

Combining Ability and Genetic Components for Length and Width of Pods in West African Okra (*Abelmoschus caillei* [A. Chev] Stevels)

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Abstract: In the tropical and subtropical regions of the world, okra pods are consumed fresh. The introduction of pure lines and hybrids with improved length and width into the cropping system, necessitate studies on the combining ability and genetic components for the length and width of pods. Seven parents and 21 F₁ generations were planted for evaluation in a randomized complete block design with two replications. The results indicated that the means squares due to GCA and SCA for length and width of pods were significant. The estimated variance due to SCA was greater than GCA variance for length and width of pods at edible stage and vice versa for length and width of pod at maturity. The study identified Parents 7, 6, 4 and 5 as best combiners for edible pod length and width, mature pod length and width. Component analysis indicated that the dominant genetic action predominate other genetic effects in the inheritance of length and width of pods. The dominance components (H₁ and H₂) were found to be greater than the additive gene effects (D). The ratio vH/D revealed overdominance loci for characters evaluated. The estimate F were positive (edible pod length and mature pod length) and negative (edible pod width and mature pod width). The proportion v4(DH₁+F)/v4(DH₁-F) was unity. While the ratio 4H₂/4H₁ = 0.25 for all characters evaluated. The non-additive genetic effects accounted for a low to moderate heritability estimate in narrow sense recorded in the study. Both Oligogenic and polygenic action were found in the study. The study indicated an empirical superiority of the possibilities of evolving pure lines and hybrid okra with improved length and width into the cropping system.

Key words: West african okra, specific combining ability, dominance ratio, additive x additive interaction effects, wr/vr regression, additive variance, non-allelic interaction

INTRODUCTION

West African Okra (*Abelmoschus caillei* [A. chev] Stevels), a fruit vegetable which is cultivated primarily for its fresh pods in the sub Sahara African states. It is biennial, self pollinated, hardy and short day crop it contains 194 chromosomes as compared with *Abelmoschus esculentus* [L.] Moench. More often the stigma remains receptive on the day of anthesis and pollination at the bud stage will not be successful. West African Okra differs from *Abelmoschus esculentus* by its intense pigmentation on plant parts (leaf vein, pods, peduncle and pods), pubescent and glabrous pods and pods in horizontal and vertical positions to Adeniji^[1] and Kehinde and Adeniji^[2].

In Nigeria, the cultivation of West African Okra traverses all agro ecological zones. Remarkably its cultivation has been noticed in high altitude areas with

elevation well over 800 meters (asl). West African Okra has a potential for a high number of flower buds, which transform into flowers and eventually pods, when compared to *Abelmoschus esculentus*. Because of its high pod yield and returns on investment, dry season farming of West African Okra for domestic consumption is on the increase. Thus attracting a higher profit as compared with investment on the first season planting. West African Okra pods are consumed fresh (a maximum of seven days after anthesis). Fresh okra pods contain 18-26% oil, 20-26% crude protein Martins *et al.*^[3]. Pods desired for seed production are allowed to dry, harvested and decortications of the pods takes place to extract the seeds. The utilization of West African Okra seeds for industrial, nutritional and biomedical purposes is limited s compared with *A. esculentus* in tropical Africa. The mucilaginous property (draw) of the pod makes the consumption of food easy.

Genetic diversity among accessions of West African Okra for length and width has been reported Ariyo *et al*^[4]. The existence of this diversity may serve as a basis for hybridization and genetic improvement in this species. Variation in length and width of pods in West African Okra may be attributed to difference in the manufacture, distribution and accumulation of photosynthate among photosynthetic parts (source and sink). A significant positive correlation between pod length and number of seeds per pod and seed per ridge may constitute basis for genetic improvement to Adeniji and Peter^[5]. Obviously, long and wide pods at edible stage, will provide for more fleshy parts for consumption. Additive genetic action in the inheritance of pod/plant, seeds/pod seed weight and pod length had been noted Adeniji and Kehinde^[6]. Genetic efforts at developing West African Okra varieties (pure lines and hybrids) with improved length and width into the cropping system is at rudimentary stage. Diallel analysis (Griffings and Haymans) have been identified as important statistical tools for evaluating combining ability and genetic components underlying inheritance of metric characters Adeniji and Kehinde^[2]. Studies on combining ability for pod yield Adeniji and Kehinde^[2] and earliness Kehinde and Adeniji^[2] in West African okra had been noted. Genetic information on the inheritance system for pod length and width in this crop is limited. This investigation was undertaken to provide genetic information on the combining ability and to evaluate genetic components underlying the inheritance of length and width of pods at edible stage and at maturity. An accomplishment of this research will provide basic information that will facilitate a release of improved varieties into the cropping system.

