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STUDIES ON GENETIC VARIABILITY FOR YIELD AND YIELD RELATED TRAITS IN PEANUT (*Arachis hypogaea* L.)

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ABSTRACT

Thirty three genotypes of peanut were evaluated during *kharif* 2019 to estimate genetic parameters *viz.*, genetic variance, heritability (broad sense) and genetic advance as per cent of mean for 19 characters. The analysis of variance revealed that highly significant differences were observed among the genotypes for all the characters studied except dry haulms yield per plant. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied implying that these characters were highly influenced by the environmental effects. High PCV and GCV values (>20%) was recorded for number of primary branches per plant and number of secondary branches per plant. High heritability (> 60%) coupled with high genetic advance as per cent of mean was recorded for specific leaf area at 45 DAS, number of primary branches per plant, hundred pod weight and hundred kernel weight indicating that these characters were governed by additive gene effects and selection of these characters is rewarding

KEY WORDS: Genetic advance, heritability, variability, peanut.

INTRODUCTION

The cultivated groundnut or peanut (*Arachis hypogaea* L.), is an annual self pollinated crop with chromosome number of 2n = 4x = 40. It is the only nut found under the soil and designated as "wonder legume". It belongs to the family Fabaceae. It is native to South America, grown throughout the tropical and sub-tropical regions of the world between the latitudes of 40° N to 40° S. It is an important oilseed crop known for its several purposes including edible oil production, direct human consumption as food and for animal consumption in the form of silage, hay and oilcake. It is a rich source of high quality oil (44-56%), protein (22-30%) on dry seed basis, carbohydrates (10-25%), vitamins (E, Z and B complex), minerals (Ca, P, Mg, Zn and Fe) and fiber. Being a legume it adds nitrogen and organic matter to the soil.

In India, peanut is cultivated in an area of 48.87 lakh ha with production of 92.52 lakh tonnes and productivity of 1893 kg ha^{-1}. In Andhra Pradesh it is grown in an area of 7.35 lakh ha with production of 10.48 lakh tonnes and productivity of 1426 kg ha^{-1} (Anonymous, 2018). Hence, increasing the productivity of peanut is one of the prime objective in plant breeding.

Effectiveness of selection depends on presence of considerable genetic variability in gene pool for evolving desirable plant types. Heritability measures the degree of resemblance between the parents and the off-springs, while genetic advance aids in exercising the necessary selection pressure. Reliable estimates of genetic variability, heritability and genetic advance will be essential for the plant breeders in determining the direction and magnitude of selection.

MATERIAL AND METHODS

Thirty three advanced breeding lines of peanut were sown during *kharif*, 2019 in a Randomized Block Design (RBD) with three replications in order to study the genetic parameters *viz.*, variability, heritability and genetic advance as per cent of mean. In each replication every genotype was sown in five rows of 5 m length with a spacing of 30 cm between the rows and 10 cm between the plants within the row. The data was collected from five randomly selected plants of each genotype in each replication for 19 characters viz., days to 50% flowering, days to maturity, SPAD chlorophyll meter reading at 45 DAS, specific leaf area at 45 DAS (cm^{2} g^{-1}), relative water content (%), plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of mature pods per plant, hundred pod weight (g), shelling per cent, hundred kernel weight (g), sound mature kernel per cent, dry haulms yield per plant (g),

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*Corresponding author, E-mail: suvarnachintha121@gmail.com harvest index (%), protein content (%), oil content (%), kernel yield per plant (g) and pod yield per plant (g).

