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Genetic Variability, Heritability and Genetic Advance as per cent of Mean for Pod Yield and its Components in Spanish Bunch Groundnut (*Arachis hypogaea* L.) in *Rabi* 2012-13

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ABSTRACT

An investigation was carried out in 20 Spanish bunch groundnut genotypes to assess the variability, heritability and genetic advance as per cent of mean for nineteen characters viz., days to 50% flowering, SPAD chlorophyll meter reading 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). The results revealed that high PCV and GCV were observed for harvest index and biological yield per plant (g) respectively. High heritability accompanied with high genetic advance as per cent of mean was recorded for SCMR at 60 DAS, SCMR at 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, kernel yield per plant (g), kernel yield per hectare (q) 100 kernel weight (g) 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, Groundnut, Heritability, Variability.

The cultivated peanut (*Arachis hypogaea* L.) is a major crop in most tropical and subtropical regions of world and in India it ranks first among edible oilseed group. Peanut seeds are of high value because of their high contents of oil (43-45%) and protein (25-30%). Genetic variability is the prerequisite for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. Hence, in present investigation an attempt was made to determine the performance of some selected Spanish bunch groundnut genotypes to assess the variability, Genotypic coefficient of variation, Phenotypic coefficient of variation, heritability in broad sense, Genetic advance and Genetic advance as per cent of mean among nineteen traits.

MATERIAL AND METHODS

The experimental material comprised of twenty Spanish bunch type of groundnut genotypes. The experiment was laid out in randomized block design with three replications at college farm, Bapatla during *Rabi* 2012-13.. Each entry was accommodated in three rows of 5.0 m length with a spacing of 30 × 10 cm. In characters like days to 50% flowering, days to maturity, shelling percentage, 100 kernel weight (g), harvest index, SPAD chlorophyll meter reading 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. 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. The data was subjected to statistical analysis and genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean were worked out as per Johnson *et al.* (1955) and Hanson (1963).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the 20 genotypes for all the characters studied indicating a high degree of variability in the material (Table 1). In the present study, the variation was also estimated character

Table 1. ANOVA for various yield and yield contributing characters of Spanish bunch groundnut in *Rabi* 2012-13.

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	0.450	12.216	6.034	20.632	13.971	11.434	0.216	0.194	0.742	0.3931
Treatments	19	10.670**	16.201**	9.812 **	72.798**	17.440 **	365.128**	56.325**	3.583**	114.069 **	3.040 **
Error	38	1.204	4.598	4.846	7.933	5.084	8.995	1.462	0.464	2.124	25.833

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	7.539	7.045	0.002	4.222	0.516	4.163	4.086	0.051	7896.662
Treatments	19	988.445 **	25.833**	0.012**	22.969**	1.781 **	15.288**	77.527**	14.944**	29228.507**
Error	38	21.020	4.100	0.001	4.782	0.216	1.980	3.907	1.765	3807.20

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

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 these traits. High PCV and GCV were exhibited by biological yield per plant (g), biological yield per hectare (q) and harvest index indicating the greater variability and scope for improvement of high yielding genotypes with desirable characters. These results were in accordance with the findings of Shoba *et al.* (2009) and John *et al.* (2011). Moderate PCV and GCV was recorded for no. of mature pods per plant, SCMR at 60 DAS 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) and Zaman *et al.* (2011). While days to 50% flowering, SCMR at 40 DAS, SCMR at 50 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), John *et al.* (2011), Zaman *et al.* (2011), Nandini *et al.* (2011) and Thirumala *et al.* (2012).

Heritability estimates were high for days to 50% flowering, SCMR at 60 DAS, SCMR at maturity, days to maturity, no. of mature pods per plant, biological yield per plant, pod yield per plant, biological yield per hectare, pod yield per hectare, harvest index, shelling percentage, kernel yield per plant, kernel yield per hectare, 100

Table 2. Estimation of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean in 20 Spanish bunch groundnut genotypes in *Rabi* 2012-13.

S. No.	Character	Mean	Range		GCV	PCV	Heritability (%)	Genetic advance	GA as % of mean
			Min.	Max.					
1	Days to 50% flowering	29.90	26.66	34.00	5.94	6.98	72.37	3.11	10.41
2	SCMR at 40 DAS (No.)	41.10	36.16	46.93	4.78	7.07	45.68	2.73	6.66
3	SCMR at 50 DAS (No.)	41.84	39.23	45.63	3.07	6.09	25.46	1.33	3.19
4	SCMR at 60 DAS (No.)	39.75	32.26	47.13	11.66	13.65	73.07	8.16	20.54
5	SCMR at 70 DAS (No.)	41.73	36.63	45.53	4.86	7.26	44.75	2.79	6.70
6	SCMR at maturity (No.)	55.82	32.86	71.96	19.51	20.24	92.96	21.63	38.76
7	Days to maturity	106.22	99.00	114.00	4.02	4.18	92.60	8.47	7.98
8	No. of mature pods per plant	6.85	5.27	9.68	14.89	17.91	69.10	1.74	25.50
9	Biological yield per plant (g)	22.74	12.50	37.68	26.86	27.62	94.61	12.24	53.83
10	Pod yield per plant (g)	5.11	3.10	6.85	18.18	22.41	65.83	1.55	30.39
11	Biological yield per hectare (q)	67.20	37.05	111.61	26.72	27.58	93.88	35.84	53.33
12	Pod yield per hectare (q)	15.08	9.26	20.24	17.83	22.32	63.85	4.43	29.36
13	Harvest index (%)	0.24	0.14	0.38	26.45	29.99	77.79	0.11	48.06
14	Shelling (%)	71.45	64.39	75.34	3.44	4.60	55.90	3.79	5.30
15	Kernel yield per plant (g)	3.65	2.27	5.14	19.77	23.53	70.62	1.25	34.23
16	Kernel yield per hectare (q)	10.79	6.78	15.25	19.51	23.47	69.13	3.60	33.42
17	100 kernel weight (g)	29.50	22.04	46.50	16.78	18.07	86.27	9.47	32.12
18	Oil content (%)	43.50	38.50	47.66	4.81	5.70	71.33	3.64	8.38
19	Oil yield per hectare (q)	469.18	280.36	646.17	19.62	23.62	69.00	157.51	33.57

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

kernel weight, oil content and oil yield per hectare indicating little influence of environment on the inheritance of these characters. Similar results were obtained by John *et al.* (2009), John *et al*. (2011), Zaman *et al.* (2011) and Nandini *et al.* (2011).

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 SCMR at 60 DAS, SCMR at maturity, no. of mature pods per plant, biological yield per plant, pod yield per plant, biological yield per hectare, pod yield per hectare, harvest index, 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), Shoba *et al.* (2009), John *et al*. (2011) and Zaman *et al*. (2011).

High heritability coupled with moderate expected genetic advance as per cent of mean was observed for days to 50% flowering 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 generations. Whereas SCMR at 40 DAS and SCMR at 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. The traits controlled by non-additive gene action can be improved by selection and intermating among selected ones in early generation followed by reselection.

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