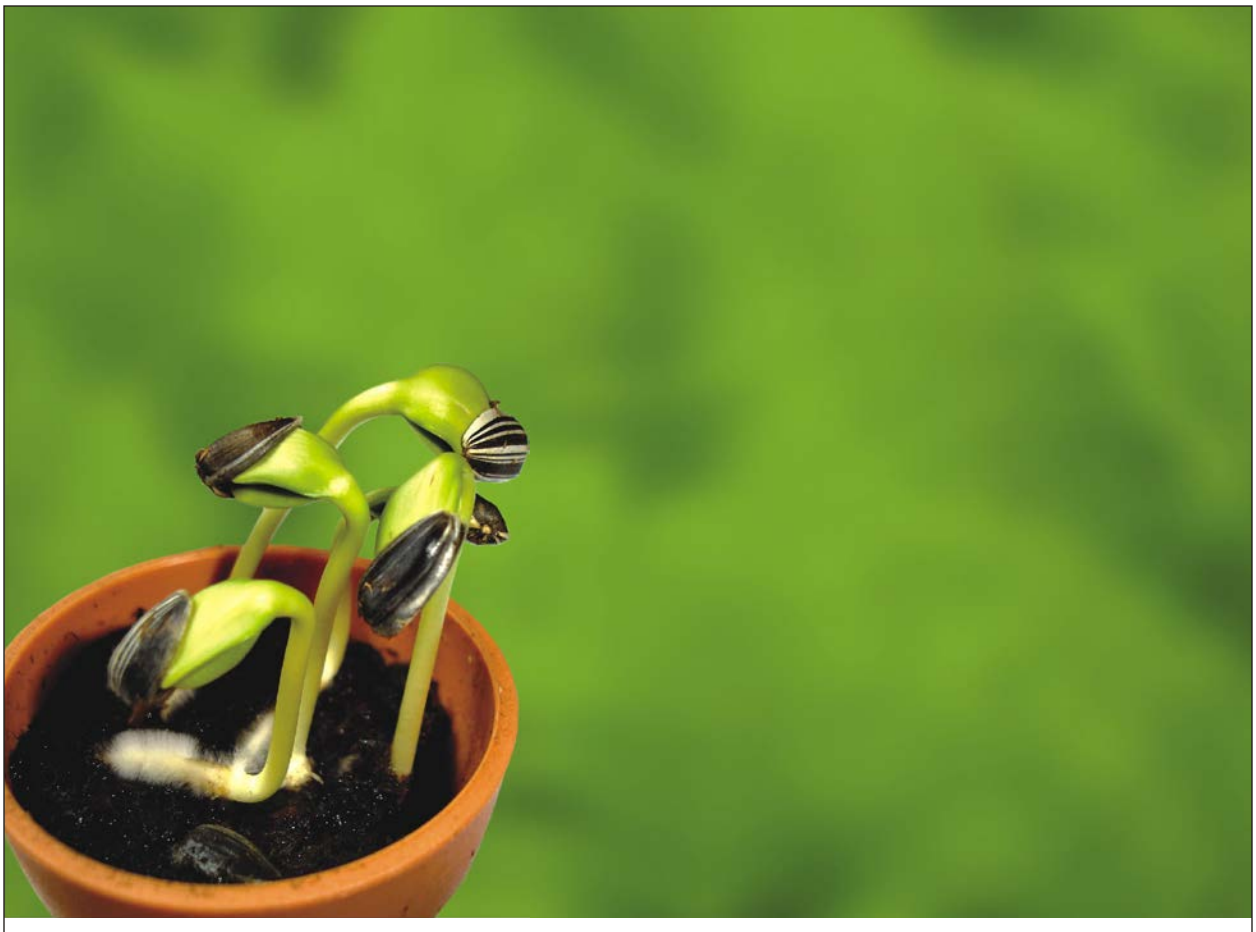

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A Quantitative Analysis of the Genetics of Yield and Yield Components in West African Okra, *Abelmoschus caillei* (A. Chev) Stevels

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ABSTRACT

The choice of an efficient breeding procedure depends to a large extent on knowledge of the genetic system controlling the character to be selected. To obtain information on the nature of gene action in West African okra, six generations of parents, first and second filial generations, back crosses 1 and 2 (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived using Generation Mean Analysis (GMA) from crosses involving fourteen selected genotypes were evaluated. The experiments were conducted at the Teaching and Research farm of the University of Agriculture, Abeokuta (7°29N, 3°30E) during the growing seasons of 2008 and 2009. The data suggest that genes influencing some of the characters are dispersed among the parental lines and those interactions are predominantly of the duplicate kind. Additive gene effects were higher than dominance gene effects for most of the traits that were evaluated. Seed yield per plant for cross NGAE-96-0062-2 X CEN 015 was controlled by complementary gene action. Days to flowering, number of pods per plant, number of seeds per pod, matured plant height and seed weight per plant for the NGAE-96-0063 X CEN 015 cross was controlled by duplicate epistatic gene actions. The presence of significant amount of all types of gene action, additive, dominance and epistasis for most of the traits has indicated that methods designed to utilize all of them such as recurrent selection and reciprocal recurrent selection has to be adopted in the breeding programme.

