Genetic studies on seed yield of West African okra [*Abelmoschus caillei* (A. Chev.) Stevels]

O.T. Adeniji[1]*, O.B. Kehinde[2], M.O. Ajala[2], and M.A. Adebisi[2]

[1]Department of Crop Science, Adamawa State University PMB 25 Mubi, Nigeria; [2]Department of Plant Breeding and Seed Technology, University of Agriculture, PMB 2240 Abeokuta, Nigeria.

Abstract

West African okra is an under-exploited vegetable crop with high pod and seed yield potentials. F_1 hybrids of eight accessions of West African okra were composited to produce F_2 seeds and backcross generations. Field evaluation of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) from five crosses was carried out in a randomized complete block design with three replications. The A, B, and C scaling tests were not significant for 100 seed weight, while significant A, B, or C scaling test for seed yield per plant was recorded. Additive gene effects [d] appeared to have contributed immensely to the inheritance of both characters. However, a non-significant interaction (i, j, l) for 100 seed weight corroborates with the results of individual A, B, and C scaling tests. A duplicate epitasis (Acc5 x Acc4) implied difficulty in evolving improved varieties. Estimates of genetic effects confirmed the preponderance of additive gene effects for 100 seed weight and seed yield per plant. High narrow sense heritability and genetic advance indicate the possibility of substantial improvement in seed yield.

Keywords: Seed weight, Genetic components, Heritability, Additive gene, Dominance.

Introduction

West African okra [*Abelmoschus caillei* (A. Chev) Stevels] is an important vegetable crop of the tropical and subtropical world. A short day plant generally with green stem (Ariyo, 1993) and having slight traces of red colour (pigmentation) in some accessions (Adeniji, 2003), it is cultivated for fresh pods, leaves, and seeds. West African Okra grows naturally in Nigeria, especially in the marginal lands along the roadsides, backyard farms, and wastelands. Dried okra seeds are used as substitutes or additives in feed compounding (Purseglove, 1974), in the preparation of okra seed meal and a number of baked products (Martin and Roberts, 1990), and in blood plasma replacement (Vickery and Vickery, 1979). Although the crop has a potential for industrial, nutritional, and biomedical purposes in the developed countries, it is under-utilized in the sub-Saharan Africa.

Varietal evaluation West African okra attempted earlier indicated a high degree of genetic diversity (Ariyo, 1993). In addition, additive genetic effects, high narrow sense heritability for length and width of pods, and seeds per ridge (Adeniji, 2003), besides high specific combining ability (SCA) for earliness (Adeniji and Kehinde, 2004) have been reported. However, genetic information on West African Okra and attempts on intraspecific hybridization are limited. Knowledge on the genetic system underlying the inheritance of seed yield is, nevertheless, fundamental. This paper provides genetic information on the inheritance pattern, genetic control, and heritability of seed yield and 100 seed weight, besides providing a framework for developing purelines and hybrids of West African okra.

Materials and Methods

Eight accessions of West African okra (Acc 1, 3, 4, 5, 7, 8, 9, and 10) showing variations in seed and pod yields were sourced from the Department of Plant

*Author for correspondence: Mobile (234)8059484626; Email<waleqed@yahoo.co.uk>.

Breeding and Seed Technology, University of Agriculture, Abeokuta. These accessions were maintained through selfing and evaluated during the planting seasons of 2002 and 2003, under rain-fed conditions. Abeokuta (7.38°N, 3,88°E, 450 m above sea level), where the present experiment was conducted, experiences a humid tropical climate. Mean annual rainfall ranges between 1340 to l850 mm and it follows a bimodal distribution pattern (March to October with a two week-long lean period in August); the main dry season is from October to March.

