

GENETIC ANALYSIS OF SOME AGRONOMIC TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)

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Abstract

A 10×10 half diallel experiment was conducted on groundnut (*Arachis hypogaea* L.) to ascertain the gene action and genetic parameters of ten traits including 50% flowering, no. of pods per plant, plant height, harvest index, pod index, 100 pod weight, 100 kernel weight, pod size, diseases infection and yield per plot. The experiments were carried out in the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh during the cropping season of 2010-2011. The estimates of gene effects indicated that significance of both additive and non-additive variance for pod size, 100 pod weight and diseases infection among the traits and presence of over dominance satisfying assumptions of diallel except dormancy. However, both the additive and non-additive gene effects together importance to control of most quantitative traits in the groundnut. The average degree of dominance (H_1/D) $1/2$ (H_1 = dominance variance, D = additive variance) was higher than one, indicating over dominance for all the traits. The narrow-sense heritability was high for 50% flowering (38%), harvest index (35%), pod size (52%), 100 pod weight (35%) and yield per plot (41%) indicating that great genetic gain could be achieved for them.

Keywords: Additive Variance, Dominance Variance, Diallel, Groundnut

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Introduction

Groundnut (*Arachis hypogaea* L.) is the second most important oilseed crop in Bangladesh after mustard/rapeseed, with an annual production of 143,000 metric tons (AIS, 2012). Its seeds contain 45-56% high quality edible oil, 25-30% protein and 20% carbohydrate together with vitamins E and B. Being a multipurpose crop. Breeding for improved and high yielding groundnut cultivars has been hampered by the lack of information on the genetics of yield and yield components (Hammons, 1973; Norden, 1973; Gibori *et al.*, 1978). Wynne and Coffelt (1973) pointed out that despite the availability of methods for characterizing the genetic variability in self-fertilizing species, little information has been obtained on the various types of gene action and their relative importance in the inheritance of important traits in groundnut. Plant breeders are primarily concerned with the improvement of those traits which are directly or indirectly related to the economic values. Such traits are generally quantitative in nature and governed by several numbers of genes each having small effect and acting in a cumulative manner called polygenes.

Among the various biometrical tools, diallel analyses furnish useful information and identification of superior parents and crosses with their gene effects. It also provides information on the nature and magnitude of genetic variance on which success of plant breeding.

Materials and Methods

The experiments were carried out in the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The parental material consisted of ten groundnut genotypes; P₁ (Dacca-1), P₂ (Zhinghabadam), P₃ (BARI Chinabadam-7), P₄ (J×57015-SL-1), P₅ (ICGV-95063), P₆ (Binachinabadam-1), P₇ (Binachinabadam-2), P₈ (Binachinabadam-3), P₉ (Binachinabadam-4) and P₁₀ (ICGV-90227). The genotypes were crossed in half diallel fashion during February to March, 2010. The F₁ seeds of all crosses along with their parents were planted in the field during 2010² 2011 for evaluation in a randomized complete block design with three replications. A unit plot

size 1.0 m x 0.8 m. One seed was sown per hole at a depth of 2.5-3.0 cm. Seeds were sown at 15 cm distances within rows of 30 cm apart from lines. All cultural practices (soil preparation, sowing, fertilizer and cultivation) followed by recommended procedures. The data were recorded on 50% flowering, no. pods/plant, plant height, harvest index, pod size, 100pod weight, 100kernel weight, pod index, diseases infection, yield per plot. The experiment was used to study additive and dominant gene effect was involved in the inheritance of this character. The genetic components were analysis by Hayman's approach

(1954b). Genetic components were also shown in Morley Jones (1965) modification of Hayman's approach.

Components of genetic variance and genetic parameters

After testing the validity of hypothesis that epistasis is absent, determination of genetic variance components along with allied genetic parameters, which were derived by Hayman (1954b). The genetic components were calculated as follows:

$D = V_{OLO} - E =$ Variance component due to additive effects of the genes.

