

# Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com



E-ISSN: 2278-4136 P-ISSN: 2349-8234 JPP 2018; 7(5): 3139-3143 Received: 23-07-2018 Accepted: 24-08-2018

#### Uma R Byadagi

M.Sc. Students, Department of Genetics and Plant Breeding University of Agricultural Sciences, Bengaluru, Karnataka, India

#### Venkataravana P

Professor of Genetics and Plant Breeding College of Sericulture, Chintamani, Karnataka, India

#### Priyadarshini SK

Assistant Professor of Genetics and Plant Breeding College of Sericulture, Chintamani, Karnataka, India

Correspondence Uma R Byadagi M.Sc. Students, Department of Genetics and Plant Breeding University of Agricultural Sciences, Bengaluru, Karnataka, India

# Genetic variability studies in F<sub>2</sub> and F<sub>3</sub> populations of three crosses of groundnut (*Arachis Hypogaea* L.)

## Uma R Byadagi, Venkataravana P and Priyadarshini SK

#### Abstract

 $F_2$  and  $F_3$  populations of three crosses *viz.*, TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 were assessed to estimate the nature and magnitude of genetic variability during *kharif* and *summer*-2017. Higher magnitudes of range and standardized range were observed for all the traits in all the three crosses. The higher estimates of GCV and PCV noticed for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>, branches plant<sup>-1</sup> and sound mature kernel percent which indicated the presence of adequate variability for these traits suggesting the ample opportunity for selection. The close correspondence between estimates of GCV and PCV indicated lesser influence of environment on traits like plant height, branches plant<sup>-1</sup> and days to first flowering in all the three crosses which is amply reflected by high broad sense heritability along with high expected GAM, suggesting the involvement of additive gene action in controlling these traits and hence, selection will be effective for these traits. A decreasing trend was observed for range, standardized range for both GCV and PCV from F<sub>2</sub> to F<sub>3</sub> generation, which explains the substantial decrease of variability in F<sub>3</sub> generation due to selection practiced in F<sub>2</sub> generation.

Keywords: Genetic variability, GCV, PCV, heritability in broad sense, GAM, additive genetic effect

#### Introduction

Groundnut (Arachis hypogaea L.), known as king of oilseeds, is an important oilseed crop in the world as well as in India. It is a highly self-pollinated crop belonging to the family Fabaceae and an allotetraploid with a chromosome number of 2n=4x=40, having 'A' and 'B' genomes, contributed by diploid progenitors A. duranensis and A. ipaensis, respectively. The hybridization between these diploid progenitors might have occurred about 3,500 years ago which lead to the origin of cultivated groundnut (Kochert et al., 1996)<sup>[10]</sup>. The seed contains about 40-54 percent oil, 25-28 percent protein and 18 percent carbohydrates in addition to minerals and vitamins. Groundnut is the third largest oilseed crop produced in the world and second largest in India. It is grown in 90 countries around the world in an area of 23.4 million hectares with 42 million tonnes production and 17.96 quintals of productivity per hectare. Groundnut is cultivated in India in an area of 5.25 million hectares with a production of 9.47 million tonnes and productivity of 18.04 quintals per hectare. Karnataka is the fourth largest producer of groundnut in India with productivity 7.32 quintals per hectare, after Gujarat, Andhra Pradesh and Tamil Nadu, respectively (Anon., 2017)<sup>[2]</sup>. Current productivity level of groundnut in Karnataka (0.73 t ha<sup>-1</sup>) is less than half of national average (1.8 t ha<sup>-1</sup>) (Anon., 2017) <sup>[2]</sup>. TMV-2, the variety developed and released in 1940 (78 years back) is still ruling despite other varieties better than TMV-2 with higher pod yield. Traders or oil mills still prefer TMV-2 variety for oil extraction because of its even-sized pods and kernels. However, the government has denotified the variety and hence it is not available in the official seed chain. There is an urgent need to develop a variety with yield potential better than that of TMV-2 but with pod and kernel type of TMV-2 so that the gap between the current productivity level of groundnut in Karnataka and national average can be reduced. Availability of natural and/or generated genetic variability is a prerequisite for any crop improvement as it provides a wide scope for the selection. The effectiveness of selection depends on the nature, extent, and magnitude of genetic variability present in the material and the degree of heritability. Existing variability has been exploited to the maximum extent by selection; thus there is a need to generate new variability in segregating populations by crossing among best available genotypes. In the present investigation carried out to create desirable variation by crossing TMV-2  $\times$  ICGV-91114, TMV-2  $\times$  TG-69 and TMV-2  $\times$  ICGV-00350 so that selection can be carried out after evaluating them for genetic variability and heritability of Characters.

