

STUDIES ON GENETIC VARIABILITY IN TWO F₃ POPULATIONS OF GROUNDNUT (*Arachis hypogaea* L.)

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ABSTRACT

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The present study aims to reveal the importance of quantitative traits and genetic variability existing in F_3 generation of two crosses, TCGS-1157 × TCGS-1073 and TCGS-1157 × TCGS-1043 of groundnut. The coefficient of variation at genotypic levels were high for number of secondary branches, number of pegs per plant, SLA, SLW, total biomass per plant, shoot weight per plant, number of mature pods per plant, mature pod weight per plant and kernel weight per plant and moderate for number of primary branches per plant, number of immature pods per plant, shelling out-turn and harvest index. Plant height and SCMR at 30 DAS and SCMR 60 DAS showed low GCV. From the results, high heritability coupled with high genetic advance observed for number of secondary branches per plant, number of pegs per plant, total biomass per plant, shoot weight per plant, mature pods per plant, harvest index, mature pod weight per plant, total biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature of pegs per plant, total biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature of pegs per plant, total biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass per plant, shoot weight per plant, mature pods per plant, biomass pe

KEYWORDS: Genetic variability, PCV, GCV, heritability, genetic advance, pod yield, groundnut.

INTRODUCTION

Groundnut is not only a major oilseed crop but also an important food crop in India. In India, groundnut occupies an area of 37 lakh ha with a production of 57 lakh tonnes and productivity of 1546 kg ha-1 in kharif season (2015-16). In rabi-summer, it is being grown in 7.4 lakh ha with production of 14.5 lakh tonnes with productivity of 1960 kg ha⁻¹ (2015-16). In Andhra Pradesh, in kharif season, it is cultivated in an area of 6.8 lakh ha with a production of 5.9 lakh tonnes and productivity of 865 kg ha⁻¹.In rabi season it is cultivated in 0.95 lakh ha with a production of 1.98 lakh tonnes and productivity of 2329kg ha⁻¹ (Anonymous, 2016). For the improvement and stabilization of yields, in these situations it is necessary to combine the good attributes from Spanish and Valencia bunch types and Virginia types to develop short duration high yielding varieties to fit into the cropping pattern of Andhra Pradesh. In this context, it is necessary to understand genetics of traits that contribute for high yield and good plant type for these two major situations-rainfed and irrigated. Hence, the present study was planned to study genetic parameters in two F₃ populations having common female parent TCGS 1157 (a high yielding short statured variety with 105-115 days duration) and male parents, TCGS 1073 and TCGS 1043.

MATERIALS AND METHODS

The present investigation was carried out at Regional Agricultural Research Station, Tirupati. The experimental material consisted of two F₃ populations viz., TCGS 1157 × TCGS 1043 and TCGS 1157 × TCGS 1073 which were derived from TCGS 1157, TCGS 1043 and TCGS 1073. The F₃ generation of two crosses were raised in unreplicated plots of 5 m length separately along with the parents during kharif, 2016. A spacing of 30 cm x 10 cm was adopted. 90-120 random competitive plants were picked up in population of each cross while 30 random competitive plants were taken in each parent for recording observations. Data was recorded for yield, harvest index and water use efficiency related traits viz., number of primary branches per plant, number of secondary branches, plant height, number of pegs, pegs to pod ratio, SLA, SLW, SCMR, total biomass per plant, shoot weight per plant, number of mature pods per plant, number of immature pods per plant, shelling out-turn, harvest index, mature pod weight per plant and kernel weight per plant. The data thus generated were subjected to statistical analysis computation of genetic variability, heritability and genetic advance estimates as per the procedures (Nadarajan and Gunasekaran, 2005).

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RESULTS AND DISCUSSION

The test of heterogeneity of crosses revealed highly significant differences among the two crosses for all 17 characters indicating presence of considerable variation in the breeding material under rainfed conditions. The estimates of genetic parameters are presented in Table 1 Since F_2 generation is a segregating population the range of variability present in all the two crosses was quite high for most of the traits suggesting the application of individual plant selection for high yield and water use efficiency.