$H_1 = V_{OLO} + 4 V_{OL1} - 4W_{OLO1} - 4W_{OLO1} - (3n - 2) E/n =$ Variance component due to dominance deviation

$H_2 = 4 V_{1L1} - 4 V_{1L1} - 2E =$ proportion of positive and negative genes in the parents

$h_2 = 4 (M_{L1} - M_{LO})^2 - 4 (n - 1) E/n^2 =$ Algebraic sum of dominance effects over all loci in heterozygous phase in all crosses

$F = 2 V_{OLO} - 4 W_{OLO1} - 2 (n - 2) E/n =$ Mean of the covariance of additive and dominance effects over all the arrays

$E = \left[\frac{\text{ErrorSS} + \text{ReplicationSS}}{df} \right] / \text{number of replications} =$ The expected environmental components

of variation

Where,

$V_{OLO} =$ Variance of parents

$V_{OL1} =$ Variance of the means of arrays

$V_{1L1} =$ Mean of all the array variances

$W_{OLO1} =$ Mean of all the covariance values

$(M_{L1} - M_{LO})^2 =$ Dominance relationship

In order to test the significance of each component: D, F, H_1 , H_2 , h_2 , E, the SE is calculated for each of them by the formula:

$$SE = (Cs^2 / n^5)^{0.5}$$

$$\text{Where, } s^2 = \frac{1}{2} [\text{var} (Wr - Vr)]$$

C= a multiplier specific to each component and was calculated as follows:

$$\text{For, } D = (n^5 + n^4) / n^5$$

$$F = (4n^5 + 20n^4 - 16n^3 + 16n^2) / n^5$$

$$H_1 = (n^5 + 41n^4 - 12n^3 + 4n^2) / n^5$$

$$H_2 = 36 n^4 / n^5$$

$$E = n^4 / n^5$$

The significance of each component was tested by t test at $(n - 2)$ df. The calculated value of 't' for each component was obtained dividing each component by their respective standard errors.

The allied genetic parameters were as follows:

$$\sqrt{(H_1 / D)} = \text{Mean degree of dominance}$$

$$H_2 / 4H_1 = \text{Proportion of dominant genes with positive and negative effect}$$

$$\frac{\sqrt{4DH_1 + F}}{\sqrt{4DH_1 - F}} = \text{Proportion of dominant and recessive genes}$$

$$h^2 / H^2 = \text{Number of gene blocks exhibiting dominance}$$

$$h^2_{ns} = \text{Heritability in narrow sense}$$

$$= \frac{D / 4}{D / 4 + H_1 / 4 + E - F / 4}$$

Morley Jones modification for diallel without reciprocal

The analysis of variance for the complete diallel table was given by Hayman (1954b). Assuming the absence of reciprocal differences. Morley-Jones (1965) brought some modification of Hayman's approach. In this modification as Hayman, determination of the sum of squares

corresponding to additive effects (a), and on the assumption of no epistasis to mean dominance (b_1), to additional dominance effects that can be accounted for genes having one allele present in only one line (b_2) and to residual dominance effects (b_3), is in essence a straight forward application of fitting constants by least squares.

Morley Jones modified analysis for diallel without reciprocals is as follows:

Item	df	Sum of squares	Mean squares
a	n-1	$\frac{1}{n+2} \text{dev}^2_{ur}$	Ma
b	n(n-1)/2	$b_1 \text{ ss} + b_2 \text{ ss} + b_3 \text{ ss}$	Mb
b_1	1	$\frac{1}{n(n^2+1)} [2X_{.} - (n+1)X.]^2$	Mb_1
b_2	n-1	$\frac{1}{n^2+4} \text{dev}^2_{tr}$	Mb_2
b_3	n(n-3)/2	Total SS- (a ss + b_1 ss + b_2 ss)	Mb_3
Error	(r-1) (t-1)	ESS	Me

Where,

a = Additive effects

b_1 = Mean dominance

b_2 = Additional dominance effects that can be accounted for genes having one allele present in only one line the remaining n-1 lines being assumed to carry the same alternative allele (dominance deviation due to arrays).

