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Research article

STUDIES ON GENETIC VARIABILITY FOR YIELD, YIELD COMPONENTS AND RESISTANCE TO KALAHASTI MALADY IN GROUNDNUT (*ARACHIS HYPOGAEA* L.).

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ABSTRACT: Twenty one crosses of groundnut derived from 7×7 diallel set without reciprocals were evaluated during *rabi* 2010-11 for variability, heritability and genetic advance. Analysis of variance for thirteen traits revealed highly significant differences among the F_2 populations tested. The estimates of GCV and PCV were high for number of secondary branches per plant, kernel yield per Plant (g), total phenols content (mg/g), pod yield per plant (g), number of kernels per plant and harvest index. High heritability coupled with high genetic advance as percent of mean for traits viz., days to 50% flowering, total phenols, number of secondary branches per plant, harvest index, kernel yield per plant and number of kernels per plant indicate that these are predominantly influenced by additive gene action and the possibility of phenotypic selection in early generations. High heritability coupled with moderate genetic advance as percent of mean for number of primary branches per plant and moderate heritability coupled with moderate genetic advance as per cent of mean for 100-kernel weight indicate the role of both additive and non additive gene action with preponderance of additive genetic variance and selection would be effective to some extent.
Key words: Groundnut, Yield, Genetic variability

INTRODUCTION

Groundnut (*Arachis hypo*gaea L.) is major oil seed crop grown in semi arid tropic areas of the world. India ranks first in area (5.64 m.*ha*) and second in production (6.96 m.tonnes). In Andhra Pradesh the area was 10.42 lakh *ha* with production of 5.40 lakh tonnes during *kharif* 2012, while the area during *rabi* was 1.16 lakh *ha* with production of 2.40 lakh tonnes with a productivity of 2069 kg per *ha* (Directorate of Economics and Statistics 2012-13).

A nematode incited problem locally called as 'Kalahasti malady' is severe and widespread in sandy loams in southern parts of Andhra Pradesh, India, since 1975-1976 during *rabi* season. Reddy *et al.* (1984) isolated the nematode and after conducting intensive pathogenicity tests and confirmed that a nematode, *Tylenchorhynchus brevilineatus* Williams was responsible for the malady. The effectiveness of the selection depends on the magnitude of genetic variability for different traits present in the population. Genetic parameters such as genotypic coefficient of variation, heritability and genetic advance serve as useful tools to quantify the genetic variability in the populations. The estimation of genotypic and phenotypic coefficient of variation indicates the amount of genetic and non-genetic variation present for different desirable traits while heritability gives an insight into the proportion of the variation which is inherent. However heritability estimate itself is not an indication of the amount of genetic progress that would result from selection.

MATERIALS AND METHODS

Field experiment was conducted during *rabi* 2010-11 at Regional Agricultural Research Station, Tirupati, Chittoor district of Andhra Pradesh. The experimental material comprised of 21 F_2 populations involving parents of seven promising parents viz., Narayani, Tirupati 4, Kalahasti, Kadiri 6, Prasuna Tirupati 3 and ICG (FDRS) 79.The data were collected on 30 randomly selected in each F_2 population in each replication and observations were recorded on days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of kernels per plant, kernel yield per plant (g),100 kernel weight (g),shelling out-turn, kalahasti malady incidence, harvest index (%), SCMR, phenols content (mg/g) and pod yield per plant (g). Analysis of variance was carried out as per the method suggested by Panse and Sukhatme (1979). Phenotypic and genotypic coefficient of variation PCV and GCV) was computed as per Burton (1952), heritability (broad sense) and genetic advance (GAM) as per Allard (1960).

RESULTS AND DISCUSSION

The Analysis of variance for thirteen characters in F_2 populations showed significant differences for all the traits (Table 1). Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits indicating the role of environment in expression of different traits. Highest GCV & PCV was registered for number of secondary branches per plant (67.02 & 79.01) followed by kernel yield per plant (26.15 & 29.25), total phenols content (23.12 & 26.43), pod yield per plant (21.51 & 29.25), number of kernels per plant (21.13 & 26.90) and harvest index (20.56) & 25.54). GCV was moderate for kalahasti malady incidence (16.20) and 100-kernel weight (12.14) while GCV was low for days to 50% flowering (9.97), number of primary branches per plant (9.50), shelling out turn (5.70), SCMR (4.94) and days to maturity (2.43).

Table 1. Analysis of variance (Mean squares) for thirteen characters among seven parents and twenty F_2 populations (*Rabi* 2010-11).

