

INTRA AND INTER-SPECIFIC CROSSES IN *Abelmoschus caillei* and *Abelmoschus esculentus* AND THE IMPLICATIONS ON POD YIELD IMPROVEMENT

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ABSTRACT

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Inter and intra specific crosses studies in *A. caillei* and *A. esculentus* and their implications on yield improvement were carried out from May to December at Research Farm of Michael Okpara University of Agriculture, Umudike using a randomized complete block design with 3 replications. The treatment consisted of 62 genotypes made up of 8 parents, 18F₁, 18F₂, 9BC₁ and 9BC₂. Results showed that the genotypes were significantly different ($P < 0.05$) in all the traits studied except for length of pod. The total variance partitioned into genetic and environmental variances and showed that large heritable variations exist within and between the species. Genotypes from intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* had higher additive variance, with narrow sense heritability values that ranged from moderate (0.500) to high (0.720), while those from intra specific crosses in *A. esculentus* had narrow sense values which ranged from small (0.200) to moderate (0.500). Okra height (0.926), number of leaves plant⁻¹ (0.951), number of pods plant⁻¹ (0.941) and weight of pods (0.800) had positive and very highly significant correlation coefficients with pod yield ha⁻¹. Breeding programme for pod yield improvement, through specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus*, faster result would be achieved by selecting okra height, number of leaves plant⁻¹, number of pods plant⁻¹ and weight of pods.

Keywords: Intra and inter specific cross, *Abelmoschus* spp, heritability, pod yield improvement.

INTRODUCTION

West African okra (*Abelmoschus caillei* (A. chev) is an important vegetable crop. A short day plant with green stem (Adeniji *et al.*, 2007) and slight traces of red colour in some accessions (Adeniji, 2003), cultivated for fresh pods, leaves and seeds. Singh and Bhatnager (1975) and Siemonsma (1982) reported that *A. caillei* contained 194 diploid chromosomes as against 130 of the conventional okra (*A. esculentus*), thereby indicating that *A. caillei* constitutes a new okra species. Due to its high yield and hardiness, it has become a major source of Okra pods in Nigeria and cultivation is progressively replacing the conventional type (Kehinde, 1999). Adeniji *et al.* (2007) reported that *A. caillei* has the potentials for industrial, nutritional and biomedical purpose in the developing countries, but is under-utilized in the sub-Saharan Africa. It has been reported that *A. caillei* is photoperiodic, which stands as the most striking difference between it and *A. esculentus* (Ariyo, 1993; Adeniji and Kehinde, 2004; Chinatu *et al.*, 2014). Yield improvement in okra is crucial since many rural dwellers in some parts of Nigeria cultivate it as an economic crop. Abdelmageed (2010) and Chinatu (2015) reported that this could only be possible through partitioning of observed variations into genetic and environmental components. An experiment that extracts estimates of genetic and environmental variances can lead to determination of broad sense heritability, which is the proportion of observed variability due to heredity (Swamy and Sathyavathi, 1977). With the introduction of backcrosses, genetic component can still be separated into additive and dominance components. Additive variance divided by phenotypic variance is regarded as narrow sense heritability (Uguru, 2000). It is a more useful concept, because it measures the relative importance of additive portion of genetic variance that can be transmitted to the next generation of offspring (Walter, 1987; Eid, 2007). Talebi *et al.* (2007) reported that the interrelationships existing between yield and its contributing components can significantly improve the efficiency of crop breeding programmes through the use of proper selection indices. Plants are selected based on traits that have positive relationship with yield, since it often lead to changes in other components due to the polygenic nature of yield (Kashian *et al.*, 2010). This study was therefore undertaken to determine the level of additive gene effects (narrow sense heritability) in crosses within and between *A. caillei* and *A. esculentus* in order to select traits that could lead to increase in okra pod yield.

