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GENETIC VARIABILITY AND HERITABILITY OF SEED YIELD COMPONENTS IN WEST AFRICAN OKRA *(ABELMOSCHUSCAILLEI [A.* CHEV] STEVELS)

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ABSTRACT

Components of genetic variation, heritability and genetic advance were evaluated in seven accessions of West Africa Okra. *(Abelmoschus caillei [A.* Chev] Stevels). Crosses among these accessions were carried out to produce F, F2 BC, and BC2. Field experiment was laid out in a randomized complete block design with two replications. Data were collected on seed yield components. The results indicated that the additive gene predominates the inheritance of these characters. Dominant gene effects were low in magnitude, unidirectional positive increasing alleles (hundred seed weight, pod length and, seeds per pod) and ambidirectional (positive increasing and negative decreasing alleles) for ridges per pod, seeds per ridge pod width and seed weight. Partial dominance, approximately complete dominance and over-dominance situation moderate the inheritance of these characters. A high additive gene estimates, narrow sense heritability and genetic advance indicated that selection in the early generations for these characters could be effective. Possibilities of developing pure lines and hybrids were found in the crosses for pod and seed yield

Keywords: West African Okra, heritability, dominance, variability

INTRODUCTION

West African Okra *(Abelmoschus caillei* [A. Chev] Stevels) is an important vegetable crop of the tropical and subtropical regions of the world. The importance of this crop lies in its mucilaginous property, which makes easy the consumption of bulky food. It is an important source of carbohydrate, protein, vitamins and minerals to the diet. West African Okra grows naturally in this environment. It is cultivated in backyard farms, along roads and on wasteland in mixed cropping. Sole production is common during the dry season. *A caillei is* essentially photoperiod sensitive, annual and relatively tolerant of insect pests and diseases. As a result of its high yield and hardiness it has become the major source of okra pods in Nigeria and its cultivation is progressively replacing the *A. esculentus [L.]* Moench (Ariyo,1993). In selfpollinated crops as West African Okra, the germplasm often exist in the form of homozygotes genotypes. However, for genetic improvement diverse genotypes are needed. This could serve as a parent stock for development of improved genotypes. Heritability specifies the proportion of the total variability that is due to genetic causes and thus a valuable tool used in conjunction with other parameters in predicting the magnitude of genetic gain that follow selection. Ariyo (1993) reported the existence of genetic variability among accessions of West African Okra. The magnitude of additive gene action relative to other gene action is particularly useful in developing pure-line varieties. Whereas, information concerning dominance and epistatic gene effects can be valuable for developing hybrid varieties. Studies on component of genetic variation, heritability and genetic advance for quantitative characters in *A. esculentus* have been reported. Additive gene action has been reported for mature pod length, width,

seeds per pod and ridges per pod (Rao, 1972; Rao and Ramu 1977; Sharma and Randhawa (1976). A high heritability estimates and genetic advance have been reported for fruit diameter and length (Malik, 1968), plant height, days to flowering (Rao 1972) in *A. esculentus.*

Genes for high yielding, hardiness and disease resistance abound in *A. caillei* intraspecific hybridization, in this species is limited as compared with *A. esculentus.* This study was initiated to estimate

1. The components of genetic variation
2. To provide heritability estimates

MATERIALS AND METHODS

Six Abelmoschus caillei accessions (P_3, P_5, P_4, P7, P_8, P,) obtained from the germplasm collection of the University of Agriculture, Abeokuta were utilized for this study. Two seeds of each accession were planted in polythene pots (25 cm length x 30 cm width) filled with sterilized soil. Five pots were allocated to each parent. Crosses among the accessions were made in the screen house in October 2000. The following crosses were made P3 x P5, P4 x P5, P7 x P8, P4 x P5, P1 x P4, F, seeds were planted in polythene pots filled with sterilized soil to produce F_2 seeds, subsequent flower buds were back crossed to produce the first backcross and second backcross generations. Parents F_1, F_2, Be, and Bc_2 from each of the five crosses were planted at the fadama, lowland ecology of the Teaching and Research farm, University of Agriculture Abeokuta (Lat 7.33°N, 2.88e 450 m asl) in October 2001. The experimental layout was a randomized complete block design with two replications. A single row of 10 meters long with inter-row spacing of 1 meter was adopted for this study. The number of rows per replication was three for each non-segregating generation, four for each backcross and F_2 generations. Two to three seeds were planted per hole with an intrarow spacing of 0.60m. A compound fertilizer N P K 15:15:15 was applied at the rate of 60 kg / hectare in two doses, first at three weeks after planting and secondly at flowering. Data were collected on individual plant basis on 96 stands for each back cross generation and 128 stands for each F_2 generation. But for the nonsegregating generations, data were consistently collected from six healthy plants in a row. The following quantitative parameters were measured; number of ridges per pod, number of seeds per pod, hundred seed weight, mature pod length, mature pod width seeds per ridge and seed weight. The pod length was measured on the longest point, while pod width as measured on the widest on the pod in centimeters. Data collected were subjected to analysis of variance ANOVA as outlined by Snedecor (1956). Six generations (P1, P2, F_1, F_2,, BC,, BC',) were analysed for variance components, E, D, H representing the environmental, additive and dominant genetic variance respectively were estimated as follows:

$$E = 1/4VP1 + 1/4VP2 + 1/2VF1$$

$$D = 4VF_2 - 2(VBC1 + VBC_2)\ H = 4(VBC1 + VBC_2 - VF_2 - E)$$

Where VP,, VP_2, V1',, VF_2, VBC_1, VBC_2 are the variances of the parents, F 1, F2 and back cross generations. Approximate variations of these variances were estimated according to the method of Schrffr (1959) The degree of dominance was estimated as /H/D.

Heritability in narrow sense was estimated following Warner (1952) method as' $h^{e}ns = [2VF_2 - (VB1 - VB_2)] / VF_2 \times 100$.

Heritability in broad sense was calculated following Mahmud and Krammer (1952) method as $VF_2 - VP, \times VP_2 / VF_2 \times 100$

RESULTS

Means and variances

The variance estimates for the pod length and pod width, ridges per pod, seeds per ridge, hundred seed weight and seed weight in the segregating generations (F_2, BC,, BC-,) were greater than the variance estimates of the non - segregating generations (P 1, P2, F,) (Table 1). This was also true for weight of hundred seeds showing that genetic variability does exist among the generation means.

The generation means (Table 2) differed significantly ($P < 0.01$) for number of ridges per pod, mature pod length and mature pod width, seeds per pod, seeds per ridge and seed weight. The non -significant difference was observed for hundred seed weight.

Genetic variability and heritabilities

Components of genetic variation, heritabilities and genetic advance for number of ridges, per pod mature pod length and mature pod width, seeds per pod, seeds per ridges, seed weight, number of seeds per pod, weight of hundred seeds are presented in Table 3. The additive gene estimates for number of ridges per pod were greater than the dominant gene estimates and environmental variation. The contribution of additive gene effects to the
total variability was maximum (80%) in P4 x P5, while the contribution of the dominant gene effects was maximum (17%) in P 1 x P4. The negative estimates of dominant gene, made impossible the estimation of dominance ratio in the cross P4 x P5. Dominance ratio range between 0.31 (P4 x P8) and 0.86 (P1 x P4). Genetic advance was maximum (2.33) in P4 x P8. The study revealed that the estimates of the additive gene effects for number of seeds per ridge, were higher than both the estimate of environmental variation and dominant gene effects except in P3 x P5. The additive gene effects accounted for between 31% and 54% of variability observed for this character. Dominant gene effects for number of seeds per ridge were low in magnitude and positive (P3 x P5, P4 x P5, P4xP8 and P1,04). The dominant gene effects contributed between 2% (P3 x P5) and 15% (PI x P4) of variability observed for this character. Dominance ratio range between 0.43 and 0.89, while its estimate in P7 x P8 was made impossible by the negative estimates of the dominant gene effects (H). Narrow sense heritability estimate for this character was maximum (51%) in P4 x P5, while genetic advance was maximum (1.34) in P7 x P8 and minimum in P7 x P8.

Components of genetic variation for number of seeds per pod indicated that the estimates of environmental variation and dominant gene effects were lower than the additive gene effects in most crosses studied. Dominant gene effects for this character were positive in direction. The dominance ratios range between 0.20 (PI x P4) and 0.82 (P3 x P5). The narrow sense heritability relatively close variation, this ranged between 47% (P4 x P8) and 69% (P7 x P8). Genetic advance was maximum (5.41) in P7xP8.