Key words: Additive, dominance, epistasis, gene action, west African Okra

INTRODUCTION

West African okra, *Abelmoschus caillei* (A. Chev) Stevels is an allopolyploid hybrid between *Abelmoschus esculentus* and *Abelmoschus manihot*. It is a short-day, annual, self-pollinating shrub cultivated for the edible fruits (pods). It belongs to the family Malvaceae. Schippers (2000) reported that It is an important vegetable crop in the Sub Saharan Africa. In Nigeria, West African okra performs very well under traditional system of farming from sea level to 800 m above sea level (Adeniji *et al*., 2007). Production and consumption of West African okra is high reflecting its role as the major vegetable crop for the majority of the rural households.

According to Olasantan and Bello (2004) over 90% of West African okra produced in Nigeria is grown by peasant farmers, intercropped with major crops such as yam, cassava and maize. FAOSTAT (2004) reported that average yield on small holder farms are currently about 2,645 kg

of tender pods/hectare among the lowest in the developing world, even though yield in the same environment can be higher. Low West African okra yields reflect frequent use of poor varieties. So the challenge of the Nigerian okra breeder is to step up yield through genetic improvement by adopting different breeding methodologies.

The breeding method to be adopted for genetic improvement of the crop depends mainly on the nature of gene action involved in the expression of the quantitative traits (Azizi *et al*., 2006). Generation mean analysis belongs to the quantitative biometric methods based on measurement of phenotypic performances on certain quantitative traits on as many as possible plant individuals in basic experimental breeding generations (Parental, filial, backcross and segregating generations. As mentioned by Kearsy and Pooni (1996), generation mean analysis is useful technique in plant breeding for estimating gene effects (additive and dominance) and their disgenic (additive x additive; Additive x dominance; Dominance x dominance) interactions responsible for inheritance of quantitative traits. According to Sharma and Sain (2003) generation mean analysis help us in understanding the performance of the parent used in the crosses and potential crosses to be used either for heterosis exploitation or pedigree selection However, Line X Tester (LxT) analysis is used to select the parents based on their combining ability but fails to detect the epistasis which remains the most complex problem and on which it is difficult to obtain reliable results. The presence or absence of epistasis can be detected by the analysis of generation means using scaling test which measures epistasis accurately whether it is complementary (additive x additive) or duplicate (additive x dominance) and (dominance x dominance) at the disgenic level (Farshadfar *et al*., 2008). Considering the fact that pod yield and it's components are the most important complex traits and their improvement is the most frequent goal of okra breeding programs in the world, selection for parental components in this study was done to fill these requirements. This investigation was undertaken to obtain information on the nature of gene action in West African okra so as to provide a basis for an evaluation of selection methods for the improvement of West African okra population. An accomplishment of this research will provide basic information that will facilitate a release of improved varieties into the cropping system.

MATERIALS AND METHODS

Study site: The experimental sites for the three experiments were chosen from both upland and inland valley (Inland valley) agro-ecological zones of derived savannah Abeokuta. The location is the Teaching and Research Farm of Federal University of Agriculture (FUNAAB), Abeokuta 7°29N, 3°30E Nigeria.

Test materials: The test materials included 14 genotypes of West African okra were selected from the genebank of National Center for Genetic Resources and Biotechnology (NACGRAB), Centre for Environment, Renewable Natural Resources Management and Development (CENRAD), Ibadan were used for the study (Table 1).

Experimental layout: The study was carried out in two phases from July, 2007 to November, 2008.

Phase I: This was conducted to produce the F_1 generation at the Teaching and Research Farm of University of Agriculture, Abeokuta during the first planting season (July, 2007).

Phase II: This was carried out at the inland valley (Inland valley) ecology of the University of Agriculture, Abeokuta, during the second planting season (December, 2007), to produce F_2 and

Table 1: Morphological characters of the accessious used to determine the gene action that control the expression of identified characters

Accessious	Stem colour	Stem pubescence	Pod colour	Pod pubescence	Pod position
CEN 001	Purple	Glaborous	GwY	Prickly	Horizontal
NGAE-96-012-2	Purple	Couspicuous	LG	Prickly	SE
AGA97/066-5780	Purple	Glaborous	DG	Downy	Horizontal
NGAE-96-0062-2	Purple	Glaborous	Green	Downy	Horizontal
NGAE-96-04	Green	Glaborous	Green	SP	SE
OAA96/175-5328	Green	Glaborous	DG	Downy	Horizontal
NGAE-96-0063	DR	SP	Green	Prickly	Erect
CEN-012	Purple	Couspicuous	Green	Prickly	Horizontal
Oja-Oba-2	Green	Glaborous	YG	SP	Horizontal
CEN 009	LP	Glaborous	Green	Downy	Horizontal
NGAE-96-0066	Purple	Glaborous	Green	SP	Horizontal
Ado-Ekiti-3	Purple	Glaborous	Green	Downy	ST
NGAE-96-0060	Purple	Glaborous	Green	Downy	Horizontal
CEN 015	LP	Glaborous	DG	Downy	SE

