

Genetic Variability Studies in large Seeded Genotypes of Peanut (*Arachis hypogaea* L.)

K. Deepthi^{1*}, K. John², D. Bharathi³ and P. Sudhakar⁴

¹P.G. Scholar, Department of Genetics and Plant Breeding,
S.V. Agricultural College, Tirupati (Andhra Pradesh), India.

²Principal Scientist (GPBR), Regional Agricultural Research Station, Tirupati (Andhra Pradesh), India.

³Senior Scientist (GPBR), Regional Agricultural Research Station, Tirupati (Andhra Pradesh), India.

⁴Controller of Examinations, ANGRAU, LAM, Guntur (Andhra Pradesh), India.

(Corresponding author: K. Deepthi*)

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ABSTRACT: Genetic studies determining the valuable confectionary characters like oil, protein, sucrose and fatty acid contents, in addition to yield components like kernel weight, shelling percentage are limited. The quality requirement of large-seeded groundnut is more precise and distinctly different from peanut as an oilseed crop. Because of the above fact, there is a necessity to evaluate the available large-seeded groundnut genotypes to know the extent of genetic variability and heritability for important confectionary characteristics. Therefore, Genetic variability analysis was carried out for physiological, yield attributes and quality traits in 26 peanut genotypes. The study indicated the existence of a considerable amount of variability for every character. High heritability estimates were recorded for sucrose content, days to maturity, sound mature kernel per cent, days to 50 % flowering, stearic acid content, dry haulms yield plant⁻¹, oil content, oleic to linoleic acid ratio, linoleic acid content, shelling per cent, kernel yield plant⁻¹, plant height, protein content, pod yield plant⁻¹, oleic acid content, specific leaf area at 45 DAS, palmitic acid content, harvest index and a number of mature pods plant⁻¹ stipulating that the effect of environment is least in the countenance of these characters. Sucrose content, dry haulms yield plant⁻¹, the number of mature pods plant⁻¹, plant height, kernel yield plant⁻¹, pod yield plant⁻¹, stearic acid content, shelling per cent and harvest index exhibited high genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean (GAM) was recorded for sucrose content, stearic acid content, dry haulms yield plant⁻¹, shelling per cent, kernel yield plant⁻¹, plant height, pod yield plant⁻¹, harvest index and the number of mature pods plant⁻¹ indicating a preponderance of additive gene action. Therefore, selection for the above characters would be more rewarding to bring improvement in peanut for physiological, yield attributes and quality traits.

Keywords: Peanut, Broad sense heritability, Genetic advance, GAM, Variability.

INTRODUCTION

Cultivated peanut (*Arachis hypogaea* L.) is an annual legume crop. It is a self-pollinated crop with a chromosome number of $2n = 4x = 40$. It is a native of South America and grown all over the tropical and subtropical regions of the world. Peanut belongs to the sub-family Papilionaceae of the family Leguminosae and it is commonly called a poor man's nut. Peanut is widely accepted as the most critical source of nutrition for both humans and animals due to its high oil (45-50%) and protein (25%) content. Apart from oil and protein, peanut contains carbohydrates (8-14%), minerals, vitamins A, B and some members of the B₂ group, mainly thiamin and niacin and are abundant in mono-unsaturated fatty acids.

As peanut is an major food crop and recently the confectionary types has presumed great importance as snack food in national and international markets, there is a necessity to enhance the quality traits of peanut. Hence selection for quality attributes in peanut is a requisite in breeding programmes.

However, genetic studies determining these valuable confectionary characters like oil, protein, sucrose and fatty acid contents, in addition to yield components like kernel weight, sound mature kernels and shelling percentage are limited. The breeding procedures involving confectionary genotypes are to be improved. The quality requirement of large-seeded groundnut is more precise and distinctly different from peanut as an oilseed crop.

