

Biological Forum – An International Journal

15(3): 95-101(2023)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Identification of High Yielding Water use Efficient F₆ and F₇ Families Derived from the Cross of GKVK-16 × KCG-2 in Groundnut (*Arachis hypogaea* L.)

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(Received: 07 January 2023; Revised: 17 February 2023; Accepted: 26 February 2023; Published: 22 March 2023) (Published by Research Trend)

ABSTRACT: 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. However, groundnut frequently experiences drought stresses for various durations and intensities. 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. Losses in yield that are due to water stress can be tackled partially by developing varieties that are better adapted to water scares conditions with yield advantage. With this background an experiment was conducted to understand the genetic potential, heritability, genetic advance and traits association of yield contributing characters for F₆ and F₇ families derived from the cross GKVK-16 × 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 2016. 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), kernel yield per plant (g), SMK% (sound mature kernel per cent), SCMR (SPAD chlorophyll meter reading) and SLA (specific leaf area) (cm²/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. Among 84 families studied 14 families have been selected based on high SCMR values, low SLA, more number of pods per plant, high shelling% and high pod yield over parents and checks were identified to be the important characters that could be used in selection for yield and the selected families will be tested further in multi rows for yield stabilization.

Keywords: GCV, PCV, Heritability, GAM, water use efficiency, Groundnut.

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 (Krapovickas and Gregory 1994). 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 (Weiss, 2000). 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 (Alam et al., 1985). 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

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semi-arid regions, where groundnut frequently experiences drought stresses for various durations and intensities (Reddy *et al.*, 2003). 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 (Kambiranda *et al.*, 2011). Losses in yield that are due to water stress can be tackled partially by developing varieties that are better adapted to water scares conditions (Ravi *et al.*, 2011).

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). Pandey et al. (2020) identified 19 major main-effect QTLs with 10.0-33.9% phenotypic variation explained (PVE) for drought tolerance- and iron deficiency tolerance- related traits, major main-effect QTLs were detected for haulm weight (20.1% PVE), SCMR (soil plant analytical development (SPAD) chlorophyll meter reading, 22.4% PVE), and visual chlorosis rate (33.9% PVE) through Genome-wide QTL discovery analysis. Nageswara Rao et al. (2001); Sheshshayee et al. (2006) 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 (Nageswara Rao et al., 2001) and reported significant and high negative inter-relationship among SLA and SCMR. Upadhyaya et al. (2002) 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. Zhang et al. (2022), identified the genotypes PI 502120 and AU-NPL 17 as water spender genotypes as they showed high yield, Δ^{13} C, photosynthesis, and stomatal conductance under drought. 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 F₆ and F₇

generation families derived from the cross of GKVK-16 × KCG-2.

MATERIALS AND METHODS

Plant material and experimental site. The present study was conducted during summer and Kharif 2016 at the experimental field, K-Block, Department of Genetics and Plant Breeding, GKVK, University of Agricultural Sciences, Bangalore. The experimental material for the present study comprised of 36 F₆ and 24 F7 families of the cross viz., GKVK-16 × KCG-2 and 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 vield 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 F7 generation. Statistical analysis of the mean data was analyzed in WINDOSTAT version 8.5 for augmented design and SPSS for descriptive statistics.

Evaluation of F₆ generation. 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 2016 with 5 m row length and 30 cm and 10 cm inter and intra row spacing respectively (Plate 1).

Evaluation of F₇ generation. Individual F₆ 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 F₇ evaluation of yield and water use efficiency-related traits as the salient features of parents and checks were given in Table 1.

Weather parameter details and recording of morphological data. Recommended fertilizer doges, cultural practices and all plant protection measures were followed to ensure a good crop stand of the F₆ and F₇ families and the monthly mean weather data for the experimental sites during the crop growth period were recorded as total rainfall (mm), the number of rainy days, the minimum and maximum temperature in °C, sunshine hours for 1hours and 2 hours (Table 2). 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: Sound mature kernel (SMK) *per cent:* was calculated by using the following formulae.

