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Research Article

Gene effects of pod yield and its components in three crosses of groundnut (*Arachis hypogaea* L.)

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Abstract:
Groundnut, (*Arachis hypogaea* L.) is a major source of vegetable oil and protein and also a major source of fodder crop. Genetic systems that control the expression of quantitative traits facilitate the choice of the most efficient breeding and selection procedure. Generation mean analysis is commonly used in studies of inheritance of quantitative traits. Four groundnut genotypes which consist of three late leaf spot and rust resistant genotypes viz., COG 0437, COG 0438 and ICGV 97150 and one susceptible genotype TMV 2 were used in the present study. The cross TMV 2 x ICGV 97150 had additive gene action for most of the traits *viz*., plant height, number of pods per plant, pod yield per plant, kernel yield per plant, hundred kernel weight and shelling percentage. Hence, early generation selection could be practiced in TMV 2 x ICGV 97150. However due to the presence of epistasis, especially for rust and LLS incidence in other two crosses *viz*., TMV 2 x COG 0437 and TMV 2 x COG 0438, selection should be postponed to later generations.

Key words:
Groundnut, generation mean analysis, additive and dominance gene effects, epistasis.

Introduction

Cultivated groundnut, (*Arachis hypogaea* L.) is an important oilseed crop. It is a major source of vegetable oil and protein, both for human beings and animals. In many drought prone areas of India, groundnut is the only source as a fodder crop, as no other fodder crop can match the drought tolerance as that of groundnut. Groundnut is an important multipurpose crop for resource less poor farmers in the semi arid tropics. Due to environmental stresses and disease pressure, average productivity is often below one tonne per hectare in groundnut.

Many traits of economic importance in groundnut are quantitatively inherited. The exploitation of genetic variability of these traits through hybridization and selection is the primary focus of most groundnut improvement programmes. A good knowledge of the genetic systems controlling expression of these characters facilitates the choice of the most efficient breeding and selection procedure. In addition to additive and dominance variation, it has been suggested that epistasis may also be involved in the inheritance of many quantitative characters in groundnut (Hammons, 1973; Wynne, 1976). But the information available on nonallelic interactions for quantitative traits in groundnut is very limited. In spite of the limited scope of exploitation of nonallelic interactions in groundnut, the information on nonallelic interactions would be of value to groundnut breeders. While variation due to dominance effects and their interactions cannot be exploited effectively in groundnut, additive x additive epistatic variation is potentially useful, as it can be fixed in homozygous cultivars.

In the present study, the generation mean analysis was employed to partition the genetic variance into additive, dominance and epistasis, which helps in formulating an effective, and sound breeding programme. Hence, F_1, F_2 and F_3 generations of three crosses *viz*., TMV 2 x COG 0437, TMV 2 x COG 0438 and TMV 2 x ICGV 97150 were raised along with the parents. Nine morphological traits were recorded from the parental and segregating generations and analysed to assess the gene action involved for various characters.

Material and Methods

The field experiment was carried out at Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Four groundnut genotypes consisting of three late leaf spot and rust resistant genotypes *viz.,* COG 0437, COG 0438, ICGV 97150 and one susceptible genotype TMV 2, and their cross combinations *viz*., TMV 2 x COG 0437, TMV 2 x COG 0438 and TMV 2 x ICGV

97150 were used in the present study. Generations *viz.,* P_1, P_2, F_1, F_2 and F_3 populations were developed for the generation mean analysis during *kharif* 2009. All the plants were raised in 1.5 m length of 30 x 20 cm spacing. A total number of nine yield and yield component traits *viz.,* plant height (cm), number of branches / plant, number of pods / plant, pod yield/plant (g), kernel yield per plant (g), shelling percentage (%), hundred kernel weight (g) and disease scoring for rust and late leaf spot was taken. Nine point disease scale (Subrahmanyam *et al.,* 1995) was used to screen the lines for sources of resistance to rust and LLS.