b_3 = Residual dominance effects

dev^2 = Sum of square of deviations from the mean

Vr = $X_i + X_{ii}$

Wr = $2(X_i + X_{ii}) - (n+2) X_{ii}$

Results and Discussion

Different components of variance were estimated using the approaches of Hayman (1954b). The application of this approach is based upon various assumptions viz. diploid segregation, homozygous parents, no multiple allelism, no reciprocal differences and independent action and distribution of non-allelic genes. Failure of any one of the assumptions invalidates drawn. For testing the validity of assumptions, 't²' test and Wr , Vr regression coefficient (b) tests were employed. The hypothesis of these tests is that if the assumptions are satisfied, the 't²' value should be non-significant and regression coefficient (b) should be significantly different from zero but not from unity (Jinks and Hayman, 1953). If the assumptions are not satisfied, the Wr - Vr is plotted against Y (Mean of array) to arrive at a decision of either using transformation of scale or dropping some of the interacting lines or crosses for satisfying the assumptions (Hayman, 1954b). In the present study the assumptions were satisfied for pod size, 100 pod weight and diseases infection. A consequence of these assumptions is that when satisfied the homogeneity of difference between Wr and Vr is

constant. Homogeneity of difference (Wr - Vr) while always implied by the validity of assumptions may also be attained in certain cases of balanced failure of these assumptions (Jinks, 1954; Hayman, 1954a). In the present study, homogeneity of difference (Wr - Vr) was constant as all the parents were situated along the regression line.

The components of additive effect (D) and dominance effects (H_1 and H_2) were significant for pod size, 100 pod weight and diseases infection, indicating importance of both additive and non-additive components in the inheritance of these traits. The magnitude of dominance (H_1) was significantly higher than additive components (D) for all the traits, indicated the presence of over-dominance for the above traits. The F component was non-significant for 50% flowering, no. of pods per plant, plant height, harvest index, 100 kernel weight, pod index and yield per plot, indicating presence of equal frequency of dominant and recessive genes for these characters. However, for pod size, 100 pod weight and diseases infection the significant F component indicated unequal frequency of dominant and recessive genes. Similar genetic

control was exhibited by the order of dominance (W_r-V_r) and array per se performance (Y_r) relationship which indicated that 50% flowering, no. of pods per plant, plant height, harvest index, 100 kernel weight, pod index and yield per plot were determined by equal proportion of dominant and recessive genes. Again exhibited that pod size, 100 pod weight and diseases infection was determined by dominant genes. From the above discussion for gene actions it is clear that both additive and non-additive components were involved in the expression at the above mentioned traits. The magnitude of dominance component was higher where they did not differ significantly. The significant values of h^2 indicated that there was significant difference between the parents and F_1 's for all the traits.

$\sqrt{H_1/D}$ value was higher than unit suggesting the presence of over dominance in expressing all the traits. The value of $H_2/4H_1$ was nearly 0.25, indicating symmetrical distribution of positive and negative alleles for no. of pods per plant, plant height, harvest index, 100 kernel weight, pod index and yield per plot while unequal value for 50% flowering, pod size, 100 pod weight and diseases infection as indicated asymmetrically distributed of positive and negative alleles.

The ratio of $[\sqrt{4DH_1 + F}] / [\sqrt{4DH_1 - F}]$ was less than unity suggesting an equal distribution of dominance and recessive genes in the parents for plant height, harvest index and yield per plot. Since the parameter h^2/H_2 had a value greater than unity, therefore the character was controlled by more than two genes or group of genes for all the traits. Heritability estimates in narrow sense. The heritability in narrow sense was high for 50% flowering (38%), harvest index (35%), 100 pod weight (35%), pod size (52%) and yield per plot (41%), and low heritability viz. no. of pods per plant (27%), plant height (24%), 100 kernel weight (15%), pod index (19%), diseases infection (17%). Presence of significant additive and non-additive gene effects was also reported by Makne and Bhale (1989), Verman *et al.* (1990), Verman and Paramasivam (1992), Makne (1992).

From the result and discussion for gene action, obviously additive and non-additive components were involved in the expression at the above mentioned traits. The magnitude of dominance component was higher except dormancy where they did not differ significantly.

