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Genetic Variability, Heritability and Genetic advance of Podyield Component traits of Virginia Bunch Groundnut (*Arachis hypogaea* L.)

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ABSTRACT

An experiment was carried out in 10 Virginia bunch groundnut genotypes to assess the variability, heritability, genetic advance and genetic advance as per cent of mean for nineteen characters viz., days to 50% flowering, SPAD chlorophyll meter reading (SCMR) at 40, 50,60,70 DAS and at maturity, days to maturity, number of mature pods per plant, biological yield per plant (g), pod yield per plant (g), biological yield per hectare (q), pod yield per hectare (q), harvest index, 100 kernel weight (g), shelling percentage, kernel yield per plant (g), kernel yield per hectare (q), oil content (%) and oil yield per hectare (q) over three seasons viz., Late Kharif (2012), Rabi (2012-13) and Summer (2013). The components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. The results revealed that highest PCV and GCV was observed for biological yield per hectare. High heritability accompanied with high genetic advance as per cent of mean was recorded for kernel yield per plant (g), kernel yield per hectare (q), 100 kernel weight and oil yield per hectare (q) indicating the preponderance of additive gene action which may be exploited through simple selection procedures.

Key words: *Genetic advance, heritability, groundnut, variability, SCMR*

INTRODUCTION

The cultivated groundnut (*Arachis hypogaea* L.) is one of the most important legume cash crop grown for its oil. Though a native of South America, the crop is cultivated in more than 90 countries around the world in an area of 23.95 M.ha with a production of 36.45 M.t and an average productivity of 1520 kg ha^{-1}. Around 90% of the total production is from developing countries located in the semi arid tropics. India and China together contribute 50% of the global pool. Groundnut is one of the most nourishing foods available in the world with 40-50% oil content, 25-28% protein content with high biological value and enriched with vitamin B and E. The basic key to bring about the genetic upgrading to a crop is to utilize the available genetic variability.

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If the variability in the population is largely due to genetic cause with least environmental effect, the probability of isolating superior genotypes is a pre requisite for obtaining higher yield, which is the ultimate expression of various yield contributing characters. For effective selection of high yielding genotypes knowledge on genetic parameters such as genetic variability, heritability, genetic advance is essential. Genetic variability for trait of interest in any breeding material is a pre- requisite as it provides the basis of selection. Heritability estimates helps in improvement of traits by utilizing heritable components of variation. Possible advance through selection based on phenotypic values can be predicted only from the knowledge of phenotypic and genotypic values. Genetic components of variation together with heritability estimates would give the best picture of the amount of advance to be expected from selection.

Hence an effort was made to investigate the extent of genetic variability and selection parameters namely heritability in broad sense and genetic advance for 19 important characters in 10 Virginia bunch type groundnut over three seasons.

MATERIAL AND METHODS

The experimental material comprised of ten Virginia bunch groundnut genotypes. The experiment was laid out in randomized block design with three replications at Agricultural college farm, Bapatla during *Late Kharif* (2012), *Rabi* (2012-13) and *Summer* (2013). The data was pooled over the three seasons. The means of the pooled data was used for statistical analysis. In each season, each entry was accommodated in three rows of 5.0 m length with a spacing of 30 × 10 cm. In case of characters like days to 50% flowering, days to maturity, shelling percentage, 100 kernel weight (g), harvest index, SPAD chlorophyll meter reading (SCMR) at 40, 50, 60, 70 DAS at maturity, kernel yield per hectare (q), biological yield per hectare (q), pod yield per hectare (q), oil yield per hectare (q) and oil content (%) were recorded on plot basis. The chlorophyll content was measured with SPAD chlorophyll meter on 5th or 6th leaf from the top of each representative plant between 10 A.M and 12 noon of the day. Oil content was estimated by using Soxhelt method as described by Sadasivam and Manickam . The amount of oil present in the sample was calculated by using the following formula –

$$\text{Oil in ground sample (\%)} = \frac{\text{Weight of oil (g)}}{\text{Weight of sample (g)}} \times 100$$

Whereas observations such as kernel yield per plant (g), number of mature pods per plant, biological yield per plant (g) and pod yield per plant (g) were recorded on 10 randomly selected plants per entry per replication. The data was subjected to statistical analysis and genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were worked out as per Burton[1]. Heritability in broad sense was estimated as per Lush[7]. Genetic advance as per cent of mean was worked out as per Johnson *et al.*[5].

RESULTS AND DISCUSSION

The analysis of variance revealed that except SCMR at 60 DAS all other characters were found to be significant (Table 1). In the present study, the variation was also estimated character wise in terms of phenotypic and genotypic coefficients of variation (Table 2). Less difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicate less influence of environment on expression of all the traits studied. High PCV and GCV was exhibited by biological yield per plant and biological yield per hectare indicating the greater variability and scope for improvement of high yielding genotypes with desirable character. These results were in accordance with the findings of Shoba *et al.*[10] and John *et al.*[3]. High PCV and moderate GCV was recorded for no. of mature pods per plant, pod yield per plant, pod yield per hectare, kernel yield per plant, kernel yield per hectare and oil yield per hectare indicating possibility for selection of good varieties with regards to the above traits. These results were in accordance with the findings of Zaman *et al*.[13], John *et al*.[3] and Vishnuvardhan *et al.*[12] While days to 50% flowering, SCMR at 40 DAS, SCMR at 50 DAS, SCMR at 60 DAS, SCMR at 70 DAS, days to maturity, shelling percentage and oil content exhibited low PCV and GCV indicating the presence of low variability among the tested genotypes. Similar results were reported by Nath and Alam[9] and Thakur *et al.*[11].