In the present study, the estimates of PCV for all the characters were little higher than the estimates of GCV, which may be due to the interaction of genotypes with the environment. The moderate to high estimate of coefficient of variation was registered for number of secondary branches, number of pegs per plant, SLA, SLW, total biomass per plant, shoot weight per plant, number of mature pods per plant, mature pod weight per plant and kernel weight per plant, moderate for number of primary branches per plant, number of immature pods per plant, shelling out-turn and harvest index indicating greater scope of selection for improvement of these characters. Similar results of high estimates of variability were reported by earlier workers for number of secondary branches (Dandu et al., 2011; John et al., 2012), SLA (Pushpa et al., 2014), total biomass per plant (Shinde et al., 2010), number of mature pods per plant and mature pod weight per plant (Padmaja et al., 2013), kernel weight per plant (Ahamed, 1995 and Vishnuvardhan et al., 2012), harvest index (Reddi et al., 1986), number of immature pods per plant (Padmaja et al., 2013), number of primary branches (Vishnuvardhan et al., 2012) and corroborates the findings of the present study.

High heritability coupled with high genetic advance as a per cent of mean were recorded for number of secondary branches per plant, number of pegs per plant, total biomass per plant, shoot weight per plant, mature pods per plant, harvest index, mature pod weight per plant, kernel weight per plant, SLA and SLW which indicated the inheritance of additive gene effects in the genetic control of these traits. Hence, simple selection can be practiced to improve these traits. This was in conformity with the findings of Dandu *et al.* (2011) for number of secondary branches Girdthai *et al.* (2012) for total biomass per plant, Riaz *et al.* (2013) for shoot weight, Sumathi and Ramanathan (1995) for number of mature pods per plant, and Jayalakshmi et al. (1998) for mature pods weight per plant. The knowledge on heritability of traits is helpful to decide the selection procedure to be followed to improve the trait in a situation. High heritability recorded in a trait indicates the low influence of environment on expression of the trait. Therefore, for improving these traits the selection will be more effective in early generation on the basis of per se performance of these traits. These traits may be improved by mass or progeny selection. High heritability recorded for pod yield per plant suggested that direct selection based on pod yield per se could be effective for its genetic improvement. High heritability coupled with moderate genetic advance as per cent of mean was recorded for SPAD chlorophyll reading and pegs/pod ratio. These are more likely to be controlled by both additive and non-additive gene effects. Hence, recombinant selection could be more effective to improve these traits.

CONCLUSION

Based on results of this study, it could be concluded that there was considerable amount of variability present in the both the crosses. To sum up, genotypic co-efficient of variation, heritability and genetic advance as percentage of mean were moderate to high in both crosses for number of secondary branches per plant, pegs per plant, total biomass per plant, shoot weight per plant, mature pods per plant, immature pods per plant, harvest index, mature pod weight per plant, kernel weight per plant, SLA and SLW indicating that these are predominantly governed by additive genetic variance. Hence, it could be inferred that simple phenotypic selection would be effective in early generations in these crosses to make improvement in the characters mentioned above. Conversely, low estimates of GCV, heritability and genetic advance as per cent of mean were registered for SCMR and pegs/pod ratio indicating little scope of improvement of these traits by selection as they are governed by the non-additive gene effects.