LG; Light green, GwP; Green with purple, PwG; Purple with Green, DG; Dark green, LP; Light purple, GwR; Green with Red, YG; Yellowish green, GwY; Green with Yellow, DgwR; Dark Green with red, SP; Slightly prickly, SE; Semi-erect

backcross generations. For each cross, two contrasting genotypes were used as parents. Each parental plant was grown in the field in a single row of 6 m length. At the onset of flowering in September, 2007, crosses were made using hand emasculation and pollination. Mature flower buds which were likely to open the next day, were selected for emasculation because the stigma of *Abelmoschus caillei* remains receptive on the day of anthesis. Ready to open staminate flowers of the male parent (P_1), were removed from the inflorescence. Simultaneously, the female flowers of the female parents (P_2) that were ready to open the following day were also identified. Undehisced anthers were also removed with forceps. Care was taken to ensure that all the anthers were removed and stigma not injured during the operation. To avoid stray pollen contamination, stigma was covered with a soda straw tube. The pollen grains of the P_1 were carefully dusted on the stigma of the female flower (P_2) to produce F_1. Crosses were identified and tagged with the date of emasculation and pollination recorded. After maturity, the F_1 progeny seeds were harvested and replanted along side with the parental genotypes. The same pollination procedure was used and the F_1 seeds crossed to P_1 and P_2 to produce backcross to better parent (BC_1) and backcross to other parent (BC_2). The F_1 seeds were also planted out in the field to raise F_2 seeds. In the early planting season of July 2008, the parental lines, F_1, F_2, BC_1 and BC_2 seeds were sown. Seeds from each of the P_1, P_2, F_1, BC_1 and BC_2 generations were planted out in a 5-single-row-plot of 6 m long, while BC_1 and BC_2 generations were planted out in a 10-single-row-plot. The F_2 generation was planted out in 20 row-plot. All the generations were arranged in a Randomized Complete Block Design with three replications. The spacing was 1 m between rows and 60 cm within row; insect pests were controlled using pyrethroid (karate EC) which was applied twice at the rate of 50 mL^{-1} per 20 L of water. Weeding was done manually when necessary. The plots of P_1, P_2 and F_1 contained 60 plants, BC_1 and BC_2 contained 120 plants, while the F_2 generations contained a total of 240 plants.

Data collection: Data were collected from all the plants for P_1, P_2, F_1, BC_1 and BC_2 but 220 plants were observed for the F_2 generation. Data from each generation were collected on number of days to 50% flowering, number of pods per plant, number of seeds per pod, matured plant height (cm) and weight of seeds per plant (g).

Statistical analysis: Quantitative data may be analyzed by Matherian technique (Mather, 1949). This analysis first requires that a scale empirically adequate for statistical purposes be obtained. Two scaling criteria, when met, satisfy this requirement.

First, the heritable effect must, on the average, be additive. This criterion can be met when Mather's A, B and C scaling test are statistically applied to the data. According to Mather (1949), the scaling test may be solved individually, or jointly as reported by Cavalli (1952). Cavalli's joint scaling test has the advantage of testing goodness of fit once, instead of in three separate instances and of making clear at once, if the fit is bad which part of the data is responsible for it.

The generation means may be influenced by six parameters: m, the mid-parent value; (d), the additive components; (h), the dominance components; (i), the additive x additive interaction; (j), the additive x dominance interaction; and (l), the dominance x dominance interaction. Cavalli's joint scaling test estimates weighted least square value of m (d) and (h) from the generation means. The weights are the reciprocals of the standard errors of the generation means. Expected generation means are then calculated using this weighted m (d) and (h) values. The comparison between the observed and expected means can then be effected by assuming the sum of squares minimized in the fitting process to be distributed as X^2 with degree of freedom equal to the number of generation means minus the number of parameters which have been fitted.

Mather's second scaling criterion calls for the contribution made by nonheritable agents to the phenotype variation to be independent of the genotype; that is there must be no genotype-environment interaction. This criterion is satisfied, in practice, if the variances of the nonsegregating generations do not differ significantly from one another.

The average of the generations were used to estimate mid-parent mean (m), additive (d) and dominance (h) gene effect by using joint-scaling test (Mather and Jinks, 1982; Cavalli, 1952), using weighted least squares.