Because of the above fact, there is a necessity to evaluate the available large-seeded groundnut genotypes to know the extent of genetic variability and heritability for important confectionery characteristics. The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or hybridization followed by selection. Hence, it is essential to study the genetic variability parameters like range, coefficient of variability, heritability and genetic advance over a mean (Parameshwarappa *et al.* 2005, Korannavar and Biradar 2019). The present investigation was taken up among twenty-six genotypes of peanut to assess the amount of genetic variability for physiological, yield attributes and quality traits in peanut.

MATERIAL AND METHODS

The present investigation was carried out among 26 peanut genotypes during *Kharif*, 2020, at a dry land farm of Sri Venkateswara Agricultural College, Tirupati using Randomized Block Design with three replications.

Observations were noted on five randomly selected plants in each genotype for SPAD chlorophyll meter reading at 45 DAS, specific leaf area at 45 DAS, relative water content, plant height, number of primary branches plant⁻¹, number of mature pods plant⁻¹, hundred pod weight, shelling per cent, hundred kernel weight, kernel yield plant⁻¹, sound mature kernel per cent, dry haulms yield plant⁻¹, harvest index, oil content, protein content, sucrose content, palmitic acid content, stearic acid content, oleic acid content, linoleic acid content, oleic to linoleic acid ratio and pod yield plant⁻¹ whereas for days to 50 % flowering and days to maturity observations were noted on a plot basis.

The variation among 26 genotypes for different characters was tested for significance by using the analysis of variance technique as given by Panse and Sukhatme (1961). The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952). Heritability in broad sense [h^2_b] was calculated by the formula given by Lush (1940) and genetic advance as given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance carried out for 24 physiological, yield attributes and quality traits revealed highly significant (1%) differences among the genotypes for the characters, *viz.*, days to 50 % flowering, days to maturity, SPAD chlorophyll meter reading at 45 DAS, specific leaf area at 45 DAS, relative water content, plant height, number of primary branches plant⁻¹, number of mature pods plant⁻¹, hundred pod weight, shelling per cent, hundred kernel weight, kernel yield plant⁻¹, sound mature kernel per

cent, dry haulms yield plant⁻¹, harvest index, oil content, protein content, sucrose content, palmitic acid content, stearic acid content, oleic acid content, linoleic acid content, oleic to linoleic acid ratio and pod yield plant⁻¹ (Table 1). These results indicated the presence of a considerable amount of genetic variation for all the 24 traits in the experimental material.

A. Variability studies

The estimates of genetic parameters *viz.*, phenotypic and genotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as per cent of mean computed for twenty-four characters in twenty-six genotypes are presented in Table 2.

The Phenotypic coefficient of variation was of high magnitude than the genotypic coefficient of variation for all the characters indicating the influence of the environment in the expression of these traits. These results are following the findings of Narasimhulu *et al.* (2012), John *et al.* (2013), Kamdi *et al.* (2017), Mahesh *et al.* (2018) and Nagaveni and Hasan Khan (2019).

The characters, sucrose content, dry haulms yield plant⁻¹, the number of mature pods plant⁻¹ and plant height showed high variability indicating an adequate amount of variation among the genotypes. Therefore, simple selection would be productive for further improvement of these characters.

Higher GCV and PCV estimates for plant height, number of mature pods plant⁻¹ and dry haulms yield plant⁻¹ were following the results obtained by Kadam *et al.* (2016) and Mahesh *et al.* (2018). High estimates of GCV for sucrose content were similar to the reports of Rathod and Toprope (2018).

The characters, specific leaf area at 45 DAS, sound mature kernel per cent, days to 50 % flowering, days to maturity, oleic acid content, protein content, linoleic acid content, palmitic acid content, SPAD chlorophyll meter reading at 45 DAS, relative water content and oil content exhibited lower estimates of both PCV and GCV.

