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Inheritance Study of Aphid (*Aphis craccivora* KOCH) and Rosette Resistance in Groundnut (*Arachis hypogaea L.*)

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Abstract This study was conducted to investigate the gene effects, heritability, genetic advance and number of effective factors controlling the inheritance of aphid and rosette resistance and other quantitative characters. Two aphid resistance, one rosette resistance, one aphid susceptible and one rosette susceptible lines were used as parents to develop F_1s, F_2s, BC_1P_1 and BC_1P_2. The seventeen generations obtained were evaluated along with three checks in three replications using randomized complete block design. The three parameter model was adequate to explain variations observed in the inheritance of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage. Non allelic interaction was significant with high narrow-sense heritability as obtained for rosette disease incidence, rosette severity index, number of matured pods per plant and net pod yield. It is possible to expect advance for these characters in further segregating generations. Wide ranges of narrow and broad sense heritability accompanied with moderate to high genetic advance except for aphid infestation index were obtained for the characters studied. The number of effective factors revealed that the understudied characters were governed by mono, oligo, and polygenes.

Keywords: *groundnut, aphid, rosette, resistance, gene effect, heritability, genetic advance, effective factors*

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1. Introduction

Groundnut is the fifth largest oil crop cultivated in more than 100 countries around the globe between Lat 40° North and South of the equator, especially in Africa, Asia, North and South America [1]. In 2015, groundnut was grown on a total area of 21.8 million hectares worldwide with an estimated production of 38.6 million tonnes (unshelled) at an average yield of 1.58 tonnes per hectare [2]. China, India, USA, Nigeria and Myanmar are the major producers of Groundnut. Developing countries in Asia, Africa and South America account for over 97 % of the world groundnut area and 95 % of total production. Nigeria and Senegal are the largest producers in West and Central Africa with 45 % Africa total production [3]. Groundnut is one of the most popular commercial crops in Nigeria. Nigeria produces 41 % of the total production in West Africa [4].

Groundnut production in Nigeria is constrained by several abiotic and biotic stresses among which is the groundnut rosette virus disease. Groundnut rosette virus disease (GRVD) has been recognized in all groundnut growing countries on the African continent, including its offshore islands such as Madagascar, but not anywhere outside Africa [5]. GRVD is responsible for an annual groundnut loss of worth US$ 150 million [1]. Nigeria alone lost about 0.7 million hectares of land to groundnut rosette virus epidemic which amounted to 250 million United States Dollars (USD) in 1975 [6]. The disease results from the synergistic interaction of three viral components; groundnut rosette virus (GRV), its satellite RNA (Sat-RNA), and groundnut rosette assistor virus (GRAV) [7]. The disease is spread by groundnut aphid.

Groundnut aphids, *Aphis craccivora* Koch, (Hemiptera: Aphididae) are an important group of insects with worldwide distribution [8]. They are herbivorous insects that can affect plants directly or indirectly by feeding on the plant's sap. Most aphid species comprise a set of closely related populations which may have diverged genetically so that they could be considered as host races, incipient or sibling species (or subspecies) [8]. Groundnut aphid is the major pest of groundnut causing yield losses by feeding on phloem sap and through transmission of virus diseases [9]

Viruses are the most difficult of all groundnut pathogens to control because no chemical substances (viricides) are available for eradicating viruses from plants [10]. Insecticides for controlling virus vectors (groundnut aphids) are expensive and hardly available to farmers. Their application also poses detrimental effect to human health and environment. Improved cultural practices are not effective because farmers are reluctant to accept and adopt those practices [1]. Host-plant resistance to *A. craccivora* in groundnut is recognized as the most effective, economic and sustainable method of limiting both the spread of the aphid and rosette viruses [9,11]. This research work focused on the studies of inheritance of aphid resistance, rosette resistance and quantitative traits in groundnut.

2. Materials and Methods

Field evaluation was conducted at the Institute of Agricultural Research (I.A.R), Samaru with an altitude of 686 m above sea level, Lat $11^0 11'$ N, long $07^0 38'$ E during the 2014 growing season in the Northern guinea savanna zone of Nigeria, with a mean annual rainfall of 1050 mm distributed within five months. The soil type is loamy. The plant materials (Table 1) for the research consisted of four entries obtained from West and Central Africa groundnut improvement program, Mali (ICGX-SM00020/5/9, ICGVIS07899, ICGX-SM0017/5/P10/P1 and ICGX-SM0020/5/P4/P1), one local variety (MANIPENTA) and three checks (SAMNUT 22, SAMNUT 23, and SAMNUT 24). Lines ICGX-SM00020/5/9 and ICGX-SM0020/5/P4/P1 were resistant to groundnut aphid, while line ICGVIS07899 was resistant to rosette whereas lines ICGX-SM0017/5/P10/P1 and MANIPENTA were susceptible to both groundnut aphids and rosette.