Action of the genes controlling quantitative characters can be described by the use of gene models. The four types of gene action *viz*., additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were estimated using five-parameter model. The variances and corresponding standard error of the means were computed from the deviations of the individual values from the pooled mean for each of the generation in each cross. The adequacy of the simple additive-dominance model in a generation was detected utilizing C and D scaling tests according to the method proposed by Mather and Jinks (1971). By using the variances of various generations for the respective mean, tests of significances were made. The t value observed for ratio C/ SE of C and D/ SE of D is compared either to the 't' table at 5 and 1 per cent level of significance. The calculated 't' value is referred to the 't' table to test the significance. In each test, the degrees of freedom are sum of the degrees of freedom of various generations involved. The additive-dominance model was considered inadequate when any one of the two scales was found to deviate significantly from zero. Mean of five generations *viz*., P_1, P_2, F_1, F_2 and F_3 could be used to estimate five parameters following a perfect fit solution given by Cavalli (1952).

Results and Discussion

The generation mean analysis is commonly employed in studies of inheritance of quantitative traits. Analysis of this technique is based on different generations of a cross *viz.,* parents, their F_1, F_2, F_3 and different back crosses.

Scaling test was performed using the mean measurements of various generations for the observed traits. As only five generations were involved, the scales C and D were calculated. The genetic parameters *viz*., (m), (d), (h), (i) and (l) provides information about the gene action involved for a particular trait under investigation. The parameters *viz*., mid parental effect (m), additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) of the three crosses presented in Table1.

The mid-parental effect (m) was significant and positive for all the crosses. For plant height, the estimates of d (4.66**±1.23) and i (9.33*±3.83) were significant in TMV 2 x COG 0437 which indicated the predominant role of additive, additive x additive gene effects. The present findings are in agreement with the results of Sangha *et al*. (1990) who reported additive x additive gene action for this trait. A simple additive-dominance model was found to be adequate for the crosses TMV 2 x COG 0438 and TMV 2 x ICGV 97150. In these crosses a greater portion of dominance effect was observed indicating the importance of dominance gene action for this character.

For number of branches per plant, in the cross TMV 2 x COG 0437, the gene effects *viz*., d (-0.45*±0.19), h (-3.98**±0.49), i (-5.10**±0.56) and l (10.06**±1.48) were significant indicating involvement of additive, dominance and dominance x dominance interactions in the control of number of branches per plant. Makne (1992) observed the involvement of both additive and non-additive gene action for number of primary and secondary branches per plant. Both additive (d) and dominance (h) effects were significant in all the crosses except TMV 2 x ICGV 97150 in which dominance effect alone was significant. Similar results of dominance gene action for this character was reported by Manoharan and Thangavelu (2009).

In the cross TMV 2 x COG 0437, the gene effects *viz.,* d (,-6.0**±0.63), h (-8.56*±3.74), i (-29.43*±3.96) and l (46.30*±12.85) were significant indicating involvement of additive, dominance and other epistatic interactions in the control of number of pods per plant and the components of (h) and (l) having opposite sign implies the involvement of duplicate epistasis in the inheritance of this trait. Duplicate epistasis observed for this trait hinders the rapid improvement by selection. This may possibly be overcome by delaying the selection to later generation when dominance effects disappear as well as by resorting to intermating of segregants in F_2 followed by recurrent selection. The selection in later generations and maintenance of large populations prior to selection may provide the maximum opportunity for advantageous combinations of genes to occur. Selection based on early generation testing would be ineffective. There was no interaction effect in the cross TMV 2 x ICGV 97150. Jivani *et al.*

(2009) noticed additive and non additive with preponderance of dominance for this trait.

For pod yield per plant, the components d (-5.48**±0.77), h (-9.82**±3.10), i (-22.89*±3.41) and l (22.12*±10.70) were significant in the cross TMV 2 x COG 0437 indicating involvement of additive, dominance and other epistatic interactions and the components of (h) and (l) having opposite sign implied the involvement of duplicate epistasis in the inheritance of this trait. In the cross TMV 2 x ICGV 97150, the component d (-3.18**±0.88) alone was significant indicating the role of additive gene action. While considering the interaction components, the cross TMV 2 x COG 0438 was significant i (-15.30**±2.4) showed the role of additive x additive gene action governing this trait. Sangha *et al*. (1990), Vindhiyavarman and Paramasivam (1992) and Ali *et al*. (1995) reported that additive gene action is involved in the inheritance of this trait.

