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## Genetic variability, heritability and genetic advance for yield and its related traits in BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> back cross generation of two crosses of groundnut (*Arachis hypogaea* L.)

Shailja Chauhan, DL Savithramma and Sritama Kundu

### Abstract

The present investigation was carried out in three backcross generations of two crosses C1 [(TMV 2 × ICGV 86699) × TMV 2] and C2 [(TMV 2 × ICGV GBFDS272) × TMV 2] in groundnut to assess the nature and extent of genetic variability, heritability and genetic advance. Most of the traits were accounted with high heritability and high GAM, which is a positive sign of least influence with the environment on population and showed presence of additive gene action. High heritability along with high GAM indicated additive gene effect, and these traits were expected to respond to selection with greater efficiency. Plant height and primary branches plant<sup>-1</sup> showed low heritability coupled with low genetic advance in all three back cross generations of both the crosses C1 and C2 indicate that the selection is not effective as non-additive genes govern the trait. Days to first flowering showed moderate heritability coupled with moderate genetic advance explaining non additive effect suggested that selection is less effective. Pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>, SMK%, Shelling% and PDI @60, 75<sup>th</sup>, 90<sup>th</sup> and 105 DAS showed high heritability coupled with high genetic advance. These traits may serve as an effective selection parameter during breeding programs for crop improvement in the future.

**Keywords:** Groundnut, variability, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, sound mature kernel (SMK)

### Introduction

Groundnut (*Arachis hypogaea* L.) is a self-pollinated annual leguminous oilseed cash crop having genome AABB and somatic chromosome number 2n = 4x = 40. It is a segmental allotetraploid belongs to family Fabaceae. This crop, popularly known as the "King" of oilseed crops or "Wonder nut", "Poor man's cashew nut" or peanut. Groundnut mainly grows throughout the tropical, sub-tropical and warm temperate regions of the world. The kernels contain 47-53 percent of edible oil; 24-36 percent of vegetable protein; 10-15 percent of carbohydrates and also good sources of minerals, vitamins and fiber (Talawar, 2004 [39], Pasupuleti *et al.*, 2016 [23]; Ondulla, 2020) [21]. Groundnut also enhance the soil fertility by fixing atmospheric nitrogen.

China is world's leading producer followed by India in groundnut production. In India, the total cultivated area under groundnut is (4.94 million hectares); production is (9.34 million tonnes, with a productivity of (1.89 million tons/hectare), (United States Department of Agriculture, 2019).

Biotic constrain is one of the major cause for low yield in groundnut. The major yield affecting diseases foliar fungal diseases, the early leaf spot (ELS) caused by *Cercospora arachidicola* and late leaf spot (LLS) caused by *Phaeoisariopsis personata* (Bert and Curtis) are the more destructive diseases (Janila *et al.*, 2013; Kirti, 2015) [9, 17]. These two diseases combined can cause pod and fodder yield loss of over 50% to 70% (Waliyar, 1991) [45].

Understanding the genetics of late leaf spot resistance components and yield and yield attributing traits is likely to contribute to enhancing breeding for these traits. Large genetic variability present in breeding material with heritable character is effective for selection of that particular trait (Padmaja *et al.*, 2015, Hugar *et al.*, 2015) [8]. Therefore, plant breeders need to require a good knowledge of genetic variability, i.e., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense, genetic advance (GA), and genetic advance as percentage of mean (GAM) improved for the genetic material at hand.

Heritability and genetic advance for breeders are highly helpful biometric tools to determine the selection's direction and extent. High heritability alone is insufficient for effective selection in advanced generations and without significant genetic advance. The high heritability and genetic advance of a given characteristic display it is driven by additive gene action and the most efficient selection condition. It is important to identify plant characteristics that affect productivity for reproductive programmes to boost groundnut production. In order to improve the efficiency of seed-selection and pod yield, knowledge on the type and scale of genetic variability and transmission of characteristics is of crucial relevance. In this study, the genetic variability, heritability and genetic advance of groundnuts were investigated.