The various genetic parameters *viz*., phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability (h^2_{bs}) in broad sense and genetic advance as per cent of mean was calculated as suggested by Burton (1952), Lush (1940), Johnson *et al*., (1955a) and Johnson *et al*., (1955b). The data analysis was carried out with WINDOWSTAT 9.2 software.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences were observed for all the characters studied except dry haulms yield per plant indicating the presence of ample amount of variability among the genotypes.(Table 1). The estimates of PCV was higher than GCV for all the characters under study (Table 2 and Fig. 1) indicating that the characters were influenced by the environment. The characters, number of primary branches per plant (GCV: 24.73%; PCV: 30.05%) and number of secondary branches per plant (GCV: 48.75 %; PCV: 74.20%) registered higher GCV and PCV (>20) values respectively indicating that these characters contributed markedly to the total variability. Similar results were reported by Mahesh *et al.* (2018), Kamdi *et al.* (2017), Bhargavi *et al.* (2017) and Gupta *et al.* (2015) for number of primary branches per plant and Korat *et al.* (2009) for number of secondary branches per plant.

Moderate GCV and high PCV was exhibited by kernel yield per plant (GCV: 17.21%; PCV: 27.84%), pod yield per plant (GCV: 15.99%; PCV: 23.95%), plant height (GCV: 15.34%; PCV: 21.31%), number of mature pods per plant (GCV: 14.21%; PCV: 25.44%) and dry haulms yield per plant (GCV: 10.49%; PCV: 26.99%).

Table 1. Analysis of variance for yield and yield attributes in peanut

S. No.	Characters	Mean sum of squares		
		Replications (df : 2)	**Treatments (df : 32)**	**Error (df : 64)**
1	Days to 50% flowering	2.192	3.773**	1.286
2	Days to maturity	55.848	69.710**	40.880
3	SCMR at 45 days after sowing	27.179	17.912**	6.213
4	Specific leaf area at 45 DAS (cm^2 g^{-1})	290.340	3535.840**	202.735
5	Relative water content (%)	57.238	47.483**	22.978
6	Plant height (cm)	28.883	132.905**	31.475
7	No. of primary branches plant^{-1}	0.942	6.737**	0.922
8	No. of secondary branches plant^{-1}	1.613	2.48**	0.755
9	No. of mature pods plant^{-1}	1.768	23.672**	10.027
10	Hundred pod weight (g)	29.464	518.534**	33.683
11	Shelling per cent	3.166	59.940**	41.130
12	Hundred kernel weight (g)	34.131	283.231**	12.110
13	Sound mature kernel (%)	7.636	40.145**	3.688
14	Dry haulms yield plant^{-1} (g)	2.570	34.692	22.609
15	Harvest index (%)	30.041	137.101**	40.158
16	Kernel yield plant^{-1} (g)	8.925	23.940**	8.387
17	Protein content (%)	0.015	0.810**	0.140
18	Oil content (%)	0.183	1.032**	0.106
19	Pod yield plant^{-1} (g)	12.960	1037.48**	607.971

