld instrument, which operates with a DC power of three Volts.

The second or third leaf from the apex was selected to record the SCMR. The selected leaf of groundnut was clamped avoiding the midrib region into the sensor head of the SPAD meter. A gentle stroke was given to record the SPAD reading and the average of such four strokes per leaflet was considered. Since groundnut is a tetra-foliate leaf, SCMR was recorded in all four leaflets and the average value was recorded. The SCMR was recorded under normal sunlight between 9.00 am to 4.00 pm.

2.5 Narrow Sense Heritability Estimates (based on Regression Co-efficient)

Narrow sense heritability estimates were performed based on the regression of F_7 on F_6, using the following formula [10].

$$\mathrm{b}\ (\mathrm{F}_7.\mathrm{F}_6) = \frac{\text{Covariance of } \mathrm{F}_7\mathrm{F}_6}{\text{Variance of } \mathrm{F}_6}$$

h^2 (ns) = b ($F_{7.}F_6$) × 0.85

Regression co-efficient between F_6 and $F_{7,}$ generations was estimated as heritability value using multiplicative factor of 6/7. Heritability estimates were computed for the selected families for all the characters.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

Analysis of variance was carried out for growth, traits related to water use efficiency, yield and its component characters and is presented in Table 1 Fig. 1. Mean sum of squares of families exhibited highly significant difference for all the traits. Further, mean sum of squares of checks *versus* families exhibited greater significant difference for all the characters like days to first flowering, plant height, branches per plant, SCMR, SLA, pod yield per plant, kernel yield per plant and sound mature kernel *per cent* except SMK *per cent*. Hence the choice of material for the study is suitable and further selections could be practiced.

3.2 Estimates of Genetic Variability Parameters

The genetic variability parameters were analyzed and presented in the Table 2. Wide range of variation was observed for the traits SLA (132 to 180.20, 98 to 156 cm^2/g with the mean of 153.47, 122.50), pods per plant (17.50 to 44.16, 18 to 49 with the mean of 28.30, 32.58), pod yield per plant (15.33 to 31.71, 13.74 to 39.25 with the mean of 22.13, 25.81), kernel yield per plant (8 to 19.46, 7.42 to 35 with the mean of 13.41 19.18), shelling% (50 to 65.29, 40.98 to 60.22 with the mean of 58.82, 52.46), SMK% (8.55 to 82, 31.77 to 60.11 with the mean of 58.49, 48.09) in F_6 and F_7 generation respectively. High GCV and PCV with narrow difference between GCV and PCV was observed for the traits Primary branches $plant^{-1}$, Pods $plant^{-1}$, Pod yield plant $^{-1}$(g), Kernel yield plant $^{-1}$(g). High heritability coupled with high GAM was observed for the traits DFF (Days to fifty *per cent* flowering), Plant height, Primary branches $plant^{-1}$, SCMR, SLA(cm^2/g), Pods $plant^{-1}$, Pod yield plant $^{-1}$(g), Kernel yield plant $^{-1}$(g), Shelling (%) and SMK (%).Similar results were reported by Meta and Monpara [11], Makhan et al. [12]; Golakia et al. [13]; John et al. [14]; Rao et al. [15] in groundnut.Similar results of High heritability coupled with high genetic advance over mean were reported by Nath et al. [16] and Golakia et al. [13] for plant height, pods per plant and pod yield per plant which indicates that these characters are under the influence of additive genetic control. Rao et al. [15] for pods per plant, Zaman et al. [17] and Rao et al. [13] for kernel yield per plant, Reddy et al. [18]; Venkataravana et al. [19] for SMK per cent.

3.3 Estimation of Correlation Coefficients

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 F_6 and F_7 generations.

Phenotypic correlation coefficients for traits related to water use efficiency, pod yield and yield and its component traits are presented in Table 3. Phenotypic correlation coefficient revealed that pod yield per plant had significant positive correlation with SCMR (0.65, 0.52), pods per plant (0.94, 0.93), kernel yield per plan (0.76, 0.92), DFF (0.20, 0.39) and plant height (0.46, 0.42), however, Pod yield per plant had significant negative correlation with SLA (-0.43, -0.36), and shelling per cent (-0.42, -0.55) in F_6 and F_7 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 Mukhtar et al. [20], Shoba et al. [21]. Koolachart et al. [22] and Thakur et al. [23]. 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 (0.41, 0.35) in F_6 and F_7 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. [24]. SLA exhibited significant negative correlation with SCMR (-0.67, -0.50), pods per pant (-0.39, -0.48), pod yield per plant (-0.43, -0.36) and kernel yield per plant (-0.43, -0.55) in F_6 and F_7 generation, suggesting the improvement of yield and water use efficiency could be done by selecting families that show low SLA. Rekha [25] and Reddy *et al.* [4] also reported similar kind of outcomes. SCMR exhibited highly significant positive association with pods per plant (0.69, 0.58), pod yield per plant (0.65, 0.52), kernel yield per plant (0.50, 0.48) and SMK *per cent* (0.48, 0.29) in F_6 and F_7 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. [26] and Rekha [25]. John et al. [14] for SCMR. This shows that selection of families whose SCMR value were higher than checks, which indirectly lead to improvement of yield in groundnut as high SCMR indicates high photosynthetic efficient genotypes with high water use efficiency. The reports of Nageshwar Rao et al. (2001), Talwar et al. [27], Rekha [25], John et al. [14] and Krishnamurthy et al. [28] also confirmed the same association in groundnut.