Table 1. Genotype, description and source of materials used in this research

Genotypes	Coding	Description	Source
Resistant lines			
ICGX-SM00020/5/9	P_1	Aphid Resistant	ICRISAT
ICGX-SM0020/5/P4/P1	P_2	Aphid Resistant	ICRISAT
ICGVIS07899	P_3	Rosette Resistant	ICRISAT
Susceptible lines			
ICGX-SM0017/5/P10/P1	P_4	Aphid Susceptible	ICRISAT
MANIPENTA	P_5	Rosette Susceptible	Local variety
Checks			
SAMNUT26	P_6	Aphid Resistant	IAR
SAMNUT23	P_7	Rosette Resistant	IAR
SAMNUT24	P_8	Rosette Resistant	IAR

ICRISAT-International Crops Research Institute for the Semi-Arid Tropics Patancheru, India. IAR-Institute for Agricultural Research, Samaru, Zaria, Kaduna State, Nigeria.

The genetic populations were developed through crossing of the resistant P_1 and susceptible P_2 parents to obtain the F_1s using biparental mating design at the screen house of Plant Science Department, Ahmadu Bello University Zaria. The F_1s were advanced to obtain the F_2s. The F_1s were also crossed to the recurrent parents to obtain BC_1P_1 and BC_1P_2 as revealed in Table 2. The resulting generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) with the three checks were evaluated in a Randomized Complete Block Design (RCBD) in three replications. One row plot each of 5m in length and an inter row and intra row spacing of 0.75m by 0.25m with an alley of 1m separating one block from the other. The rows containing the genotypes under test were flanked by two infector rows of MANIPENTA, a highly susceptible cultivar. This technique, called infector-row technique was described by [10]. MANIPENTA was sown two weeks earlier to allow buildup of infestation. *Aphis cracccivora* were collected from infested groundnut *Arachis hypogaea* and cowpea *Vigna unguiculata* plants in fields within Zaria and environments. These colonies were maintained on susceptible local groundnut genotype MANIPENTA. Three wingless (apterae) aphids were introduced on the tender leaves of 14 day-old seedlings of each of the twenty genotypes under trial. Each genotype was observed for the presence or absence of the aphids. Plants with no aphids were re-infested 7days after the first infestation. It was rare to find plants without aphids in choice test because the aphids were free to roam to find suitable plants within the field. No measure was taken to confine the aphids within the field. Data were collected from 40 plants for non-segregating populations (P_1, P_2 and F_1) while 100 plants and 80 plants were considered for F_2 and BC_1 P_1, BC_2 and P_2 segregating populations respectively. Plant height, Days to 50% flowering, Days to maturity, Number of mature pods per plant, Number of seeds per pod were counted while Shelling percentage, Net pod yield, and Hundred seed weight were measured using Mottler PM16-N weighing balance (ISC070501 Model).

2.1. Rosette Severity Index

The disease severity was recorded as the amount of plant tissue that was diseased with green or chlorotic rosette. Reaction to rosette was scored based on the scale of 1 (No apparent rosette symptoms), 3 (10% -20% rosette symptoms), 5 (20% -60% rosette symptoms) and 7 (60% - 80% rosette symptoms). Disease severity index was then obtained using the formula described by [12].

$$DSI = \sum\left(\frac{s \times n}{t \times 3}\right) \times 100, \quad (1)$$

$$DSI = Disease\ Severity\ Index, \quad (2)$$

$$s = Score\ (class), \quad (3)$$

$$n = Number\ of\ plants\ in\ class, \quad (4)$$

$$t = Total\ number\ of\ plants, \quad (5)$$

2.2. Rosette Disease Incidence

The ratio of number of plants that showed green or chlorotic conditions to the total number of plants in the

row were expressed in percentage. The percent disease incidence was scored based on the scale of Less than 10% (Highly resistance), 11-30% (Resistant), 31-50% (Moderately resistance) and more than 50% (Susceptible) as recommended by ICRISAT [1].

2.3. Aphid Infestation Index

Aphid infestation index for each line was calculated by the Formula and scale (Table 2 - Table 3) developed by [13,14]

$$DI = \sum \frac{SV \times NA}{4 \times NP} \times 100 \quad (6)$$

$$DI = Aphid\ damage\ index, \quad (7)$$

$$SV = Scale\ value, \quad (8)$$

$$NA = Total\ number\ of\ aphids\ in\ the\ category, \quad (9)$$

$$NP = Total\ number\ of\ plants. \quad (10)$$

2.4. Statistical Analysis

Data collected from different genetic populations were subjected to appropriate genetic analysis using (SASQUANT) joint scaling tests, six parameter model, broad sense heritability, narrow sense heritability, genetic advance and effective factors. Joint scaling test of [15] was performed to estimate the three-parameter model consisting of mid-parental value (m), dominance (h) and additive (d) gene effects following the weighted least square method proposed by [16]. Adequacy of three-parameter model was tested using chi-square test for goodness of fit at degrees of freedom. Broad sense heritability and narrow sense heritability were estimated as suggested by [17]. Expected gain in selection from selecting desirable F_2 plants to generate F_3 populations or from the segregating population to the next generation was computed as per cent of means based on the formula and procedure suggested by [18]. Effective factors (EF) were estimated using five methods. Method 1 (EF_1) was proposed by [17], method 2 (EF_2) was proposed by [19], methods 3 to 5 were proposed by [20]. All of the formulas assume segregating genes are not linked, all the genes have equal effects on characters studied, epistatic effects are absent, dominance effects are absent, and genotype x environment effects are absent [17]

2.4.1. Scaling Tests

Joint scaling test of [15] was performed to estimate the three-parameter model consisting of mid-parental value (m), dominance (h) and additive (d) gene effects following the weighted least square method proposed by [16]. Adequacy of three-parameter model was tested using chi-square test for goodness of fit at degrees of freedom, where n is the number of generation from which the three parameters were estimated.