#### Material and Methods

The experiment was carried out during *kharif*- 2017 at the field unit of ARS, Chintamani and National Seed Project, J Block, UAS, GKVK, Bengaluru. The crop was grown by following all the agronomic practices as per the package of practices recommended for Eastern Dry Zone of Karnataka (Anon., 2016)<sup>[11]</sup>. The material for the present investigation consisted of F<sub>2</sub> and F<sub>3</sub> populations of three connected crosses *viz.*, TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 where, TMV-2 was the common female parent, which is comparatively low yielding but has desirable pod type and kernel type. It was crossed to the three high yielding varieties, ICGV-91114, TG-69 and ICGV-00350. Parent material was obtained from AICRP on Groundnut, ARS, Chintamani.

The  $F_2$  plants derived from each of the three connected crosses and their parents were grown in plots of 18 m<sup>2</sup> area with a spacing of 0.3×0.2 m. The parents were evaluated in Randomised Block Design with three replications. Both the parents and  $F_2$  population were evaluated during kharif- 2017 at the field unit of ARS, Chintamani. In total, 189  $F_2$  plants from cross TMV-2 × ICGV-91114, 196 from cross TMV-2 × TG-69 and 200  $F_2$  plants from cross TMV-2 × ICGV-00350 were available for recording observations.

The top 25 genotypes bearing TMV-2 pod type were selected based on kernel yield from each of the three crosses. The selected  $F_2$  plants were forwarded to  $F_3$  and evaluated on plant-to-row progeny basis in Augmented Design along with checks TMV-2, GKVK-5 and KCG-6 during *summer*-2017 at experimental field unit of National Seed Project, UAS, GKVK, Bengaluru. The data was recorded on individual plants in the  $F_2$  generation and on five plants randomly selected from each of the parents in each of the three replications.

In the  $F_3$  generation, five plants randomly selected from each of the family or progeny row, and checks from each block were considered for recording the observations. The genotypic and phenotypic co-efficient of variations was computed as suggested by Robinson *et al.*, (1949) <sup>[13]</sup>. Heritability and genetic advance were worked out as per the method outlined by Hanson *et al.*, (1956) <sup>[6]</sup>. The Analysis of variance was performed following Augmented Design as suggested by Federer (1961) <sup>[4]</sup>, using WINDOSTAT 8.5 version for  $F_3$  population.

### **Results and Discussion**

### Mean performance of parents

The results revealed that the parents differed significantly for days to first flowering, pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup> indicating the diverse nature of parents used in hybridization. The mean performance of the parents ranged from 31.13 (ICGV-91114) to 36.53 (ICGV-00350) for days to first flowering, and from 16.20 (ICGV-00350) to 22.60 (ICGV-91114) for pods plant<sup>-1</sup>. The mean values for pod yield plant<sup>-1</sup> ranged from 10.67 (ICGV-00350) to 15.33 (TMV-2) and for kernel yield plant<sup>-1</sup> from 6.93 (ICGV-00350) to 10.03 (TG-69). However, no significant difference was noticed for plant height, branches plant<sup>-1</sup>, shelling percent and sound mature kernel percent, among the four parents (Table 1).