3.4 Estimation of Parent-offspring Correlation, Regression and Heritability in F_6 and F_7 Generations

Data presented in the Table 4 indicates the presence of significant positive correlation coupled with higher magnitude of parent-offspring regression observed for the traits like days to first flowering (r=0.61, b=0.44), plant height (r=0.71, b=0.56), SCMR (r=0.38, b=0.70), pods per plant (r=0.60, b=0.56), pod yield per plant (r=0.53, b=0.67) and kernel yield per plant (r=0.27, b=0.21) respectively. Further high narrow sense heritability was observed for traits like days to first flowering (75.23), plant height (48.31), SCMR (59.79), pods per plant (47.61), and pod yield per plant (57.34) respectively.

Lush [29] defined heritability in broad and narrow sense and emphasized that characters are subjected to different amount of non-heritable variation. The broad sense heritability includes genotypic variance and phenotypic variance, but genotype variance includes both dominance and additive variance and hence not a reliable index for practicing selections. While narrow sense heritability includes additive variance and phenotypic variance, hence, additive variance is a reliable index of the total genotypic variance, and selections will be effective for forwarding the lines to next generation. Hence, a comparison was made between narrow sense and broad sense heritability.

Estimation of parent-offspring correlation, regression and heritability exhibited significant positive intergeneration correlation coupled with higher magnitude of parent-offspring regression between F_6 and F_7 generation for the traits like days to first flowering, plant height, SCMR, pods per plant, pod yield per plant and kernel yield per plant, this suggests that these characters could be used as selection criteria for selection of superior families from F_7 generation. Further high broad sense heritability coupled with high narrow sense heritability has been observed for traits like Days to fifty *per cent* flowering, plant height, SCMR, pods per plant, pod yield per plant, indicated the characters are governed by additive gene action. The higher value of narrow sense heritability suggests that there is predominance of additive gene action in the inheritance of the trait and hence effective selection can be made in the early generation. It helps in estimating the performance of the future generations depending on present generation. Hence, performance of future generations can be estimated depending on the traits having higher value of Narrow sense heritability further improvement of pod yield upon selection could be possible. These findings were supported by Kulkarni et al. [30] and Reddy et al. [31]. Overall three superior families were noticed with more pods plant^{-1}, high pod yield plant^{-1}, high kernel yield^{-1}, high shelling (%), high SMK (%), high SCMR value, and low SLA value (Table 5, Fig. 2).

Table 1. Estimation of Analysis of variance (ANOVA)

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$_6$	2.00	14.33	13.87	0.40	12.91	52.64	29.31	43.16	40.49	11.06	68.76*
	F$_7$	1.00	12.00	28.20	0.53	20.01	54.50	31.52	33.14	39.36	17.69	85.80*
Checks	F$_6$	2.00	12.33	15.04	0.64	54.74	71.40	11.47	21.51	34.65	40.66	55.81
	F$_7$	2.00	10.66	23.74	1.38	32.90	94.00*	20.20	18.78	14.14	32.18	62.83
Families	F$_6$	11.00	22.56**	94.82**	7.59**	180.62**	594.25**	66.16**	139.76**	117.10**	139.94**	91.40**
	F$_7$	11.00	33.36**	104.74**	8.33**	229.74**	651.84**	76.44**	104.86**	127.15**	129.38**	98.51**
Checks *vs.* Families	F$_6$	22.00	48.89**	231.42**	33.45**	528.18**	887.73**	238.88**	357.85**	552.73**	289.41**	331.53**
	F$_7$	22.00	40.11**	387.69**	29.93**	562.87**	2450.25**	183.24**	389.40**	423.19**	335.08**	205.11**
Error	F$_6$	18.00	0.66	2.71	0.08	3.11	6.82	6.90	5.93	3.28	2.85	20.35
	F$_7$	18.00	1.20	1.82	0.05	2.41	4.66	7.88	7.45	2.04	4.55	11.49