Table 1. Means + variance estimates for 7 characters computed for six generations from five crosses of West African Okra

Generation	Mean	variance	Mean	variance	Mean	variance	Mean	variance	Mean	variance	Mean	variance	Mean	variance
P8	9.07	a12	1175	1 H3	9112	612	157	015	083	006	9.28	1 0.21	146.01	16.50
P7	**718**	017	910	0.72	84.40	6.76	5.04	0.07	8.47	0.12	11.10	0.14	134.30	
F2	7.91	1.34	10.35	1.621	85.40	2040	4.97		6.0	1.86		2.07	138, ~F	AF
	716	1.11	10.13			1541	4.60	039	10.90	1.28	10.6	1.08	**1022**	2
	7.92		9.77	0 4.9	51.42	1122	1 168	037	717	1.09	7.86	1.93	14~.2i	21.36
P8	9.07	0.12	10.75		91,12	6.72	4.57		12.83	006	L.28	0.21	14611	1600
Fl	1 7.79	0.42	914	0.83	4.00	18.58	1.78	0.47	914	0.32		0.60	13227	1 Tl 8
F2	W75		'.72	1			4.98	1.41	11.10	.11		072	1027	**08192**
			10.43	1.07		119	4.66					131	12817	19.16
P5	ibig	1.30	10.40	1.07		2.01	5.11	0.14	11.04	015		0.22	136.07	4.90
	7.66	0.85	50	118	ION	FTOO	4.~8----------	DA3	9089--019		918	tZ	02.67	208
F2	9.80	1.48	10.40	1.34	51.73	1 12.45	5.05	04	90	0.98	12.66	0.45	162.01	28.00
1	806	133	113D	1 12	1.3					008	1216	0.4	15407	1860
	9.5	1.16	9.96	1.05	076			0.57	9.61	0.34 _ 9,82		1.34	152.01	22.00
	*19	130	1a4O	1107	8944 j	2.01	1	0.14	11.04	0.15	12.32	A	14567	i
						2.10		Oil	.20	0.09	7.91	0.21	146.40	4.90 1
Fl			9.94	092		7.40	4.72	0.29	9.75					
42	7.41	1.31	9.78	1.59	77.53	1 14.85	4.96	0.69	9.46	1.01	10.45	1.30	152.72	32.32
Bl		1.11	9.08	1.19	9639	1 10.04	4.80	0.55	926	015	12.04	117	23	1
B2	7.28		9.40	1.29	5018	11.75	4.96	0.40	917	too	1025	110	151.23	2920
Pi	7.13	0.29	9.41	0.81	53.18	57	1 5.08	020	991	0.15	10-52	0.50		4110
P4	7.05	K3	922	013	62.30		5.03	0.11	9.20	0.09	7.91	a2l	14HO	
Fl	933	017	813	HiS	5615	7.90	4:57	~FT-	778	017	822	117	16116	2301
F2	a89	1.22	1110	117	50.80	15.00	515	0.66	915	157	7.89	1.34	209LO	4033
B 1	30	1 0.87	.56		52399	11.19	4.57	0.43	8.19	0. 56	t~T4	0.91	127.00	33.93

Mpl = Mature pod length; Mpw = mature pod width; Rpp = ridges per Pod; Spp = seeds per pod; Spr = seeds per ridge; wt.

100 seed. = 100seed weight; 3xx~seed weight.

Table 2. Analysis variance for 7 characters of six generation derived from crosses of West African Okra, A *caillei* [A.Chev] Stevels. The values are mean square.

Sources of Variation	DF	MPL	MPW	RPP	SPR	SPP	100WT	SDW
Generations	29	5.10	4.03*	2.28**	2.47**	557.13	1.18	5527.95
Error	_, 29	0.08	1 1.58	#0.54	0.76	17.96	7	268.58

* ** = 1%, 5% level of probability
MpI = Mature pod length; Mpw = mature pod width; Rpp = ridges per Pod; Spp = seeds per pod; Spr = seeds per ridge; 100wt. = 100 seed weight; Sdw = seed weight

The estimates of additive gene effects for seed weight were greater than the estimates of environmental variation and dominant gene effects. Estimates of dominant gene effects were high, positive (PI x P4, P7 x P8) and negative (P3 x P5, P4 x P5, P4 x P8). The additive gene effects accounted for between 21% (P 1 x P4) and 68% (P4 x P8) while the dominant gene effects contributed between -0.30% (P3 x P5) and 35% (P1 x P4). The narrow sense heritability estimates presented a very large variation; this ranges between 21% (P1 x P4) and 67% (P4 x P8).