The information on gene action controlling the inheritance of the characters under study was obtained from six parameters model suggested by [21] using the means of the generations (P_1, P_2, F_1, F_2, BC_1P_1, BC_1P_2) as shown below:

$$Mean\ effect = m, \quad (11)$$

$$Additive = d, \quad (12)$$

$$Dominance = h, \quad (13)$$

$$Additive\ x\ Additive = i, \quad (14)$$

$$Additive\ x\ Dominance = j, \quad (15)$$

$$Dominance\ x\ Dominance = l, \quad (16)$$

$$m = \overline{F_2}, \quad (17)$$

$$d = \overline{BCP_1} - \overline{BCP_2}, \quad (18)$$

$$h = 2\overline{BCP_1} + 2\overline{BCP_2} + \overline{F_1} - 4\overline{F_2} - \tfrac{1}{2}\overline{P_1} - \tfrac{1}{2}\overline{P_2}, \quad (19)$$

$$i = 2\overline{BCP_1} + 2\overline{BCP_2} - \tfrac{1}{2}\overline{P_1} + \tfrac{1}{2}\overline{P_2}, \quad (20)$$

$$j = \overline{BCP_1} - \overline{BCP_2} - \tfrac{1}{2}\overline{P_1} + \tfrac{1}{2}\overline{P_2}, \quad (21)$$

$$l = \overline{P_1} - \overline{P_2} + \tfrac{1}{2}\overline{F_1} + 4\overline{F_2} - 4\overline{BCP_1} - 4\overline{BCP_2}. \quad (22)$$

Table 2. Information of parents, F_1s, F_2s and backcrosses developed

Female Parent	Male Parent	F_1	F_2	BC_1P_1	BC_1P_2
P_1	P_4	$P_1 \times P_4$	$(P_1 \times P_4) \times (P_1 \times P_4)$	$(P_1 \times P_4) \times P_1$	$(P_1 \times P_4) \times P_4$
P_2	P_4	$P_2 \times P_4$	$(P_2 \times P_4) \times (P_2 \times P_4)$	$(P_2 \times P_4) \times P_2$	$(P_2 \times P_4) \times P_4$
P_3	P_5	$P_3 \times P_5$	$(P_3 \times P_5) \times (P_3 \times P_5)$	$(P_3 \times P_5) \times P_3$	$(P_3 \times P_5) \times P_5$

Table 3. Aphid Damage index (D.I) based on four-point scale

Scores	symptoms description	No. of Aphids
0	No aphid.	< 1
0.5	Fewer than 10ahids per plant, no colony formed.	< 10
1.0	Plant appears healthy.	11- 100
1.5	Plant appears healthy	101 – 150
2.0	Aphids mostly on young leaves, or tender stem, plant appear healthy.	151 – 300
2.5	Plants appear healthy.	301 – 500
3.0	Plants appear healthy, young leaves and tender stems are covered with aphids, leaves appear slightly curly and shiny.	501 – 800
3.5	Plants appear stunted, leaves appear curled and slightly yellow, no sooty mould and few cast skin.	>800
4.0	Plants appear stunted, leaves appear severely curled and yellow and are covered with sooty mould and cast skin.	>800

The variances of the estimates of gene effects were obtained as follows:

$$V_m = V(F_2) \tag{23}$$

$$V_d = V(BCP_1) + V(BCP_2) \tag{24}$$

$$V_h = 4V(BCP_1) + 4V(BCP_2) + V(F_1) + 16(F_2) + 1/2V(P_1) + 1/2V(P_2) \tag{25}$$

$$V_i = 4V(BCP_1) + 4V(BCP_2) + 16V(F_2), \tag{26}$$

$$V_j = V(BCP_1) + V(BCP_2) + 1/2V(P_1) + 1/2V(P_2) \tag{27}$$

$$V_l = V(P_1) + V(P_2) + 4V(F_1) + 16(F_2) + 16V(BCP_1) + 16V(BCP_2). \tag{28}$$

Standard error was obtained by taking the square root of the respective variances

2.4.2. Heritability

Broad sense heritability and narrow sense heritability were estimated following the formula suggested by [17] using the following relation:

$$H_b^2 = \frac{\sigma_{F2}^2 - \sigma_E^2}{\sigma_{F2}^2} \times 100, \tag{29}$$

Where,

$$H_b^2 = broad\ sense\ heritability, \tag{30}$$

$\sigma^2 F_2$ =variance of F_2 population of a set, (31)

$$\sigma_E^2 = environmental\ variance, \tag{32}$$

The narrow sense heritability were computed using the formula

$$H_{(N)} = \frac{\sigma_A^2}{\sigma_{F_2}^2} \times 100, \tag{33}$$

Where,

σ_A^2 =additive variance as a component of genetic effect, (34)