Shelling percent =
$$\frac{\text{Kernel weight (g)}}{\text{Pod weight (g)}} \times 100$$

SMK (%) = $\frac{\text{Number of well developed kernels}}{\text{Total number of kernels}}$

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). Amongst several leaf characters, leaf thickness and chlorophyll content determine the leaf transmittance characters. 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 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.

RESULTS AND DISCUSSION

Analysis of variance revealed a significant difference for all the characters among families in the cross GKVK-16 \times KCG-2. Further, checks vs families exhibited greater significant difference for days to first flowering, plant height, primary branches per plant, pods per plant, SCMR, SLA, pod yield per plant, kernel yield per plant and SMK (%) except plant height in F₇populationas shown in the Table 3. Thus, indicating the presence of a sufficient amount of genetic variability for all the studied traits. Hence the result indicates that choice of material for the study is suitable and further selections could be practiced for crop improvement in achieving desirable traits

Estimates of Genetic variability parameters. High GCV and PCV coupled with the narrow difference between GCV and PCV for kernel yield per plant, pods per plant and shelling per cent in F₆ and F₇ generations of the cross GKVK-16 × KCG-2 (Table 4) which suggest that expression of pods per plant, kernel yield per plant, shelling per cent and SMK per cent are less influenced by the environment, therefore, these characters could be used for selection of superior families as selection criteria. Similar findings of higher estimates of GCV and PCV for kernel yield per plant and pod yield per plant were reported by Giri et al. (2009); Sridevi et al. (2022). The high estimates of GCV and PCV for the above-mentioned traits suggest the presence of a higher magnitude of variation for these traits. Thus individual plant selection can be practiced for these characters. Whereas Chauhan et al. (2022) reported high GCV, PCV for shelling %, kernel yield per plant and pod yield per plant in BC_1F_1 , BC_1F_2 and BC₁F₃ populations. In literature similar results were reported by Meta and Monpara (2010), Makhan et al. (2003); Golakia et al. (2005); John et al. (2005); Rao et al. (2012) in groundnut. High broad-sense heritability accompanied with high genetic advance as per cent mean was recorded for pods per plant, pod yield per plant, SMK per cent, kernel yield per plant and shelling per cent in F₆ and F₇ generation of the cross GKVK-16×KCG-2 (Table 4). This indicates that the heritability is mostly due to additive gene effects and there is a lot of scope for improvement of these traits in the future breeding programme. Similar results were reported by Nath and Alam (2002); Golakia et al. (2005) for plant height, pods per plant and pod yield per plant which indicates that these characters are under the influence of additive genetic control and selection will be effective and may rapidly contribute to yield. Rao et al. (2012) for pods per plant, Padmaja et al. (2013a) for pod yield per plant, Zaman et al. (2011); Rao et al. (2012) for kernel yield per plant, Reddi et al. (1991); Venkataravana et al. (2000) for SMK per cent.

Phenotypic correlation coefficients. Phenotypic correlation coefficients for growth, traits related to water use efficiency, pod yield and yield and its component traits was estimated in F₆ and F₇ generation and results are presented in Table 5. DFF showed significant positively correlation with primary branches per plant, (r= 0.27, 0.45), SLA (r= 0.34, 0.40), pods per plant (r= 0.45, 0.56), pod yield per plant (r= 0.22, 0.38), kernel yield per plant (r= 0.43,0.37). Whereas, DFF showed a negative correlation with shelling%. Plant height exhibited significant positive correlation with SCMR (r= 0.41, 0.48), pods per plant (r= 0.22, 0.34), pod vield per plant (r= 0.39, 0.41), kernel vield per plant (r= 0.40, 0.48), SMK% (r= 0.43, 0.21). Primary branches per plant showed a significant positive correlation for all traits except SLA and shelling%. SCMR exhibited significant positive correlation with, pods per plant (r= 0.46, 0.53), pod yield per plant (r= 0.69, 0.66), kernel yield per plant (r= 0.67, 0.51), shelling% (r= 0.33, 0.42) however it exhibited the presence of significant negative correlation with SLA (r= -0.70, -0.81). SLA showed a significant negative

