Agric. Sci. Digest., 37(4) 2017 : 310-313
Print ISSN:0253-150X / Online ISSN:0976-0547

AGRICULTURAL RESEARCH COMMUNICATION CENTRE
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Genetic variability studies in Virginia bunch groundnut (*Arachis hypogaea* L.)

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Received: 22-11-2016 Accepted: 20-10-2017 DOI: 10.18805/ag.D-4524

ABSTRACT

An investigation was carried out in 10 Virginia bunch groundnut genotypes to assess the variability, heritability and genetic advance as per cent of mean for nineteen characters. Analysis of variance revealed highly significant differences among the genotypes for all the characters studied. The PCV was generally higher than the GCV for all the characters studied, which indicate that the variation was not only due to genotypes but also due to influence of environment on the trait. The results revealed that high PCV and GCV was observed for oil yield per hectare (q). High heritability accompanied with high genetic advance as per cent of mean was recorded for biological yield per plant (g), pod yield per plant, kernel yield per plant (g) and 100 kernel weight (g) indicating the preponderance of additive gene action which may be exploited through simple selection procedures.

Key words: Genetic Advance, Groundnut, Heritability, SCMR, Variability.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) also known as peanut or earthnut, is regarded as one of the most important protein rich seed and it occupies the fifth position as oilseed crop after soyabean, cotton seed, rape seed and sunflower seed (Nath and Alam 2002). Peanut seeds are of high value because of their high contents of oil (43-54%) and protein (25-30%). The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and genetic advance as per cent of mean helps in choosing the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance as per cent of mean present in the available genotypes. Hence, in present investigation an attempt was made to determine the performance of some selected Virginia bunch groundnut genotypes to assess the variability of the important traits.

MATERIALS AND METHODS

The experimental material comprised of ten Virginia bunch groundnut genotypes. The list of genotypes together with their pedigree and source of origin is presented in Table 1. The experiment was laid out in randomized block design with three replications at Agricultural College Farm, Bapatla, during *Late Kharif* 2012 (December – March). Each entry was accommodated in three rows of 5.0 m length with a spacing of 45 × 15 cm. All recommended agronomic practices were followed for reaping good crop. 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 and SPAD chlorophyll meter reading 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 (1992). The amount of oil present in the sample was calculated by using the following formula –

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

Where as 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. Pod yield per hectare was computed from pod yield per plot and expressed in quintals per hectare. The formula used is-

$$\text{Pod yield per hectare} = \frac{\text{Yield per plot (g) *}}{\text{Plot area}} \times 10000 \text{ m}^2$$

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Table 1: List of Virginia bunch genotypes used in the present investigation together with their pedigree and source.

Name of thegenotype	Habit group	pedigree	Source
ICGV99073	VB	Germplasm collections	ICRISAT, Patancheru, Hyderabad
Kadiri-3	VB	Selection from Rohut-33	ARS, Kadiri
Kadiri-7 Bold	VB	Germplasm collections	ARS, Kadiri
Kadiri-8 Bold	VB	Germplasm collections	ARS, Kadiri
K-1578	VB	Germplasm collections	ARS, Kadiri
K-1581	VB	Germplasm collections	ARS, Kadiri
K-1454	VB	Germplasm collections	ARS, Kadiri
K-1620	VB	Germplasm collections	ARS, Kadiri
ICGV86564	VB	Germplasm collections	ICRISAT, Patancheru, Hyderabad
K-1628	VB	Germplasm collections	ARS, Kadiri

VB – Virginia bunch
ARS – Agricultural Research Statio

Where as * Yield per plot = Mean pod yield (g) × Plant stand at harvest (no.)

RESULTS AND DISCUSSION

The data was subjected to statistical analysis and genetic parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were worked out as per Burton (1952). Heritability in broadsense was estimated as per Lush (1940). Genetic advance as per cent of mean was worked out as per Johnson *et al.* (1955).

The analysis of variance revealed significant differences among all the 10 genotypes for all the characters studied, indicating a high degree of variability in the material (Table 2). In the present study, the variation was also estimated character wise in terms of phenotypic and genotypic coefficients of variation (Table 3). Less difference between GCV indicate less influence of environment on expression of these traits. High PCV and moderate GCV was exhibited by 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 trait. These results were in accordance with the findings of John *et al*. (2011) and Vishnuvardhan *et al.* (2012). Moderate PCV and GCV was recorded for biological yield per plant, pod yield per plant, biological yield per hectare, pod yield per hectare, harvest index and 100 kernel weight indicating the greater role of environment interaction with genetic factors in their variability expression. These results were in accordance with the findings of Sudhir *et al.* (2008), Korat *et al*. (2009), John *et al*. (2011) and Zaman *et al*. (2011) for 100 kernel weight. While 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 John *et al*. (2009), Zaman *et al.* (2011) for days to 50% flowering.