Broad-sense (H_B) and narrow sense (H_N) heritabilities were estimated as suggested by Wright (1968) as:

$$H_B = \{V_{F2}-[(V_{p1} +V_{p2} +2V_{F1})/4]\}/V_{F2}$$

Heritability in the narrow sense was computed as suggested by Warner (1952) as:

$$H_N = [V_{F2}- (V_{BC1} +V_{BC2})/2]/V_{F2}$$

RESULTS

Means along with their respective standard errors for the five characters studied in nine crosses of West African okra are presented in Table 2. The means of the F_1 with respect to all the characters studied were higher than the means of the better parents except for mean seed weight (27.57) in cross NGAE-96-0060 X NGAE-96-0062-2 which tended towards the mean of the smaller parent NGAE-96-0062-2 (P_2). The mean values recorded for these characters in the F_2 and backcross one (BC_1) were larger and closer to the mean values of the parent except for seed weight in cross NGAE-96-0060 X NGAE-96-0062-2, that recorded lower (27.57) but closer to the mean value (30.43) of P_2. The mean values of BC1 for matured plant height in cross CEN001 X Ado-Ekiti-3, number of pods per plant in cross NGAE-96-04 X OAA96/175-5328 and seed weight per plant in cross NGAE-96-0063 X CEN015 were higher than what were obtained in the two parents. Whereas, all the characters in BC_2 recorded mean values that fell between the figures obtained for P_1 and P_2.

Table 2: Means and standard errors, of five West African okra characters in nine crosses

Characters	Parental combination	P_1	P_2	F_1	F_2	BC_1	BC_2
Days to	NGAE-96-012-2 (G2)	90.33±0.52(G2)	79.00±0.51(G6)	93.00±0.42	93.00±0.09	88.67±0.10	83.67±0.08
50% Flower	X CEN001(G6)						
Number of	AGA97/0665780(G10)	14.33±0.68(G10)	6.67±0.34(G14)	19.67±1.67	15.33±0.13	14.20±0.22	16.77±0.19
Pods/PLT	X NGAE-96-0062-2(G14)						
	NGAE-96-04(G7)	13.70±0.41(G7)	5.87±1.03(G9)	12.37±1.12	17.07±0.12	16.93±0.20	9.10±0.18
	X OAA96/175-5328(G9)						
Number of	NGAE-96-0063(G19)	93.30±0.617(G19)	90.40±0.718(G5)	100.70±1.19	93.80±0.20	88.10±0.23	70.80±0.20
Seeds per pod	X CEN012(G5)						
	Oja-Oba-3(G22)	96.13±0.85(G22)	65.70±0.715(G13)	90.10±0.909	110.13±0.150	88.43±0.225	96.17±0.182
	X CEN009(G13)						
Matured	NGAE-96-0066(G15)	203.67±1.17(G15)	193.00±0.91(G9)	207.33±0.73	210.33±0.16	200.67±0.23	188.67±0.20
plant height	X OAA96/175-5328(G9)						
	CEN001(G6)	190.33±1.11(G6)	180.00±0.93(G24)	194.67±1.30	194.92±0.14	199.00±0.22	133.69±0.23
	X Ado-Ekiti-3(G24)						
Seed weight	NGAE-96-0060(G17)	32.53±0.47(G17)	30.43±0.27(G14)	27.57±0.45	30.67±0.05	29.07±0.08	32.47±0.08
per Plant	X NGAE-96-0062-2(G14						
	NGAE-96-0063(G19)	30.40±0.36(G19)	28.60±0.31(G8)	32.70±0.53	26.50±0.07	32.60±0.09	24.60±0.08
	X CEN015(G8)						

Where P_1 = Male parent, P_2 = Female parent; F_1 = (P_1xP_2); F_2 = Selfed F_1; $BC_1 = P_1 x (P_1xP_2)$; $BC_2 = P_2x(P_1xP_2)$

The variances of the F_2 generation for all characters were higher than the variances in the other generations. Number of seeds per pod for example recorded the highest variance (43.78) for the cross NGAE-96-0063 X CEN012 followed by matured plant height (36.1) for NGAE-96-0066 X OAA96/175-5328 and number of pods per plant (29.03) for the cross AGA97/066-5780 X NGAE-96-0062-2. In all, the F_1 generation recorded the lowest variance for all the characters in the four generations (Table 3).

The additive and dominance gene effects were observed to control the variation in the traits. Additive gene effects (D) were larger relative to dominance (H) in all crosses for number of seeds per pod (11.72 and 36.30) and matured plant height (9.42 and 39.52). In most cases, the m, d, h values were significantly different from zero (Table 4). This indicates that the generation means do not depends solely upon the additive and dominance effects of the genes, suggesting nonallelic interaction (epistasis) to be the major influence in the determination of the traits. Ideally, it would be advantageous to eliminate this interaction, thereby obtaining a system for which the additive-dominance model is adequate. Numerous transformations were tried on the data for this purpose, non yielded a nonsignificant chi-square.

Mather's second scaling criterion calls for the variances of the nonsegregating generation to be equal. The F ratio of the raw data of some of the characters was significant, suggesting that genotype x environment interactions were present. A log transformation reduces the F ratio to a nonsignificant values, thereby satisfying the second criterion for an adequate scale.