The components d (-4.64**±0.79), h (-7.07**±2.59), i (-18.26*±2.88) and l (18.94*±8.93) were significant in the cross TMV 2 x COG 0437 indicating involvement of additive, dominance and other epistatic interactions for kernel yield per plant and the components of (h) and (l) having opposite sign showed the involvement of duplicate epistasis in the inheritance of this trait. In the cross TMV 2 x COG 0438, the component d (-3.00**±0.60) was higher in magnitude than h (-4.99**±1.78) indicating the preponderance of additive gene action and the significant i (-13.18*±1.95) showed the additive x additive interaction governing this trait. The cross TMV 2 x ICGV 97150 had shown the significant d (-1.84**±0.50) which implied the role of additive gene action for this trait. Venkateswarlu *et al.* (2007) reported additive and non additive gene action for this trait.

For shelling percentage, the estimates of h (-9.87*±4.18), i (-18.43** ± 5.46) and l (56.72* ± 13.89) were significant in TMV 2 x COG 0438 which indicated the predominant role of dominance, additive x additive and dominance x dominance gene action and the components of (h) and (l) having opposite sign implied the involvement of duplicate epistasis in the inheritance of this trait. Vindhiyavarman and Paramasivam (1992) reported that additive and non-additive gene action were equally important for this trait. The crosses TMV 2 x COG 0438 and TMV 2 x ICGV 97150 had shown significant (h) effect *viz.*, -9.87*±4.18 and 16.56*±6.37 which indicated the dominance gene action governing this trait. The results were in accordance with the results of Manoharan and Thangavelu (2009). Jivani *et al.* (2009) noticed that additive and non additive gene action with preponderance of dominance for this trait.

For hundred kernel weight, the estimates of d (-4.71*±2.14), h (-11.42**±3.53) and i (-12.67* ± 4.86) were significant in the cross TMV 2 x COG 0437 which indicated the predominant role of additive, dominance and additive x additive gene effects. The presence of additive x additive gene effect was observed in the crosses TMV 2 x COG 0437 and TMV 2 x COG 0438. Jivani *et al.* (2009) reported additive and non additive gene effects with preponderance of dominance for this trait.

For rust severity score, it was observed that additive, dominance and epistatic effects in all the crosses and the opposite signs of the components (h) and (l) had shown the duplicate epistasis for all the crosses. The component (i) was positive and significant which implied alleles with positive effects were more often dominant for all the crosses. The magnitude of dominance was more than additive indicating the preponderance of dominance. For interaction components, the magnitude of the component (i) was more than (l) indicating the importance of additivity. Venkataravana and Injeti (2008) noticed that high heritability coupled with high genetic variation for rust and pod yield indicating that additive gene effect was operating for these characters.

For LLS severity score the component (h) had higher magnitude than the component (d) indicated the predominant nature of dominance for all the crosses. The two types of epistatic effects *viz*., (i) and (l) were controlling the trait in crosses TMV 2 x COG 0437 and TMV 2 x ICGV 97150. The significant value of i (8.56 **±0.75) in the cross TMV 2 x COG 0438 showed the additive x additive gene effect. For interaction components, the component (i) was more than (l) implied importance of additivity in the crosses TMV 2 x COG 0437 and TMV 2 x ICGV 97150 and also the opposite signs of the components (h) and (l) had shown the duplicate epistasis.

The presence of duplicate epistasis would be detrimental for rapid progress, making it difficult to fix genotypes with increased level of character manifestation because the positive effect of one parameter would be cancelled out by the negative effect of another. Hence, early generation intermating besides accumulating the favourable genes and maintaining heterozygosity in the population are likely to throw out desirable recombinants. The characters plant height and 100 kernel weight were under the control of additive or additive type of epistasis. All other characters including the foliar disease incidence had epistatic gene action which includeed additive as well as dominance type gene interaction. The cross TMV 2 x ICGV 97150 had additive gene action for most of the traits except, number of branches, rust and LLS incidence. Hence early generation selection could be practiced in TMV 2 X ICGV 97150 for most of the characters due to the presence of additive gene action. However due to the presence of epistasis, especially for rust and LLS incidence in other two crosses, selection should be postponed to later generations.