$\sigma_{F_2}^2$ =variance of the F_2 population of a cross. (35)

Additive variance (σ_A^2) as a component of genetic effect was computed using the formula

$$\sigma_A^2 = 2\sigma_F^2 - \left(\sigma_{B1}^2 + \sigma_{B2}^2\right), \tag{36}$$

Where,

σ_F^2 = variance of the F_2 population of a cross, (37)

σ_{B1}^2 = variance of backcross to parent 1 population, (38)

σ_{B2}^2 = variance of backcross to parent 2 population, (39)

2.4.3. Genetic Advance

Expected gain in selection from selecting desirable F_2 plants to generate F_3 populations or from the segregating population to the next generation would be computed as per cent of means based on the formula and procedure suggested by [18] as:

$$G_s = k * \sigma^2{}_F * h^2, \tag{40}$$

Where:

G_s = expectation of genetic advance under selection, (41)

k=Standardized selection differential,

at 10% selection intensity=1.755, (42)

$\sigma^2{}_F$ =variance of the F_2 population of a cross, (43)

h^2 =narrow sense heritability. (44)

2.4.4. Number of Effective Factors

This is the estimated minimum number of genes controlling the expression of a character. Effective factors (EF) were estimated using five methods. Method 1 (EF_1) was proposed by [17], method 2 (EF_2) was proposed by [19], methods 3 to 5 were proposed by [20].

$$EF_1 = \frac{(P_2 - P_1)^2 \left[1.5 - 2h(1-h)\right]}{8\left[\sigma_{F2}^2 - 0.25\left(\sigma_{P1}^2 + \sigma 2\sigma_{F1}^2\right)\right]}, \tag{45}$$

where

$$h = \frac{F_1 - P_1}{P_2 - P_1}, \tag{46}$$

$$EF_2 = \frac{\left[0.5(P_2 - P_1)\right]^2}{\left[2\sigma_{F2}^2 - \left(\sigma_{B1}^2 + \sigma_{B2}^2\right)\right]}, \tag{47}$$

$$EF_3 = \frac{(P_2 - P_1)^2}{8\left[\sigma_{F2}^2 - 0.25\left(\sigma_{P1}^2 + \sigma_{P2}^2 + 2\sigma_{F1}^2\right)\right]}, \tag{48}$$

$$EF_4 = \frac{(P_2 - P_1)^2}{8\left[2\sigma_{F2}^2 - \left(\sigma_{B1}^2 + \sigma_{B2}^2\right)\right]}, \tag{49}$$

$$EF_5 = \frac{(P_2 - P_1)^2}{8\left[\sigma_{B1}^2 + \sigma_{B2}^2 - \left(\sigma_{F1}^2 + 0.5\sigma_{P1}^2 + 0.5\sigma_{P2}^2\right)\right]}, \tag{50}$$

Where

P_1=mean of parent 1 population, (51)

P2=mean of parent 2 population, (52)

F1=mean of first filial generation population, (53)

σ_{P1}^2 = variance of parent 1 population, (54)

σ_{P2}^2 = variance of parent 2 population, (55)

σ_{F1}^2 = variance of first filial generation population, (56)

σ_{F2}^2 = variance of second filial generation pop., (57)

σ_{B1}^2 = variance of backcross to parent 1 population, (58)

σ^2_{B2} = variance of backcross to parent 2 population, (59)

All of the formulae assume segregating genes are not linked, all the genes have equal effects on characters studied, epistatic effects are absent, dominance effects are absent, and genotype x environment effects are absent [17].

3. Results

The result of the Joint scaling test (three parameter model), six parameter model, broad sense heritability, narrow sense heritability and genetic advance is shown in Table 4.

3.1. Gene Effects

In the present study, determination of mode of inheritance according to generation mean is based, according to [22] and [23], on parameters, which reflect mutual relationships between homozygous parents and their progenies for a particular quantitative characteristic. The method is in fact based on the existence of connections among mean generation values, which are dependent solely on additive and dominant gene effects. There are several ways to test these relationships as well as the verity of the hypothesis that these relationships depend solely on additive and dominant genes. One of them is [15] joint scaling test. The joint scaling test is considered more appropriate than Mather's scaling test for checking the adequacy of the additive-dominant model. The test estimates, the parameters |m|, |d| and |h| were obtained from means of the six generations followed by a comparison of the observed generation means with expected values derived from the estimates of the three parameters.

The sum contributions of the six generations for all the eleven characteristics in the three sets of crosses representing chi-square values for three degrees of freedom were significantly different from zero. This implies the inadequacy of the additive-dominant model and indicates that additive and dominant genes do not exclusively control the expression of the studied characteristics but non-allelic interactions were also present.

The six-parameter model [21] was fitted to establish the presence of effects of the non-allelic interaction on the expression of the studied characteristics. The six parameters were evaluated based on the mean values of the parents, F_1, F_2 and reciprocal backcrosses to recurrent parents.