MATERIALS AND METHODS

Accessions of West African Okra (P1, P2, P3, P4, P5, P6 and P7), sourced from the germplasm collection of the University of Agriculture, Abeokuta were utilized for this study. These accessions have shown diversity for length and width and have been maintained through selfing. Hybridization among the accession were made in the screen house following a 7×7 diallel pattern without reciprocals to produce F₁ seeds. Field evaluation of the parents and F₁ generations were conducted at the Teaching and Research farm, University of Agriculture Abeokuta, Nigeria (Lat, 7.53°N, 3.38°E, 450 m asl) The experimental layout was a randomized complete block design with two replications. Each row was 10 meters long and inter-row spacing of 1 meter. Two seeds were planted per hole, later thinned to one plant per stand. The number of rows for each generation was 3% and five rows

for each F₁ generation. The plots received fertilizer equivalent N; P: K 15:15:15 at the rate of 60 kg ha⁻¹, 2-3 weeks after planting and at flowering. All agronomic activities were carried out.

Field observations were made from 64 stands for each parent and 128 stands for each F₁ generation. Length and width of pods at edible stage were estimated by tagging fifteen flowers per plant at anthesis. Seven days after anthesis the length and width of pods were measured. The pod length and width at maturity were measured by randomly harvesting fifteen pods per plant and measuring the length and width. In both cases, the length was measured on the longest point on the pod and the width on the widest point on the pod in centimeters. Data collected were subjected to analysis of variance and test of significance to meet the pre-requisite for further analysis. Subsequently, plot means were analyzed for combining ability in the parents and in the F₁ generations following the method 2 model 1 of Griffings^[7] to estimate the genetic and environmental components of complex population variances. Pod length and width at edible stage and maturity in the parents and F₁ generations were analyzed for genetic parameters following the method of Haymans^[8], which is the most sensitive means available to detect non additive variation and dominance. Further analysis as correlation and regression between parental order of mean (V_r) and parental order of dominance (W_r+V_r), the covariance of the array (W_r) and the variance of the array (V_r) for pod length and width at edible and at maturity were carried out. The estimate D, F, H₁ and H₂ were calculated as specified by Hayman^[8]. The ratio 1/4 (H₂/H₁) was used to calculate the average frequency of the negative versus positive alleles in the parents Crumpaker and Allard^[9]. If the distribution is equal among the parents, the ratio is expected to be 0.25. Heritability in narrow sense was calculated by the method of Crumpaker and Allard^[9]. The effective factors for length and width of pods at edible and maturity stages were estimated as Effective factors = (Overall progeny mean-parental mean)²/1/4H₂

RESULTS AND DISCUSSION

The estimated means squares of the combining ability and the estimate of genetic components Table 1 showed that the means squares due to GCA were greater than the SCA mean squares for the length and width of pods at edible stage and at maturity. The values of the GCA and SCA for edible pod length, mature pod length and width were statistically significant (p<0.05). This explains a greater role of both the additive and non additive gene effects in the inheritance of these characters. But the

Table 1: Mean squares and estimates of genetic components from the analysis of variance for combining ability for length and width of pods in a 7x7 diallel crossing (Griffings Model 1 Method 2)

	Edible pod length	Edible pod width	Mature pod length	Mature pod width
GCA	1.62**	0.56	230.28**	52.80**
SCA	0.40**	0.13	18.35**	3.97**
Error	0.08	0.009	0.005	0.13
O ² gca	0.17	0.06	25.59	5.86
O ² sca	0.32	0.12	18.35	3.84
O ² A	0.34	0.12	50.18	11.72
O ² D	0.32	0.12	18.35	3.84
O ² A/D	1:1	1:1	2.78	3.00

