

Heritability and Genes Governing Number of Seeds per Pod in West African Okra *Abelmoschus caillei* (A. Chev.) Stevels.

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Abstract

Heritability and genetic action moderating the inheritance of number of seeds per pod was investigated in four crosses of West African Okra accessions. Parents with variation for number of seeds per pod were used in hybridization process. Generations developed (Parents, F₁, F₂, BC₁ and BC₂) were planted for evaluation in a randomized complete block design with four replications. The results showed the adequacy of the additive – dominance model for one out of the four crosses (Acc6 x Acc1) and the inadequacy of the model for the remaining crosses. This was ascribed to significant estimates of A, B and C scaling test. The results of the generation mean analysis indicated that the additive genetic effect (d) significantly accounted for a large proportion of variability observed for number of seeds per pod in the crosses evaluated. The narrow sense heritability estimates were moderately high in all the crosses. An additive genetic effect suggests that selection among the segregating population could provide an average improvement in the performance of seed yield in subsequent generations.

Keywords: West African Okra, Additive gene action, Generation means, Seed yield, Heritability, Genetic components.

1. Introduction

West African Okra belongs to the family Malvaceae. It is photoperiod sensitive (short day) and cultivated primarily for its fresh pods and leaves. Nutritionally, okra pods contain 88ml water, 2.1g protein, 0.2g fat, 8g carbohydrate and 332.72mg vitamins in 100g of edible portion (Berry *et al.*, 1988). Genetic studies in West African Okra are limited. Ariyo (1993) reported the existence of genetic diversity in West African Okra accessions. Studies conducted by Adeniji and Kehinde (2003) and Adewusi (2011) indicated that west African okra are either pigmented or non –pigmented ; pubescent or glabrous and arranged in vertical or horizontal direction.

Heritability of metric characters has been identified as a genetic relationship between the parents and the offspring. These genetic components have been widely used to assess the degree to which a character is transmitted from parent to the offspring. Information on heritability could as well indicate the possibility and extent to which improvement in a character is possible. More often in biological research, broad and narrow sense heritabilities are used to evaluate the proportion of heredity and environment in the expression of a character. In West African Okra, high narrow sense heritability has been reported for pod length, pod width, plant height and number of seeds per pod (Adeniji, 2003). West African Okra Pods are consumed fresh (a maximum of 7 days after anthesis) obviously a high number of pods per plant is a desirable horticultural characteristic for genetic improvement in West African Okra. This present study was carried out to evaluate the mode of inheritance and genetic control of number of seeds per pod and heritability estimates for number of seeds per pod in West African Okra.

2. Materials and Methods

2.1 Experimental materials, location and design

Six accessions of West African okra (Acc1, Acc6, Acc8, Acc5, Acc11 and Acc12) were sourced from the germplasm collection of the National Centre for Genetic Resources and Biotechnology (NACGRAB), Moor plantation, Ibadan. Two to three seeds of each accession were planted in polythene pots filled with sterilized soil. Five pots were allotted to each of the parentals. Single crosses without reciprocals were carried out among the accessions to produce the F₁ generation seeds. Mature flower buds which are likely to open the next day were selected for emasculation because the stigma of *Abelmoschus caillei* remains receptive on the day of anthesis. Flower buds for emasculation were held gently to avoid stress on the fragile attachment of the buds. A slight ring was made at the base of the flower bud with a blade for easy removal of the petals and calyx sheath to expose the stamina tubes and the stigma. The pollens were then dusted on the stigma. F₁ seeds were planted in pots and each F₁ plant was allowed to self pollinate to produce F₂ seeds. Subsequent flower buds were back crossed to the parents. Field evaluation of the parentals, F₁, F₂, BC₁ and BC₂ were carried out in 2007 at the Farm Centre of the Federal Polytechnic Ilaro, Ilaro, Ogun State, Nigeria.

The experimental layout was a randomized complete block design with four replications. A single row plot of 10metres long with an inter row spacing of 1metre was adopted. The number of rows for each replication was one for each of the Parents and the backcrosses, two for the F_1 s and four for the F_2 s. Two to three seeds of each generation were planted per hole, with an intra row spacing of 0.60 metre and later thinned to one plant per stand. The plots received equal dosage of Fertilizer (NPK 15:15:15) at the rate of 60kg/ha, 3 weeks after planting and at flowering.

2.2. Data collection and analysis

Number of seeds per pod was recorded using 24 stands for each parent and backcross generation, 48 stands for each F_1 generation and 96 stands for each F_2 generation. Number of seeds per pod was determined by counting the number of seeds of four randomly selected pods per plant.