The joint scaling test showed that the estimate of three parameter model was adequate to explain the gene effects controlling days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage in the three sets of groundnut crosses confirming significant additive and dominance gene effects.

Based on the joint scaling test, the three parameter model was inadequate to confirm the gene effects controlling rosette disease incidence, rosette severity index and net pod yield in the three sets of groundnut crosses. Therefore, six parameter model was fitted to estimate gene effects that govern the expression of these characters.

The joint scaling test revealed inadequacy of the three parameter model to explain the gene effects governing the expression of aphid infestation index, matured pods per plant and hundred seed weight in two groundnut sets. It was also deficient in explaining the gene effect governing the manifestation of days to maturity (χ^2=9.2**) in one groundnut set hence, the six parameter model was used to elucidate the type of gene effect responsible for the manifestation of these characters.

In the six parameter model, additive x additive gene effect was significant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for rosette disease incidence and rosette severity index. It was significant in ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1 for rosette severity index and in ICGVIS07899 x Manipenta for matured pods per plant and net pod yield. Additive x dominance gene effect was significant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for matured pods per plant and net pod yield.

3.2. Broad and Narrow Sense Heritability

The estimates of heritability and genetic advance for the eleven characters in the three sets of crosses are presented in Table 4. Estimates of heritability of a character that was less than 40% was considered low, 41 to 59% was considered moderate and above 60% high. Similarly, an estimate of genetic advance that was less than 10% was considered low, 11 to 20% moderate and above 20% high.

High broad sense heritability estimates were noted for days to fifty percent flowering (83 to 93%), number of seeds per plant (79 to 88%) in the three groundnut sets of crosses. Broad sense heritability ranged from 0.03 to 56% in plant height. Moderate to high estimates (46 to 69%) were recorded for shelling percentage in two sets. Aphid infestation index, days to maturity and hundred seed weight showed moderate (50 to 54%) broad sense heritability in one out of the three sets of crosses.

High narrow sense heritability (65 to 95%) was exhibited in the three sets of groundnut crosses for rosette disease incidence, rosette severity index, net pod yield, number of seeds per plant and hundred seed weight. Moderate narrow sense heritability (40 to 53%) was recorded for days to fifty percent flowering, aphid infestation index, plant height and shelling percentage while low narrow sense heritability was noticed for days to maturity and matured pods per plant.

3.3. Genetic Advance

High genetic advance (20.1 to 32.3) was obtained in the three sets of groundnut crosses for rosette disease incidence, plant height, shelling percentage, and hundred seed weight. Moderate to low (15.8 to 21.5) estimate was recorded for days to fifty percent flowering. Moderate values were obtained for rosette severity, days to maturity, matured pods per plant, net pod yield and number of seeds per plant. Aphid infestation index recorded low genetic advance.

Table 4. The estimates of gene effects, heritability and genetic advance for aphid infestation index, rosette disease incidence, rosette severity index and other quantitative characters from the three sets of crosses evaluated at Samaru in 2014

Characters	Days to fifty percent flowering			Aphid infestation index (%)			Rosette disease incidence (%)		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	4.20±2.8**	39.6±1.7**	34.8±1.6**	7.2±3.9	2.9±1.1	17.3±17.1	25.4±6.1**	13.5±4.7**	43.6±15.8**
D	-2.7±1.4	-1.3±0.8	0.9±0.8	0.8±1.9	-1.5±0.6**	25.8±8.4**	5.1±3.0	-3.5±2.3	17.2±7.7
H	-6.9±3.1	-0.4±1.8	1.6±1.8	-2.2±4.3	-1.5±1.2	-40.1±19.0*	2.0±7.1	15.4±5.2**	7.7±17.9
χ^2	1.7	0.6	1.9	12.7**	0.01	186.9**	26.1**	29.2**	44.5**
Gene effects estimated from six parameter model									
M	-	-	-	-14.2±16.5	0.2±5.1	24.8±77.6	-35.7±19.2	-31.4±16.1	-199±76.9
D	-	-	-	-0.1±1.9	-1.5±0.6	28.3±9.4**	5.9±2.1	-4.4±2.1	19.9±8.6
H	-	-	-	53.3±41.8	3.4±13.0	-92.3±196.4	122.6±46.8	124.2±43.9	164.0±187.0
I	-	-	-	21.3±16.0	2.8±4.9	-5.8±75.0	62.0±18.7**	45.0±17.6	62.4±74.8
J	-	-	-	18.2±12.2	-0.7±3.8	-52.8±57.5	-20.4±12.8	14.8±12.0	-46.4±50.9
L	-	-	-	-34.9±27.6	-1.5±8.6	57.8±129.6	-49.7±30.3	-64.3±28.2	-94.4±120.5
H%	91	83	93	0.0[x]	50	0.0[x]	0.0[x]	0.0[x]	0.0[x]
h%	53	40	46	47	51	48	74	65	69
GA	21.5	15.8	18.6	4.9	6.3	5.6	32.3	26.6	29.5