Genetic variability observed for hundred seeds weight showed that the additive gene effects were greater than both the environmental variation and dominant gene effects. Additive gene effects was maximum (2.22) in P4 x P8. The additive gene contribution to variability observed for this character was maximum 78% (P4 x P8). While dominant gene effects contribution was maximum (14%) in P 1 x P4. Dominant estimates were positive and low in magnitude for all the crosses studied; the dominance ratio was less than 1.0 in all the crosses evaluated. The cross (P4 x P8) recorded the maximum broad sense heritability (90%) estimate. Narrow sense heritability was maximum (79%) in P4 x P8, while genetic advance was maximum (1.92) in P4 x P8. The estimates of the additive gene effects were positive and greater than the estimates of the dominant gene effects and environmental variation for mature pod length and width. The contribution of the additive gene effects to variation observed for pod length and width was maximum (67% in P3 x P5, and 74% in P8 x P7 respectively. The estimates of dominant gene effects were positive for pod length, positive and negative for pod width. The contribution of the dominant gene effects to the variability observed for pod width, was 61% in P7 x P8 and 20% for pod length. The dominance ratio range between 0.37 and 0.83 for pod length and 0.47 and 1.18 for pod width. Similarly, narrow sense heritability was maximum (75%) pod length and 73% for pod width in P1xP

DISCUSSION

Significant difference ($P<0.05$) observed for most characters (Table 2) showed the magnitude of variability among generations evaluated. This agrees with the findings of Ariyo (1993), in *Abelmoschus esculentus*. The failure to detect significant difference among the generations for hundred seed weight could be attributed to a nearly equal parental means

Table 3. Components of genetic variation for seven characters computed for six generations from five crosses of West African Okra

Crosses				~H/D Hb			
Number of ridges per pod							
I P3 x P5							
P4 x P5	0.85	0 94± 0.74		0.88 ®		32	0.80
P7 x P8	0.74	0.98± 0.79		72		37	0.89
P4 x P8	0.38	1.54± 0.98	-0.32± 0.57	0.74	89	57	1.35
P 1 x P4	0.32	3.20± 1.30	0.84±1.09	90		80	2 33
	0.44	1.14 ±0.88				47	1.06
Number of seeds per ridge							
23 x P5							
P4 x P5	0.90	0.52± 0.66				28	0 67
P7x P8	0.89	1 28 ±0.83		0.38	67	44	1 27
_x P8	0.84	1.66± 0.88		0.43	48		1.34
P1 x P4	0.73_	1.92 ±0.69	0.12 ±0.68	58			0.71
	0.89	1.40 ±0.99	0.24± 0.75	0.46	48		1.04
Number of seeds per pod				0.89	56		
W P3 x P5	5.06	20.16 ±3.6				37	4.78
P4 x P5		15.10 ±3.18		0.82	84		4.23
P7 _x P8	3.89	28.34± 4.06		0.75	86		5.41
P4 x P8	111.50	20 82± 3.28		0.57	91	54	4.53
P 1 x P4 _	5.61	18.40± 3.06		0.30	83	53	
Seeds weight		32.00± 15.61	13.41 ±4.09	0.23	70	69	4.87
P3 x P5						47	
		39.48± 14.0				61	
		45.74± 6.89					
P4 x P5_		38.90± 14.88					6.32
P7 x P8	26 26			60			6 07
	18.76	13.48± 18.62		0.41	54		
P4 x P8						49	7 34
PI x P4	14 09	0.87± .065		69		49	
	14 30	0.58± 0.69					2 45
Weight of 100 seeds		0.88 ±0.67		1.83	61	67	
P3 x P5		2.22 ± 1 05				21	
P4 x P5		0.60 ±0.62	22.68± 3.0	0.39	61		0 79
P7 x P8	0.27			0.49	80		1.06
P4 x P8	021			0.21	84	57 y	
P 1 x P4	0.15	1.76 ±1.08		0.13	90		
Mature pod length	0.30	1.10 ±0.71		0.77		62	1.92
P3 x P5	0.27						0.75
P4 x PS		2.02 ±1.20					
		2.70 ±1.20		0.83	91	79	
P7 x P8	0.42			0.54	89	45	1.48
P4 x P8	0.47	2.36 ±1.17					1.08
P 1 x P4	0.68			0.51	98		
Mature pod width	0.42	1.82 ±0.81		0.37	95		1.43
P3 x F5	0.20	0.86 ±0.85		0.57	93		2.04
P4 x PS						50	1.97
4._	0.70					48	
	0.75			82			1.61
				65		75	0.77
						67	
			1.20 ±1.02				
			0.32 ±0.97				
			1.68± 1.24				
			0.36±1..36				
			1.20± 1.01				
P7 x P8	0.81	2.26 ±1.12	0.52 ±1.18				1.62
P4 x P8	0.41					59	1.59
P 1 x P4	0.76					73	I.74s

E = Environmental variation, H = Dominant gene effects D = Additive gene effects. /H/D = D dominance ratio, Hb = Broad sense heritability, Hn = Narrow sense heritability, G.A = Genetic Advance.