The individual scaling tests of Mather (1949) were employed to test their fitness to the additive-dominance model. The generation mean analysis was calculated using the method of Mather and Jinks (1971) where m is the mid-point, d is the additive genetic effects, h is the 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. P_1 is the parent with a high mean value while P_2 is the parent with a lower mean value. BC_1 and BC_2 are corresponding backcrosses to parent 1 and 2 respectively. The significant tests for the various genetic effects for this model were determined by computing the standard error (SE) from the variance of each corresponding population mean.

The variance components E , D and H representing the additive variance, dominance variance and environmental variance were calculated as specified by Scheffe (1959). Broad sense and narrow sense heritability estimates were estimated as specified by Warner (1952).

3. Results and discussions

Table 1 shows the estimate of generation means and within plot variance for seed yield in the crosses of West African Okra. Under additive gene action, the F_1 mean is expected to be midway between the means of their parental combinations (Mather and Jinks, 1971). This observation is true for the cross Acc8 x Acc5. However, the F_1 means for other crosses tend towards the parent with a lower number of seeds per pod. This could imply a dominance of a low number of seeds per pod in this cross (Acc8 X Acc5). The F_1 mean for the number of seeds per pod was less than the mid parent in all the crosses evaluated.

The F_2 means were intermediate between the better parent value and the mid-parent value. The high variance estimates recorded for the F_2 generation revealed that a substantial estimate of the genetic variability for number of seeds does exist among the segregating F_2 generations. Thus providing a framework to advance selection for genetic improvement in seed yield.

Table 2 shows the individual scaling test for number of seed per pod in four crosses of West African Okra. The mean values of number of seeds per pod subjected to the individual scaling test of Mather (1949) showed that the A, B and C scaling test for cross Acc6 x Acc1 were not significantly different from zero indicating the adequacy of the additive dominance model in explaining the inheritance pattern for number of seeds per pod while in the other three crosses, a significant estimates of the A, B or C scaling tests entities recorded suggest the presence of epistasis on the scale of measurement used and the inadequacy of the additive- dominance model. It further indicates that the mean value for number of seeds per pod is not free from linkage bias.

Table 3 shows the estimates of genetic effect using Six parameter model of the Parents, F_1 , F_2 , BC_1 and BC_2 for seed yield in crosses of West African Okra. The Six Parameter model (Mather and jinks 1971) for seed yield indicated that the estimates of the additive gene effect (d) were significant for all the crosses evaluated.

This foregoing genetic information implies that the additive gene action form a high proportion of the mean effects and also the most important factor contributing to the genetic control of this character. The breeding implication of this is that early selection among the segregating population could be worthwhile. Adeniji and Kehinde (2003) noted the preponderance of additive gene action in the inheritance of pod length and width, seeds per pod and seeds per ridge. A significant estimate of the dominant gene effect (h) was also recorded in two crosses (Acc6 x Acc12 and Acc11 x Acc12); with the estimate recorded for Acc11 x Acc12 indicating that dominance was in the direction of the lesser parent. A significant interaction component (i,j,l) was recorded in Acc11 x Acc12 implying that all the three epistatic terms were important in the expression of seed yield in this cross. The additive x dominance digenic interaction were negative in all the crosses evaluated and significant for three crosses implying the potential for depression in seed yield. A duplicate type of epistasis was recorded in Acc6 x Acc12; Acc8 x Acc5 and Acc11 x Acc12 indicating the complex nature of inheritance of seed yield. It also indicated that difficulties might be encountered in the process of evolving and developing varieties with improved seed yield. However, the other crosses used in this study could be desirable for improvement in seed yield. A non- significant interaction component (i,j,l) for seed yield in cross Acc6 x Acc1 indicated no evidence of non-allelic gene interaction implying additivity in the inheritance of this trait and the adequacy of additive –

dominance model which is consistent with the results of the individual Scaling tests A,B and C.

The result of the component analysis for number of seed per pod (Table 4) showed that the estimates of the additive gene effect (D) were greater in magnitude as compared with the dominant gene effect (H) and environmental variation(E) across loci in all the crosses evaluated. This suggests the preponderance of the additive gene effects in the inheritance of this trait. In addition, the presence of dominance was indicated by the estimated value of $\sqrt{H/D}$ which was between 0.29 and 0.64, suggesting partial dominance loci in the inheritance of number of seeds per pod in the crosses. This indicates the possibility of developing hybrid varieties for seed yield in West African Okra.