Table 1: Mean performance of pod yield and its attributes for parents used in the crosses

Parents	Plant height (cm)	Branches plant <sup>-1</sup>	Days to first flowering	Pods plant <sup>-1</sup>	Pod yield plant <sup>-1</sup> (g)	Kernel yield plant <sup>-1</sup> (g)	Shelling %	SMK %
TMV-2	31.07	4.67	34.20	22.60	15.33	9.00	57.25	70.80
ICGV-91114	30.47	4.73	31.13	20.53	14.70	9.83	67.44	81.71
TG-69	30.07	4.53	33.40	19.80	14.80	10.03	67.87	83.43
ICGV-00350	32.13	4.73	36.53	16.20	10.67	6.93	65.40	72.93
CD @ 5%	2.29	0.61	0.88	1.63	2.28	2.42	9.68	16.86
CD@ 1%	3.47	0.93	1.33	2.47	3.46	3.66	14.67	25.55
Overall mean of parents	30.94	4.67	33.82	19.78	13.88	8.95	64.49	77.22

### **Analysis of Variance**

Significant mean sum of squares noticed for all the traits due to progenies suggested the existence of significant variability among the progenies for all the traits in all the three crosses except for shelling percent in cross TMV-2 × ICGV-91114, branches plant<sup>-1</sup> in cross TMV-2 × TG-69 and for sound mature kernel percent in cross TMV-2 × ICGV-00350 (Table 2). This variability noticed can be attributed to the segregation of genes as  $F_3$  is an early segregating generation.

Further, the significant mean sum of squares due to checks vs. progenies (between  $F_3$  progeny rows) observed for all the traits in  $F_3$  progenies of all the three crosses except for traits

plant height, kernel yield plant<sup>-1</sup> in crosses TMV-2 × ICGV-91114 and TMV-2 × ICGV-00350, for sound mature kernel percent in crosses TMV-2 × ICGV-91114 and TMV-2 × TG-69 and for branches plant<sup>-1</sup>, pods plant<sup>-1</sup> in cross TMV-2 × TG-69, suggested the presence of adequate variability between the progenies as well. The significant differences were also noticed between the checks for branches plant<sup>-1</sup>, days to first flowering and shelling percent in all the three crosses (Table 2). The significant variability found among and also between the F<sub>3</sub> progenies adequately provided statistical validity for evaluating these progenies further for pod yield and its component traits in all the three crosses.

Table 2: ANOVA for pod yield and its attributing traits in F<sub>3</sub> generation of three crosses C<sub>1</sub>, C<sub>2</sub> and C<sub>3</sub>

Source of variation	Crosses	Blocks	Progenies + Checks	Checks	Progenies	Checks vs. Progenies	Error
Degrees of freedom		7	27	2	24	1	14
	C1	20.02**	11.12*	9.88	13.82*	13.64	4.04
Plant height(cm)	C2	16.58*	23.79 ***	9.88	22.80 ***	116.27***	4.038
	C3	8.80	16.82 **	9.88	16.78 **	17.88	4.038
	C1	0.78	1.40**	8.65***	0.78*	3.91**	0.29
Branches plant <sup>-1</sup>	C2	0.78	1.20 **	8.65 ***	0.67	1.06	0.29
	C <sub>3</sub>	0.74	1.59 ***	8.65 ***	0.99*	3.67 **	0.29
Days to 50% flowering	C1	5.14	8.55**	21.29**	5.87*	55.38***	2.48