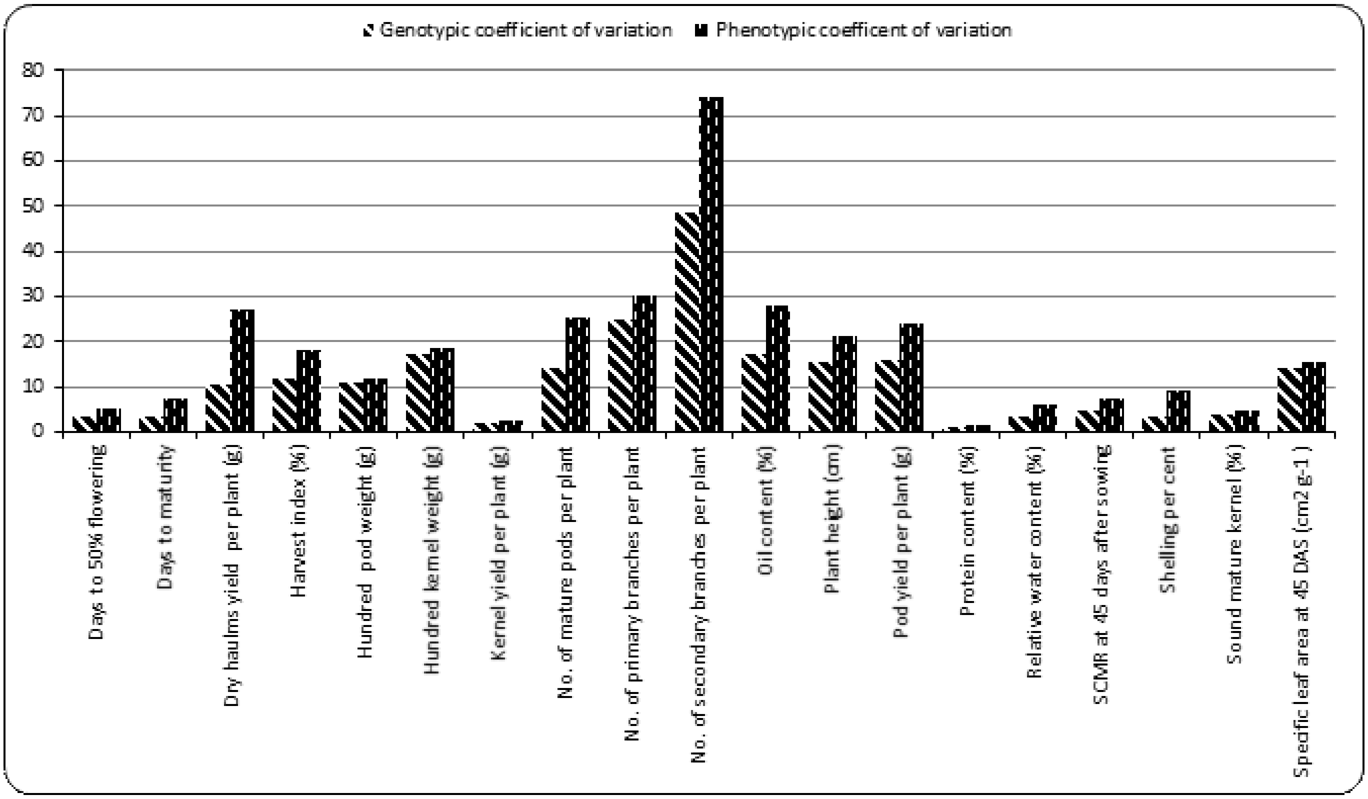

Fig. 1. Genotypic and phenotypic coefficent of variation for physiological, yield and quality traits in peanut.