With the effects of nonallelic interaction on the observed means delineated and the genotype x environment interaction detected and eliminated by a log transformation, it is possible to estimates the magnitude of each parameter influencing the characters and to test it's significant from zero. The model was extended to a six-parameter model including three interaction terms (i), (j) and (l) using the methodology described by Jinks and Jones (1958) (Table 5) in which additive

Table 3: Within family variance of nine crosses of West African okra

		Generations					
Characters	Parental combination	P1	P2	F1	F2	BC1	BC2
Days to 50%	NGAE-96-012-2 (G2)	10.4(G2)	10.1(G6)	8.40	19.50	12.40	9.30
Flower	X(CEN001(G6)						
Number of	AGA97/0665780(G10)	13.6(G10)	6.81(G14)	23.33	29.03	26.10	22.80
Pods/PLT	XNGAE-96-0062-2(G14						
	NGAE-96-04(G7)	8.1(G7)	20.6(G9)	22.40	27.40	24.40	21.70
	XOAA96/175-5328(G9)						
Number of	NGAE-96-0063(G19)	12.33(G19)	14.36(G5)	23.86	43.78	28.13	24.15
Seeds per pod	XCEN012(G5)						
	Oja-Oba-3(G22)	16.99(G6)	14.30(G24)	18.19	32.99	27.06	21.82
	XCEN009(G13)						
Matured plant height	NGAE-96-0066(G15)	23.4(G15)	18.2(G9)	14.60	36.10	27.50	23.80
	XOAA96/175-5328(G9)						
	CEN001(G6)	23.4(G15)	18.2(G9)	14.60	36.10	27.50	23.80
	XAdo-Ekiti-3(G24)						
Seed Yield per Plant	NGAE-96-0060(G17)	9.30(G17)	5.30(G14)	9.00	11.60	10.00	9.40
	XNGAE-96-0062-2(G14)						
	NGAE-96-0063(G19)	7.23(G19)	6.26(G8)	10.60	16.11	11.51	9.93
	XCEN015(G8)						
Number of plants sampled		60	60	60	220	120	120.00

Table 4: Joint scaling test using weighted least square means with three parameter model m,d, h of Mather and Jinks (1982), Singh and Chaudhary (1996)

Characters	Parental combination	m	D	H	X^2
Days to 50% Flower	NGAE-96-012-2 (G2)	84.44±0.42	5.66±0.32	8.19±0.80	34.85
	X CEN001(G6)				
Number of Pods/PLT	AGA97/0665780(G10)	10.46±0.46	3.38±0.39	9.78±0.95	2.85
	X NGAE-96-0062-2(G14				
	NGAE-96-04(G7)	10.54±0.51	5.48±0.43	7.34±1.03	137.94
	X OAA96/175-5328(G9)				
Number of Seeds per pod	NGAE-96-0063(G19)	84.65±0.70	11.72±0.52	2.60±1.34	11.82
	X CEN012(G5)				
	Oja-Oba-3(G22)	86.21±0.58	36.30±0.47	20.31±1.13	48.99
	X CEN009(G13)				
Matured plant height	NGAE-96-0066(G15)	197.27±0.58	9.42±0.48	7.80±1.10	97.92
	X OAA96/175-5328(G9)				
	CEN001(G6)	176.87±0.66	39.52±0.49	6.60±1.30	67.26
	X Ado-Ekiti-3(G24)				
Seed Yield per Plant	NGAE-96-0060(G17)	32.33±0.36	2.37±0.29	-3.46±0.72	22.14
	X NGAE-96-0062-2(G14)				
	NGAE-96-0063(G19)	27.76±0.40	4.74±0.31	0.64±0.81	20.06
	X CEN015(G8)				

(d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) effects were each calculated. The additive, dominance and epistatic type of gene interaction in each cross for different traits were found to be different from the expected. The dominance x dominance

Table 5: Genetic component estimates of six generation means fitted to six parameter model of Hayman (1958), Jinks and Jones (1958) in nine crosses of West African okra

Characters	Parental combination	m	d	H	I	J	L
Days to 50%	NGAE-96-012-2 (G2)	111.99±1.55	5.67±0.51**	-56.96±3.86**	-27.32±1.46**	-1.33±1.32	37.97±2.65**
Flower	X CEN001(G6)						
Number of	AGA97/0665780(G10)	9.88±2.00	3.83±0.51**	12.01±5.16**	0.62±1.93	-2.52±1.63	-2.22±3.78
Pods/plt	X NGAE-96-0062-2(G14						
	NGAE-96-04(G7)	26.01±1.97	3.91±0.60**	-22.11±5.11**	-16.22±1.88**	7.83±1.72*	8.47±3.75*
	X OAA96/175-5328(G9)						
Number of	NGAE-96-0063(G19)	149.04±2.38	1.43±0.85	-172.74±6.01**	-57.20±2.22**	31.80±2.15**	124.40±4.22**
Seeds per pod	X CEN012(G5)						
	Oja-Oba-3(G22)	152.25±2.13	15.22±0.72**	-106.31±5.46**	-71.33±2.01**	-14.96±1.92**	44.17±3.82**
	X CEN009(G13)						
Matured	NGAE-96-0066(G15)	260.97±2.20	5.33±0.72	-148.93±5.60	-62.64±2.08	13.33±1.95	95.29±3.80
plant height	X OAA96/175-5328(G9)						
	CEN001(G6)	298.50±2.11	5.17±0.78*	-311.50±5.50**	-113.34±1.96**	120.33±2.10**	207.67±4.04**
	X Ado-Ekiti-3(G24)						
Seed Yield	NGAE-96-0060(G17)	31.08±1.29	1.05±0.43*	1.85±3.36	0.40±1.22	4.70±1.17**	-5.37±2.44
per Plant	X NGAE-96-0062-2(G14						
	NGAE-96-0063(G19)	21.31±1.45	0.92±0.45	9.49±3.69*	8.20±1.37**	14.10±1.24**	1.90±2.75
	X CEN015(G8)						