Two seeds per accession were sown in polythene pots (750 cm^2) filled with sterilized topsoil (15 pots per accession). At flowering, five crosses were made (Acc l x Acc4, Acc8 x Acc4, Acc9 x Acc10, Acc3 x Acc5, and Acc8 x Acc7). The parents and the F_1 seeds were planted in a screen-house and were allowed to self-pollinate to produce F_2 seeds. Subsequent flower buds were backcrossed to either parents to produce backcross generations 1 and 2 respectively. The field evaluation of the parents F_1, F_2, BC_1, and BC_2 was carried out in a randomized complete block design with three repli-cations. A single row (10 m) formed a plot; 1.5 m wide buffer strips separated the plots and 2 m wide alleys separated the replications. Two seeds were planted per hole made 0.60 m apart and later thinned to a single seedling per hole. The plots received NPK equivalent of 15:15:15 at 60 kg ha^{-1} 2 to 3 weeks after planting and at flowering.

Data collection and analysis

The data on seed yield and 100 seed weight were collected on individual plant basis from 64 stands each for parent 1, parent 2, and F_1, 128 stands for F_2, 238 stands for BC1 (backcross generation 1), and 128 stands for BC_2. For determining the weight of 100 seeds, 15 pods were randomly harvested at maturity from each plant (960 pods per parent). Harvested pods from each generation were decorticated before seed extraction. From each sample, 100 clean seeds were counted and weighed on a sensitive balance (Mettler PE, 2000). For determination of the seed yield per plant, pods harvested at maturity were decorticated and the seeds extracted

and weighed. Mean weight of 100 seeds and seeds yield per plant for each generation (P_1, P_2, F_1, F_2 BC_1, BC_2) were determined. Using the Generalized Linear Model (GLM) procedure of SAS (1997), analysis of variance was conducted to determine whether differences existed among the generations. Separate analysis for each population was also done for the two traits to determine the within plot variances. The plot means were subjected to individual scaling tests (A, B and C of Mather and Jinks, 1949), as given below:

$$A = 2BC_1 - P_1 - F_1$$
$$B = 2BC_2 - P_2 - F_2$$
$$C = 4F_2 - 2F_1 - P_1 - P_2$$

The generation mean analysis was performed by fitting the six-parameter model suggested by Mather and Jinks (1949):

$$m = 1/2P_1 + 1/2\ P_2 + 4F_2 - 2B_1 - 2B_2$$
$$[d] = ½\ P_1 - 1/2\ P_2$$
$$[h] = 6B_1 - 6B_2 - 8F_2 - F_1 - 1/2P_1 - 1/2\ P_2$$
$$[i] = 2B_1 + 2B_2 - 4F2$$
$$[j] = 2B_1 - 2B2 - P_2$$
$$[l] = P_1 + P_2 + 2F_2 + 4F_2 - 4B1 - 4B_2$$

Where *m* is the mid-point, *d* is the pooled additive genetic effect, *h* is the pooled dominance genetic effects, *i* is the additive x additive genetic effects, *j* is the additive x dominance genetic effects, and *l* is the dominance x dominance genetic effects. The environmental (E), additive (D), and dominance genetic (H) effects across loci were estimated according to Scheffe (1959) where:

$$E = 1/4V_{P1} + 1/4V_{P2} + 1/2\ V_{F1}$$
$$D = 4V_{F2} - 2(V_{BC1} + V_{BC2})$$
$$H = 4(V_{BC1} + V_{BC2} - V_{F1} - E)$$

The degree of dominance was estimated as H/D. Broad-sense and narrow-sense heritabilities were estimated based on the additive and dominance genetic effects (Warner ,1952), standard error of heritability in narrow-sense as per Ketata et al. (1976), and genetic advance following Allard (1960).

Results and Discussion

Mean square estimates (Table 1) showed that seed yield differences between the generations were significant ($p<0.01$). Variance estimates of the segregating generations were greater than that of F_1 and the parents (Table 2) implying that genetic diversity for seed yield and 100 seed weight was considerable. The A, B, and C scaling tests were not significantly different from zero for the 100 seed weight (Table 3). This indicates the possibility of explaining inheritance within the framework of additive and dominance scales. However, the generation means were free from linkage bias. Significance of the A, B, C tests for seed yield in the crosses evaluated suggests epistasis on the scale of measurement used. Since each test has its own expectation in terms of the magnitude of epistatic effects, there was no concordance among the A, B, and C tests.