Characters	Rosette severity index (%)			Plant height (cm)			Days to maturity		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	38.2±13.2**	15.5±11.1	42.7±19.5*	35.3±3.5**	38.2±3.1**	32.0±3.0**	105.4±4.1**	110.7±4.2**	101.8±4.7**
D	3.7±6.3	-6.7±5.2	21.9±9.3	-0.8±1.8	2.7±1.6	-1.6±1.5	-6.7±2.0*	-2.6±2.1	3.4±2.3
H	-0.7±15.3	27.7±12.6*	22.3±22.4	-0.8±3.9	-2.5±3.4	7.3±3.3	-7.0±4.4	-6.4±4.5	-2.3±5.0
χ^2	342.6**	480.7**	554.2**	3.2	3.3	0.1	4.1	4.5	9.2**
Gene effects estimated from six parameter model									
M	-100.6±40.5	-95.3±34.7**	-94.3±78.3	-	-	-	106.8±11.5**	86.6±17.2**	130.7±17.9**
D	5.1±4.8	-8.9±4.2	25.1±9.4	-	-	-	-6.8±1.4**	-3.7±2.1	4.8±2.2*
H	316.8±102.8**	291.7±87.7**	376.9±197.7	-	-	-	-37.4±28.8	57.4±42.4	-81.0±44.5
I	139.5±39.1**	111.0±33.4**	134.7±75.5	-	-	-	0.7±11.2	23.6±16.6	-28.2±17.4
J	-33.8±30.0	35.2±25.6	-60.7±57.6	-	-	-	3.6±8.3	16.9±12.1	-22.4±12.7
L	-1634.0±69.4	-148.0±59.1	-223.9±133.0	-	-	-	38.2±18.7	-41.5±27.4	52.5±28.8
H%	0.0[x]	0.0[x]	0.0[x]	0.03	18	56	54	0.0[x]	0.0[x]
h%	94	95	93	52	49	49	29	33	31
GA	14.3	15.3	14.8	20.7	20.1	20.4	10.1	12.2	11.2

Characters	Number of mature pods per plant			Net pod yield			Number of seeds per plant		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	14.6±5.4	150±4.4**	24.5±7.4*	7.6±4.2	14.1±3.8**	16.1±1.4**	14.6±1.4**	16.5±1.1**	17.1±1.0**
D	111.0±2.6**	6.3±2.1**	-5.8±3.6	1.9±2.2	3.03±1.90	-5.4±3.0	-0.1±0.7	0.9±0.6	-1.3±0.5**
H	5.7±6.0	8.7±5.0	-12.8±8.3	10.3±4.9*	11.0±4.3	-9.9±6.4	1.4±1.6	-1.1±1.2	-0.4±1.2
χ^2	14.9**	5.1	24.9**	18.4**	8.7*	15.6**	0.3	0.8	0.2
Gene effects estimated from six parameter model									
M	40.0±16.2	11.9±19.1	-65.6±26.2	30.2±12.1	17.7±15.5	-42.5±20.2	-	-	-
D	12.4±1.7**	7.0±3.4**	-6.2±2.9*	4.0±1.6	4.1±2.0	-5.2±2.7	-	-	-
H	-32.0±41.2	33.9±48.4	212.2±66.5**	-30.1±29.6	14.0±37.7	128.7±48.6	-	-	-
I	-26.8±15.8	1.9±18.6	90.0±25.5**	-23.5±11.7	-4.4±15.0	58.6±19.5**	-	-	-
J	-36.8±12.0**	17.3±14.0	12.5±19.3	-28.00±8.2**	-12.9±10.4	-1.6±13.3	-	-	-
L	2.1±27.1	-29.1±31.8	-134.5±43.6*	12.2±19.3	-11.1±24.5	-79.7±31.2	-	-	-
H%	0.0[x]	0.0[x]	0.0[x]	0.0[x]	0.0[x]	0.0[x]	79	88	86
h%	30	35	33	89	87	74	75	71	85
GA	9.9	12.1	11.0	15.3	16.1	15.7	17.5	16.1	15.7

Characters	Shelling percentage (%)			Hundred seed weight (g)		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from three parameter model						
M	72.6±2.4**	70.8±3.4**	73.9±3.4**	40.8±4.5**	56.6±5.3**	39.1±2.2**
D	2.2±1.2	0.9±2.1	-2.9±1.6	-14.3±2.0**	-6.5±2.5	-3.1±1.0**
H	-1.1±2.6	-2.8±4.8	-8.9±3.7	4.2±6.0	-1.5±7.0	-18.1±3.2**
χ^2	1.8	1.9	3.4	18.8**	24.5**	2.5
Gene effects estimated from six parameter model						
M	-	-	-	79.6±23.7**	52.3±23.6*	9.8±11.4
D	-	-	-	-14.4±1.9**	-7.2±2.0**	-3.0±0.8**
H	-	-	-	-113.7±64.2	-31.3±63.6	50.8±32.1
I	-	-	-	-35.3±23.4	5.6±23.3	29.6±11.3
J	-	-	-	3.3±19.5	11.0±19.3	-11.4±10.1
L	-	-	-	93.3±43.9	54.9±43.5	-31.2±22.5
H%	69	0.0[x]	46	0.0[x]	0.0[x]	20
h%	51	47	53	62	68	72
GA	25.3	23.0	24.1	21.6	25.5	23.5

Cross 1=ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, Cross 2=ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1, Cross 3=ICGVIS07899xManipenta. Estimate of gene effects were significantly different from zero at 0.05(*) and 0.01(**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, χ^2=chi square, H=broad sense heritability, h=narrow sense heritability, GA=genetic advance, (x) value assumed to be zero due to negative estimate.