MATERIALS AND METHODS

The study was carried out at the Western Farm of Michael Okpara University of Agriculture, Umudike from 2009 to 2011. Umudike lies within longitude 07° 33' E and latitude 05° 29' N, with an altitude of 122m above sea level, with bimodal peaks of rainfall, with sandy-loamy soil, (National Root Crop Research Institute, Umudike, Meteorological station). The planting materials, 4 varieties of *A. caillei* (NGAE-96-012-1, OJA- OBA 4, NGAE-96 - 0067 and OWODE) and 4 varieties of *A. esculentus* (NG/SA/07/0516, NGB/06/080, NG/SA/07/0522 and

NG/SA/07/0528) collected from National Biotechnology centre, Ibadan, were used in the hybridization. The F₁ hybrids were backcrossed with parents to raise backcross1 (BC₁) and backcross2 (BC₂) seeds while those not backcrossed were selfed to raise F₂ seeds. Comparison blocks were established to evaluate the traits of the genotypes. The treatments consisted of 62 genotypes made up of 8 parents, 18F₁, 18F₂, 9BC₁ and 9BC₂ generations, in a randomized complete block design replicated 3 times. The following data were collected: okra height, number of leaves plant⁻¹, number of branches plant⁻¹, number of flowers, plant⁻¹ number of pods plant⁻¹, length of pods, weight of pods plant⁻¹, fresh pod yield (Kg/ha). Data were subjected to analysis of variance and means separated through Duncan Multiple Range Test, (Snedecor and Cochran, 1989). The gross variability was partitioned into genetic and non-genetic components. The additive component (1/2D) of the genetic variation was obtained as: $1/2D = 2VF_2 - (VBC_1 + VBC_2)$. Where VF₂=second filial generation variances; VBC₁= Backcross 1 variance and VBC₂=Backcross -2 variances. Environmental variance (VE) was obtained as:

$$VE = \frac{VP_1 + VP_2 + VF_1}{3}$$

VP₁, VP₂, and VF₁ were parent-1, parent-2 and F₁ variances, respectively.

Dominance (1/2H) was obtained as; $1/2H = VBC_1 + VBC_2 - (1/2D + 2VE)$. Narrow sense heritability was obtained as:

$$\frac{1/2D}{1/2D + 1/4H + VE}$$

Hanson et al., (1956)

RESULTS

The genotypes were significantly different ($p < 0.05$) in all the traits studied except for length of pods, (Table 1). Pod yield varied from 2014.22 to 8440.32 kg ha⁻¹. This showed high variation in among the gene types in fresh pod yield ha⁻¹. Chinatu (2015) had reported that high genetic variation existed between *A. caillei* and *A. esculentus*, due difference in their genetic composition (Table1). Environmental variance was smallest for both intra and inters specific crosses in *A. caillei* and *A. esculentus* indicating that height of the plants was determined by genetic factor. In the intra-specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability ranged from 0.282 (Small) to 0.471 (moderate) values. In intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently higher than dominance, narrow sense heritability values which ranged from 0.529 (moderate) to 0.763 (high) and 0.488 (moderate) to 0.701 (high) values, respectively. This implies that heritable trait can be transferred faster through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties than intra specific crosses in *A. esculentus*. Heritable variation (additive gene effect) was larger in inter specific crosses in *A. caillei* and *A. esculentus* and intra specific crosses in *A. caillei* than in intra specific crosses in *A. esculentus*.

Tables 5 to 7 show that environmental variance was smallest for both intra and inter specific crosses in *A. caillei* and *A. esculentus* indicating that number of leaves plant⁻¹ was determined by genetic factor. In the intra-specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability values ranged from 0.346 (small) to 0.489 (moderate). In intra specific crosses in *A. caillei* and inter-specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently higher than dominance, narrow sense heritability ranged from 0.511 (moderate) to 0.706 (high) and 0.514 (moderate) to 0.729 (high) values, respectively. Additive gene effect was more pronounced in inter specific crosses between *A. caillei* and *A. esculentus* and intra specific crosses in *A. caillei* than in intra specific crosses in *A. esculentus*. This implies that the heritable trait (number of leaves plant⁻¹) can be transferred faster through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties than intra specific crosses in *A. esculentus*.

Tables 8 to 10 indicated small value for environmental variance for both intra and inter specific crosses in *A. caillei* and *A. esculentus* implying that number of pods plant was determined by genetic factor. In the intra-specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability values ranged from 0.444 to 0.620 (moderate). In intra specific crosses in *A. caillei* and inter-specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently higher than dominance, narrow sense heritability values ranged from 0.565 (moderate) to 0.808 (high) and 0.446 (moderate) to 0.742 (high), respectively. Additive gene effect was more pronounced in inter specific crosses between *A. caillei* and *A. esculentus* and intra specific crosses in *A. caillei* than in intra specific crosses in *A. esculentus*. This showed that the heritable trait (number of pods per plant) can be transferred faster through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties than intra specific crosses in *A. esculentus*.