To this effect, the aim of the present study was to assess genetic variability of three BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> back cross-generation of two crosses in groundnut based on LLS resistance components, morpho-physiological traits (yield and yield components). Genotypic and phenotypic variations and genetic advance have been reported for several traits in groundnut (Korat *et al.*, 2009<sup>[15]</sup>; Zaman *et al.*, 2011<sup>[48]</sup>; Rao *et al.*, 2014<sup>[26]</sup>; Yusuf *et al.*, 2017)<sup>[47]</sup>.

### Method and Materials

The experiment was carried out for BC<sub>1</sub>F<sub>1</sub> population of both the crosses C1 [(TMV2 × ICGV86699) × TMV2] and C2 [(TMV2 × GBFDS272) × TMV2] along with checks were in non-replicated trail. The BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> population were laid out in augmented design, where parents and checks were replicated for the crosses C1 [(TMV2 × ICGV86699) × TMV2] and C2 [(TMV2 × GBFDS272) × TMV2]. The crop were raised during *Kharif* 2019, Summer 2020 and *Kharif* 2020, at the Department of Genetics and Plant Breeding, UAS, GKVK, Bangalore in green grouse (BC<sub>1</sub>F<sub>1</sub> population) as well in field (BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> population). Throughout the crop growth period, appropriate cultural practices were followed.

### Observations recorded

Observations were recorded on individual plant basis for days to first flowering, plant height (cm), number of primary branches, number of pods plant<sup>-1</sup>, pod weight (g), kernel weight (g), pod yield plant<sup>-1</sup>(g) and kernel yield plant<sup>-1</sup> (g), shelling percent, sound mature kernel (SMK) percent and late leaf spot disease.

Various genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense, and genetic advance as a percent of mean were calculated using standard statistical methods. Genetic parameters such as phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were computed (Burton and De vane, 1953) to enable comparison of phenotypic and genotypic variance across traits. Sivasubramanian and Madhavamenon (1973)<sup>[36]</sup> categorized GCV and PCV as less than 10% as low; 10- 20% as moderate as and higher than 20% as high. As suggested by Robinson *et al.* (1949)<sup>[29]</sup>, the heritability range was classified as: less than 30% - Low heritability; 30%-60% - Moderate heritability; more than 60% - High heritability and expected genetic advance as *per cent* mean (GAM) were estimated (Johnson *et al.*, 1955) grouped GAM as less than 10% - Low GAM; 10%-20% - Medium GAM; more than 20% - High

GAM using mean trait values of each plant from the back cross population. Analysis was done using INDOSTAT 8.5 software package (WINSTAT, 2010) for all three back cross populations.

### Results and Discussion

The genetic improvement of any crops depends on the amount of genetic variability and the extent of heredity. In self-pollinated crops, hybridization is one of the methods by which favourable genes available in different genotypes could be combined into one genotype through genetic recombination. The development of genetic variability through hybridization and selection complements natural variability to improve crops. It also helps in analysing and understanding the gene action that controls these economic traits. Information about the type and extent of variability present in the population due to genetic and non-genetic causes is an essential requirement for a systemic breeding program.

In the present study, the phenotypic and genotypic coefficients of variation exhibited a wide range for all characters. The results on mean and variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h<sup>2</sup>) in broad sense and genetic advance as per cent of mean (GAM) in all the nine crosses for yield and foliar diseases are presented in Table 1 and fig 1. The outcome of the genetic analysis in all three back cross population of both crosses C1 and C2 for first flowering, plant height (cm), primary branches plant<sup>-1</sup>, pod yield plant<sup>-1</sup> (g), kernel yield plant<sup>-1</sup> (g), sound mature kernel percentage, shelling percentage and late leaf spot disease scores are summarized briefly as follows.

#### 1. Days to first flowering

The estimates of GCV and PCV indicated the difference between GCV and PCV is narrow in all three BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> populations suggesting there is a less influence of environmental Vasanthi *et al.* (2015)<sup>[42]</sup> reported low GCV and PCV in groundnut for days to first flowering. Moderate heritability coupled with moderate GAM were observed in all three BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> populations. The non-additive effect suggested that selection was less effective. Vasanthi *et al.* (2015)<sup>[42]</sup> reported Moderate heritability coupled with moderate GAM in 50 *per cent* flowering in groundnut.