Table 5. Estimates of effective factors (EF) for aphid, rosette and other quantitative characters from the three sets of crosses evaluated at Samaru in 2014

S/No.	Character(s)	Cross	EF1	EF2	EF3	EF4	EF5	Mean
1	Days to fifty percent flowering	C1	2.30	2.01	0.44	0.50	0.39	1.13
		C2	0.25	0.50	0.09	0.13	0.07	0.21
		C3	0.05	0.26	0.05	0.06	0.04	0.09
2	Aphid infestation index (%)	C1	-2.47	0.00	0.00	0.00	0.00	-0.49
		C2	0.34	1.22	0.24	0.30	0.20	0.46
		C3	0.56	2.97	0.55	0.74	0.44	1.05
3	Rosette disease incidence (%)	C1	3.97	4.05	1.20	1.01	1.48	2.34
		C2	0.76	2.61	0.74	0.65	0.85	1.12
		C3	4.04	0.07	0.02	0.02	0.02	0.83
4	Rosette severity index (%)	C1	19.59	9.15	2.82	2.29	3.69	7.51
		C2	4.96	15.47	4.88	3.87	6.60	7.15
		C3	18.43	1.02	0.32	0.26	0.42	4.09
5	Plant height (cm)	C1	0.03	0.06	0.02	0.02	0.02	0.03
		C2	0.58	1.88	0.42	0.47	0.38	0.75
		C3	1.52	0.39	0.09	0.10	0.09	0.44
6	Days to maturity	C1	4.46	16.22	2.19	4.06	1.50	5.69
		C2	1.19	3.88	0.62	0.97	0.45	1.42
		C3	1.10	7.36	1.08	1.84	0.77	2.43
7	No of matured pods per plant	C1	-12.50	-20.50	-8.93	-5.12	-34.84	-16.38
		C2	3.15	14.23	1.95	3.56	1.34	4.85
		C3	7.87	12.35	1.56	3.09	1.05	5.18
8	Net pod yield (g)	C1	6.59	3.76	1.37	0.94	2.50	3.03
		C2	4.19	3.38	1.23	0.85	2.26	2.38
		C3	10.29	5.82	2.12	1.46	3.87	4.71
9	Number of seeds per plant	C1	0.24	0.01	0.00	0.00	0.00	0.05
		C2	0.10	0.27	0.09	0.07	0.12	0.13
		C3	0.16	0.49	0.16	0.12	0.22	0.23
10	Shelling percentage	C1	0.30	0.88	0.20	0.22	0.19	0.36
		C2	0.60	0.55	0.12	0.14	0.10	0.30
		C3	0.96	1.16	0.26	0.29	0.23	0.58
11	Hundred seed weight (g)	C1	5.94	32.77	5.91	8.19	4.63	11.49
		C2	2.12	6.67	1.34	1.67	1.11	2.58
		C3	2.31	1.19	0.23	0.30	0.19	0.84

EF1=Effective Factors (Wright,1968), EF2=Effective Factors (Mather and Jinks 1981), EF2 to EF3=Effective factors (Lande, 1981), C1=ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, C2=ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1, C3=ICGVIS07899xManipenta

3.4. Estimates of Number of Effective Factors

Estimates of the minimum number of genes (effective factors) controlling the eleven characters obtained using the five methods are presented in Table 5 estimates over all the three sets of crosses ranged from 0.05 to 2.30 for days to fifty percent flowering, from -2.47 to 2.97 for aphid infestation index, from 0.02 to 4.05 for rosette disease incidence and from 0.26 to 18.43 for rosette severity index. It ranges from 0.02 to 1.88 for plant height, from 0.62 to 16.22 for days to maturity and from -34.84 to 14.23 for number of matured pods per plant. The estimate for net pod yield ranged from 0.85 to 10.29, for number of seeds per plant it ranged from 0.00 to 0.49, for shelling percentage it ranged from 0.10 to 1.16 and for hundred seed weight it ranged from 0.23 to 32.77.

Mean estimates of the minimum number of genes for each set of cross ranged from 0.09 to 1.13 for days to fifty percent flowering, from -0.49 to 1.05 for aphid infestation index, from 0.83 to 2.34 for rosette disease incidence and from 4.09 to 7.51 for rosette severity index. The mean estimate for plant height ranges from 0.03 to 0.75, for days to maturity it ranged from 1.42 to 5.69, for number of matured pods per plant it ranged from -16.38 to 5.18 and for net pod yield it ranged from 2.38 to 4.71. It ranged from 0.05 to 0.23 for number of seeds per plant, from 0.30 to 0.58 for shelling percentage and from 0.84 to 11.49 for hundred seed weight.

