

Genetic variability Studies for Yield Contributing, Kernel Size and Quality Traits in Peanut (*Arachis hypogaea* L.)

G. Sreevidya^{1*}, P. Shanthi¹, A. Srividhya², S. Vasundhara³, M. Vishnuvardhan Kumar⁴,
K. Girish Kumar¹, V. Uday⁵ and P. Jashuva⁶

¹Department of Genetics and Plant Breeding,

S.V. Agricultural College, ANGRAU, Tirupati (Andhra Pradesh), India.

²Department of Genetics and Plant Breeding,

RARS, Tirupati (Andhra Pradesh), India.

³Department of Seed Science and Technology

S.V. Agricultural College, ANGRAU, Tirupati (Andhra Pradesh), India.

⁴Department of Genetics and Plant Breeding,

Agricultural College, Bapatla (Andhra Pradesh), India.

⁵Department of Biotechnology,

Jaya College of Arts and Science (Andhra Pradesh), India.

⁶Department of Molecular Biology and Biotechnology,

S.V. Agricultural College, ANGRAU, Tirupati (Andhra Pradesh), India.

(Corresponding author: G. Sreevidya*)

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ABSTRACT: The research work was carried out at Dry land farm, Regional Agricultural Research Station (RARS), Tirupati during *Kharif*, 2022 comprising of thirty genotypes and genetic parameters viz., genetic variability, heritability (broad sense) and genetic advance as per cent of mean were estimated for ten characters. Analysis of variance showed that there were significant differences for all the ten characters studied indicating the presence of variability among the genotypes. Among all the characters studied, phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) suggesting that the environment strongly influenced these characters. Pod yield plant⁻¹ and Kernel yield plant⁻¹ exhibited high PCV and GCV values (>20%) indicating that these traits can be considered for direct selection which leads to genetic improvement. Pod yield plant⁻¹, kernel yield plant⁻¹, 100 pod weight, 100 kernel weight and kernel length were governed by additive gene action which indicates selection of these traits is rewarding as they recorded higher estimates for both heritability (>60%) and high genetic advance as per cent of mean.

Keywords: Peanut, Genetic variability, Heritability, Genetic advance.

INTRODUCTION

The cultivated peanut (*Arachis hypogaea* L.) is a self-pollinated legume crop and allotetraploid with $2n=4x=40$ and is called as king of oilseeds. Groundnut originated from the Greek words 'Arachis' and 'Hypogaea'. 'Arachis' means legume and 'Hypogaea' means below ground which means pods are formed in the soil and exhibit the phenomenon of geocarpy. Groundnut can be divided botanically into two subspecies viz., *hypogaea* and *fastigiata*, differing in their alternate and sequential branching pattern respectively. The subspecies *hypogaea* is further divided into *hypogaea* (Virginia) and *hirsuta* while *fastigiata* is divided into *fastigiata* (Valencia), *vulgaris* (Spanish), *peruviana*, and *aequatoriana* (Krapovickas and Gregory 1994).

India is the second largest producer of groundnut after China, followed by United States and Nigeria (Tiwari *et al.*, 2018).

However according to the analysis conducted it was identified that in India there is a negative trend in the growth rate of area and production whereas productivity of groundnut increased over the years (Shruthi *et al.*, 2017).

Genetic variability estimates help in parental selection and is also useful in the selection of individuals that can perform well across different environmental conditions. Kernel yield is a complex character that is polygenic and highly influenced by the environment. Thereby, selection based only on the yield restricts the improvement of kernel size (Mubai *et al.*, 2020). However, selection based on the highly heritable yield attributes is most effective in improving yield and which in turn used to calculate the breeding value of individuals. Combined approach of high broad sense heritability and high genetic advance as per cent of mean determines the simultaneous improvement of multiple desirable traits.