*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

Table 2. Estimates of genetic variability parameters

Traits		Mean	Range		Standardized Range	GCV (%)	PCV (%)	$h^2_{(bs)}$%	GAM%
	Crosses		Min.	Max.					
DFF	F_6	30.25	29.00	32.00	0.10	02.31	02.57	89.93	10.53
	F_7	30.44	26.00	35.00	0.30	04.23	05.63	75.23	21.76
Plant height (cm)	F_6	37.83	34.28	41.33	0.19	04.65	05.03	92.50	05.44
	F_7	36.08	12.40	49.36	01.02	19.09	21.83	87.49	25.86
Primary branches plant^{-1}	F_6	04.73	03.20	05.55	0.50	12.77	15.11	84.56	07.65
	F_7	04.86	03.12	07.56	0.91	13.46	15.26	88.23	17.75
SCMR	F_6	38.02	32.00	43.66	0.31	08.42	10.69	78.83	08.55
	F_7	42.98	35.00	55.36	0.47	06.12	06.99	87.63	19.74
SLA(cm^2/g)	F_6	153.47	132.00	180.20	0.31	06.65	9.26	71.86	13.70
	F_7	122.50	98.00	156.00	0.47	08.18	09.08	90.10	16.86
Pods plant^{-1}	F_6	28.30	17.50	44.16	0.94	19.29	24.52	78.68	29.64
	F_7	32.58	18.00	49.00	0.95	17.81	25.20	70.69	35.14
Pod yield plant $^{-1}$(g)	F_6	22.13	15.33	31.71	0.74	19.72	24.14	81.72	30.69
	F_7	25.81	13.74	39.25	0.99	17.91	19.56	91.60	24.83
Kernel yield plant $^{-1}$(g)	F_6	13.41	08.00	19.46	0.85	23.08	29.09	79.37	11.61
	F_7	19.18	07.42	35.00	01.44	26.35	31.89	82.64	10.93
Shelling (%)	F_6	58.82	50.00	65.29	0.26	7.01	08.97	78.21	12.61
	F_7	52.46	40.98	60.22	0.37	06.46	09.16	70.55	13.31
SMK (%)	F_6	58.49	8.55	82.00	01.26	24.65	26.87	91.76	50.79
	F_7	48.09	31.77	60.11	0.59	17.66	18.06	97.82	36.40

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 3. Estimation of phenotypic correlation coefficients

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	0.48**	0.30**	0.32**	0.22*	0.32**	0.20*	0.41**	0.32**	0.30*
	F_7	0.57**	0.36**	0.21*	0.17	0.26*	0.39**	0.39**	0.25*	0.43**
Plant height(cm)	F_6	1.00	-0.20*	0.35*	0.32*	0.41*	0.46**	0.51**	-0.45**	0.48*
	F_7	1.00	-0.32**	0.42	0.35*	0.32**	0.42**	0.45**	-0.37**	0.20*
Primary branches plant $^{-1}$	F_6		1.00	0.39*	-0.18	0.58**	0.32**	0.52**	0.32**	0.45**
	F_7		1.00	0.25*	-0.20	0.46**	0.25*	0.65**	0.44**	0.36*
SCMR	F_6			1.00	-0.67*	0.69**	0.65**	0.50*	-0.58**	0.48*
	F_7			1.00	-0.5**	0.58**	0.52**	0.48*	-036**	0.29*
SLA(cm^2/g)	F_6				1.00	-0.39*	-0.43**	-0.43**	-0.24*	0.18
	F_7				1.00	-0.48**	-0.36**	-0.55**	-0.37**	0.07
Pods plant $^{-1}$	F_6					1.00	0.94**	0.62**	-0.45**	0.21
	F_7					1.00	0.93**	0.87**	-0.35**	0.10
Pod yield plant $^{-1}$(g)	F_6						1.00	0.76**	-0.42**	0.24*
	F_7						1.00	0.92**	-0.55**	0.33**
Kernel yield plant $^{-1}$(g)	F_6							1.00	0.41**	0.25*
	F_7							1.00	0.35**	0.36**
Shelling (%)	F_6								1.00	0.65**
	F_7								1.00	0.49**
SMK (%)	F_6									1.00
	F_7									1.00

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

Table 4. Estimation of parent-offspring correlation, regression and heritability

Traits	Regression components			
	R	**B**	$h^2_{(bs)}$	$h^2_{(ns)}$
DFF	0.61*	0.44	75.23	38.08
Plant height (cm)	0.71**	0.56	87.49	48.31
Primary branches plant $^{-1}$	0.25*	0.15	88.23	13.13
SCMR	0.38*	0.70	87.63	59.79
SLA(cm^2/g)	0.14	0.21	90.10	18.61
Pods plant $^{-1}$	0.60**	0.56	70.69	47.61
Pod yield plant $^{-1}$(g)	0.53**	0.67	91.60	57.34
Kernel yield plant $^{-1}$ (g)	0.27*	0.21	82.64	18.34
Shelling (%)	0.05	0.12	70.55	10.88
SMK (%)	0.28*	0.29	97.82	25.08