4. Discussion

The results of joint scaling test indicated that the three parameter model was adequate to explain variations observed in the inheritance of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage in the three sets of groundnut crosses studied. The estimates for the gene effects revealed that both the additive and dominance gene effects contributed significantly to the inheritance of the characters studied. This finding is explicit from the chi-square analysis which showed insignificance in the three sets tested. However, the three parameter model was inadequate to explain the variations observed in the inheritance of rosette disease incidence, rosette severity index and net pod yield in the groundnut three sets; rosette disease incidence, rosette severity index and net pod yield in two groundnut sets and days to maturity in one groundnut set. To improve these

characters, selection in the early generations will be desirable. Six parameter model was used to establish the presence of the effects of the non-allelic interaction on the expression of the studied characteristics. Non allelic gene interactions were significant for number of matured pods per plant, net pod yield, rosette severity index and rosette disease incidence. Selection in the early generations will be ineffective and so must be delayed till later generations.

With the exception of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage the directions of dominance (h) and dominance x dominance (l) for all the characters studied were in opposite directions i.e. when h is positive, l is negative and vice versa. This suggests duplicate type of gene interaction.

Heritability estimate gives information on transmissibility of the quantitative characters and are important for effective breeding strategy. The magnitude of the heritability is used to predict the behavior of succeeding generations through the use of appropriate selection criteria to access the level of genetic improvement. Genetic advance on the other hand provides explicit information and precise view of segregating generations for selection. High heritability along with high genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics.

The moderate to high broad sense heritability estimates obtained from days to fifty percent flowering, number of seeds per plant, plant height and shelling percentage indicate that the genotypic variances were higher than the phenotypic variances. The genetic variation was large due to major genes controlling the characters which can easily be inherited thus selection would be effective in the desired direction for each of the characters in the groundnut sets of crosses tested [24].

The moderate to high narrow sense heritability that was exhibited in all the characters except days to maturity and matured pods per plant indicate the preponderance of additive gene effect in the three sets of groundnut crosses studied. The variation shown in the heritability estimates may also be due to the fact that only one environment was used thus the genotype x environment estimates was not obtained. This had been reported to cause bias in the estimate of heritability [25]. However, the high heritability values indicated that the characters studied were highly transmissible and selection can be done to improve these characters.

Similarly, the characters studied showed moderate to high genetic advance except for aphid infestation index. According to [26], characters with high heritability accompanied with high genetic advance also result in better genetic gain through selection.

Wide ranges obtained for number of effective factors could be as a result of the failure to meet some of the under lying assumptions of the five methods. The presence of dominant genes as can be deduced from the adequacy of the three parameter model in the joint scaling test for days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage rendered the estimates of the number of effective factors less reliable. The presence of epistasis as can be deduced from the six parameter model for rosette disease incidence, rosette severity index, matured pods per plant and net pod yield rendered the estimates of number of effective factors less reliable. Secondly, genes may be inherited in blocks of DNA segregates and may be estimated as though they are inherited as single strands of DNA. However, based on the present study mean estimates of number of effective factors showed that approximately one gene controls the expression of days to fifty percent flowering and plant height in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, aphid infestation index and shelling percentage in ICGVIS07899xManipenta. An approximate of two genes controls the expression of rosette disease incidence in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1. These suggest that few genes were responsible for the manifestation of these characters hence, the evidence of monogenic and oligogenic inheritance. This result was in concordance with [27] who showed that resistance to aphid vectors is controlled by a single recessive gene while resistance to groundnut rosette virus is controlled by two recessive genes [28]. The expression of number of matured pods per plant and net pod yield in ICGVIS07899xManipenta were controlled by about five genes. Days to maturity, rosette severity index and hundred seed weight in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1 were controlled by about six, eight and eleven genes respectively. These suggest that many genes were responsible for the manifestation of these characters hence, the evidence of polygenic inheritance.

5. Conclusions

In conclusion, in the set of crosses where non allelic interaction was significant with high narrow-sense heritability as obtained for rosette disease incidence (i=62.0±18.7**, h^2=74% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1), rosette severity index (i=139.5±39.1**, h^2=94% and 111.0±33.4**, h^2=95% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1 and ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1), number of matured pods per plant (i=90.0±25.5**, h^2=33% in ICGVIS07899xManipenta, j=-36.8±12.0**, h^2=30 % in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, l=-134.5±43.6*, h^2=33% in ICGVIS07899 x Manipenta) and net pod yield (i=58.6±19.5**, h^2=74% in ICGVIS07899xManipenta, j=-28.00±8.2**, h^2=89% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1), it is possible to expect advance for these characters in further segregation generations. Crosses where non allelic interaction was not significant to explain all variation in generation means along with low heritability imply more complex nature of inheritance and/or influence of the environment on the expression of these characters. The number of effective factors revealed that days to fifty percent flowering, aphid infestation index, plant height, number of seeds per plant and shelling percentage were controlled by mono genes. Rosette disease incidence was controlled by oligogenes while rosette severity index, days to maturity, number of matured pods per plant, net pod yield and hundred seed weight are controlled by polygenes. This study revealed that the parents used had no complete resistance to aphid and rosette resistance. Therefore, it is necessary to study resistance of the sets of crosses using molecular marker and transgenic approaches to obtain more stable and reliable sources of resistance.

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