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correlation for all traits except plant height and primary branches per plant. Further, it also showed the existence of a significant positive correlation with DFF (r= 0.34, 0.40). Pods per plant exhibited a significant positive correlation with all traits except SMK% where it has shown a significant negative correlation with SLA (r= -0.06, -0.14). Pod yield per plant exhibited a significant positive correlation with all traits except SLA and shelling *per cent* where it showed a significant negative correlation in both F₆ and F₇ generation with the value of SLA (r= -0.74, -0.68) and shelling% (r= -0.56, -0.45). Kernel yield per plant showed a significant positive correlation with all the traits except SLA (r= -0.61, -0.57). Shelling % showed significant positive correlation with SCMR (r= 0.33, 0.42). 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. Kernel yield per plant (r= 0.52, 0.62) SMK% (r= 0.23, 0.29), whereas it found significant negative correlation with SLA (r= -0.22, -0.33), pods per plant (r= -0.25, -0.46), pod yield per plant (r= -0.56, -0.45). SMK% exhibited significant positive correlation with plant height (r= 0.43, 0.21), primary branches per plant (r= 0.31, 0.51), pod yield (r= 0.41, 0.65), kernel yield per plant (r= 0.37, 0.52), John et al. (2019), SMK% (r= 0.23, 0.29) and significant negative correlation with SLA (r= -0.32, -0.28). These results are in accordance with the reports of Sridevi et al. (2022); Reddy et al., (2017); Mukhtar et al. (2011); Shoba et al. (2012). Koolachart et al. (2013); Thakur et al. (2013). This indicates that selection of traits for low SLA leads to improvement in yield. From F7 generation fourteen

superior families from cross GKVK-16×KCG-2 were selected for multi-location evaluation (Table 6, Plate 2).



Plate 1: Field view of F7 generation of groundnut crop.



Plate 2: Selected superior families in F7 generation.

Genotypes	SCMR	SLA (cm²/g)	Pods/ plant	Pod yield (g/pt)	SMK (%)
GKVK-16	42.45	153.04	30.55	28.00	75.00
KCG-6	45.39	142.00	30.14	29.28	65.12
KCG-2	44.25	136.20	22.00	20.29	81.00
TMV-2	35.38	152.15	18.00	15.00	60.75

Table 1: Salient features of parents and checks used in the study.
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Table 2:	Monthly	Mean	Weather	Data of H	Experimenta	al Sites E	During Ci	rop Gro	wth Perio	od for the	e Year 201	6.
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Month	Total Rainfall	Rainy days	Tem (⁰ C	ւթ Հ)	Sun shine	RH (%)		
	(mm)	(100.)	Max	Min	Hours	I hr	II hr	
JAN	2.4	0	27.5	14.7	7.6	90	47	
FEB	0	0	31.2	16.2	9.0	85	38	
MAR	4.2	1	34.0	19.9	8.2	86	37	
APR	1.2	0	35.8	23.1	9.1	84	37	
MAY	112.6	6	33.1	21.4	7.8	88	42	
JUNE	140.4	13	28.4	19.9	4.7	92	55	
JULY	271.4	11	27.6	19.3	4.1	94	58	
AUG	28.0	2	28.1	19.5	5.7	92	54	
SEP	51.4	5	27.8	19.0	3.5	92	54	
OCT	31.0	3	29.6	18.0	7.9	85	48	
NOV	0	0	29.6	16.2	8.5	82	43	
DEC	64.4	3	27.2	14.7	6.9	88	46	
TOTAL	707	44	30.0	18.5	6.9	88	47	