#### 2. Plant height (cm)

All three generations showed narrow differences between GCV and PCV, indicating that the trait is less influenced by the environment and less variability for the trait in all the population. Low heritability coupled with low genetic advance was also observed in all the three generations indicating that the trait is governed by non-additive gene action and that selection is ineffective. The results are the agreement with Sarvamangla (2009), John *et al.* (2011)<sup>[12]</sup>, Thakur *et al.* (2011)<sup>[40]</sup>, Vishnuvardhan *et al.* (2012)<sup>[44]</sup> and Mahalakshmi *et al.* (2018)<sup>[19]</sup> in groundnut.

#### 3. Primary branches plant<sup>-1</sup>

Low heritability coupled with low genetic advance found in all three populations indicate that selection is not effective as the trait is governed by non-additive genes. These results were found to be in accordance with the results of Channayya (2009), Sudha *et al.* (2012)<sup>[37]</sup>, John *et al.* (2011)<sup>[12]</sup>, Vishnuvardhan *et al.* (2012)<sup>[44]</sup> and Savita *et al.* (2014)<sup>[34]</sup>.

#### 4. Pods plant<sup>-1</sup> (g)

In all, the three generations showed narrow differences between GCV and PCV, indicating the trait had a low environmental effect. High heritability with high GAM indicated that the trait is controlled by additive gene action and that selection for this trait is effective. Similar results were obtained by John *et al.* (2011) [13], Alam *et al.* (2013) +, Yadav *et al.* (2014) [46], Satish *et al.* (2014) [32] and Mahalakshmi *et al.* (2018) [19] in groundnut.

#### 5. Pod yield plant<sup>-1</sup>

In all the three BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> populations, there was less difference between GCV and PCV, indicating the trait had low environmental effect. High heritability with high GAM character indicates the predominant role or additive gene action suggesting that selection will be rewarding to obtain higher yield in groundnut. The results obtained by Zaman *et al.* (2011) [48], Rao *et al.* (2012) [25], Yadav *et al.* (2014) [46], Satish *et al.* (2014) [32], Sanjeev Kumar *et al.* (2015) [30] and Mahalakshmi *et al.* (2018) [19] support these findings.

#### 6. Kernel yield plant<sup>-1</sup> (g)

The genetic estimates were high GCV and PCV with high heritability coupled with high GAM was found in all three generations *viz.*, BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> of both the crosses C1 and C2.

There is narrow difference noticed in all three generation for GCV and PCV value indicating there is less influence of environment for controlling the trait. High heritability coupled with high GAM-indicated additive gene plays important role and selection is effective. Kumar and Rajamani (2004) [16], Ravi Kumar (2005) [28], John *et al.* (2007) [12], Rout *et al.* (2010), Rao *et al.* (2012) [25], Zaman *et al.* (2011) [48] and Mahalakshmi *et al.* (2018) [19] obtained high GCV and PCV with high heritability coupled with high GAM for kernel yield plant<sup>-1</sup> in groundnut.

#### 7. Sound mature kernel (%)

Sound mature kernel showed high GCV and PCV of both C1 and C2 crosses with high heritability coupled with high genetic advance in all three generations.

GCV and PCV showed narrow differences in all three generations and this trait is less influenced by environment and selection is effective because trait is controlled by additive gene action because high heritability coupled with high genetic advance as *per cent* mean. Similar findings reported by Shinde *et al.* (2010) [35], Jogloy *et al.* (2011), Pradhan and Patra (2011) [24], Vishnuvardhan *et al.* (2012) [44] and Gupta *et al.* (2015) [7] high GCV and PCV and high heritability coupled with high genetic advance for sound mature kernel.

#### 8. Shelling percentage (%)

In BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub>, populations of both C1 and C2 crosses, the values of GCV and PCV are high with high heritability added with high GAM.