Broad sense heritability estimates were never below 86% but the narrow sense heritability estimates ranged between 70 and 90%. A high estimate of broad and narrow sense heritabilities for number of seeds per pod indicated that selection in the early generations for this character will be highly effective in developing a breeding strategy and a good genetic base for seed improvement in *Abelmoschus caillei*. High estimates of broad and narrow sense heritabilities for number of seeds per pod observed in this study corroborates the findings of Adeniji and Kehinde (2003) in *Abelmoschus caillei*. A high estimate of narrow sense heritability recorded in all the crosses shows that a large proportion of phenotypic variability for this character was additive. This in turn suggests that early generation selection is worthwhile for genetic improvement. High estimates of broad and narrow sense heritabilities for number of seeds per pod observed in this study corroborates the findings of Martin et al.,(1981) in *Abelmoschus esculentus* (L) Moench. High estimates of narrow sense heritability shows that selection in the F₂ generation would lead to a substantial genetic improvement in seed yield. Hence, the prospect of formulating a breeding strategy for seed improvement

4. Conclusion

The study indicated that additive genetic effect governed the inheritance of number of seed per pod in West African Okra. The presence of a higher estimate of additive gene effect for number of seeds per pod in this study may result in an estimation of the actual number of segregating genes. Broad sense heritability estimates were greater than the narrow sense heritability for this trait. The high narrow sense heritability recorded in this study provide the possibility of developing a breeding plan and a good genetic base as well as evolving improved pure lines and hybrids in West African Okra. The cross Acc 11 xAcc12 amongst others, may be ideal for future hybridization and genetic improvement in *Abelmoschus caillei* for number of seeds per pod.

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Table 1: Estimates of generation means and within plot variance for number of seeds per pod in four crosses of West African Okra.

ACC ₆ 67.59 ± 7.42	ACC ₆ 48.28 ± 10.38	ACC ₈ 53.29 ± 5.69	ACC ₁₁ 45.42 ± 0.00
ACC ₁₂ 52.83 ± 11.65	ACC ₁ 29.71 ± 7.08	ACC ₅ 38.62 ± 9.20	ACC ₁₂ 35.78 ± 0.86
F ₁ 53.35 ± 4.29	F ₁ 35.50 ± 27.00	F ₁ 38.34 ± 10.92	F ₁ 43.15 ± 6.89
F ₂ 60.46 ± 27.57	F ₂ 40.02 ± 53.33	F ₂ 38.58 ± 64.37	F ₂ 37.98 ± 32.65
BC ₁ 66.47 ± 5.08	BC ₁ 40.51 ± 4.78	BC ₁ 44.04 ± 48.04	BC ₁ 20.58 ± 0.00
BC ₂ 65.63 ± 10.89	BC ₂ 34.55 ± 21.12	BC ₂ 48.22 ± 5.30	BC ₂ 4.06 ± 12.76
MP 60.21	MP 38.99	MP 45.96	MP 40.60

MP =Mid – parent

Table 2: A, B and C Scaling test for number of seeds per pod in four crosses of West African Okra.

Acc6 x Acc12	Acc6 x Acc1	Acc 8xAcc5	Acc11 x Acc12
A=12.00±3.019**	A= -2.76±3.756	A=-3.55±7.232	A= -49.68±1.056**
B=25.08±3.718**	B= 3.89±5.449	B=19.48±3.237**	B= 3.19± 3.840
C=1 4.72± 10.944	C= 11.09±19.081	C=14.275± 16.377	C= -15.58± 11.745

** Significance (P<0.01)

Table 3: The estimates of genetic effects using Six Parameter model of the Parents, F₁, F₂, BC₁ and BC₂ for seed yield in crosses of West African Okra.

Acc6 x Acc12	Acc6 x Acc1	Acc8 x Acc5	Acc11 x Acc12
m 37.85±11.301	49.035±18.966	15.746±17.546	69.24±11.989
d 7.38±1.092**	9.285±1.044**	7.335±0.985**	4.820±0.230**
h74.94±24.464**	22.285±39.756	68.715±38.811	-98.95±25.319**
i 22.36±11.255	9.96±18.937	30.208±17.519	-28.64±11.987*
j 13.08±4.558**	-6.65±5.502	23.03±7.572**	-50.6±3.609**
l 59.44±13.556**	8.83±21.627	46.141±21.953**	72.86±13.756**

Table 4: Components of genetic variation for number of seeds per pod in four crosses of West African Okra.

Genetic component	Acc6 x Acc12	Acc6xAcc1	Acc8xAcc5	Acc 11 x Acc 12
E	6.913	17.865	9.338	3.660
D	78.340	161.520	150.800	105.080
H	19.068	67.060	33.082	8.840
√H/D	0.493	0.644	0.468	0.290
H _B	0.864	0.872	0.900	0.937
H _N	0.770	0.700	0.811	0.900

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