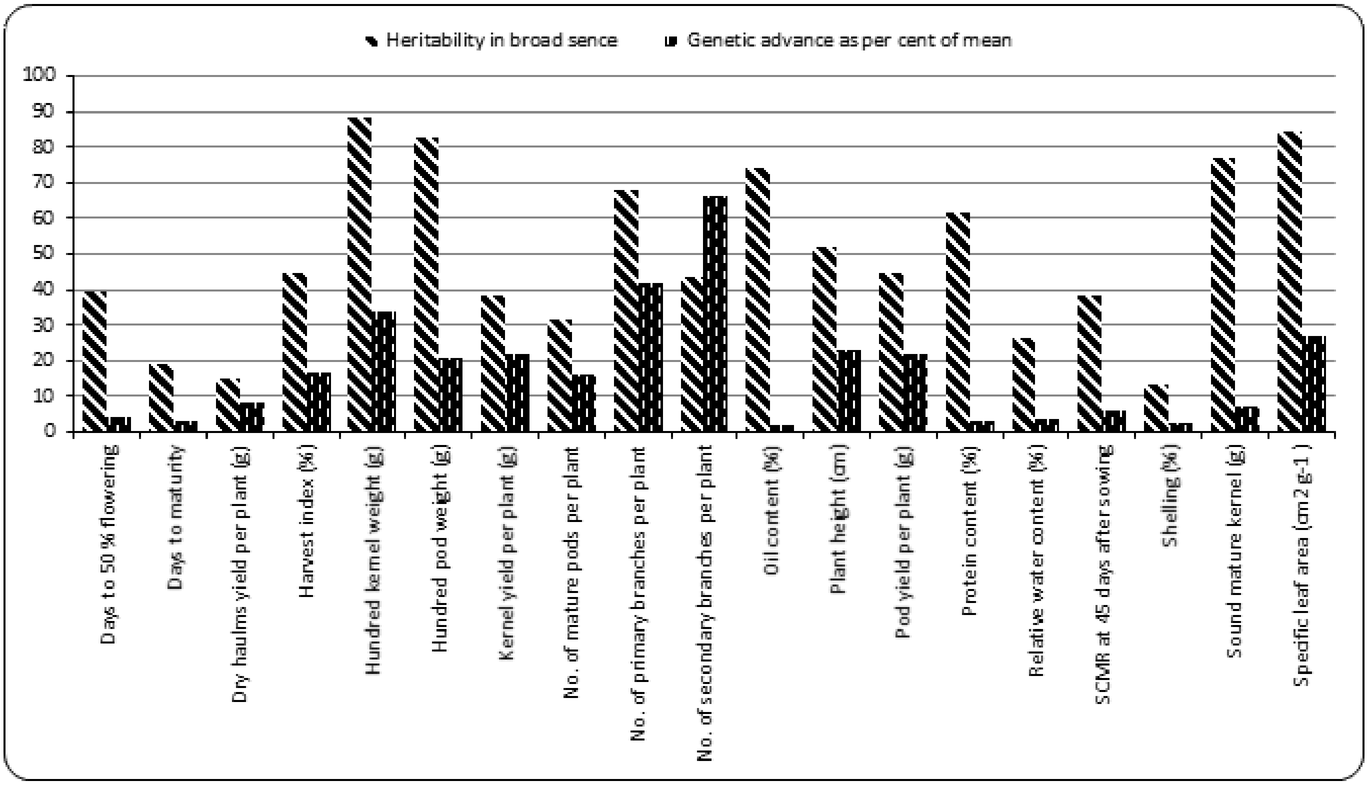

Fig. 2. Heritability in broad sence and genetic advance as per cent of mean for physiological, yield and quality traits in peanut

Table 2. Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for yield and yield attributes in peanut

S. No.	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as per cent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50% flowering	27.62	25.67	30.00	0.83	2.12	3.30	5.27	39.21	1.18	4.25
2.	Days to maturity	96.13	91.00	108.33	9.61	50.49	3.25	7.44	19.03	2.79	2.92
3.	SCMR at 45 days after sowing	43.00	39.10	47.70	3.90	10.11	4.59	7.40	38.56	2.53	5.88
4.	Specific leaf area (cm^2 g^{-1})	235.61	162.89	286.23	1111.03	1313.77	14.15	15.38	84.57	63.14	26.80
5.	Relative water content (%)	90.59	79.32	96.01	8.17	31.15	3.16	6.16	26.23	3.02	3.33
6.	Plant height (cm)	38.16	26.47	51.97	33.81	65.29	15.34	21.31	51.79	8.62	22.74
7.	No. of primary branches plant^{-1}	5.63	4.13	9.93	1.94	2.86	24.73	30.05	67.76	2.36	41.94
8.	No. of secondary branches plant^{-1}	1.56	0.00	2.87	0.57	1.33	48.75	74.20	43.17	1.03	65.98
9.	No. of mature pods plant^{-1}	14.99	10.02	20.47	4.54	14.57	14.21	25.44	31.21	2.45	16.36
10.	Hundred pod weight (g)	115.88	92.67	138.67	161.61	195.30	10.97	12.06	82.75	23.82	20.56
11.	Shelling per cent	76.55	62.33	83.67	6.27	47.40	3.27	8.99	13.23	1.88	2.45
12.	Hundred kernel weight(g)	54.50	42.33	75.00	90.37	102.48	17.44	18.57	88.18	18.39	33.74
13.	Sound mature kernel (%)	88.33	82.00	96.00	12.15	15.84	3.95	4.51	76.72	6.29	7.11
14.	Dry haulms yield plant^{-1} (g)	19.18	8.87	25.87	4.02	26.63	10.49	26.99	15.12	1.61	8.41
15.	Harvest index (%)	47.07	35.32	66.31	32.32	72.48	12.08	18.09	44.59	7.82	16.61
16.	Protein content (%)	25.60	24.30	26.33	0.22	0.36	1.85	2.36	61.40	0.76	2.98
17.	Oil content (%)	47.35	45.67	48.37	0.31	0.42	1.17	1.36	74.32	0.99	2.08
18.	Kernel yield plant^{-1} (g)	13.23	8.29	21.50	5.18	13.57	17.21	27.84	38.20	2.90	21.91
19	Pod yield plant^{-1} (g)	17.16	11.27	26.27	7.64	17.14	15.99	23.95	44.58	3.80	21.99