Table 1. Means square for weight of hundred seeds and seed weight in six generations of West African Okra.

Source of variation	Df	Weight of 100 seeds	Seed weight
Generation	29	1. 18ns	5527.25**
Error	29	0.77	268.36

**= Significant at 1% level of probability.

A comparison of the generation mean analysis data in Table 4 indicates that estimates of the additive gene effects [d] were greater in magnitude than their corresponding dominance effects [h] for 100 seed weight and seed yield per plant. Therefore, additive genes are the most important factors contributing to the genetic control of these characters. This is consistent with the findings of Kulkarni et al. (1978) for pod yield in *Abelmoschus esculentus* and Adeniji (2003) for earliness in West African okra. Further, in situations where additive gene effects moderate the inheritance pattern, early selection among the segregating population could be worthwhile.

The dominant gene effects [h] were negative and non-significant for 100 seed weight. However, significant and non-significant, positive, and negative estimates of [h] were recorded for seed yield. Dominance in the direction of lesser parent is undesirable. A non-significant interaction component (*i, j, l*) for 100 seed weight (Acc9 x Acc10, Acc5 x Acc3, Acc4 x Acc5, Acc1 x Acc4) and seed yield (Acc9 x Acc10, Acc5 x Acc3, and Acc1 x Acc 4) indicated no evidence of non-allelic interaction, implying additivity in the inheritance of 100 seed weight and seed yield. This is consistent with the results of the individual scaling test A, B, and C.

Table 2. Means± within plot variance for 100 seed weight and seed yield in six generations of West African okra.

			Weight of 100 seeds (g)					
Acc 1	5.86±0.20	Acc8	4.57±0.15	Acc9	5.11±0.17	Acc3	5.43±0.17	Acc8	5.43±0.04
Acc4	4.03±0.11	Acc4	4.03±0.11	Acc 10	4.08±0.13	Acc5	5.13±0.17	Acc7	4.57±0.15
F_1	4.57±0.33	F_1	4.74±0.47	F_1	4.72±0.29	F_1	4.96±0.13	F_1	4.64±0.03
F_2	26.45±0.66	F_2	4.94±0.41	F_2	4.98±0.69	F_2	5.23±0.67	F_2	4.97±0.60
BC_1	5.01±0.99	BC_1	4.66±0.91	BC_1	4.86±0.55	BC_1	5.28±0.42	BC_1	4.68±0.37
BC_2	4.54±0.18	BC_2	4.63±0.81	BC_2	4.96±0.40	BC_2	4.51±0.57	BC_2	4.60±0.34
			Seed yield per plant (g)					
Acc3	168.01± 31.74	Acc8	145.07±14.70	Acc5	4.40±:4.90	Acc3	68.01±31.74	Acc8	134.02± 6.74
Acc4	126.07±:4.90	Acc4	135.41±16.90	Acc4	135.41±4.90	Acc4	26.07±29.36	Acc7	116.30±16.50
F_1	142.07±10.29	F_1	121.27±17.41	F_1	I61.86±23.91	F_1	142.07±25.08	F_1	132.07±20.20
F_2	162.01±32.33	F_2	152.72 ±29.947	F_2	228.00±40.21	F_2	162.01±26.01	F_2	138.21±36.21
BC_1	155.61 ±29.20	BC_1	130.00 ±10.16	BC_1	65.00±33.90	BC_1	155.61±13.00	BC_1	140.01±28.21
BC_2	152.61±:28.20	BC_2	128.13±19.33	BC_2	127.77±27.02	BC_2	152.61±13.00	BC_2	152.61±23.59

'Acc' refers to the accession numbers; F_1 and F_2= first and second filial generations, BC_1 and BC_2= back cross generations 1and 2.

Table 3. A, B, and C scaling test for 100 seed weight and seed yield in six generations of West African okra.