Environmental variances were smallest for both intra and inter specific crosses in *A. caillei* and *A. esculentus* indicating that pod-length was influenced more by genetic factor (Tables 11 to 13). In the intra-specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability values ranged from 0.262 (small) to 0.476 (moderate). In intra specific crosses in *A. caillei* and inter-specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently at par with

dominance, narrow sense heritability values ranged from 0.290 (small) to 0.421 (moderate) and 0.257 (small) to 0.0.492 (moderate) respectively. It shows that dominant variation was a major component of heritable variation. Hence, narrow sense heritability was small. This implies that heritable traits in pod-length can only be transferred after several generations of crosses in both intra specific and inter specific crosses between *A. caillei* and *A. esculentus*.

Table 1: Mean of agronomic traits of parents, F1, F2 and backcrosses in *A. caillei* and *A. esculentus*

Genotypes	Plant Height(cm)	No of leaves plant ⁻¹	No of pods plant ⁻¹	Length of pods(cm)	Weight of pods (g)	Fresh pod yield (kg ha ⁻¹)
Parents						
OWODE	130.10 ^{cdefgh}	95.43 ^k	12.43 ^{bcd}	11.03 ^a	19.77 ^{abc}	4355.77 ^{lm}
NGAE-96-012-1	209.70 ^{rstu}	167.40 ^{stu}	19.07 ^{kl}	11.23 ^a	21.96 ^c	7387.20 ^{tv}
NGAE-96-0067	199.33 ^{qu}	154.50 ^{qrs}	18.50 ^{hijkl}	10.50 ^{as}	21.02 ^{abc}	6913.24 ^{rst}
OJA-OBA4	115.40 ^{bc}	77.00 ^j	10.33 ^{abcde}	8.50 ^a	17.31 ^{abc}	3173.21 ^{defgh}
NG/SA/07/0516	74.10 ^a	34.73 ^a	6.00 ^a	11.27 ^a	19.36 ^{abc}	2065.07 ^a
NG/SA/07/0528	83.10 ^a	38.87 ^{ab}	6.33 ^a	10.77 ^a	19.12 ^{abc}	2235.86 ^{ab}
NG/SA/07/0522	120.90 ^{cd}	55.90 ^{def}	10.10 ^{abcde}	11.00 ^a	17.24 ^{abc}	3090.28 ^{defg}
NGB/06/080	123.50 ^{cd}	60.20 ^{defg}	10.60 ^{abcde}	9.77 ^a	17.63 ^{abc}	3321.10 ^{efgh}
F₁ hybrids						
OWODExNGAE-96-012-1	210.40 ^{qrst}	153.57 ^{qr}	17.50 ^{fghijkl}	11.70 ^a	21.09 ^{abc}	6608.21 ^{qrs}
NGAE-96-012-1 x OWODE	259.70 ^y	171.70 ^y	20.80 ^k	11.70 ^a	21.98 ^c	8440.32 ^w
NGAE-96-0067 x OWODE	251.30 ^y	170.60 ^y	18.70 ^{ghijkl}	11.82 ^a	21.72 ^c	7225.44 ^{stv}
NGAE-96-012-1 x OJA-OBA4	247.60 ^{xy}	169.30 ^y	20.80 ^{kl}	11.75 ^a	21.86 ^c	8083.34 ^{vw}
OJA-OBA4 x NGAE-96-012-1	201.70 ^{qr}	140.00 ^p	16.53 ^{efghijkl}	11.23 ^a	20.66 ^{abc}	6117.55 ^{pq}