MATERIAL AND METHODS

Thirty diverse genotypes of groundnut were sown during *kharif* 2022 in a Randomized Block Design (RBD) with two replications in Regional Agricultural Research Station (RARS), Tirupati to analyze the variability, heritability and genetic advance as per cent of mean. In each replication, every genotype was sown in 2 rows of 3 m in length with a spacing of 30 cm between rows and 10 cm between plants within the row. All necessary cultural operations along with proper plant protection measures were taken to control insect pests. Observations were recorded for thirty genotypes separately on randomly chosen five competitive plants in each genotype in each replication for ten characters *viz.*, pod yield plant⁻¹, kernel yield plant⁻¹, 100 pod weight, 100 kernel weight, shelling percentage, sound mature kernel percentage, kernel length, kernel breadth, oil content, protein content.

Analysis of variance was calculated using the mathematical model proposed by Panse and Sukhatme (1961). Phenotypic and genotypic coefficients of variation were calculated based on the formula given by Burton (1952). Broad sense heritability (h^2_{bs}) and genetic advance as per cent of mean were estimated as suggested by (Johnson *et al.*, 1955). WINDOSTAT 9.2 software was utilized to undergo statistical analysis.

RESULTS AND DISCUSSION

Analysis of variance showed that there were significant differences at 1% level for all the ten characters studied (Table 1) and the results obtained were similar to Kumar *et al.* (2019); Mahesh *et al.* (2018).

PCV and GCV revealed that there exist environmental influences on characters as the estimates of PCV were higher than GCV estimates for all characters studied (Table 2). Higher GCV and PCV (>20%) were identified for the characters Pod yield plant⁻¹ (GCV: 27.64%, PCV: 28.4%) and Kernel yield plant⁻¹ (GCV: 25.84%, PCV: 28.01%) which indicates the presence of significant amount of variability for these traits within the population. Higher GCV and PCV were identified for Pod yield plant⁻¹ was similarly reported by Shinde *et al.* (2019); Yadav *et al.* (2014); Yadlapalli (2014); John *et al.* (2006).

Moderate GCV and PCV were observed for 100 pod weight (GCV: 18.16%, PCV: 18.68%), 100 kernel

weight (GCV: 12.65%, PCV: 13.46%), kernel length (GCV: 10.74%, PCV: 11.88%). 100 kernel weight exhibiting moderate GCV and PCV were reported by Shinde *et al.* (2019) and Rao *et al.* (2014) whereas 100 pod weight and 100 kernel weight showing moderate GCV and PCV were given by Pradhan *et al.* (2011). Low GCV and PCV were contributed by the remaining characters. Shelling percentage exhibiting low GCV and PCV was similarly reported by Pradhan *et al.* (2011). The coefficient of variation provides information only about the overall variability of a trait but whether such variability is due to genetic or environmental factors can be clarified with heritability estimates.

High heritability was observed for all the characters *viz.*, protein content (98.98%), oil content (98.63%), pod yield plant⁻¹ (94.72%), 100 pod weight (94.54%), 100 kernel weight (88.37%), kernel yield plant⁻¹ (85.15%), kernel length (81.76%), kernel breadth (77.58%) and shelling percentage (73.50%) except sound mature kernel percentage (46.66%). Broad sense heritability was higher for pod yield plant⁻¹, 100 kernel weight, were earlier reported by Yadlapalli (2014); John *et al.* (2006).

High heritability combined with high genetic advance as per cent of mean revealed the preponderance of additive gene action and thus result in the selection of those traits in the early generations itself which were recorded for pod yield plant⁻¹ (h^2_{bs} = 94.72%, GAM= 55.4%), kernel yield plant⁻¹ (h^2_{bs} = 85.15%, GAM= 49.13%), 100 pod weight (h^2_{bs} = 94.54%, GAM= 36.38%), 100 kernel weight (h^2_{bs} = 88.37%, GAM= 24.5%) and kernel length (h^2_{bs} = 81.76%, GAM= 20.01%). High heritability coupled with high genetic advance as per cent of mean for pod yield plant⁻¹ and kernel yield plant⁻¹ were reported by Narasimhulu *et al.* (2012). Heritability and genetic advance as per cent of mean were higher for pod yield plant⁻¹, kernel yield plant⁻¹ and 100 kernel weight which were in accordance with the results of Rao *et al.* (2014). High heritability coupled with high genetic advance as per cent of mean for pod yield plant⁻¹ was similarly reported by Yadlapalli (2014). In the current study the estimates for 100 kernel weight was in accordance with Donkor *et al.* (2022); Pradhan *et al.* (2011); Mahalakshmi *et al.* (2005).