Weight of 100 seeds (g)				
Acc1 x Acc4	Acc 9 x Acc10	Acc5 x Acc4	Acc5 x Acc3	Acc8 x Acc7
A= 0.37±1.24ns	A=–0.45±l.85ns	A=–5.23±1.15ns	A=–0.32±:0.79ns	A=–0.32±0.79ns
B=–0.46±0.43ns	B=–0.05±1.23ns	B=–0.15±0.86ns	B=0.11±0.84ns	B= 0.11±0.84ns
C=1.36±2.73ns	C=0.84±5.72ns	C=0.34±2.83ns	C=1.82±2.90ns	C=0.99±2043ns
Seed yield per plant (g)				
A= 29.95±ll.48*	A=–24.48±:9.98*	A=–0.11±3.19ns	A= 26.06±l1.24*	A= 29.95±11.48*
B=38.67±2.24*	B=–12.14±10.51ns	B=–1.68±14.55*	B= 35.88±10.86*	B= 38.87±12.24*
C=38.23±26.40ns	C=53.23±26.56*	B= 90.33±24.20*	C=95.82±2.42ns	C= 38.20±26.40ns

'Acc' refers to the accession numbers; A, B and C are the individual scaling tests of Mather and Jinks (1949); *= Significant at 5% level of probability; ±= Standard deviation; ns= not significant.

The additive x dominance digenic interaction effects [*j*] were positive and negative for seed yield, indicating the presence of duplicate epistasis in the cross Acc5 x Acc4. The breeding implication is that difficulties might be encountered in the process of evolving varieties with improved seed yield. However, the other crosses used in this study could be desirable for improvement in seed yield. The magnitude of dominance x dominance digenic interaction effects [*l*] was relatively large for seed yield, although they were statistically significant and non-

significant in the crosses evaluated. Significant estimate of *I* (additive x additive interaction) suggest an enhancing effect in the inheritance of 100 seed weight. In addition, positive and significant *j* (additive x dominance interaction) in the cross Acc5 x Acc4 indicates the potential for enhancing seed yield in the subsequent generations.

Furthermore, the components of genetic variation (Table 5) indicate that the estimates of additive genetic effects across loci (D) were greater in magnitude than

Table 4. Gene effect using six-parameter model of the parents, F_1, F_2, BC_1, and BC_2 for weight of 100 seeds and seed weight in six generations of West African okra.

Weight of 100 seeds (g)					
Gene effects	Acc1x Acc4	Acc9 x Acc10	Acc5 xAcc4	Acc5xAcc3	Acc8xAcc7
M	6.50±3.02ns	6. 14±5.24ns	10.20±3.08ns	6.48±3.10*	6.13±2.88*
[d]	0.03± 0.11ns	0.23±0.10ns	0.04±0.10ns	0.16±0.09*	0.23±0.08*
[h]	–3.46±4.71ns	–3.24±11.05ns	–1.05±5.88ns	–3.17±5.98ns	–3.08±5.75ns
[i]	–1.44±2.45ns	–1.34±5.69ns	–0.32±3.08ns	–1.20±3.10n	11.32±2063*
[j]	–0.92±1.48ns	0.52±2.44ns	–0.40±1.57ns	–0.80±1.43ns	2.96±1.09ns
[I]	1.66±5.16ns	1. 84±7.46ns	0.38±4.05ns	1.18±4.05ns	1.65±3.70ns
Seed yield per plant (g)					
M	97.65±19.56ns	142.60±27.58*	413.00±30.21 *	167.92±4.96*	2.3 72±4.96*
[d]	8.75±2.88ns	4.13±3.03ns	7.13±4.86ns	7.97±2.92ns	0.23±0.08*
[h]	127.5±265.40ns	37.00±27.38ns	–565.22±47.29*	2.21±57.74ns	–119.93±57.49*
[i]	27.62±28.18ns	–1.86±27.38ns	–251.60±70.79*	–38.88±24.65ns	3.83±13.70ns
[j]	–5.93±28.10ns	–4.61±18.51ns	61.75±8.39*	61.13±14.79ns	3.83±13.70ns
[I]	–99.84±39.00ns	–35.81±39.05ns	313.91±42.54*	–30.92±39.97ns	129.56±34.22*