Chavadhari *et al.* (2017) and Yusuf *et al.* (2017) reported moderate values of GCV and high PCV for plant height. Moderate GCV and moderate PCV was exhibited by specific leaf area at 45 DAS (GCV: 14.15%; PCV: 15.38 %), harvest index (GCV: 12.08%; PCV: 18.09%), hundred pod weight (GCV: 10.97%; PCV: 12.06%) and hundred kernel weight (GCV: 17.44%; PCV: 18.57%). Moderate variability for hundred kernel weight was reported by Nayak *et al.* (2018), Nagaveni and Hasan (2019), Rathod and Toprope (2018) and Bhakal and Lal (2017). Similar results for hundred pod weight was reported by Korat *et al.* (2010) and Mahesh *et al.* (2018). Moderate variability for harvest index and specific leaf area at 45 DAS was reported by Nagaveni and Hasan (2019).

High heritability was recorded by hundred kernel weight (88.18%), followed by specific leaf area (84.57%), hundred pod weight (82.75%), sound mature kernel per cent (76.72%), oil content (74.32%), number of primary branches per plant (67.76%) and protein content (61.40%) indicating that the effect of environment is least in expression of these characters.

Heritability in broad sense includes both additive and epistatic gene effects, it will be reliable only if accompanied by high genetic advance (Fig. 2). High heritability coupled with high genetic advance as per cent of mean were recorded for the characters *viz.,* specific leaf area at 45 DAS (h^2_{bs}= 84.57%, GAM= 26.80%), number of primary branches per plant (h^2_{bs}= 67.76%, GAM= 41.94%), hundred kernel weight (h^2_{bs}= 88.18%, GAM= 33.740%) and hundred pod weight (h^2_{bs}= 82.75%, GAM= 20.56%) indicating the preponderance of additive gene action in expression of these characters and selection would be effective for improvement of these characters. High heritability coupled with high genetic advance as per cent of mean for number of primary branches per plant was reported by Waidkar *et al.* (2018), Mahesh *et al.* (2018) and Vasanthi *et al.* (2015a). High heritability coupled with high genetic advance as per cent of mean for hundred kernel weight were also reported by Satish (2014), Patil *et al.* (2014), Rao *et al.* (2014), Gupta *et al.* (2015), Vasanthi *et al.* (2015a), Bhargavi *et al.* (2017), Mahesh *et al.* (2018) and Kakeeto *et al.* (2019). In the present study the estimates for hundred pod weight was in accordance to results reported by Nath and Alam (2002), Gupta *et al.* (2015), Chavadari *et al.* (2017) and Kumar *et al.* (2019).

CONCLUSION

High heritability coupled with high genetic advance as per cent of mean was observed for specific leaf area at 45 DAS, number of primary branches per plant, hundred kernel weight and hundred pod weight indicating the preponderance of additive gene action in governing these traits and direct selection would be rewarding for crop improvement. It was also observed that the trait number of primary branches per plant possessed higher estimates of GCV, PCV, heritability and genetic advance as per cent of mean implying that these traits were predominantly under the control of additive gene action and genetic improvement can be achieved through simple selection for these traits.

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