	C2	13.95**	8.52 **	21.29 **	8.49 *	53.32 ***	2.48
	C3	25.96 ***	12.56 **	21.29 **	10.24 **	204.50 ***	2.48
	C1	111.83*	209.43***	84.16	221.54***	937.21***	26.92
Pods plant <sup>-1</sup>	C <sub>2</sub>	145.08 **	126.84 **	84.16	175.94 ***	34.34	26.92
	C3	110.02 *	243.41 ***	84.16	254.62 ***	1048.04 ***	26.92
	C1	74.64*	141.61***	42.13	160.59***	319.79**	24.32
Pod yield plant <sup>-1</sup> (g)	C <sub>2</sub>	67.70*	79.49 *	42.13	95.36 **	159.71 *	24.32
	C3	104.47**	161.47 ***	42.13	191.14 ***	331.82 **	24.32
	C1	34.55	57.35*	5.45	70.63**	31.52	17.01
Kernel yield plant <sup>-1</sup> (g)	C <sub>2</sub>	37.90	38.00	5.45	42.57 *	205.98 **	17.01
	C <sub>3</sub>	66.35 *	66.07 **	5.45	90.48 **	13.19	17.01
	C1	41.65	71.57**	244.01***	25.77	842.25***	15.46
Shelling %	C <sub>2</sub>	27.84	86.58 ***	244.01 ***	39.32 *	825.71***	15.46
-	C3	78.39 **	106.36 ***	244.01 ***	48.89 *	1483.87 ***	15.46
SMK %	C1	48.99	104.91**	25.33	118.03***	49.54	21.38
	C <sub>2</sub>	64.24 *	71.92 *	25.33	87.36 **	1.61	21.38
	C3	33.05	50.05 *	25.33	47.52	149.01 *	21.38

\*: Significant at P=0.05, \*\*: Significant at P=0.01 and \*\*\*: Significant at P=0.001

C1 - TMV-2×ICGV-91114, C2 - TMV-2×TG-69 and C3 - TMV-2× ICGV-00350

# Genetic variability studies in $\mathbf{F}_2$ and $\mathbf{F}_3$ populations of the three crosses

On comparing the trait means of  $F_2$  population with the  $F_3$  progeny means, a large shift of trait mean values was observed from  $F_2$  to  $F_3$  generation for all the traits in all the three crosses as expected (Table 3). This shift can be accountable to the selection practiced in  $F_2$  population based on TMV-2 pod type and kernel yield and the correlated response of other traits to the selection.

Among the crosses in  $F_2$  population mean performance of cross TMV-2 × ICGV-00350 was higher for branches plant<sup>-1</sup>, days to first flowering, pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup>, indicating that, this cross is better

performing compared to other two crosses. Among the three crosses, cross TMV-2 × TG-69 manifested higher mean values for plant height, shelling percent and sound mature kernel percent. However in F<sub>3</sub> progenies of cross TMV-2 × ICGV-00350 were late maturing than the other two crosses studid in this investigation. TMV-2 × ICGV-91114 and TMV-2 × ICGV-00350 cross F3 progenies had high number pods plant<sup>-1</sup>, higher pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup> than cross TMV-2 × TG-69, but TMV-2 × ICGV-91114 cross F3 progenies recorded low readings for shelling percent and sound mature kernel percent were than TMV-2 × TG-69 and TMV-2 × ICGV-00350 (Table 3).