Lower estimates of GCV and PCV for days to 50 % flowering were by the results of Vasanthi *et al.* (2015), Kadam *et al.* (2016), Chavadhari *et al.* (2017), GonyaNayak *et al.* (2018) and Mahesh *et al.* (2018). The low variability estimates recorded for SPAD chlorophyll meter reading at 45 DAS and days to maturity were confirmed with the findings of Rathod and Toprope (2018) and Gonya Nayak *et al.* (2018). Jayalakshmi *et al.* (2003) showed similar results for specific leaf area at 45 DAS. Lower estimates of GCV and PCV for protein content and oil content were confirmed with the findings of Vasanthi *et al.* (2015), Omprakash and Nadaf (2017) and Mahesh *et al.* (2018), whereas low variability for relative water content and sound mature kernel per cent were similar with the findings of Nagaveni and Hasan Khan (2019).

Table 1: Analysis of variance for physiological, yield attributes and quality traits in 26 genotypes of peanut.

Sr. No.	Characters	Mean sum of squares		
		Replications (df:2)	Treatments (df:25)	Error (df:50)
1	Days to 50% flowering	0.205	6.660**	0.205
2	Days to maturity	0.935	123.502**	1.455
3	SPAD chlorophyll meter reading at 45 DAS	1.108	6.556**	3.714
4	Specific leaf area at 45 DAS (cm ² g ⁻¹)	37.072	618.035**	79.521
5	Relative water content (%)	6.743	8.858**	4.469
6	Plant height (cm)	47.246	233.358**	27.051
7	Number of primary branches plant ⁻¹	0.286	0.903**	0.425
8	Number of mature pods plant ⁻¹	2.265	42.076**	7.177
9	Hundred pod weight (g)	365.020	653.869**	129.836
10	Shelling per cent	1.799	213.409**	22.368
11	Hundred kernel weight (g)	25.893	109.350**	25.347
12	Kernel yield plant ⁻¹ (g)	0.716	13.913**	1.489
13	Sound mature kernel (%)	3.193	100.678**	2.397
14	Dry haulms yield plant ⁻¹ (g)	16.958	206.185**	10.493
15	Harvest index (%)	9.861	137.845**	22.468
16	Oil content (%)	0.798	3.431**	0.321
17	Protein content (%)	0.141	4.122**	0.485
18	Sucrose content (%)	0.065	9.362**	0.026
19	Palmitic acid (%)	0.018	0.616**	0.094
20	Stearic acid (%)	0.008	0.384**	0.014
21	Oleic acid (%)	0.495	12.054**	1.453
22	Linoleic acid (%)	0.230	8.923**	0.905
23	Oleic to Linoleic acid ratio (%)	0.0003	0.032**	0.003
24	Pod yield plant ⁻¹ (g)	4.298	41.540**	5.001

*Significant at 5 % level; **Significant at 1% level

B. Heritability

High heritability estimates were recorded for sucrose content, days to maturity, sound mature kernel per cent, days to 50% flowering, stearic acid content, dry haulms yield plant⁻¹, oil content, oleic to linoleic acid ratio, linoleic acid content, shelling per cent, kernel yield plant⁻¹, plant height, protein content, pod yield plant⁻¹, oleic acid content, specific leaf area at 45 DAS, palmitic acid content, harvest index and the number of mature pods plant⁻¹. The characters *viz.*, hundred pod weight and hundred kernel weight exhibited moderate heritability. The characters, the number of primary branches plant⁻¹, relative water content and SPAD chlorophyll meter reading at 45 DAS exhibited lower heritability estimates.

C. Genetic advance

High genetic advance was exhibited for the character's specific leaf area at 45 DAS and hundred pod weight, whereas dry haulms yield plant⁻¹, plant height, shelling per cent, days to maturity, sound mature kernel per cent and harvest index recorded moderate genetic advance. The characters *viz.*, hundred kernel weight, pod yield plant⁻¹, number of mature pods plant⁻¹, sucrose content, kernel yield plant⁻¹, oleic acid content, linoleic acid content, days to 50% flowering, protein content, oil content, relative water content, SPAD chlorophyll

meter reading at 45 DAS, palmitic acid content, stearic acid content, number of primary branches plant⁻¹ and oleic to linoleic acid ratio recorded low genetic advance.