LITERATURE CITED

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Character	Mean	Range	Phenotypic variance	Genotypic variance	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability %	Genetic advance	Genetic advance as % of mean
Primary branches per plant									
$TCGS-1157 \times TCGS-1073$	4.68	2-8	0.98	0.37	21.20	13.07	38.04	0.78	16.61
$TCGS-1157 \times TCGS-1043$	4.58	3-7	0.54	0.13	16.05	7.77	23.45	0.36	7.75
Secondary branches per plant									
$TCGS-1157 \times TCGS-1073$	3.41	0-7	2.40	1.04	45.51	29.98	43.39	1.39	40.68
$TCGS-1157 \times TCGS-1043$	3.31	9-0	1.21	0.12	33.20	10.66	10.32	0.23	7.06
Plant height (cm)									
$TCGS-1157 \times TCGS-1073$	30.77	22-52	18.62	8.54	14.02	9.50	45.87	4.08	13.25
$TCGS-1157 \times TCGS-1043$	30.17	20-39	17.56	8.42	13.62	9.43	47.93	4.14	13.45
Pegs number per plant									
$TCGS-1157 \times TCGS-1073$	27.54	11-56	64.75	52.99	29.22	26.43	81.83	13.56	49.25
$TCGS-1157 \times TCGS-1043$	26.53	9-68	69.20	51.98	31.35	27.17	75.12	12.87	48.52
Pegs/Pod									
$TCGS-1157 \times TCGS-1073$	1.86(7.81)	6.38-10.18	0.54	0.06	9.41	3.14	11.10	0.17	2.15
$TCGS-1157 \times TCGS-1043$	1.97(8.03)	6.18-11.24	0.73	0.62	10.61	9.83	85.89	1.51	18.77
Total biomass per plant (g)									
$TCGS-1157 \times TCGS-1073$	22.95	8.80-48.70	36.99	26.62	26.50	22.48	71.96	9.02	39.28
$TCGS-1157 \times TCGS-1043$	19.24	8.30-48.60	43.28	32.40	34.19	29.59	74.87	10.15	52.74
Shoot weight per plant (g)									
$TCGS-1157 \times TCGS-1073$	15.78	5.40-53.50	49.07	41.74	44.38	40.93	85.07	12.28	77.78
$TCGS-1157 \times TCGS-1043$	11.68	4.90-34.00	23.75	15.77	41.73	34.01	66.41	6.67	57.09
Mature pods per plant									
$TCGS-1157 \times TCGS-1073$	10.24	3.00-22.00	16.37	9.74	39.51	30.48	59.51	4.96	48.44
$TCGS-1157 \times TCGS-1043$	10.34	3.00-20.00	11.26	3.36	32.45	21.04	42.05	2.91	28.11
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Character	Mean	Range	Phenotypic variance	Genotypic variance	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability %	Genetic advance	Genetic advance as % of mean
Immature pods per plant									
$TCGS-1157 \times TCGS-1073$	4.90	1.00-11.00	4.52	0.48	43.39	14.18	10.68	0.47	9.55
TCGS-1157 × TCGS-1043	3.39	1.00-9.00	3.25	0.27	53.19	15.34	8.32	0.31	9.12
Shelling out-turn (%)									
$TCGS-1157 \times TCGS-1073$	58.33(49.83)	29.40-57.07	18.52	15.08	8.64	7.79	81.40	7.22	14.48
$TCGS-1157 \times TCGS-1043$	54.70(47.72)	33.67-55.37	26.96	23.72	10.88	10.21	87.99	9.41	19.72
Harvest index (%)									
$TCGS-1157 \times TCGS-1073$	43.29(41.09)	30.74-55.06	23.60	20.52	11.82	11.02	86.95	8.70	21.17
$TCGS-1157 \times TCGS-1043$	47.26(43.40)	29.76-55.26	28.83	25.61	12.37	11.66	88.84	9.83	22.64
Mature pod weight per plant (g)	t (g)								
$TCGS-1157 \times TCGS-1073$	8.60	2.10-18.70	7.55	4.34	31.96	24.22	57.41	3.25	37.79
$TCGS-1157 \times TCGS-1043$	10.76	2.70-20.00	10.76	7.08	41.57	33.71	65.78	4.45	56.33
Kernel weight per plant (g)									
$TCGS-1157 \times TCGS-1073$	5.01	1.10-10.80	2.86	2.02	33.78	28.38	70.61	2.46	49.13
$TCGS-1157 \times TCGS-1043$	4.23	1.10-12.10	2.87	1.94	40.04	32.94	67.67	2.36	55.82
SCMR (30 days)									
TCGS-1157 × TCGS-1073	45.35	30.50-66.80	14.47	10.05	8.39	6.99	69.45	5.44	12.00
$TCGS-1157 \times TCGS-1043$	43.79	6.3-55.1	15.40	5.74	8.96	5.47	37.26	3.01	6.88
SCMR (60 days)									
$TCGS-1157 \times TCGS-1073$	48.47	30.00-58.70	29.41	20.30	11.19	9.30	69.03	7.71	15.91
$TCGS-1157 \times TCGS-1043$	47.65	32.40-58.40	21.64	7.96	9.76	5.92	36.77	3.52	7.39
SLA									
$TCGS-1157 \times TCGS-1073$	145.96	41.18-342.90	2140.28	1434.08	31.70	25.95	67.00	63.86	43.75
$TCGS-1157 \times TCGS-1043$	148.00	72.57-371.50	1510.65	931.07	26.26	20.62	61.63	49.35	33.34
SLW									
$TCGS-1157 \times TCGS-1073$	0.01	0.00292-0.02	0.0000063	0.0000045	33.18	28.04	71.42	0.003695	48.81
TCGS-1157 × TCGS-1043	0.0072	0.00269-0.01378	0.0000031	0.0000019	24.67	19.14	60.23	0.002201	30.61

Studies on genetic variability in two F3 populations of groundnut (Arachis hypogaea L.)

Table 1. Cont...

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