Note: r- Inter-generation correlation, b-regression, $h^2_{(bs)}$ - Heritability in broad sense, $h^2_{(ns)}$ - Heritability in narrow sense

Table 5. Performance of Selected superior families in F_7 generation for water use efficiency related traits, pod yield and its component traits

Sl. No	Name	SCMR	SLA(cm^2/g)	Pods plant $^{-1}$	Pod yield plant $^{-1}$ (g)	Kernel yield per plant (g)	Shelling%
1	C3-32-1-7-4-1	51.00	110.00	67.00	55.33	43.00	58.61
2	C3-130-5-6-2-4	48.00	114.00	54.00	49.00	31.40	58.97
3	C3-88-4-5-1-3	42.00	121.00	53.00	48.33	35.25	56.37
	GKVK-6	32.33	163.00	22.00	15.60	8.00	51.28
	KCG-2	38.10	150.00	25.00	19.10	15.33	49.60
	KCG-6	39.11	145.66	34.00	28.36	20.69	53.78

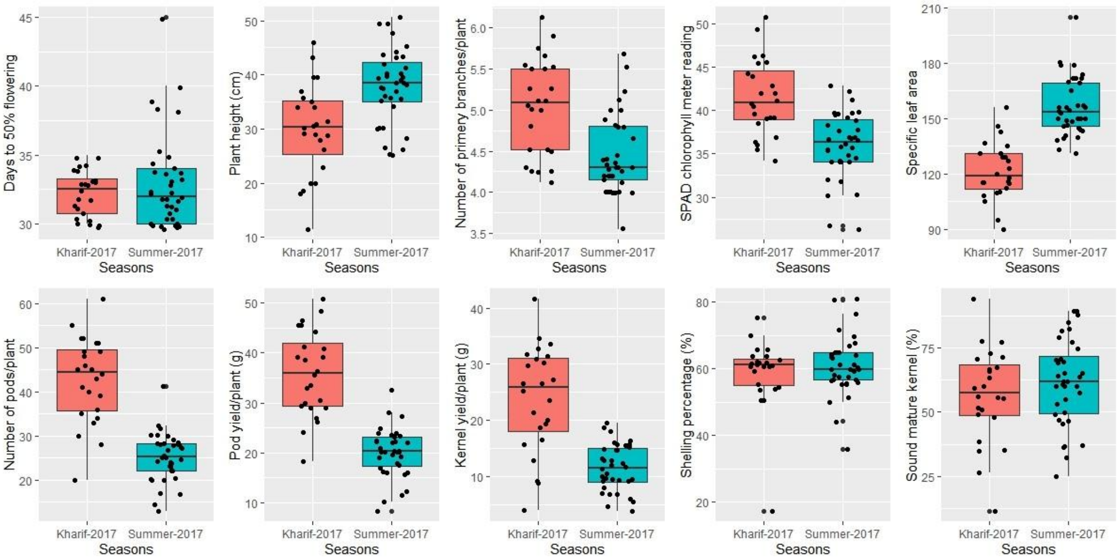

Fig. 1. Box plot showing variation for trait studied in the *Kharif* and summer seasons

Fig. 2. Selected superior plants for yield traits

4. CONCLUSIONS

Analysis of variance for all the characters studied in both F_6 and F_7 generations revealed highly significant differences among the families suggesting the presence of sufficient amount of variability. Further, genetic variability estimates such as PCV and GCV coupled with high heritability and genetic advance as *per cent* mean for kernel yield per plant, pod yield per plant and sound mature kernel percentage, SLA indicating the presence of sufficient variability and involvement of additive gene action in both F_6 and F_7 generations for these traits. Days to first flowering SCMR exhibited lower PCV and GCV estimates and thus indicating less variation for this trait. Phenotypic correlation coefficient depicted significant positive association of SCMR, pods per plant and kernel yield per plant with pod yield per plant. SLA exhibited significant negative association with pod yield per plant and SCMR. Therefore, superior genotypes for high yield and water use efficiency were selected depending on the relationship between SLA, SCMR and pod yield. Three superior families were noticed with more pods plant^{-1}, high pod yield plant^{-1}, high kernel yield^{-1}, high shelling (%), high SMK (%), high SCMR value, and low SLA value. Further, these superior families also revealed the presence of high parent offspring regression and intergeneration correlation, implying increased efficiency of selection for most of the traits considered and these were identified to be the important characters that could be used in selection for yield.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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