sv	Generations	Df	DFF	Plant height (cm)	Primary branches plant ⁻¹	SCMR	SLA (cm²/g)	Pods Plant ⁻¹	Pod yield plant ⁻¹ (g)	Kernel yield plant ⁻¹ (g)	Shelling (%)	SMK (%)
Disaira	F ₆	5.00	14.58	45.34	0.23	17.84	130.23	40.46	184.16	139.98	150.62	115.53
DIOCKS	F7	3.00	10.52	57.82**	0.38	15.68*	160.82	436.54*	214.21	133.34	129.31	156.71*
Chaolic	F ₆	2.00	22.88	22.17	0.42	31.11	42.59	312.41	140.62	111.00	162.11	107.27
Checks	F ₇	2.00	14.08	31.82	0.50	11.89*	81.82	348.60	280.44	141.20	239.04	108.89
Familias	F ₆	35.00	32.30**	67.83**	7.33**	33.04**	855.44**	536.75**	644.54**	532.98**	759.39**	402.95**
Fammes	F ₇	23.00	41.38**	49.05**	8.29**	25.38**	849.05**	608.82**	608.22**	635.65**	538.51*	645.96**
Checks	F ₆	70.00	72.67**	227.12**	14.65**	364.06**	1342.25**	1463.76**	1016.29**	1660.04**	664.93**	4141.66**
<i>vs.</i> Families	F7	46.00	69.01**	40.39	12.58**	411.99**	1244.36**	1338.13**	2555.88**	2424.28**	690.58**	4668.19**
Eman	F ₆	20.00	5.42	5.29	0.185	8.17	6.57	16.71	16.63	22.16	18.99	10.58
EII0I	F ₇	12.00	3.86	5.49	0.22	2.27	5.49	17.11	12.04	10.03	27.48	19.56

Table 3: Analysis of variance for growth, traits related to water use efficiency, pod yield and its component characters in F₆ and F₇ generations of the cross GKVK-16 × KCG-2 in groundnut.

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 4: Estimates of genetic variability parameters for growth, traits related to water use efficiency, pod yield and its component characters in F₆ and F₇ generation in the cross GKVK-16×KCG-2 of groundnut.

Tuoita	Creases	Maan	Range		Standardized	CCV(q)	$\mathbf{PCV}(0)$	h^2	CAMØ
Trans	Crosses	Mean	Min.	Max.	Range	GCV (%)	FCV (%)	<i>n</i> (bs) /0	GAM%
DEE	F ₆	30.91	29.00	36.00	0.23	03.56	05.74	62.09	08.53
DFF	F ₇	34.36	30.00	45.00	0.10	10.28	11.67	88.09	04.35
Diant haight(am)	F ₆	32.85	20.12	45.45	0.77	10.73	14.19	75.62	22.10
Flant height(chi)	F ₇	32.87	19.66	45.45	01.15	15.58	18.32	85.06	32.09
Drimory bronch as alonts	F ₆	05.11	03.64	06.20	0.50	08.08	10.56	76.57	07.95
Primary branches plant.	F ₇	04.92	03.06	06.5	0.64	09.11	11.67	78.09	24.35
SCMD	F ₆	38.95	32.63	48.03	0.40	06.17	08.79	70.27	05.48
SCMR	F ₇	44.07	32.09	59.08	0.42	08.70	09.90	87.95	17.93
$SI \wedge (am^2/a)$	F ₆	154.56	129.00	186.50	0.37	14.71	16.39	89.75	30.30
SLA (clif/g)	F ₇	144.03	93.00	198.00	0.54	14.42	18.18	79.35	29.72
Pode plant	F ₆	31.42	20.00	41.60	0.69	13.65	17.81	76.65	17.12
Fous plant	F ₇	41.31	16.70	74.00	01.55	23.41	31.18	75.11	35.39
Bod wield plant-l(a)	F ₆	30.95	20.12	45.33	0.81	17.83	21.44	83.17	21.40
Fou yield plain (g)	F ₇	42.88	13.59	88.45	01.59	19.29	26.47	72.88	34.28
Kamal yield alant: (a)	F ₆	26.34	13.81	40.00	0.99	15.86	20.81	76.25	11.25
Kernel yield plant (g)	F ₇	22.51	02.14	54.62	01.72	26.94	36.82	73.19	47.94
Shalling $(0')$	F ₆	60.27	48.39	92.4	0.73	11.65	12.48	93.42	13.45
Shennig (%)	F ₇	58.88	15.46	69.84	0.33	29.01	35.91	80.80	30.19
SMR (0/)	F ₆	64.24	39.58	90.22	0.79	16.56	20.69	80.06	17.08
SIVIK (%)	F ₇	43.69	14.00	80.23	01.17	57.17	60.99	93.74	117.79

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 5: Phenotypic correlation coefficients for traits related to growth, water use efficiency, pod yield and its component traits in F₆ and F₇ generation of the cross GKVK-16×KCG-2 in groundnut.