There is narrow difference noticed in all three generations where GCV and PCV value indicating there is less influence of environment and high heritability coupled with high GAM,

indicating that the trait is controlled by additive gene action and selection is rewarded for high yielding in groundnut. High GCV, PCV with high heritability and high GAM was earlier reported by John *et al.* (2007) [12], Savalia *et al.* (2009), Sumathi and Murlidharan (2009), Channayya *et al.* (2011) [4], Zaman *et al.* (2011) [48], Yadav *et al.* (2014) [46] and Mahalakshmi *et al.* (2018) [19] in groundnut.

#### 9. Percent disease incidence (PDI @ 60, 75, 90 and 105 DAS)

The higher estimates of GCV and PCV with narrow difference in BC<sub>1</sub>F<sub>1</sub> and BC<sub>1</sub>F<sub>3</sub> populations of both C1 and C2 crosses found with high heritability coupled with high genetic advance as *per cent* mean at PDI @ 60, 75, 90 and 105 DAS. As per the results obtained for the late leaf spot disease, LLS disease resistance is controlled by additive gene action in BC<sub>1</sub>F<sub>1</sub> and in BC<sub>1</sub>F<sub>3</sub> populations of both the crosses C1 and C2. Selection is rewarding for LLS disease resistance as PDI. According to Varshney *et al.* (2013) [41], disease score is the best selection criteria in the field for used in breeding program due to high heritability and its measures, which is accordance with the present results.

The values high PCV and GCV values coupled with high heritability and GAM values. Indicated that selection is effective. Dwivedi *et al.* (2002) [6], Khedekar (2008), Venkataravana and Injeti (2008) [43], Dolma *et al.* (2010) [5], Narasimhulu *et al.* (2013) [20], Padmaja *et al.* (2013) [22] and Ashish *et al.* (2014) were also suggested. The higher estimates of GCV and PCV with high heritability with high GAM for PDI in groundnut.

Comparing characters using GCV is preferable since it only considers heritable factors, whereas PCV estimates also consider environmental factors. Burton suggested that the genomic coefficient of variation (GCV) in conjunction with heritability estimates would provide the clearest picture of the degree of genetic gain that may be anticipated because of selection. The GCV alone is not relevant for selection. It is possible to determine the type of gene action governing a given trait by comparing relative heritability estimates and predicted genetic advance expressed as a percentage of the mean. High genetic progress and heritability values for any attribute suggest that selection and additive gene action will be successful in enhancing these qualities.

For the three backcross populations BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub>, and BC<sub>1</sub>F<sub>3</sub> of the two crosses C1 [(TMV 2 ICGV 86699) TMV 2] and C2 [(TMV 2 ICGV GBFDS272) TMV 2] high PCV and GCV values were reported for Kernel yield plant<sup>-1</sup>, SMK %, shelling percentage, and PDI @60, 75th, 90th, and 105th DAS. This showed that these characters' variation contributed significantly to overall variability and that selecting for these traits would only be effective if the environment had a smaller influence on the trait. In light of these characters, there was considerable scope for choices.

In terms of heritability and genetic advance as a percentage of mean (GAM), high values were observed for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>, SMK percentage, shelling percentage, and PDI @60, 75, 90, and 105 DAS in all the backcross populations. As previously observed, additive genes mostly regulated these qualities, suggesting that selecting for such features could help enhance groundnut.

**Table 1:** Genetic variability parameters for morph-metric traits a yield and yield related traits in backcross BC<sub>1</sub>F<sub>1</sub>, BC<sub>1</sub>F<sub>2</sub> and BC<sub>1</sub>F<sub>3</sub> populations of the cross C1 [(TMV 2 × ICGV86699) × TMV 2] and C2 [(TMV 2 × GBFDS272) × TMV 2] in groundnut