Table 2: Estimates of GCA (gi) of seven parents of West African Okra accessions

	Edible pod length	Rank	Edible pod width	Rank	Mature pod length	Rank	Mature pod width	Rank
G1	0.24	2	0.35	4	0.12	7	0/24	3
G2	0.22	3	0.02	7	0.41	4	0.12	5
G3	-0.16	6	-0.03	6	-0.93	2	0.09	6
G4	0.13	7	0.38	2	1.40	1	-0.25	2
G5	0.17	5	-0.36	3	=0.37	6	1.61	1
G6	-0.20	4	-0.45	1	-0.90	3	0.18	4
G7	0.40	1	-0.26	5	-0.38	5	-0.03	7
	Se (gi) = 0.17		Se (gi) = 0.09		Se (gi) = 0.12		Se (gi) = 0.12	
	LSD5% = 0.34		LSD5% = 0.19		LSD5% = 0.24		LSD5% = 0.25	
	LSD1% = 0.45		LSD1% = 0.23		LSD1% = 0.30		LSD1% = 0.32	

estimated SCA means squares for edible pod width was non significant. As such, the estimated variance due to GCA and additive variance for mature pod length and width were greater than the estimated variance due to SCA and dominant variance. This affirms the role of additive gene action in relation to other gene action in the inheritance of pod length and width at maturity. But the SCA variance and dominant variance for pod length and width at edible stage and maturity were numerically greater than the GCA variance and additive variance, thus indicating a greater deviation from additivity. This is an implication that dominant genetic action was more important in the inheritance of edible pod length and width. The ratio of additive variance to dominant variance was equal in proportion for edible pod length and width Table 1.

This investigation elucidated that combining ability estimates in the parents Table 2 identified parents 7, 2 and 1 as best combiners for edible pod length. Parents 6, 4 and 5 as best combiners for edible pod width. In addition, parents 4, 3, 6 and parents 5, 4, and 1 were identified as best combiners for mature pod length and mature pod width, respectively. The high GCA effect recorded in this study is squal to the presence of additive gene effects and additive x additive interaction effects in the parents. However, these parents could be selected for breeding experiment aimed at improving length and width of pods at edible stage and at maturity. But parents 4, 2, 7 and 5 recorded a low GCA values for pod length and width at edible stage and length and width of pods at maturity. Other parental accessions were intermediate in the performance for measured parameters. The specific combining ability Table 3 indicated that the

cross $P_4 \times P_7$ (0.60), $P_2 \times P_6$ (-0.57) had the highest SCA values for edible pod length. Similarly, the cross $P_2 \times P_3$ (-1.42), $P_1 \times P_6$ (-1.32) were best specific combiners for edible pod width. The cross $P_4 \times P_6$ (-6.42), $P_1 \times P_5$ (-6.27) for mature pod length and the cross $P_1 \times P_5$ (1.77), $P_3 \times P_8$ (1.60) for mature pod width recorded a high SCA values. This is an indicative of the preponderance of dominant interaction effects in these cross combinations for these characters. The cross $P_2 \times P_3$ is the best combiners for edible pod width and $P_2 \times P_3$ as poor combiners x poor combiners.

The study identified that the cross ($P_1 \times P_6$) as best combiners x best combiners and the cross ($P_2 \times P_3$) as poor combiners x poor combiners for edible pod width. In addition, the cross $P_4 \times P_6$ and $P_1 \times P_5$ were identified as best combiners x best combiners and poor combiners x poor combiners respectively for mature pod length. For mature pod width, the cross $P_1 \times P_5$ was identified as best combiners x best combiners, $P_1 \times P_6$ as best combiners x intermediate combiners and $P_2 \times P_5$ poor combiners x best combiner. While the cross $P_1 \times P_3$ was identified as best combiners x poor combiners for mature pod length. Hybridization between best combiners x best combiners for edible pod width ($P_1 \times P_6$), mature pod length ($P_1 \times P_5$) may introduce transgressive segregants in advance generations. However, this genetic situation is moderated additive x additive type of gene action. Negative estimates of SCA values recorded in this study indicated a partial dominance situation across loci.