Traits	Generations	Plant height(cm)	Primary branches plant ⁻¹	SCMR	SLA (cm²/g)	Pods Plant ⁻¹	Pod yield plant ⁻¹ (g)	Kernel yield plant ⁻¹ (g)	Shelling (%)	SMK (%)
DEE	F ₆	0.15	0.27*	0.10	0.34**	0.45**	0.22*	0.43**	-0.15	0.14
DFF	F7	0.14	0.45**	0.14	0.40**	0.56**	0.38**	0.37*	-0.12	0.19
Plant	F ₆	1.00	-0.47**	0.41**	-0.14	0.22*	0.39**	0.40**	-0.22*	0.43**
height(cm)	F ₇	1.00	-0.35*	0.48**	-0.19	0.34**	0.41**	0.48**	-0.18	0.21*
Primary branches	F ₆		1.00	0.26*	-0.15	0.23*	0.27*	0.62**	-0.11	0.31**
plant ⁻¹	F7		1.00	0.36**	-0.18	0.36**	0.50**	0.53**	-0.19	0.51**
SCMR	F ₆			1.00	-0.70**	0.46**	0.69**	0.67**	0.33**	0.10
	F7			1.00	-0.81**	0.53**	0.66**	0.51**	0.42**	0.18
ST A (2/-)	F ₆				1.00	-0.36**	-0.74**	-0.61*	-0.22*	-0.32*
SLA (clii /g)	F7				1.00	-0.41**	-0.68**	-0.57**	-0.33**	-0.28*
Dodo plant 1	F ₆					1.00	0.34*	0.33*	-0.25*	-0.06
Pous plant	F7					1.00	0.27*	0.48**	-0.46**	-0.14
Pod yield	F ₆						1.00	0.76**	-0.56**	0.41**
plant ⁻¹ (g)	F ₇						1.00	0.84**	-0.45**	0.65**
Kernel yield	F ₆							1.00	0.52**	0.37**
plant ⁻¹ (g)	F7							1.00	0.62**	0.52**
Shalling (%)	F ₆								1.00	0.23*
Snelling (%)	F7								1.00	0.29*
SMIZ (07)	F ₆									1.00
SMK (%)	F ₇									1.00

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

Sr. No	Name	SCMR	SLA (cm²/g)	Pods plant ⁻¹	Pod yield plant ⁻¹ (g)	Kernel yield per plant (g)	Shelling %
1.	C1-213-2-1-1-2	47.72	104	54.00	48.36	32.05	65.86
2.	C1-74-4-3-3-2	46.96	110	61.00	56.61	42.85	58.02
3.	C1-213-6-2-7-2	55.36	116	72.00	62.28	52.90	84.93
4.	C1-213-6-2-2-4	59.80	93	52.00	48.50	35.20	76.12
5.	C1-213-2-8-4-16	46.08	136	69.00	61.79	45.34	74.38
6.	C1-40-1-5-1-8	47.50	114	69.00	63.60	40.00	59.52
7.	C1-74-4-3-3-1	44.38	118	64.00	57.81	39.66	55.91
8.	C1-213-6-2-7-1	45.14	116	57.00	47.48	42.12	88.76
9.	C1-47-9-10-1-1	52.58	119	62.00	56.24	48.16	85.63
10.	C1-40-1-5-1-7	48.20	121	59.00	49.56	34.98	70.58
11.	C1-137-4-7-5-9	51.50	116	74.00	57.39	34.62	60.12
12.	C1-137-4-7-5-3	49.38	124	56.00	45.52	37.54	52.14
13.	C1-46-1-10-1-9	52.06	132	67.00	58.91	36.93	62.72
14.	C1-137-4-7-5-1	48.60	145	60.00	57.66	36.36	60.00
	GKVK-16	42.57	155	30.00	20.10	15.20	50.23
	KCG-2	40.00	158	24.00	19.11	12.39	49.77
	TMV-2	32.00	160	20.00	15.33	8.00	42.36

 Table 6: Performance of selected superior families in F7 generation for water use efficiency related traits, pod yield and its component traits in the cross GKVK-16 × KCG-2 of groundnut.