Where, m = mean, d = additive, h = dominance, I = additive x additive, j = additive x dominance, l = dominance x dominance

(l) interaction was larger than the additive x additive (i) and additive x dominance (j) effects, while for main effects the dominance components (h) was greater than the additive (d) components. Opposite signs with (i) and (l) indicated duplicate gene action. This applied to all characters except seed weight per plant for the cross NGAE-96-0063 X CEN015. Additive gene effect was observed to be significantly lower and positive (5.67) relative to dominance effect (h) that was larger and equally significant but with negative value in the cross involving days to 50% flowering. In the same cross, significant i (-27.32) and l (37.97), disgenic epistatic term were observed. For seed weight per plant also, additive gene effect was observed to be significantly lower and positive (1.05) relative to dominance effect (h) that was larger (1.85) in the cross NGAE-96-0060 X NGAE-96-0062-2. In the same cross, only significant j (4.70) disgenic epistatic term was observed.

The estimates of the environmental variance, additive (D), dominance, (H) and direction of dominance (F), degree of dominance $(H/D)^{1/2}$, broad (Hb) and narrow sense (H) heritability are presented in Table 6. The adequacy of additive-dominance model was further tested by portioning the variations to show type of allelic and non-allelic relationship. Both the additive (D) and dominance (H) components were greater than zero and therefore found significant for all the characters studied. D was higher for all the traits except number of seeds per pod for the NGAE-96-0063 X CEN012 cross, matured plant height for the CEN001 X Ado-Ekiti-3 cross and seed weight per plant for the NGAE-96-0063 X CEN015 cross where H was greater than D. Positive direction of dominance (F), of individual gene interaction was recorded for number of pods per plant for the cross AGA97/066-5780 X NGAE-96-0062-2, number of seeds per pod for the cross Oja-Oba-3 X CEN009, matured plant height in cross CEN001 X Ado-Ekiti-3 and seed weight per plant for the cross NGAE-96-0060 X NGAE X NGAE-96-0062-2. It is also of note that the degree of dominance may not be unidirectional as revealed in the negative F ratios for number of days to flowering, number of pods per plant for the cross NGAE-96-04 X OAA96/175-5328, matured plant height for the cross NGAE-96-0066 X OAA96/175-5328 and seed weight per plant for NGAE-96-0063 X

Table 6: Estimates of environmental (E) and additive (D), dominance (H), direction of dominance (F), degree of dominance ($H/D^{1/2}$), broad and narrow sense heritability (Hb;Hn) for five characters in nine crosses of West African okra

	Parental combination	E	D	H	F	$H/D^{1/2}$	Hb	Hn
Days to 50% flowering	NGAE-96-012-2 (G2) XCEN001(G6)	9.31	34.63	-28.40	-3.07	-0.91	52.18	44.36
Number of pods per plant	AGA97/0665780(G10) X NGAE-96-0062-2(G14	16.77	18.32	12.41	3.22	0.82	42.23	15.78
	NGAE-96-04(G7) X OAA96/175-5328(G9)	18.35	17.23	1.58	-2.69	0.30	32.93	15.88
Number of seeds per pod	NGAE-96-0063(G19) X CEN012(G5)	26.36	70.57	-71.43	-3.99	-1.01	57.51	40.29
	Oja-Oba-3(G22) X CEN009(G13)	19.42	34.21	-14.13	5.24	-0.64	48.72	25.92
Matured plant height	NGAE-96-0066(G15) X OAA96/175-5328(G9)	17.72	41.90	-10.20	-3.67	-0.49	50.97	28.95
	CEN001(G6) X Ado-Ekiti-3(G24)	25.19	24.55	-28.06	6.35	-1.07	25.49	10.98
Seed weight per plant	NGAE-96-0060(G17) X NGAE-96-0062-2(G14	8.18	7.63	-1.50	0.59	-0.44	29.74	7.21
	NGAE-96-0063(G19) X CEN015(G8)	10.92	21.56	-22.38	-1.58	-1.02	46.17	33.46

CEN015. It therefore suggested dominance towards the smaller parents. Heritability in the narrow sense ranged from 7.21% for the cross NGAE-96-0060 X NGAE-96-0062-2 for seed weight per plant to 44.36% for days to flower.