Heritability in broadsense and genetic advance as per cent of mean is given in Table 3. Heritability estimates were high for days to 50% flowering, SCMR at maturity, days to maturity, biological yield per plant, pod yield per plant, biological yield per hectare, pod yield per hectare, kernel yield per plant, kernel yield per hectare, 100 kernel weight, oil content and oil yield per hectare indicating little influence of environment on the inheritance of these characters. Similar results was obtained by John *et al.* (2009)

Heritability estimates along with genetic advance as per cent of mean are more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability and genetic advance as per cent of mean were high for biological yield per plant, pod yield per plant, pod yield per hectare, kernel yield per plant, kernel yield per hectare, 100 kernel weight and oil 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 Sudhir *et al.* (2008) and Zaman *et al*. (2011).

High heritability coupled with moderate expected genetic advance as per cent of mean was observed for days to maturity, SCMR at maturity, biological yield per hectare and oil content indicating the role of both additive and non-additive gene actions in the inheritance of these traits and improvement can be brought about using breeding methods like diallel selective mating or bi-parental mating followed by selection in advanced generation. Where as SCMR at 40, 50, 60 and 70 DAS expressed moderate heritability accompanied with low genetic advance as per cent of mean indicating these traits are governed by non-additive gene action with little influence of environment in its inheritance. The traits controlled by non-additive gene action can be improved by selection and intermating among selected ones in early generation followed by reselection.

Table 2: ANOVA for various yield and yield contributing characters of Virginia bunch groundnut in *Late Kharif* 2012

Source of variation	df	Days to 50%	SCMR at 40 DAS flowering	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	Pod y ield/plant (g)
	1	2	3	4	5	6	7	8	9	10	
Replication	2	5.200	0.292	15.665	2.052	9.052	1.374	0.133	0.246	1.080	0.444
Treatments	19	26.522**	13.058*	16.874*	14.970*	13.209*	56.550**	26.963**	1.210**	20.438**	3.036 **
Error	38	1.533	4.644	6.101	5.835	4.977	6.351	2.207	0.308	1.587	0.262

Source of variation	df	Biological yield/hectare (q)	Pod yield/hectare	Harvest index	Shelling (%)	Kernel yield/plant (g)	Kernel yield/hectare	100 Kernel weight (g)	Oil content (%)	Oil yield /hectare (q)
		11	12	13	14	15	16	17	18	19
Replication	2	2.928	1.053	0.0004	2.190	0.121	0.263	28.284	0.281	519.57
Treatments	19	34.394**	5.241 **	0.0033**	14.847*	1.487**	2.550**	363.781**	36.722**	4552.516**
Error	38	3.468	0.465	0.0007	9.138	0.160	0.282	12.39	2.226	656.55

*= significant at 0.05 level
**= significant at 0.01 level

Table 3: 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 *Late Kharif* 2012

Character	Mean	Range		GCV	PCV	Heritability (%)	Genetic advance	GA as % of mean
		Min.	Max.					
Days to 50% flowering	30.10	27.66	36.00	9.58	10.43	84.45	5.46	18.15
SCMR at 40 DAS (No.)	39.88	36.70	44.20	4.19	6.84	37.65	2.11	5.30
SCMR at 50 DAS (No.)	43.16	40.26	48.53	4.38	7.21	37.05	2.37	5.50
SCMR at 60 DAS (No.)	45.01	41.00	48.20	3.87	6.62	34.29	2.10	4.67
SCMR at 70 DAS (No.)	43.11	39.60	46.30	3.84	6.44	35.54	2.03	4.71
SCMR at maturity (No.)	43.70	37.53	49.73	9.36	10.99	72.49	7.17	16.41
Days to maturity	123.66	119.66	128.00	2.32	2.61	78.90	5.25	4.25
No. of mature pods per plant	5.96	4.77	6.84	9.19	13.07	49.40	0.79	13.30
Biological yield per plant (g)	22.80	19.64	27.16	10.99	12.30	79.83	4.61	20.23
Pod yield per plant (g)	5.71	3.90	6.83	16.82	19.05	71.89	1.74	30.58
Biological yield per hectare (q)	29.77	25.79	35.37	10.78	12.46	74.82	5.72	19.21
Pod yield per hectare (q)	7.45	5.10	8.89	16.91	19.22	77.40	2.28	30.65
Harvest index (%)	0.25	0.19	0.29	11.80	15.71	56.40	0.04	18.25
Shelling (%)	64.57	61.25	67.54	2.13	5.14	17.23	1.17	1.82
Kernel yield per plant (g)	3.70	2.39	4.60	17.97	20.98	73.33	1.17	31.70
Kernel yield per hectare (q)	4.83	3.13	6.00	17.99	21.08	72.82	1.52	31.63
100 kernel weight (g)	60.66	41.40	74.46	17.84	18.76	90.43	21.20	34.95
Oil content (%)	41.72	36.06	46.93	8.12	8.87	83.78	6.39	15.32
Oil yield per hectare (q)	201.24	123.34	256.58	18.13	22.15	66.98	61.53	30.57

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

CONCLUSION

The present study clearly showed that biological yield per plant, pod yield per plant, harvest index, kernel yield per plant and 100 kernel weight were more variable characters among these genotypes. The estimates of heritability and genetic advance as per cent of mean were high for biological yield per plant, pod yield per plant, kernel yield per plant and 100 kernel weight indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through simple selection procedures.

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