Heritability estimates were high for kernel yield per plant, kernel yield per hectare and oil yield per hectare indicating little influence of environment on the inheritance of these characters. Similar results were obtained by John *et al.*[4] and Narasimhulu *et al.*[8].

Heritability estimates along with genetic advance as per cent of mean are more helpful in predicting the gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as per cent of mean was recorded in kernel yield per plant, kernel yield per hectare, 100 kernel weight and oil yield per hectare indicating the preponderance of additive gene action in governing the inheritance of this character and offers scope for improvement through simple selection procedures. Similar results were reported by John *et al*.[4] and Thakur *et al*.[11].

Moderate heritability coupled with high genetic advance as per cent of mean for biological yield per plant, pod yield per plant, biological yield per hectare and pod yield per hectare indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through simple selection procedures. These findings were in agreement with Shoba *et al*.[10] and John *et al*.[3].

Whereas moderate heritability accompanied with low genetic advance as per cent of mean was observed in days to 50% flowering, days to maturity, shelling percentage and oil content indicating the preponderance of non additive gene action as well as influence of environment. The improvement of this trait might be possible through heterosis breeding. Similar result was reported by Korat *et al.*[6] and Zaman *et al.*[13].

Table 1: ANOVA for various yield and yield contributing characters of Virginia bunch groundnut in pooled environment

Source of variation	df	Days to 50% flowering	SCMR at 40 DAS (No.)	SCMR at 50 DAS (No.)	SCMR at 60 DAS (No.)	SCMR at 70 DAS (No.)	SCMR at maturity (No.)	Days to maturity	No. of mature pods /plant	Biological yield/plant (g)	Pod yield/plant (g)
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Replication	2	6.100	1.526	1.455	0.860	3.019	8.211	0.933	0.171	2.401	0.330
Treatments	19	27.980**	29.311**	37.944**	23.852	25.714*	124.741**	30.455**	11.759**	271.452 **	17.215**
Error	38	3.610	7.958	8.573	12.086	10.981	34.42	5.425	1.406	19.289	1.182

Source of variation	df	Biological yield/hectare (q)	Pod yield/hectare (q)	Harvest index	Shelling (%)	Kernel yield/plant (g)	Kernel yield/hectare (q)	100 Kernel weight (g)	Oil content (%)	Oil yield/hectare (q)
		11	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
Replication	2	10.827	1.151	0.0001	3.257	0.207	0.648	44.71	1.496	1561.828
Treatments	19	469.114 **	29.621**	0.0095**	73.887**	9.625**	16.612**	616.448**	46.508**	25705.378**
Error	38	35.572	2.191	0.0026	9.078	0.63033	1.111	34.54	4.331	1620.220

*= significant at 0.05 level

**= significant at 0.01 level

Table 2: Estimation of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean in 10 Virginia bunch groundnut genotypes in pooled data

S. No.	Character	Mean	Range		GCV	PCV	Heritability (%)	Genetic advance	GA as % of mean
			Min.	Max.					
1	Days to 50% flowering	33.26	31.00	37.11	4.94	7.55	42.85	2.21	6.67
2	SCMR at 40 DAS (No.)	41.79	39.68	44.78	3.68	7.69	22.97	1.52	3.63
3	SCMR at 50 DAS (No.)	43.45	40.60	47.62	4.15	7.91	27.57	1.95	4.49
4	SCMR at 60 DAS (No.)	45.84	43.70	49.08	2.49	7.98	9.76	0.73	1.60
5	SCMR at 70 DAS (No.)	45.50	42.52	47.98	2.81	7.80	12.97	0.94	2.08
6	SCMR at maturity (No.)	54.48	45.61	58.08	5.81	12.23	22.57	3.10	5.69
7	Days to maturity	123.76	120.00	126.44	1.34	2.31	33.89	2.00	1.61
8	No. of mature pods per plant	7.55	6.31	9.79	14.20	21.17	44.99	1.48	19.62
9	Biological yield per plant (g)	26.26	17.65	35.14	20.15	26.18	59.22	8.39	31.95
10	Pod yield per plant (g)	7.35	4.72	9.60	18.13	23.39	60.10	2.13	28.96
11	Biological yield per hectare (q)	34.19	22.86	45.75	20.29	26.75	57.52	10.84	31.70
12	Pod yield per hectare (q)	9.61	6.18	12.59	18.15	23.80	58.18	2.74	28.52
13	Harvest index (%)	0.28	0.24	0.34	9.64	20.33	22.49	0.02	9.42
14	Shelling (%)	68.11	62.73	71.86	3.93	5.92	44.23	3.67	5.39
15	Kernel yield per plant (g)	5.04	3.21	6.97	19.84	25.11	62.43	1.62	32.29
16	Kernel yield per hectare (q)	6.59	4.21	9.14	19.89	25.51	60.77	2.10	31.94
17	100 kernel weight (g)	55.91	41.55	69.61	14.38	17.81	65.18	13.37	23.91
18	Oil content (%)	40.59	36.84	44.71	5.33	7.39	51.97	3.21	7.91
19	Oil yield per hectare (q)	265.88	167.46	367.89	19.45	24.65	62.29	4.10	31.63

GCV= Genotypic coefficient of variation
PCV= Phenotypic coefficient of variation
GA= Genetic advance

CONCLUSION

High heritability coupled with high genetic advance as per cent of mean was recorded in kernel yield per plant, kernel yield per hectare, 100 kernel weight and oil yield per hectare indicating the preponderance of additive gene action in governing the inheritance of this character and offers scope for improvement through simple selection procedures. Hence these characters should be taken into account for further improvement of the genotypes.

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