Character	Replications df=2	Treatments df=27	Error df=54
Days to 50% flowering	0.23	30.59**	0.19
Days to maturity	0.57	21.00**	0.41
Number of primary branches per plant	0.60	0.69**	0.11
Number of secondary branches per plant	2.07	5.43**	0.62
Number of kernels per plant	21.00	43.16**	7.40
Kernel Yield per Plant (g)	3.58	7.99**	1.31
100 kernel weight (g)	6.53	63.83*	15.23
Shelling out-turn	27.81	66.93**	33.44
Kalahasti malady incidence	0.02	0.72**	0.13
Harvest index (%)	20.35	172.69**	26.45
SCMR	0.54	17.50**	3.18
Phenols content (mg/g)	0.10	12.57**	1.17
Pod yield per plant (g)	3.75	15.64**	3.45

Table 2: Genetic parameters for thirteen characters among seven parents and twenty one F_2s (*Rabi* 2010-11)

S.No.	Character	Mean	Genotypic coefficient of variation %	Phenotypic coefficient of variation (%)	Heritability (Broad sense) (%)	Genetic advance	Genetic advance as percentage of mean (%)
1	Days to 50% flowering	31.94	9.97	10.06	98.17	6.50	20.34
2	Days to maturity	107.86	2.43	2.50	94.35	5.24	4.86
3	Number of primary branches per plant	4.62	9.50	12.01	62.58	0.72	15.49
4	Number of Secondary branches per plant	1.89	67.02	79.01	71.95	2.21	117.11
5	Number of kernels per plant	16.34	21.13	26.90	61.70	5.59	34.19
6	Kernel yield per Plant (g)	5.70	26.15	29.25	62.96	2.44	32.59
7	100- kernel weight (g)	33.15	12.14	16.91	51.53	5.95	17.95
8	Shelling out-turn	58.62	5.70	11.39	25.03	3.44	5.87
9	Kalahasti malady incidence	2.73	16.20	0.33	59.51	0.70	25.74
10	Harvest index	33.95	20.56	25.54	65.00	11.58	34.11
11	SCMR	44.20	4.94	6.38	59.94	3.48	7.88
12	Total phenols content (mg/g)	8.43	23.12	26.43	76.51	3.51	41.65
13	Pod yield per plant (g)	9.37	21.51	29.25	54.08	3.05	32.59

The utility of heritability is increased when used in conjunction with the selection differential, the amount the mean of selected lines exceeds the mean of the entire group i.e., genetic advance under selection. High heritability coupled with high genetic advance as percent of mean for traits viz., days to 50% flowering (98.17 & 20.34), total phenols content (76.51& 41.65), number of secondary branches per plant (71.95 & 117.11), harvest index (64.82 & 34.11), kernel yield per plant (62.96 & 32.59) and number of kernels per plant (61.70 & 34.19) indicate that these are predominantly influenced by additive gene action.

Greater genetic advance as per cent of mean (GAM) for number of secondary branches in this study corroborates with the report of Jayalakshmi (1997). High heritability coupled with moderate genetic advance as percent of mean for number of primary branches per plant (62.58 % & 17.95%) and moderate heritability coupled with moderate genetic advance as per cent of mean for 100-kernel weight (51.53% & 17.95%) indicate the role of both additive and non additive gene action with preponderance of additive genetic variance.

Cahaner (1978) in a study of F_2 generation of a set of diallel crosses, Jogloy *et al.* (2011) in a study of 200 lines of ten crosses (F_6 generation), Jayalakshmi *et al*. (1998) in a study of F_4 population of two crosses, Padmaja *et al.* (2013) in a study of 106 recombinant inbred lines reported high GCV, heritability and genetic advance for pod yield/plant which are in line with the results in the present study. Manoharan *et al.* (1990) and Vasanthi and Reddy (2002) reported moderate to high heritability and genetic advance for kernel yield. Girdthai *et al.* (2012) reported high heritability for Harvest Index and SCMR in a study of 140 lines derived from $F_{4:6}$ and $F_{4:7}$ generations of four crosses. Upadhyaya *et al.* (2010) studied gene action controlling the inheritance of SCMR in two crosses and observed that SCMR at 60 DAS is under the control of dominance effects with duplicate epistasis and suggested to defer selection to later generations. Results of present study are in conformity with earlier reported results. Rufus (2009) reported moderate to high GCV for all the traits except shelling out-turn and harvest index in a study of F2 generation of ten crosses. Results of present study are in conformity with earlier findings.

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