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Table 1. Estimates of genetic parameters for nine morphological traits of crosses *viz*., TMV 2 x COG 0437, TMV 2 x COG 0438 and TMV 2 x ICGV 97150 in groundnut

Traits	Crosses	m	d	h	i	l
Plant height (cm)	C1	24.42 **±0.73	4.66 **±1.23	0.40 ±2.65	9.33 *±3.83	-14.82 ±9.69
	C2	25.94 **±0.78	0.48 ±1.19	1.28 ±2.40	-	-
	C3	24.41 **±0.77	-2.03 ±1.16	0.78 ±2.39	-	-
Number of branches /plant	C1	4.14 **±0.11	-0.45 *±0.19	-3.98 **±0.49	-5.10 **±0.56	10.06 **±1.48
	C2	4.25 **±0.13	-0.95 **±0.17	-0.93 *±0.43	-	-
	C3	4.09 **±0.10	0.0±0.28	-2.06 **±0.45	-2.06 **±0.57	3.75 **±1.37
Number of pods/plant	C1	14.87 **±0.94	-6.0 **±0.63	-8.56 *±3.74	-29.43 *±3.96	46.30 *±12.85
	C2	14.71 **±0.81	-5.00 **±0.80	-8.09 **±2.42	-19.13 *±2.71	10.66 ±7.97
	C3	14.11 **±0.92	-4.85 **±0.84	1.95 ±2.77	-	-
Pod yield/plant (g)	C1	12.50 **±1.00	-5.48 **±0.77	-9.82 **±3.10	-22.89 *±3.41	22.12 *±10.70
	C2	12.95 **±0.76	-4.00 **±0.59	-5.09 *±2.27	-15.30 **±2.4	5.30 ±7.48
	C3	11.32 **±0.75	-3.18 **±0.88	1.45 ±2.26	-	-
Kernel yield/plant (g)	C1	9.22 **±0.86	-4.64 **±0.79	-7.07 **±2.59	-18.26 *±2.88	18.94 *±8.93
	C2	8.86 **±0.56	-3.00 **±0.60	-4.99 **±1.78	-13.18 *±1.95	10.79 ±5.76
	C3	8.18 **±0.63	-1.84 **±0.50	2.80 ±1.82	-	-
Shelling percentage (%)	C1	71.25 **±1.73	-4.06 ±2.82	-1.86 ±5.04	-	-
	C2	67.52 **±1.49	-1.09 ±2.76	-9.87 *±4.18	-18.43**±5.46	56.72 *±13.89
	C3	71.05 **±2.06	1.71 ±2.16	16.56 *±6.37	15.14*±7.47	-27.66±23.05
Hundred kernel weight (g)	C1	31.78 **±1.34	-4.71 *±2.14	-11.42**±3.53	-12.67 *±4.86	-8.22 ±12.07
	C2	33.02 **±1.01	-1.97 ±2.02	-2.96 ±2.98	-11.88 *±4.26	11.54 ±9.61
	C3	30.54**±0.83	2.28*±1.27	0.18±2.89	-	-
Rust severity score	C1	7.11 **±0.23	3.45 **±0.05	14.79 *±0.52	18.30 *±0.61	-26.68 **± .94
	C2	5.52 **± 0.32	2.95 **±0.05	8.25 **±0.72	10.99 *±0.82	-6.14 *±2.62
	C3	6.18 **±0.25	3.45 **±0.05	7.01 **±0.74	12.61 *±0.78	-15.74 **±2.50
LLS severity score	C1	7.19 **±0.24	3.45 **±0.05	12.58**±0.55	16.10 *±0.64	-22.59 **±2.05
	C2	5.75 **±0.28	2.95 **±0.05	5.82 **±0.67	8.56 **±0.75	-2.22 ±2.39
	C3	6.20 **±0.24	2.95 **±0.05	5.66 **±0.70	10.76 *±0.75	-13.15 **±2.41

*, ** Significant at 5 and 1% level, respectively

C1- TMV 2 x COG 0437, C2- TMV 2 x COG 0438, C3- TMV 2 x ICGV 97150