Table 1: Analysis of variance for yield contributing, kernel size and quality traits in groundnut.

Sr. No.	Character	Mean sum of squares		
		Replications	Treatments	Error
		df=1	df=29	df=29
1.	Pod yield plant ⁻¹ (g)	0.020	9.490**	0.250
2.	Kernel yield plant ⁻¹ (g)	0.040	3.870**	0.310
3.	100 pod weight (g)	0.920	479.260**	13.460
4.	100 kernel weight (g)	3.260	52.890**	3.260
5.	Shelling percentage	3.260	35.370**	5.400
6.	Sound mature kernel (%)	2.810	22.060**	8.020
7.	Kernel length (mm)	0.006	5.550**	0.550
8.	Kernel breadth (mm)	0.140	0.490**	0.060
9.	Oil content (%)	0.930	7.220**	0.040
10.	Protein content (%)	1.990	6.740**	0.030

** Significant at 1% level

Table 2: Mean, range, coefficient of variation, heritability (broad sense) and genetic advance a sper cent of mean for ten characters in 30 groundnut genotypes.

Sr. No.	Character	Mean	Range		Variance		Coefficient of variance		Heritability (Broad sense) (%)	Genetic Advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1.	PYP	7.78	3.70	12.20	4.62	4.88	27.64	28.40	94.72	4.31	55.40
2.	KYP	5.16	2.30	7.60	1.78	2.09	25.84	28.01	85.15	2.54	49.13
3.	100 PW	84.02	66.47	130.86	232.90	246.36	18.16	18.68	94.54	30.57	36.38
4.	100KW	39.37	31.50	53.00	24.81	28.08	12.65	13.46	88.37	9.65	24.50
5.	SP	70.00	60.50	77.00	14.99	20.39	5.53	6.45	73.50	6.84	9.77
6.	SMK	92.25	85.57	96.79	7.02	15.04	2.87	4.20	46.66	3.73	4.04
7.	KL	14.72	12.99	19.63	2.50	3.06	10.74	11.88	81.76	2.95	20.01
8.	KB	8.46	7.62	9.84	0.22	0.28	5.48	6.22	77.58	0.84	9.94
9.	Oil	47.04	42.66	51.26	3.59	3.64	4.03	4.06	98.63	3.88	8.24
10.	Protein	23.86	20.52	29.21	3.36	3.39	7.68	7.72	98.98	3.76	15.74

PYP : Pod Yield Per Plant (g); **SP**: Shelling Percentage **Oil** : Oil content(%)
KYP : Kernel Yield Per Plant (g); **SMK** : Sound Mature Kernel(%); **Protein** : Protein content(%)
100 PW : Hundred Pod Weight (g); **KL**: Kernel Length(mm)
100 KW : Hundred Kernel Weight(g); **KB** : Kernel Breadth(mm)

CONCLUSIONS

The higher estimates of GCV and PCV were found for Pod yield plant⁻¹ and Kernel yield plant⁻¹ which make these particular traits appropriate for selection. High heritability combined with high genetic advance as per cent of mean were recorded for Pod yield plant⁻¹, kernel yield plant⁻¹, 100 pod weight, 100 kernel weight and kernel length indicating the dominance of additive gene effects and hence direct selection can be used to enhance these traits.

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Conflict of Interest. None.

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