Genetic advance as per cent of mean. Higher genetic advance as per cent of mean was recorded for sucrose content, dry haulms yield plant⁻¹, the number of mature pods plant⁻¹, plant height, kernel yield plant⁻¹, pod yield plant⁻¹, stearic acid content, shelling per cent and harvest index. The characters exhibited a moderate genetic advance as per cent of mean, oleic to linoleic acid ratio, sound mature kernel per cent, hundred pod weight, days to 50% flowering, hundred kernel weight, days to maturity and specific leaf area at 45 DAS. The characters *viz.*, the number of primary branches plant⁻¹, linoleic acid content, oleic acid content, protein content, palmitic acid content, oil content, SPAD chlorophyll meter reading at 45 DAS and relative water content exhibited low genetic advance as per cent of mean.

High heritability coupled with high genetic advance as per cent of mean was recorded for sucrose content, stearic acid content, dry haulms yield plant⁻¹, shelling per cent, kernel yield plant⁻¹, plant height, pod yield plant⁻¹, harvest index and number of mature pods plant⁻¹ indicating preponderance of additive gene action and hence phenotypic selection would be more effective for improvement of these characters.

Table 2: Estimates of genetic parameters for physiological, yield attributes and quality traits in 26 genotypes of peanut.

Sr. No.	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50% flowering	24.10	22.00	27.00	2.15	2.35	6.08	6.36	91.30	2.88	11.97
2.	Days to maturity	116.29	105.00	123.00	40.68	42.13	5.48	5.58	96.54	12.91	11.10
3.	SPAD chlorophyll meter reading at 45 DAS	47.18	44.36	50.96	0.94	4.66	2.06	4.57	20.32	0.90	1.91
4.	Specific leaf area at 45 DAS (cm ² g ⁻¹)	223.37	186.53	248.72	179.50	259.02	5.99	7.20	69.30	22.97	10.28
5.	Relative water content (%)	88.00	84.32	91.67	1.46	5.93	1.37	2.76	24.66	1.23	1.40
6.	Plant height (cm)	40.14	18.46	50.16	68.76	95.82	20.65	24.38	71.77	14.47	36.04
7.	Number of primary branches plant ⁻¹	5.03	4.13	6.20	0.15	0.58	7.92	15.18	27.22	0.42	8.51
8.	Number of mature pods plant ⁻¹	14.14	8.33	28.46	11.63	18.81	24.11	30.67	61.84	5.52	39.07
9.	Hundred pod weight (g)	156.48	132.65	183.59	174.67	304.51	8.44	11.15	57.36	20.62	13.17
10.	Shelling per cent	55.79	43.21	72.41	63.68	86.04	14.30	16.62	74.00	14.14	25.34
11.	Hundred kernel weight (g)	66.32	58.01	78.43	28.00	53.34	7.97	11.01	52.49	7.89	11.90
12.	Kernel yield plant ⁻¹ (g)	10.27	7.17	16.72	4.14	5.63	19.79	23.08	73.55	3.59	34.97
13.	Sound mature kernel (%)	83.90	72.42	92.65	32.76	35.15	6.82	7.06	93.18	11.38	13.56
14.	Dry haulms yield plant ⁻¹ (g)	23.58	8.73	42.13	65.23	75.72	34.24	36.89	86.14	15.44	65.47
15.	Harvest index (%)	45.27	28.37	61.28	38.45	60.92	13.69	17.24	63.12	10.14	22.41
16.	Oil content (%)	48.26	46.64	50.29	1.03	1.35	2.10	2.41	76.30	1.83	3.79
17.	Protein content (%)	26.33	24.43	29.10	1.21	1.69	4.18	4.94	71.39	1.91	7.27
18.	Sucrose content (%)	2.77	0.10	7.91	3.11	3.13	63.56	63.83	99.16	3.61	130.40
19.	Palmitic acid (%)	11.07	9.92	11.79	0.17	0.26	3.76	4.67	64.78	0.69	6.24
20.	Stearic acid (%)	2.14	1.71	2.85	0.12	0.13	16.33	17.29	89.16	0.68	31.76
21.	Oleic acid (%)	43.34	40.58	48.57	3.53	4.98	4.33	5.15	70.86	3.25	7.52
22.	Linoleic acid (%)	38.32	33.99	40.99	2.67	3.57	4.26	4.93	74.69	2.91	7.59
23.	Oleic to Linoleic acid ratio (%)	1.13	0.99	1.42	0.00	0.01	8.76	10.06	75.92	0.17	15.73
24.	Pod yield plant ⁻¹ (g)	18.68	10.86	28.00	12.17	17.18	18.67	22.17	70.89	6.05	32.38