DISCUSSION

The fact that the values obtained for the characters in all the crosses in the F_1 generations were higher than those in the two parents suggests heterosis. Heterosis may results from overdominance of gene pairs, from dispersion of the dominant increasing alleles in the parental lines, or from a combination of the two. Estimates of (h) and (l) show these two parameters to be of opposite sign for all the characters. This suggests that the predominant type of interaction in the system is of the duplicates, dominant epistatic, or recessive suppressor kind. Any of these kinds of gene action could produce heterosis if the genes were dispersed in the parental lines but no heterosis if the genes were associated. This shows that better progress from selection is expected in a future selection. The mean values of the F_2 for number of pods per plant for the AGA97/066-5780 X NGAE-96-0062-2 and NGAE-96-04 X OAA96/175-5328 crosses indicated transgressive segregation towards over dominance resulting in production of higher pod number from the progenies. The transgressive segregation contradict with the reports of Adeniji *et al.* (2007). The large variance of the F_2 populations for all the characters implied that the selection for these traits can be successful. All the three kinds of genetic effect (additive, dominance and epistasis) appeared to have played a role in the inheritance of West African okra plant traits in the nine crosses although the greater portion was additive. Similar results were also reported by Vicharat (1990) on *A. esculentus* and of Adeniji *et al.* (2007) on *A caillei*. Understanding the genetic determination of traits helps the breeder in formulating breeding techniques for combining desirable characters, dispersed in two or more genotypes into one (Singh and Chaudhary, 1996). According to Tefera *et al.* (1995),

comparison of varieties released from direct selection of germplasm and hybridization indicated that recombinant inbred varieties yielded 9% higher than the former.

According to Mather and Jinks (1982), opposite signs of additive x additive (i) and dominance x dominance (l) indicated prevalence of duplicate epistasis and complementary epistasis when the signs are the same. This is true for seed weight per plant for the NGAE-96-0063 X CEN015 cross. The complementary effect of these traits will produce new recombinants capable of improving yield. The duplicate nature of the gene action in the inheritance of days to flower, height at maturity, number of pods per plant, number of seeds per pod in all the crosses and seed weight per pod for the NGAE-96-0060 X NGAE-96-0062-2 cross would tend to hinder progress at increased level of manifestation. Similar result was also reported by Adeniji *et al.* (2007) on West African okra. Falconer and Mackay (1996) reported that in self- pollinated plant like West African okra, epistasis is more important than dominance which last for a short time with progressive selfing but non allelic interaction can generate different phenotypes some of which represent real genetic advance over their parents. However, Moreno-Gonzalez and Cubero (1993) reported that where epistasis is more important, recurrent selection and reciprocal recurrent selection have been recommended as efficient techniques for selecting desirable cultivar.

The components of genetic variation for all the characters in all the crosses except number of seeds per pod for the NGAE-96-0063 X CEN012 cross, matured plant height for the CEN001 X Ado-Ekiti-3 cross and seed weight per plant for the NGAE-96-0063 X CEN015 cross indicated the preponderance of the additive gene effect. This indicated that additive genes contributed more to the inheritance of these characters than other effects. Consequently, the segregating generation may be suitable for rapid improvement leading to the isolation of homozygous pure lines, after a period of selfing. Dominance was unidirectional negative decreasing alleles at all loci for all the characters except number of pods per plant where unidirectional positive increasing alleles were observed. According to Mehta *et al.* (2007) negative F values indicate gene interaction towards smaller parents. Therefore in breeding for earliness, increased pod number, seed number per pod, seed weight per plant with short plant, CEN 001, OAA96/175-5328, CEN012 and CEN015 could serve as a reliable parent stock. A partial dominance situation indicated that most of the phenotypes were intermediate between homozygous parents in the expression of pod number per plant for the cross NGAE-96-0063 X OAA96/175-5328 cross, seed number per pod for the Oja-Oba-3 X CENOO9 cross, matured plant height for the NGAE-96-066 X OAA96/175-5328 cross and seed weight per plant for the NGAE-96-0060 X NGAE-96-0062 cross. However, an approximately complete dominance situation showed that generations were closer to the dominant parents with early maturity and higher pod number. An overdominance situation observed for number of seeds per pod for the NGAE-9600063 X CEN012 cross, matured plant height for the CEN001 X Ado-Ekiti-3 cross and seed weight per plant for the NGAE-96-0063 X CEN015 cross showed that the phenotypic values of the heterozygotes is higher to either of the homozygous parents. Over dominant loci are not always stable during hybrid development. Therefore, the possibility of hybrid development for these characters may look theoretically feasible. Nevertheless, it is not economically feasible because of the huge cost and labour required during hybridization and more importantly West African okra is a selfer. The lowest additive genetic variation for seed weight per plant for the NGAE-96-0060 X NGAE-96-0062-2 cross; indicated environmental influence on the weight of West African okra seed. However, number of seeds per pod for the NGAE-96-0063 X CEN012 cross was under additive genetic control. Narrow sense heritability is important for breeding programs, because it estimates the relative importance of the additive portion of the genetic variance that can be transmitted to

the next generation. In previous study, Falconer and Mackay (1996) reported that the low narrow sense heritability might be caused by low additive effects and high dominance gene action. The ineffectiveness of direct selection in the early generation of these characters in development of inbred lines was manifest in the low narrow sense heritability estimates which ranged from 7.21% for seed weight per plant for the cross NGAE-96-0060 X NGAE-96-0062-2 to 44.3% for days to flower.