		Maar	_		Raı	nge	Standardized range			
Traits	Crosses	Mear	1	Minimum		Maximum		Standardized range		
		F <sub>2</sub>	F3	F <sub>2</sub>	F3	F <sub>2</sub>	F3	F <sub>2</sub>	F3	
	C1	29.89	39.51	20.00	30.50	45.00	47.40	0.84	0.43	
Plant height(cm)	C <sub>2</sub>	31.68	37.49	19.00	29.00	46.00	44.00	0.85	0.40	
	C <sub>3</sub>	31.39	41.77	21.00	34.80	40.00	49.60	0.61	0.35	
	C1	4.07	5.95	1.00	4.00	6.00	7.50	1.23	0.59	
Branches plant <sup>-1</sup>	C2	4.20	5.67	3.00	4.20	7.00	7.00	0.95	0.49	
	C3	4.27	5.93	3.00	3.67	7.00	7.60	0.94	0.66	
	C1	32.84	43.96	29.00	40.00	37.00	49.00	0.24	0.20	
Days to 50% flowering	C2	33.77	43.92	29.00	40.00	38.00	51.00	0.27	0.25	
	C3	35.40	45.92	33.00	42.00	37.00	51.00	0.11	0.20	
	C1	12.00	35.53	1.00	10.00	29.00	60.00	2.33	1.41	
Pods plant <sup>-1</sup>	C2	13.22	28.46	3.00	3.60	39.00	59.60	2.72	1.97	
	C3	15.13	36.03	5.00	8.67	36.00	70.60	2.05	1.72	
	C1	8.74	28.83	0.60	6.26	20.00	49.64	2.22	1.50	
Pod yield plant <sup>-1</sup>	$C_2$	8.22	20.11	1.50	1.70	23.00	41.04	2.62	1.96	
	C3	11.10	28.92	3.00	5	31.00	55.02	2.52	1.73	
	C1	5.81	19.48	0.50	3.52	15.50	33.50	2.58	1.54	
Kernel yield plant <sup>-1</sup>	$C_2$	5.85	13.77	1.00	1.02	16.00	26.36	2.56	1.84	
	C3	7.43	18.87	1.50	3.13	22.00	36.78	2.76	1.78	
Shelling %	C1	65.05	67.36	22.22	57.43	89.66	75.29	1.04	0.27	
	$C_2$	70.81	67.45	45.45	57.16	88.89	77.36	0.61	0.30	
	C <sub>3</sub>	64.35	64.64	25.00	48.42	85.71	83.66	0.94	0.55	
	C1	80.29	84.29	0.00	48.07	100.00	100.00	1.25	0.62	
SMK %	C <sub>2</sub>	86.97	85.94	0.00	64.15	100.00	98.00	1.15	0.39	
	C3	79.15	82.81	0.00	68.31	100.00	93.63	1.26	0.31	

Table 3: Estimates of mean, range and standardized range for pod yield and its attributing traits in F2 and F3 population of three crosses.

C1 - TMV-2×ICGV-91114, C2 - TMV-2×TG-69 and C3 - TMV-2× ICGV-00350

High magnitudes of both range and standardized range were noticed for all the traits in both  $F_2$  and  $F_3$  populations of all the three crosses except for days to first flowering. Highest

standardized range was observed for traits like pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup>. But there was significant decreasing trend of standardized range from  $F_2$  to

 $F_3$  generation was noticed for all traits except for days to first flowering in all three crosses (Table 3), which explains the substantial decrease of variability in  $F_3$  generation due to selection practiced in  $F_2$  generation.

In the present investigation, higher estimates of GCV and PCV were noticed for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup>, the most important yield traits, in both  $F_2$  and  $F_3$  population of all the three crosses and for branches plant<sup>-1</sup> and sound mature kernel percent in  $F_2$  population of cross TMV-2 × ICGV-91114 and TMV-2 × ICGV-00350.

In F<sub>2</sub> population, moderate estimates of GCV and PCV were noticed for plant height in all the three crosses, branches plant<sup>-1</sup> in cross TMV-2 × TG-69, shelling percent in cross TMV-2 × ICGV-91114 and TMV-2 × ICGV-00350 and for sound mature kernel percent in cross TMV-2 × TG-69. However, moderate PCV was observed for plant height in cross TMV-2 × TG-69, branches plant<sup>-1</sup> in all the three crosses and for sound mature kernel percent in cross TMV-2 × ICGV-91114 in F<sub>3</sub> population. Low magnitudes of GCV and PCV noticed for days to first flowering suggested less variability expressed for this trait in both F<sub>2</sub> and F<sub>3</sub> populations of all the three crosses (Table 4). Similar findings were reported by Jayalakshmi *et al.* (1998) <sup>[8]</sup>, Rudraswamy *et*  al. (1999) <sup>[14]</sup> and Dolma et al. (2010) <sup>[3]</sup> for pod yield and kernel yield plant<sup>-1</sup>. The results for plant height at harvest (moderate GCV) and for days to first flowering (low GCV) were in agreement with the results reported earlier by Mohan et al. (2012) <sup>[12]</sup>. A decreasing trend was observed for both GCV and PCV from  $F_2$  to  $F_3$  generation, which again reiterated the substantial decrease of variability in F<sub>3</sub> generation due to selection practiced in F<sub>2</sub> generation. Further close correspondence between estimates of GCV and PCV indicated the lesser influence of environment on growth traits like plant height, branches plant<sup>-1</sup> and days to first flowering in all the three crosses which is amply reflected by high broad sense heritability along with high expected GAM (except days to first flowering) in both  $F_2$  and  $F_3$  populations. On the contrary, wider differences between the estimates of GCV and PCV indicated larger influence of environment for the expression of yield traits like pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant-1, which is amply reflected by comparatively low broad sense heritability in  $F_2$  and  $F_3$ populations of cross TMV-2  $\times$  ICGV-91114 and TMV-2  $\times$ TG-69. However, high magnitude of broad sense heritability accompanied with