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. 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 F₆ and F₇ 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. From the overall study fourteen superior families from cross GKVK-16×KCG-2 were selected from F7 generation for multi-location evaluation.

Acknowledgement. I extremely thank Department of genetics and plant breeding, University of Agricultural Sciences, Bangalore for providing facilities for conducting the trial.

Conflicts of Interest. None.

REFERENCES

- Alam, M. S., Rahman, A. R. M. S. and Khair, A. B. M. A. (1985). Genetic variability and charachter association in groundnut (*Arachis hypogaea* L. of Bangladesh]. *Bangladesh Journal of Agriculture* (*Bangladesh*).
- Chauhan, S., Savithramma, D. L. and Kundu, S. (2022). Genetic variability, heritability and genetic advance for yield and its related traits in BC1F1, BC1F2 and

BC1F3 back cross generation of two crosses of groundnut (Arachis hypogaea L.).

- Giri, R. R., Toprope, V. N. and Jagtap, P. K. (2009). Genetic variability, character association and path analysis for yield, its component traits and late leaf spot, *Phaeoisariopsis personata* (Berk and curt), in groundnut. *International Journal of Plant Sciences* (*Muzaffarnagar*), 4(2), 551-555.
- Golakia, P. R., Makne, V. G. and Monpara, B. A. (2005). Heritable variation and association in Virginia runner and Spanish bunch group of groundnut. *National Journal of Plant Improvement*, 7(1), 50-53.
- John, K., Madhavi Santhoshi, M.V. and Rajasekhar, P. (2019). Correlation and path analysis in groundnut (Arachis hypogaea L.). International Journal of Current Microbiology and Applied Sciences, 8(12), 1521-1529.
- John, K., Vasanthi, R. P., Venkateswarlu, O. and Sudhakar, P. (2005). Genetic variability and correlation studies among F1s and parents in groundnut (*Arachis* hypogaea L.). Legume Research-An International Journal, 28(4), 262-267.
- Kambiranda, D. M., Vasanthaiah, H. K., Katam, R., Ananga, A., Basha, S. M. and Naik, K. (2011). Impact of drought stress on peanut (*Arachis hypogaea* L.) productivity and food safety. *Plants and environment*, 1, 249-272.
- Koolachart, R., B. Suriharn, S. Jogloy, N. Vorasoot, S. Wongkaew, C. C. Holbrook, N. Jongrungklang, T. Kesmala. and A. Patanothai (2013). Relationships between physiological traits and yield components of peanut genotypes with different levels of terminal drought resistance. SABRAO Journal of Breeding and Genetics, 45(3), 422-446.
- Krapovickas, A. and Gregory, W. C. (1994). Taxonomia Del Genero Arachis (leguminosae). *Bonplandia*, 1-186.
- Makhan Lal, Roy, D. and Ojha, O. P. (2003). Genetic variability and selection response for root and other characters in groundnut (*Arachis hypogaea* L.). Legume Research, 26(2), 128-130.
- Meta, H. R. and Monpara, B. A. (2010). Genetic variation and trait relationships in summer groundnut, (Arachis

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Biological Forum – An International Journal 15(3): 95-101(2023)

hypogaea L.). Journal of Oilseeds Research, 27(1), 8-11.