Characters	Crosses	BC <sub>1</sub> F <sub>1</sub> Population				BC <sub>1</sub> F <sub>2</sub> Population				BC <sub>1</sub> F <sub>3</sub> Population			
		GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)	GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)	GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)
DFE	C1	5.56	6.41	35.32	10.94	4.32	6.48	33.83	10.7	5.99	6.73	34.00	10.72
	C2	6.89	8.04	36.09	11.08	5.41	6.74	33.77	11.44	5.07	6.53	33.79	10.39
PH (cm)	C1	14.24	15.61	5.67	6.4	3.75	6.04	4.82	6.17	2.95	4.28	5.02	5.38
	C2	4.60	7.20	11.42	6.12	5.41	7.45	4.93	9.36	5.65	6.92	5.18	9.19
PB/P	C1	4.60	7.20	24.74	9.68	6.8	8.93	18.85	9.45	8.32	9.37	29.41	9.37
	C2	9.95	10.33	26.77	9.96	8.11	11.89	21.19	9.31	4.44	8.6	29.02	8.63
P/P	C1	41.84	48.44	74.61	44.46	39.32	42.93	71.32	60.09	32.82	33.77	78.05	33.89
	C2	50.88	58.70	74.14	52.49	24.99	29.17	76.67	60.32	32.8	35.5	76.38	38.63
PY/P (g)	C1	46.03	48.55	61.82	34.56	32.21	33.19	60.96	32.49	34.08	36.58	78.02	37.34
	C2	56.63	58.70	64.52	32.10	30.42	32.21	73.55	27.82	34.66	36.51	77.24	38.67
KY/P (g)	C1	51.47	59.44	68.04	34.33	34.46	35.07	65.15	45.05	52.2	57.55	63.47	47.56
	C2	32.18	32.1	63.3	38.86	36.04	36.3	66.55	49.17	39.71	42.93	68.23	45.09
SMK%	C1	55.99	58.87	71.75	29.9	31.3	33.06	58.29	9.91	37.11	33.42	70.38	9.01
	C2	54.48	57.44	70.97	27.13	32.76	34.14	55.79	7.06	32.45	30.41	73.09	9.03
SH%	C1	41.66	47.02	66.9	46.45	5.02	54.27	62.69	24.54	66.15	62.37	62.29	30.78
	C2	48.13	53.73	63.29	40.07	67.52	49.3	67.66	27.74	60.63	63.95	66.24	46.9
PDI@ 60	C1	79.71	82.92	70.68	20.72	-	-	-	-	73.34	74.25	7.3	19.25
	C2	56.23	67.32	70.75	29.58	-	-	-	-	56.4	66.44	6.2	36.39
PDI@ 75	C1	59.03	61.21	69.51	47.65	-	-	-	-	52.67	55.28	10.85	32.48
	C2	62.74	65.02	50.59	84.04	-	-	-	-	40.44	45.09	10.07	95.76
PDI@ 90	C1	47.62	52.98	80.79	58.17	-	-	-	-	47.64	52.13	14.06	44.96
	C2	74.38	77.9	47.99	87.26	-	-	-	-	37.4	40.9	14.01	90.3
PDI@105	C1	48.97	51.55	90.24	55.82	-	-	-	-	42.15	46.72	17.21	50.39
	C2	71.48	87.76	48.23	93.07	-	-	-	-	36.33	38.46	17.64	90.58