Table 4: Estimates of parameter	rs specifying variability	for pod yield and its attr	ributing traits in F2 and	l F3 population of the three crosses
---------------------------------	---------------------------	----------------------------	---------------------------	--------------------------------------

Troite	Crosses	PCV%		GCV	%o	h <sup>2</sup> (BS)		Expected GAM	
1 raits		F <sub>2</sub>	F3	F <sub>2</sub>	F3	F <sub>2</sub>	F3	F <sub>2</sub>	F3
	C1	15.67	7.91	12.66	6.06	65.31	58.63	21.08	9.55
Plant height(cm)	$C_2$	15.89	10.34	13.47	8.84	71.88	63.12	23.53	15.57
	C3	14.16	8.12	12.17	6.54	73.97	64.87	21.57	10.85
	C1	25.75	12.80	20.79	9.02	65.18	49.63	34.58	13.09
Branches plant <sup>-1</sup>	$C_2$	26.38	12.62	18.03	8.29	46.70	43.12	25.38	11.21
	C3	28.73	14.14	21.08	10.81	53.85	48.46	31.86	17.02
	C1	5.90	4.81	5.05	3.21	73.19	44.44	8.89	4.40
Days to 50% flowering	$C_2$	6.78	5.58	5.97	4.27	77.51	58.64	10.82	6.74
	C <sub>3</sub>	3.86	5.77	4.64	3.29	72.64	64.67	5.78	7.69
	C1	40.51	33.40	31.58	30.04	60.78	50.89	50.72	45.65
Pods plant <sup>-1</sup>	$C_2$	45.45	37.54	33.45	32.82	54.17	46.42	50.72	49.10
	C <sub>3</sub>	38.77	35.13	33.72	32.04	75.64	63.20	60.42	60.20
	C1	44.17	35.39	30.98	28.66	42.11	36.63	38.31	25.87
Pod yield plant <sup>-1</sup>	$C_2$	44.68	40.38	32.07	24.08	29.05	23.10	26.74	22.48
	C3	49.48	38.18	41.44	34.16	70.12	60.06	71.48	62.97
	C1	48.92	35.72	31.12	28.77	40.46	34.85	40.78	37.72
Kernel yield plant <sup>-1</sup>	$C_2$	46.51	41.07	28.09	20.03	18.55	16.79	17.77	15.58
	C3	54.48	40.97	43.76	34.68	64.50	51.65	72.40	60.47
	C1	19.15	7.13	17.27	12.9	81.26	16.52	32.06	2.43
Shelling %	$C_2$	11.22	8.04	9.22	5.54	67.63	47.45	15.63	7.86
	C3	16.51	9.16	14.90	6.84	81.41	55.85	27.69	10.53
	C1	26.96	10.48	26.31	8.92	95.24	72.57	52.89	15.66
SMK %	C2	16.51	9.01	14.95	7.23	81.93	64.36	27.87	11.95
	C3	28.12	7.31	27.69	4.72	96.94	41.70	56.15	6.28

 $C_1$  - TMV-2×ICGV-91114,  $C_2$  - TMV-2×TG-69 and  $C_3$  - TMV-2× ICGV-00350

high expected GAM was recorded for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup> in F<sub>2</sub> and F<sub>3</sub> populations of cross TMV-2 × ICGV-00350 indicating that selection for these traits would be effective in this population. Similar results are reported by Meta and Monpara (2010) <sup>[11]</sup> for plant height, Zaman *et al.* (2011) <sup>[15]</sup> for branches plant<sup>-1</sup> and days to first flowering, John and Raghava (2014) <sup>[9]</sup> for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup> and kernel yield plant<sup>-1</sup>.