Haymans^[8] approach to the understanding of the underlying genetic components to a set of diallel identified parents 4, 6, 5 and 2 to have recorded the lowest $Wr + Vr$ estimates (parental order of dominance) for edible

Table 3: Specific combining ability for length and width of pods of West African Okra (*A. caillei*)

Cross	Edible pod length	Edible pod width	Mature pod length	Mature pod width
1x2	0.45	0.20	-4.84	-0.60
1x3	0.02	0.75	-5.29	-0.15
1x4	-0.31	0.28	-4.39	0.50
1x5	0.46	-0.13	-6.77	1.77
1x6	-0.07	-1.32	-5.69	-0.84
1x7	-0.42	-0.07	-1.81	0.37
2x3	0.41	-1.42	-5.55	0.34
2x4	0.23	0.55	-4.41	-0.34
2x5	-0.38	-0.34	-5.85	-1.05
2x6	-0.57	-0.41	-2.29	-0.25
2x7	0.16	-0.22	-4.58	-0.34
3x4	-0.32	-0.11	-5.79	-0.23
3x5	-0.07	-0.01	-4.73	1.64
3x6	0.01	0.07	-4.65	-0.46
3x7	0.10	-0.01	-4.36	-1.28
4x5	0.08	0.20	-4.32	-0.04
4x6	-0.01	-0.61	-6.42	0.76
4x7	0.06	-0.47	-4.94	-0.16
5x6	-0.01	0.41	-6.01	1.81
5x7	-0.28	0.26	-0.67	1.45
6x7	-0.04	0.57	-1.09	-0.35
	SE(si = 0.35)	SE(si = 0.12)	SE(si = 0.45)	SE(si = 0.45)
	LSD5% = 0.70	LSD5% = 0.24	LSD5% = 0.90	LSD5% = 0.90
	LSD1% = 0.93	LSD1% = 0.31	LSD1% = 1.20	LSD1% = 1.20

pod length and width and mature pod length and width at maturity. Hence they contain dominant alleles for these characters. However, parents 5, 2, 1 and 3 had the highest estimates of $W_r + V_r$ for edible pod length and width, mature pod length and width. This could be explained as the presence of recessive alleles in the parents. The correlation between W_r (covariance between the parents and their offspring) and V_r (variance of the array) for edible pod length was significant ($r = 0.71^*$), while its regression was 0.51^* . Similarly, the regression of W_r/V_r for mature pod width was 0.82^* and the correlation was of W_r/V_r was 0.70^* . The regression analysis ordinarily suggest that the assumption of a simple additive-dominance model in the inheritance of edible pod length and mature pod width was adequate. In another study, Adeniji and Kehinde^[10] had noted the adequacy of the additive- dominance model in the inheritance of pod yield in West African Okra. A positive intercept (a) for edible pod width (0.31), edible pod length (0.15) and mature pod length (1.42) identified these characters to be dominant at the loci in the crosses evaluated. A negative intercept for pod width at maturity ($a = 0.29$) indicated an incomplete dominance situation at the loci. The correlation coefficient between the parental order of dominance ($W_r + V_r$) and the parental measurement (Y) was positive for mature pod length ($r = 0.52$). This posited that the parents with dominant genes for mature pod length and edible pod width had the lowest $W_r + V_r$ values. They contain mostly dominant genes.

In study, the correlation coefficient was not significant, thus indicating the presence of dominant genes, which increase pod length at maturity and pod