- Mukhtar, A. A., Tanimu, B. S., Ibrahim, B. S., Abubakar, I. U. and Babaji, B. A. (2011). Correlations and path coefficients analysis between pod yield and some quantitative parameters in ground nuts (*Arachis hypogaea* L.). *International Journal of Science and Nature*, 2(4), 799-804.
- Nageswara Rao, R. C., Talwar, H. S. and Wright, G. C. (2001). Rapid assessment of specific leaf area and leaf nitrogen in peanut (*Arachis hypogaea* L.) using a chlorophyll meter. *Journal of Agronomy and Crop Science*, 186(3), 175-182.
- Nath, U. K. and Alam, M. S. (2002). Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea L.*). *Journal of Biological Sciences*, 2(11), 762-764.
- Padmaja, D., Eswari K. B., Rao, B. M. V. and Reddy, S. M. (2013a). Genetic variability, heritability for late leaf spot tolerance and productivity traits in a recombinant inbred line population of groundnut (*Arachis* hypogaea L.). IOSR Journal of agriculture and veterinary science, 5, 36-41.
- Pandey, M. K., Gangurde, S. S., Sharma, V., Pattanashetti, S. K., Naidu, G. K., Faye, I., Hamidou, F., Desmae, H., Kane, N.A., Yuan, M. and Vadez, V. (2020). Improved genetic map identified major QTLs for drought tolerance-and iron deficiency tolerancerelated traits in groundnut. *Genes*, 12(1), p.37.
- Rao, V. T., Bhadru, D., Murthy, K. G. K. and Bharathi, D. (2012). Genetic variability and association among the various characters in groundnut (*Arachis hypogaea* L). *International journal of Applied Biology and Pharmaceutical*, 3, 337-341.
- Ravi, K., Vadez, V., Isobe, S., Mir, R. R., Guo, Y., Nigam, S. N., Gowda, M. V. C., Radhakrishnan, T., Bertioli, D. J., Knapp, S. J. and Varshney, R. K. (2011). Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). *Theoretical and Applied Genetics*, *122*, pp.1119-1132.
- Reddy, A. T., Sekhar, M. R., Vijayabharathi, A., Pathy, T. L., Reddy, G. L. and Jayalakshmi, V. (2017). Studies on combining ability and heterosis for yield and its

component traits in groundnut (Arachis hypogaea L.). International Journal of Current Microbiology and Applied. Science, 6(12), 551-559.

- Sheshshayee, M. S., Bindumadhava, H., Rachaputi, N. R., Prasad, T. G., Udayakumar, M., Wright, G. C. and Nigam, S. N. (2006). Leaf chlorophyll concentration relates to transpiration efficiency in peanut. *Annals of Applied Biology*, 148(1), 7-15.
- Shoba, D., Manivannan, N. and Vindhiyavarman, P. (2012). Correlation and path coefficient analysis in groundnut (Arachis hypogaea L.), Madras Agricultural Journal, 99(1-3), 18-20.
- Sridevi, S., Meenakumari, B., Manivannan, N. and Ravichandran, V. (2022). Assessment of genetic variability, character association and path analysis of kernel yield and yield components in groundnut (Arachis hypogaea L.). Electronic Journal of Plant Breeding, 13(2), 476-481.
- Thakur, S. B., Ghimire, S. K., Chaudhary, N. K., Shrestha, S. M. and Mishra, B. (2013). Variability in groundnut (Arachis hypogaea L.) to Cercospora Leaf spot disease tolerance. International Journal of Life Sciences Biotechnology and Pharm Research, 2, 254-262.
- Upadhyaya, H. D., Bramel, P. J., Ortiz, R. and Singh, S. (2002). Developing a mini core of peanut for utilization of genetic resources. *Crop Science*, 42(6), 2150-2156.
- Venkataravana, P., Sheriff, R. A., Kulkarni, R. S., Shankaranarayana, V. and Fathima, P. S. (2000). Correlation and path analysis in groundnut (*Arachis* hypogaea L.). Mysore Journal of Agricultural Sciences, 34(4), 321-325.
- Weiss, E. A. (2000). Oilseed crops (Second Ed.). Blackwell Science Ltd., London.
- Zaman, M. A., Tuhina-Khatun, M., Ullah, M. Z., Moniruzzamn, M. and Alam, K. H. (2011). Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). *The Agriculturists*, 9(1-2), 29-36.
- Zhang, Q., Dang, P., Chen, C., Feng, Y., Batchelor, W., Lamb, M. and Sanz-Saez, A. (2022). Tolerance to mid-season drought in peanut can be achieved by high water use efficiency or high efficient use of water. *Crop Science*, 62(5), 1948-1966.

How to cite this article: Padmashree R., Shanthala J., Honnappa M., D. L. Savithramma, Sanjeevkumar R., E. Gangappa and A.G. Shankar (2023). Identification of High Yielding Water Use Efficient F_6 and F_7 Families Derived from the Cross of GKVK-16 × KCG-2 in Groundnut (*Arachis hypogaea* L.). *Biological Forum – An International Journal*, *15*(3): 95-101.