The parents used in hybridization were diverse in nature with respect to traits, days to first flowering, pods plant<sup>-1</sup>, pod yield and kernel yield plant<sup>-1</sup>. The mean performance of cross TMV-2  $\times$  ICGV-00350 was comparatively greater than the other two crosses for yield traits like pods plant<sup>-1</sup>, pod yield

plant<sup>-1</sup> and kernel yield plant<sup>-1</sup> in both  $F_2$  and  $F_3$  populations, indicating that this cross was high yielding compared to other two crosses. Moderate to high estimates of GCV and PCV along with high heritability and high expected GAM were observed for plant height, branches plant<sup>-1</sup> and shelling percent suggesting that these traits are governed by additive gene action, hence selection on these traits will be effective to enhance productivity of groundnut.

#### References

 Anonymous. Package of practice book, Univ. Agric. Sci. Bengaluru, 2016, 157-162.

- 2. Anonymous. Status paper on oil seeds, Ministry of Agriculture, Govt. of India, 2017, 23.
- 3. Dolma T, Reddi Sekhar M, Raja Reddy. Genetic variability, correlation and path analysis for yield, its components and late leafspot resistance in Groundnut (*Arachis hypogaea* L.). J Oilseeds Res. 2010; 27(2):154-157.
- 4. Federer WT. Augmented designs. Hawaiian Planters' Record. 1956; 55:191-208.
- 5. Govindaraju D, Atzmon G, Barzilai N. Genetics, lifestyle and longevity: Lessons from centenarians. Appl. Transl. Genome. 2015; 4:23-32.
- 6. Hanson CH, Robinson HR, Comstock RS. Biometrical studies of yield in segregating population of Korea Lespedeza. Agron. J. 1956; 48:268-272.
- 7. Hawkes JG. The importance of genetic resources in plant breeding. Biol. J Linnean Soc. 1991; 43:3-10.
- 8. Jayalakshmi V, Reddy PV, Asalatha M, Vasanthi RP. Genetic variability for water use efficiency traits in Groundnut. Legume Res. 1998; 21(1):8-12.
- 9. John K, Raghava RP. Variability, heritability and genetic advances for water use efficiency traits in Groundnut (*Arachis hypogaea* L.). Int. J. Curr. Sci. 2014; 13:1-5.
- Kochert G, Stalker HT, Gimenes M, Galgaro L, Lopes CR, Moore K. RFLP and cytogenetic evidence on the origin and evolution of allotetraploid domesticated peanut (*Arachis hypogaea* L.). Am. J. Bot. 1996; 83:1282-1291.
- 11. Meta HR, Monpara BA. Genetic variation and trait relationship in summer Groundnut (*Arachis hypogaea* L.). J Oilseeds Res. 2010; 27(1):8-11.
- Mohan K, Vishnuvardhan RP, Vasanthi K, Hariprasad R and Bhaskar Reddy B V, Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). Int. J. Appl. Biol. Pharma. Technol. 2012; 3(1):390-394.
- Robinson HF, Comstock RE, Harvey P. Estimation of heritability and degree of dominance in corn. Agron. J 1949; 41:353-359.
- 14. Rudraswamy P, Nehru SD, Kulkarni RS, Manjunath A. Estimation of genetic variability and inbreeding depression in six crosses of groundnut (*Arachis hypogaea* L.). Mysore J. Agric. Sci. 1999; 33(2):248-252.
- Zaman MA, Tuhina KM, Ullah MZ, Moniruzzamn M, Alam KH. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). The Agriculturists. 2011; 9(1&2):29-36.