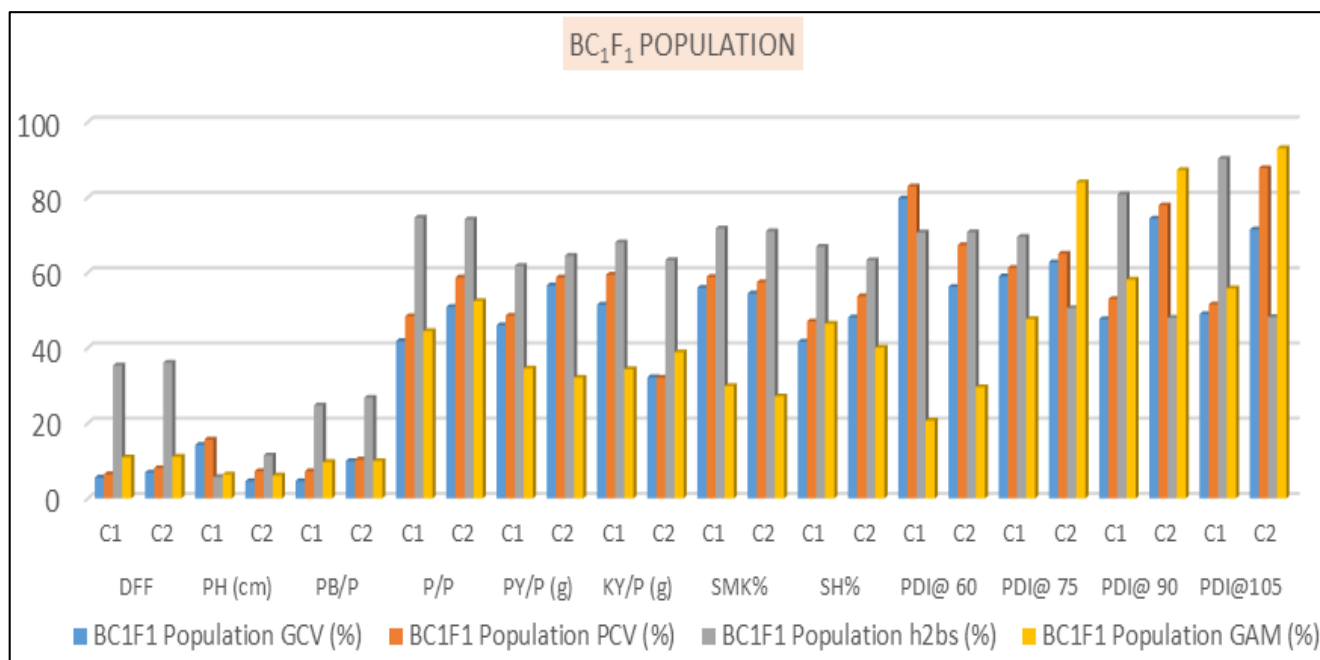
DFE- Days to first flowering, pH- Plant height (cm), PB/P- Primary branches plant<sup>-1</sup>

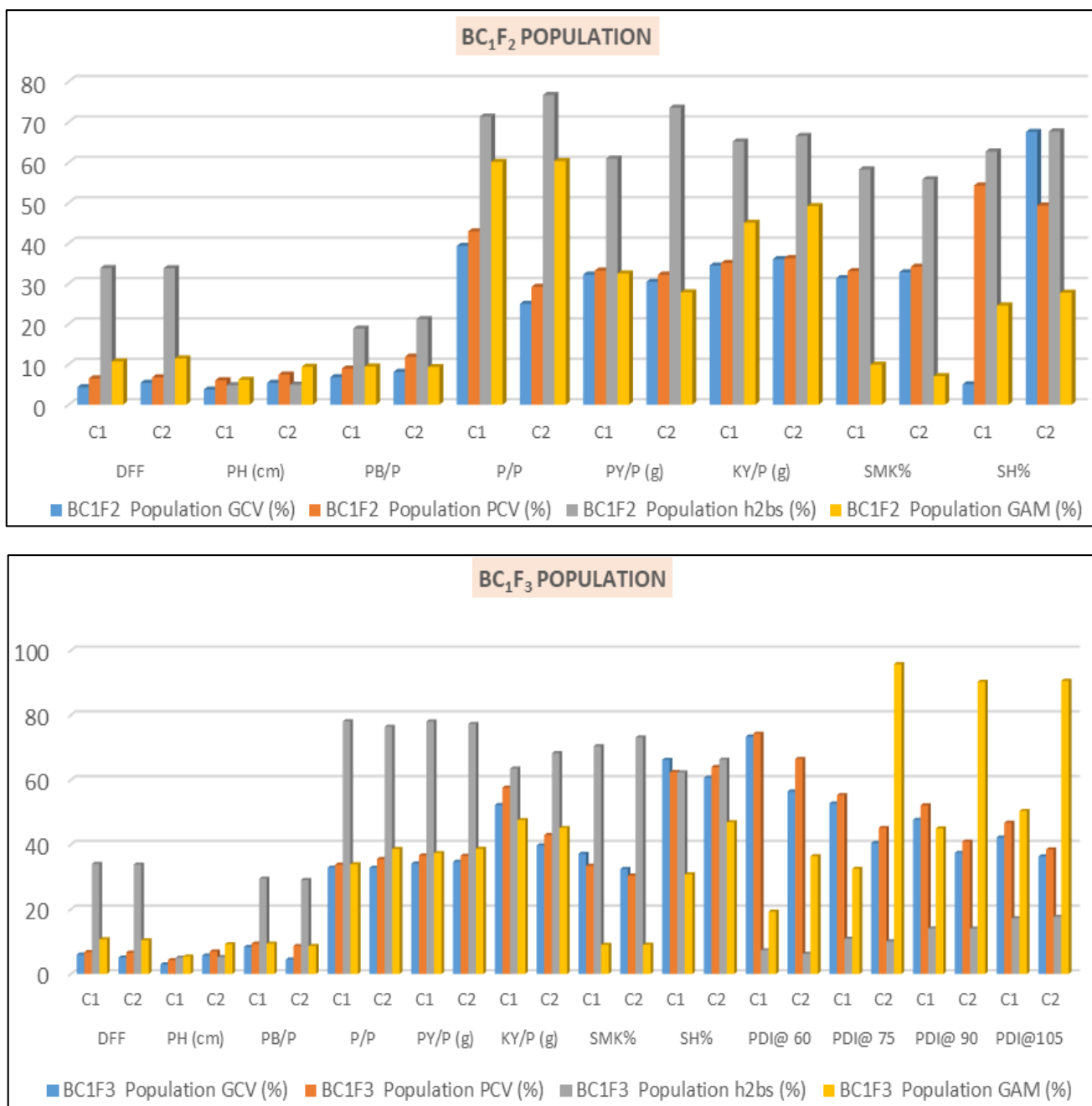
P/P- Pods plant<sup>-1</sup> (g), PY/P-Pod weight (g), KY/P- Kernel weight (g)