'Acc' refers to the accession numbers; *significant at 5% level of probability; ns= not significant; M = generation mean; [d] = additive genetic effect; [h] = dominance genetic effects; [i[additive x additive genetic interaction effect; [j] = additive x dominance interaction effects; [I] = dominance x dominance interaction effects.

the dominant genetic effects (H) and environmental variation (E) for 100 seed weight (Acc1 x Acc4, Acc8 x Acc4, Acc4 x Acc5, Acc8 x Acc7 Acc5 x Acc3) and seed yield (Acc8 x Acc4, Acc5 x Acc3, Acc8 x Acc7). A partial dominance situation (H/D< 0.70) and approximately complete dominance situation *(*H/D = 0.7 to 1.0) moderate the inheritance of 100 seed weight and seed yield. A partial dominance situation (Acc8 x Acc 4, Acc 4 x Acc5. Acc 5 x Acc3, Acc8 x Acc7) and seed yield (Acc8 x Acc7) also explain that 100 seed weight as well as seed yield were intermediate between the parents.

However, an approximately complete dominance situation for 100 seed weight (Accl x Acc4), and an over-dominance loci (Acc8 x Acc7) were observed. This explains the possibility of developing purelines and hybrids for seed yield in West African okra. The floral biology of West African okra could limit this task; hence, a greater manipulation of hybridization is required. The estimates of dominance ratio (Acc8 x Acc4, Acc5 x Acc4, Acc5 x Acc3) for seed yield were invalidated by a negative estimate of H. A negative estimate of dominance might be due to epistasic gene action in the cross

combinations. Apparently, broad-sense heritability estimates were greater in magnitude than narrow-sense heritability for both 100 seed weight and seed yield.

The estimates of narrow-sense heritability ranged between 0.51 and 0.79 for 100 seed weight and between 0.29 and 0.60 for seed yield per plant. Sood et al. (1993) also reported high estimates of heritability for 100 seed weight in *A. esculentus*. A high estimate of narrow-sense heritability and genetic advance in all the crosses for 100 seed weight and two crosses for seed weight shows that a large proportion of phenotypic variability for these character was additive. This in turn suggests that early generation selection is worthwhile for genetic improvement. A moderate heritability estimate (Acc4 x Acc5, Acc8 x Acc7) for seed yield may be attributed to the large environmental variations in F_2 population.

Overall, the study indicated that genetic diversity exists among the generations evaluated. The additive genetic effects moderate the inheritance of 100 seed weight, while non-additivity (dominance and epistasis) was an important inheritance mechanism for seed yield. The high additive genetic effects observed translate into high

Table 5. Components of genetic variation for 100 seed weight and seed yield in West African Okra.

Source of variation	Weight of 100 seeds (g)				
	Acc 1 x Acc4	Acc8 x Acc4	Acc4 x Acc5	Acc5 x Acc3	Acc8 x Acc7
E	0.27	0.30	0.21	0.27	0.15
D	0.60	2020	.0.85	0.78	0.88
H	0.36	0.04	0.20	0.12	0.04
H/D	0.77	0.13	0.49	0.39	0.21
Hb	0.51	.079	0.70	0.61	0.75
Hn	0.59	0.78	0.62	0.57	0.75
GA	0.65	1.92	1.06	0.97	1.17
	Seed yield per plant (g)				
E	14.30	14.09	0.21	21.11	18.76
D	13.38	38.90	26.26	32.00	45.74
H	49.12	-18.28	34.48	-36.44	-18.56
H/D	1.82	-	-	-	0.41
Hb	0.61	0.29	0.69	0.57	.054
Hn	0.21	0.67	0.49	0.57	0.49
GA	20.45	7.34	6.32	5.21	6.09

'Acc' refers to the accession numbers; E= Environmental variation. D= Additive genetic effects, H= Dominance effects H/D Dominance ratio Hb = Broad sense heritability, Hn = Narrow sense heritability, GA= Genetic advance.

narrow-sense heritability for 100 seed weight. A high narrow-sense heritability and genetic advance provide the possibility of evolving improved purelines and hybrids will be rapid.

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