High heritability coupled with high genetic advance as per cent of mean for number of mature pods plant⁻¹ was also reported by Chavadhari *et al.* (2017) and Mahesh *et al.* (2018). Similar results for plant height were reported by Rao *et al.* (2014) and Yusuf *et al.* (2017). Narasimhulu *et al.* (2012) reported similar results for shelling per cent. High heritability coupled with high genetic advance as per cent of mean for kernel yield plant⁻¹ and pod yield plant⁻¹ were similar to the findings of Rao *et al.* (2014), Gupta *et al.* (2015), Rajarathinam *et al.* (2017) and Bugati *et al.* (2020). Mahesh *et al.* (2018) and Nagaveni and Hasan Khan (2019) reported similar results for dry haulms yield plant⁻¹. High heritability coupled with high genetic advance as per cent of mean for harvest index are by the reports of Vasanthi *et al.* (2015) and Chavadhari *et al.* (2017). Yusuf *et al.* (2017) reported similar results for stearic acid content. High heritability coupled with high genetic advance as per cent of mean for sucrose content conforms to the reports of Rathod and Toprope (2018). High heritability coupled with moderate genetic advance as per cent of mean was exhibited by characters *viz.*, days to maturity, sound mature kernel per cent, days to 50 % flowering, oleic to linoleic acid ratio and specific leaf area at 45 DAS. This finding obviates simple selection and necessitates recombination breeding with a postponement of selection at later generations.

High heritability coupled with moderate genetic advance as per cent of mean for sound mature kernel per cent were similar to the reports of Kumar *et al.* (2019). Similar results were reported for days to 50 % flowering by John and Reddy (2014).

Characters *viz.*, oil content, linoleic acid content, protein content, oleic acid content and palmitic acid content recorded high heritability coupled with low genetic advance as per cent of mean, which indicated the presence of non-additive gene action. High heritability is exhibited due to the favourable influence of environment rather than genotype and hence selection for such traits may not be rewarding. High heritability coupled with low genetic advance as per cent of mean for protein and oil content were also reported by Kumar *et al.* (2019).

Moderate heritability and moderate genetic advance as per cent of mean were recorded for the characters, hundred pod weight and hundred kernel weight, indicating that both additive and non-additive gene actions have a role in inheritance and phenotypic selection would be adequate to some extent. Similar kinds of results for moderate heritability coupled with moderate genetic advance as per cent of mean for hundred pod weight and hundred kernel weight was reported by Patil *et al.* (2014) and Shinde *et al.* (2019).

Low heritability and low genetic advance as per cent of mean were recorded for characters *viz.*, then umber of

primary branches plant⁻¹, relative water content and SPAD chlorophyll meter reading at 45 DAS, which indicates that these characters were highly influenced by environmental effects and selection would be ineffective. Low heritability and low genetic advance as per cent of mean for SPAD chlorophyll meter reading at 45 DAS and relative water content were similar to the findings of Srivalli and Nadaf (2016).

CONCLUSION

The present study revealed a higher magnitude of variability for most of the yield and quality traits, which is also accompanied by high heritability and genetic advance. High heritability coupled with high genetic advance as per cent of mean was observed for sucrose content, stearic acid content, dry haulms yield plant⁻¹, shelling per cent, kernel yield plant⁻¹, plant height, pod yield plant⁻¹, harvest index and the number of mature pods plant⁻¹. This indicates that these characters were under additive genetic control and selection for genetic improvement will be worthwhile and may rapidly contribute to yield and quality improvement.

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