CONCLUSION

The generation mean analysis has brought out that individual crosses greatly differed for gene action and on the overall basis all the types of gene action, additive, dominant and epistasis were important. The additive gene effect for some traits would enhance pure line breeding. Days to flower, number of pods per plant, number of seeds per pod, matured plant height and seed weight per plant for the cross NGAE-96-0063 X CEN015 are controlled by duplicate epistasis gene action and therefore would ensure successful hybridization effort in a meaningful West African okra improvement programme. The presence of significant amount of all types of gene action, additive, dominance and epistasis are important for most of the traits has indicated that methods designed to utilize all of them such as recurrent selection and reciprocal recurrent selection has to be adopted in the breeding programme.

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REFERENCES

Adeniji, O.T., O.B. Kehinde, M.O. Ajala and M.A. Adebisi, 2007. Genetic studies on seed yield of West African okra (*Abelmoschus caillei* (*A. chev.*) stevels). J. Trop. Agric., 45: 36-41.

Azizi, F., A.M. Rezai and G. Saeidi, 2006. Generation mean analysis to estimate genetic parameters for different traits in two crosses of crom. J. Agric. Sci. Tech., 8: 153-169.

Cavalli, L.L., 1952. An Analysis of Linkage in Quantitative Genetics. In: Quantitative Inheritance, Rieve, C.R. and C.H. Waddington (Eds.). HSMO, London, pp: 135-144.

Falconer, D.S. and T.F.C. Mackay, 1996. Introduction to Quantitative Genetics. 4th Edn., Benjamin Cummings, England, ISBN-13: 9780582243026, Pages: 464.

Farshadfar, E., M. Aghaie, M. Sharifi and A. Yaghotipoor, 2008. Assessment of salt tolerance inheritance in barley via generation mean analysis. J. Biol. Sci., 8: 461-465.

Hayman, B.I., 1958. The separation of epistasis from additive and dominance variation in generation means. Heredity, 12: 371-390.

Jinks, J.L. and R.M. Jones, 1958. Estimation of the components of heterosis. Genetics, 43: 223-234.

Kearsy, M.J. and H.S. Pooni, 1996. The Genetic Analysis of Quantitative Traits. 1st Edn., Chapman and Hall, London, UK., pp: 46.

Mather, K. and J.L. Jinks, 1982. Biometrical Genetics. 3rd Edn., Chapman and Hall, London, Pages: 396.

Mather, K., 1949. Biometrical Genetics. Dover Press, New York, USA.

Mehta, N., B.S. Asati and S.R. Mamidwar, 2007. Heterosis and gene action in okra. Bangladesh J. Agric. Res., 32: 421-432.

Moreno-Gonzalez, J. and J.I. Cubero, 1993. Selection Methods. In: Plant Breeding: Principles and Prospects, Hayward, M.D., I. Romagosa and N.O. Bosemark (Eds.). Chapman and Hall, London, UK., ISBN-13: 9780412433900, pp: 281-313.

Olasantan, F.O. and N.J. Bello, 2004. Optimum sowing dates for okra (*Abelmoschus esculentus*) in monoculture and mixture with cassava (*Manihot esculenta*) during the raining season in the South-Western Nigeria. J. Agric. Sci. Cambridge, 142: 49-58.

Schippers, R.R., 2000. African Indigenous Vegetables: An Overview of the Cultivated Species. Natural Resources Institute/ACP-EU Technical Centre for Agricultural and Rural Cooperation, Chatham, United Kingdom, Pages: 214.

Sharma, S.N. and R.S. Sain, 2003. Genetic architecture of grain weight in durum wheat (*Triticum durum*) under normal and late sown environments. Wheat Inform. Serv., 96: 28-32.

Singh, S. and B.S. Chaudhary, 1996. Variability, heritability and genetic advance in cultivars of rice (*Oryza sativa*). Crop Res., 12: 165-167.

Tefera, H., M. Ayele and K. Assefa, 1995. Improved varieties of tef (*Eragrostis tef*) in Ethiopia. Releases of 1970-1995, Research Bulletin No 1, Debre Zeit Agricultural Research Center, Alemaya University of Agriculture, Debre Zeit, Ethiopia, pp: 32.

Vicharat, C., 1990. Genetic variation influence on plant characters and yield of okra (*Abelmoschus esculentus* (L) Moench). Kasetsart University, Bangkok, Thailand, pp: 58. ht://agrifao.org/agris-search/search/display.do?f=1996%2FTH%2FTH96012.xml%3BTH9520510.

Warner, J.N., 1952. A method of estimating heritability. Agron. J., 44: 427-430.

Wright, S., 1968. The Genetics of Quality Variability. In: Evolution, Genetics and Population: Genetics and Biometrics Foundation, Wright, S. (Ed.). Vol. 1. University of Chicago Press, Chicago, IL., USA., ISBN-13: 9780226910383, pp: 371-420.