width at edible stage in the parental genotypes. A positive intercept of W_r/V_r regression (1.42) for mature pod length indicated the preponderance of dominant alleles at the loci for mature pod length. The correlation coefficient between $W_r + V_r/Y_r$ was negative; this provides that parents with recessive genes recorded a high estimate of $W_r + V_r$. While parents with increasing genes (positive) recorded the lowest $W_r + V_r$ estimate and contain mostly dominant alleles. Therefore a high manifestation of mature pod width and edible pod length was governed by recessive alleles. The results of the correlation coefficient between per se performance and GCA effects for edible pod length ($r = 0.18$), edible pod width ($r = 0.11$), mature pod length (0.94^*) and mature pod width ($r = 0.99^{**}$) observed in this study, explained that an independent mechanism exist in the genetic system for the inheritance of pod length and width of the pods at edible stage. This could however make breeding for these characters difficult. But a high predictability of the performance of pod length and width in the F_1 can be done satisfactorily. The results obtained in the combining ability was further strengthened the graphical relationship between the per se performance and the GCA values for pod length and width at edible stage Fig. 1 and 2. This showed that parents 7 had a high GCA value and considerably high per se performance for length at edible stage. In addition, parents 6 recorded a negative but a high GCA values. This parent could be selected for hybridization, when improvement in pod length and width at edible stage is desirable. The ordination of the GCA effects and per se performance for pod length and width at maturity

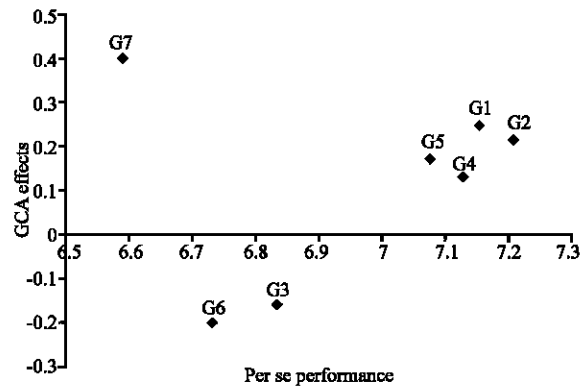


Fig. 1: Relationships between GCA effects and per se performance for Edible Pod length

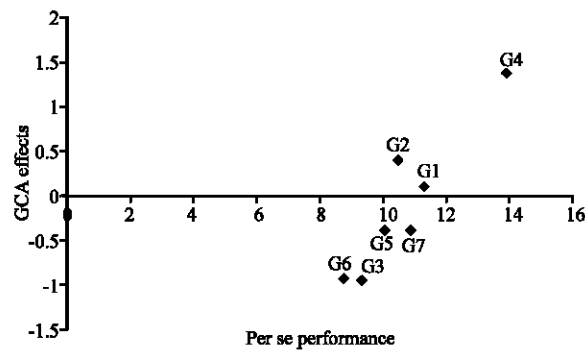


Fig. 2: Relationships between GCA effects and per se performance for Mature Pod length

Fig. 3 and 4 identified parents 4, 3, 6 and 5 to have a high estimates of GCA values and parental mean for both character. This further corroborates finding in this study that additive and additive x additive interaction effects moderates the inheritance of these character.

Haymans^[6] components analysis of combining ability Table 4 in West African Okra indicated that additive genetic variance (D) was greater than the environmental variance (E) for pod length and width at edible stage and at maturity ($D > E$). The estimate of additive genetic variance was less than the dominance variance ($D < H_1$ and H_2) for these character. This confirm the of dominance genetic effects in the inheritance of these character. Among the dominance components (H_1 and H_2), the magnitude H_1 was greater than H_2 ($H_1 > H_2$) for pod length at edible stage. A situation wherein H_1 was greater than H_2 ($H_1 > H_2$) for pod length indicated that the positive and negative alleles at the loci for length of pods were not equal in proportion. However, a situation wherein $H_1 > D$ for characters evaluated suggest overdominance effects. Similarly, estimates of the ratio $vH/D = 2.60, 1.29, 1.23, 1.09$ for edible pod length and width, mature pod length and

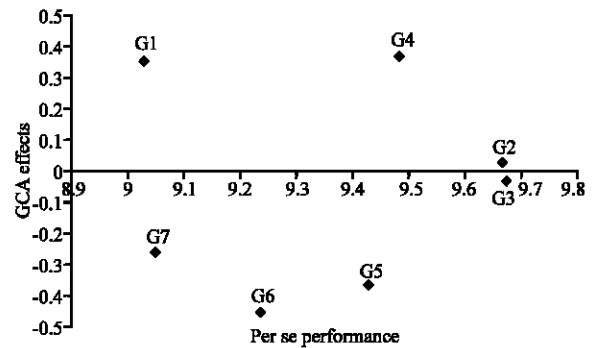


Fig. 3: Relationships between GCA effects and per se performance for Edible Pod width