Components of genetic variation for hundred seed weight, number of seeds per ridge mature pod length mature pod width, number of seeds per pod, number of ridges per pod and seed weight showed that the estimates of the additive gene effects and its percentage contribution to variability for these characters were greater than the estimates of the dominant gene effects and environmental variation. The preponderance of additive gene effects predominates inheritance of these characters. Our observations agree with Rao and Ramu (1977) and Padda and Dhanker (1980) in *A. esculentus.* A high additive gene effects and a low estimates of environmental variation observed in this study could give to the isolation of homozygous lines for genetic improvement in these characters. Therefore, a repeated selection may not be necessary.

Dominance components were ambidirectional with alleles from both parents contributing to the inheritance of seed weight, ridges per pod, seeds per ridge, while dominance were unidirectional, positive increasing alleles with alleles from the larger parent contributing to the inheritance of number of seeds per pod. In addition, a partial dominance situation (/H/D<0.69) observed across loci moderate the inheritance of ridges per pod (P3 x P5, P4 x P5, P4 x P8), seed weight (P7 x P8), hundred seed weight (P3 x P5, P4 x P5, P7 x P8, P4 x P8), and seeds per pod (P4 x P8, P 1 x P4), pod length (P4 x P5, P7 x P8, P4 x P8, P1 x P4), and pod width P7 x P8) for these characters. This indicated that these phenotypes (ridges per pod, seeds per ridge, seed weight, hundred seed weight, seeds per pod) are intermediate in expression of these characters between the two homozygous parents involved in each cross.

An approximate complete dominance situation (/H/D<0.69) moderate the inheritance of ridges per pod (P3x P5, P7 x P8), seeds per ridge (P1 x P4) weight of hundred seeds (P 1 x P4), and seeds per pod (P3 x P5, P4 x P5) pod width (P4 x P8,) and pod length (P3 x P5). This showed that the expression of these phenotypes were closer to the homozygous dominant parents. The superiority for these characters could be retained in a single line, which may be ideal for development of pure line for genetic improvement in seed weight. An over dominance situation (/H/D 1.001.25) for seeds weight (P1 x P4), and pod width (P4 x P8) observed in this study may be ideal for development of hybrid for pod and seed yield. But the superiority for this characters can be captured in a single line after a series of replicated family trials The over dominance situation observed across loci for seed weight and pod width may suggest that the phenotypic measurement of the heterozygotes population are superior to either of the two parents Dominance was unidirectional positive increasing alleles to the larger patents for mature pod length, but an ambidirectional dominance with alleles from both parents govern the inheritance of mature pod width. A partial dominance situation and approximately complete dominance moderate the inheritance of pod length A low narrow sense heritability estimates (28-44%) for seeds per pod, ridges per pod, weight of hundred seed weight, mature pod width, number of seeds per ridge in some crosses showed the ineffectiveness of direct selection among segregation generations. Therefore, a replicated family trails and a backcross procedure for these characters could be ideal for genetic improvement.

In addition a high heritability estimates for weight of hundred seeds in this study

agrees with Padda *et al.,* (1970). A high additive gene estimates, broad sense and narrow sense heritability for hundred seed weight, number of ridges per pod, number seeds per ridge, pod length and pod width indicated that selection in the early generations for these characters should be highly effective in developing a breeding strategy and a good genetic base for seed improvement in *A. caillei.* High estimates of broad and narrow sense heritability for number of seeds per pod observed in this study corroborates the findings of Martin *et al.,* (1981) in *A esculentus..* High estimates of narrow sense heritability and genetic advance for seed weight agreed in showing that selection in the F_2 generation would lead to a substantial genetic improvement in seeds yield. Hence the prospect of formulating a breeding strategy for seed improvement.

CONCLUSION AND RECOMMENDATION

The study showed that the additive gene effects predominate the inheritance of number of seeds per pod, seeds per ridge, ridges per pod, seed weight, mature pod length and mature pod width and hundred seed weight. But environmental variation was minimal. Dominant gene effects were ambidirectional for inheritance of seed weight, mature pod width, number of ridges per pod, number of seeds per pod. A partial dominance and complete dominance situation moderate the inheritance of these characters. An over-dominance situation across loci was responsible for inheritance of seed weight in P 1 xP4.

Broad sense heritability estimates were greater than the heritability in narrow sense for most characters, a moderate to high and a high additive gene effects observed in this study for, most characters could be ideal for foe developing a breeding plan and a good genetic base for yield improvement in A. *caillei.* The cross (P7 x P8) amongst others may be ideal for future hybridization and genetic improvement in *A. caillei* for number of ridges per pod, number of seeds per pod, hundred seed weight and seed weight

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