SMK % - Sound mature kernel percentage, SP%- Shelling percentage

PDI@ 60- percent disease incidence at 60<sup>th</sup> DAS, PDI@ 75- percent disease incidence at 75<sup>th</sup> DAS

PDI@ 90- percent disease incidence at 90<sup>th</sup> DAS, PDI@ 105- percent disease incidence at DAS





**Fig 1:** Graphical representation of genetic parameters for 11 characters in three back cross BC1F1, BC1F2 and BC1F3 populations of the cross C1 [(TMV 2 × ICGV86699) × TMV 2] and C2 [(TMV 2 × GBFDS272) × TMV 2] in groundnut

**Conclusion**

The present study indicated that most traits were under the influence of genetic control and could be improved through classical selection. It also had high PCV and GCV values coupled with high heritability and GAM for all the three back-cross population of both cross C1 and C2. Thus, results clearly indicated that there is a presence of a wide spectrum of genetic variation and the higher estimates of heritability implied that the environmental effects least influence these characters. Kernel yield per plant, SMK percentage, shelling percentage and PDI @60, 75th, 90th and 105 DAS showed high GCV and PCV with narrow difference indicated there is narrow difference noticed in all three generations where GCV and PCV value indicating there is less influence of environment. High heritability along with high GAM indicated the presence of additive gene effect and these traits were expected to respond to selection with greater efficiency.

Plant height and primary branches per plant showed low heritability coupled with low genetic advance in all three back cross-generation of both the crosses C1 and C2 indicate that the selection is not effective as non-additive genes govern the trait. Days to first flowering, showed moderate heritability coupled with moderate genetic advance explaining non-additive effect suggested that selection is less effective. Pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup>, kernel yield plant<sup>-1</sup>, SMK percentage, shelling percentage and PDI @60, 75<sup>th</sup>, 90<sup>th</sup> and 105 DAS showed high heritability coupled with high genetic advance. The traits with high heritability coupled with GAM under investigation could successfully be used in selection for further crop improvement. Genetic differences among back cross populations give great opportunities to use these populations as a source of genetic material for the further crop improvement in groundnut.

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