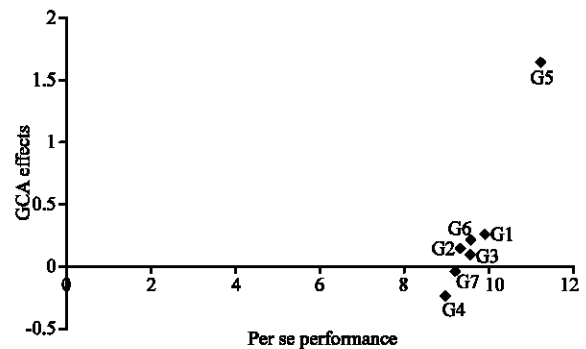


Fig. 4: Relationships between GCA effects and per se performance for Matured Pod width

width, respectively, further confirm overdominance loci. An overdominance loci provides that hybrids with considerable length and width could be released into the cropping system. Apparently, estimates of F were positive for edible pod length (0.27), mature pod length (0.05) and negative for edible pod width (-0.08) and mature pod width (-1.40).

A positive estimate of F could be explained as a greater frequency of dominant increasing alleles than decreasing alleles in the parental accessions for pod length. While a negative estimate of F showed a high frequency of dominant decreasing alleles than dominant increasing alleles in the parental accessions for pod width. The proportion of dominant to recessive genes in the parental accessions $v4 (DH_1) + F/v4 (DH_1 - F) = 1.00$ was unity for length and width of pods. This is a clear manifestation that there were in excess dominant genes in the genetic system of inheritance of pod length and width at edible stage and at maturity in the parental accessions. The estimate of the proportion of dominant and recessive genes in the parents H_2/H_1 was 0.25 for pod length and width at edible stage and at maturity. Therefore, the loci exhibiting positive and negative genes were equally distributed in the parents for these characters. Narrow

Table 4: Components of Genetic and Environmental Variation and other statistics in a 7×7 diallel cross evaluated for length and width of Pods in West African Okra according to Hayman^[9]

	Edible pod length	Edible pod width	Mature pod length	Mature pod width
E	0.06	0.04	0.15	0.04
D	0.35	0.73	2.50	0.76
H ₁	2.38	1.22	3.80	1.93
H ₂	0.20	0.25	3.86	2.22
H ₂ /4H ₁	0.25	-0.08	0.25	0.29
F	0.27	1.29	0.05	-1.40
vH ₁ /D	2.60	0.98	1.23	1.59
v ₄ (DH ₁ +F)/ v ₄ (DH ₁ -F)	1.01	0.98	1.00	1.00
Hn	0.51	0.35	0.37	0.20
K	2.30	2.60	5.20	5.50

E = Environmental variation, D = Additive variation, H₁ and H₂ = Dominance components, H₂/4H₁ = Proportion of dominant and recessive genes, F = Frequency of dominance, vH₁/D = Degree of dominance, vH₁/D = Degree of dominance, v₄(DH₁+F)/v₄(DH₁-F) = The proportion of dominant and recessive genes in the parent

sense heritability estimates were low (0.20) to moderate (0.37). This could be ascribed to a high magnitude of non additive genetic effects. A moderate narrow sense heritability estimate (0.51) showed that an average performance of the total phenotypic variability in diallel analyses for edible pod length was additive. Therefore, mass selection strategy could be ideal for genetic improvement in pod length at edible stage. While emphasis pedigree, sib test or progeny test may be necessary to make a satisfactory improvement in length and width of pod at maturity and pod with at edible stage. This is because a large proportion of phenotypic observed was due to non additive genetic effects.

The study indicated a minimum of two genes moderate the inheritance of length and width of pods at edible stage. Thus suggesting an oligogenic action. While a maximum of six genes moderate the inheritance of length and width of pods at maturity, revealing a polygenic action.

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