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Table 1. Components of variance and genetic parameters for different quantitative traits of 10×10 half diallel cross of groundnut

Components	50% Flowering	No. of pod splant ⁻¹	Plant height	Harvest index	Pod size	100Pod weight	100Kernel weight	Pod index	Diseases infection	Yieldplot ⁻¹
D	8.25 ±4.03	1.69 ±7.05	10.04 ±59.84	25.42 ±23.46	0.46*** ±0.05	281.75** ±67.38	7.19 ±4.65	26.23 ±15.29	182.76*** ±28.05	2846.48 ±1939.04
F	13.90 ±9.29	0.43 ±16.26	-28.93 ±138.06	-21.81 ±55.05	0.48*** ±0.11	404.22* ±155.46	8.66 ±10.74	5.77 ±35.27	307.83** ±64.72	-20.14 ±4473.95
H ₁	46.58** ±8.57	61.89** ±15.0	509.81** ±127.37	216.78** ±50.78	0.85*** ±0.10	717.79** ±143.42	85.78*** ±9.90	128.71** ±32.54	398.10*** ±59.71	17854.78** ±4127.43
H ₂	30.73** ±7.28	48.41** ±12.75	466.34** ±108.25	194.93** ±43.16	0.53*** ±0.09	448.70** ±121.89	76.87*** ±8.42	123.52** ±27.66	244.64** ±59.71	14956.05** ±3507.86
h ²	3506.82** ±4.88	423.41** ±8.33	1646.79** ±72.46	3421.17** ±28.89	8*** ±0.06	6322.56** ±81.59	443.55*** ±5.63	4270.00*** ±18.51	1080.90*** ±64.72	61629.40** ±2348.02
E	0.50 ±1.21	7.21** ±2.12	10.35 ±18.04	15.22 ±7.19	0.004 ±0.01	23.02 ±20.13	2.24 ±1.40	21.14** ±4.61	5.41 ±8.46	302.57 ±584.64
$\sqrt{H_1 / D}$	2.38	6.44	7.23	2.93	1.36	1.6	3.5	2.22	1.48	2.5
$H_2 / 4H_1$	0.16	0.2	0.23	0.22	0.16	0.16	0.22	0.24	0.15	0.21
$\frac{\sqrt{4DH_1 + F}}{\sqrt{4DH_1 - F}}$	2.1	1.01	0.65	0.74	2.24	2.63	1.41	1.1	3.66	1
h ² /H ₂	114.69	8.82	3.54	17.59	15.08	14.11	5.81	34.73	4.43	4.12
h ² ns	0.381	0.27	0.244	0.35	0.52	0.351	0.15	0.19	0.17	0.41

*and ** indicating significance at 0.05 and 0.01 level of probability, respectively

Table 2. Hayman analysis of variances (MS) following Morley jones modification for different morpho-physiological agronomic traits in 10×10 half diallel cross of groundnut

Source	df	50% flowering	No. of pods plant ⁻¹	Plant height	Harvest index	Pod size	100 Weight	Pod weight	100 kernel weight	Pod index	Diseases infection	Yieldplot ⁻¹
a	9	64.78**	110.85**	602.12**	559.56**	2.57**	1232.03**	59.68**	236.42**	313.82**	44166.83**	
b	45	29.99**	55.83**	378.74**	189.20**	0.52**	454.39**	76.08**	143.97**	259.26**	12435.09**	
b ₁	1	353.05**	66.28 ^{ns}	603.68**	1163.13**	0.18 ^{ns}	1143.66**	1325.34**	825.57**	2384.15**	18.88	
b ₂	9	47.41**	59.19*	155.30**	106.37*	1.18**	898.48**	34.25**	82.75 ^{ns}	506.54**	98.87.92**	
b ₃	35	16.29**	54.67***	429.77**	182.67**	0.36**	320.50**	51.14**	140.27**	134.96**	13444.83**	
Error	108	2.07	28.02	29.23	45.79	0.07	69.62	6.10	70.71	14.81	925.33	

*and ** indicating significance at 0.05 and 0.01 level of probability, respectively
df→degree of dominance