NG/SA/07/0516 x NGB/06/080	127.56 ^{def}	61.50 ^{efgh}	9.20 ^{abcde}	11.40 ^a	16.28 ^{ab}	3122.84 ^{defgh}
NGB/06/080 x NG/SA/07/0516	146.30 ^{hijklm}	74.00 ^{hij}	12.53 ^{bcd}	10.98 ^a	16.05 ^a	3197.28 ^{defg}
NG/SA/07/0522 x NG/SA/07/0516	147.70 ^{ijklmn}	72.30 ^{hij}	10.50 ^{abcde}	11.07 ^a	16.42 ^{abc}	3122.84 ^{defg}
NG/SA/07/0528 x NGB/06/080	137.30 ^{defghijk}	61.37 ^{efgh}	9.83 ^{abcde}	11.65 ^a	17.01 ^{abc}	2842.75 ^{bcd}
NGB/06/080 x NG/SA/07/0528	153.50 ^{klmn}	76.70 ^{ij}	12.85 ^{bcd}	10.95 ^a	16.04 ^a	3242.83 ^{defgh}
NGAE-96-012-1 x NGB/06/080	243.37 ^{wx}	167.17 ^{stu}	21.16 ^l	11.60 ^a	19.63 ^{abc}	7384.37 ^{tv}
NGB/06/080 x NGAE-96-012-1	149.20 ^{klmn}	107.40 ^j	13.96 ^{cd}	11.17 ^a	18.54 ^{abc}	4422.72 ^{lm}
NGAE-96-0067 x NG/SA/07/0516	229.37 ^w	167.47 ^{tu}	19.97 ^{kl}	10.90 ^a	20.35 ^{bc}	7224.75 ^{stv}
NG/SA/07/0516 x NGAE-96-0067	179.00 ⁱ	111.60 ^{lm}	9.60 ^{abcd}	11.68 ^a	19.83 ^{abc}	3408.82 ^{efghi}
F₂						
OWODExNGAE-96-012-1	194.97 ^p	120.13 ^{mn}	14.37 ^{defghij}	11.37 ^a	20.64 ^{abc}	5262.79 ^{no}
NGAE-96-012-1 x OWODE	222.83 ^{uv}	161.53 ^{stu}	19.60 ^{kl}	11.70 ^a	21.98 ^c	7658.81 ^{uv}
NGAE-96-0067 x OWODE	218 ^{rstuv}	144.37 ^{pq}	17.17 ^{ghijkl}	7.4 ^a	21.50 ^{bc}	6622.48 ^{qrs}
NGAE-96-012-1 x OJA-OBA4	217.23 ^{stuv}	162.87 ^{stu}	19.70 ^{kl}	11.10 ^a	20.77 ^{abc}	7274.12 ^{stuv}
OJA-OBA4 x NGAE-6-012-1	149.80 ^{klmn}	102.00 ^{kl}	12.03 ^{bcd}	10.57 ^a	19.04 ^{abc}	4049.03 ^{ijkl}
NG/SA/07/0516 x NGB/06/080	102.47 ^b	48.63 ^{bcd}	7.63 ^{ab}	11.67 ^a	17.41 ^{abc}	2335.11 ^{abc}
NGB/06/080 x NG/SA/07/0516	130.43 ^{defgh}	66.67 ^{ghi}	11.03 ^{abcde}	10.63 ^a	16.72 ^{abc}	3271.27 ^{defgh}
NG/SA/07/0522 x NG/SA/07/0516	128.5 ^{cdefg}	66.53 ^{fghi}	11.00 ^{abcde}	11.05 ^a	16.20 ^{ab}	3175.10 ^{defgh}
NG/SA/07/0528 x NGB/06/080	115.85 ^{bc}	46.50 ^{bc}	8.07 ^{abc}	11.40 ^a	17.93 ^{abc}	2564.59 ^{abcd}
NGB/06/080 x NG/SA/07/0528	132.40 ^{defghij}	69.03 ^{ghi}	11.20 ^{abcde}	10.84 ^a	17.10 ^{abc}	3395.47 ^{efgh}
NGAE-96-012-1 x NGB/06/080	217.53 ^{stuv}	160.63 ^{stu}	20.15 ^{kl}	11.37 ^a	19.94 ^{abc}	7124.69 ^{stuv}
NGB/06/080 x NGAE-96-012-1	134.87 ^{defghij}	82.90 ^j	11.25 ^{abcde}	10.67 ^a	19.36 ^{abc}	3850.22 ^{hijkl}
NGAE-96-0067 x NG/SA/07/0516	215.73 ^{rstuv}	155.63 st	18.37 ^{ghijkl}	10.87 ^a	20.40 ^{abc}	6642.51 ^{qrs}
NG/SA/07/0516 x NGAE-96-0067	103.73 ^{cd}	50.33 ^{cd}	7.50 ^{ab}	11.47 ^a	20.17 ^{abc}	2682.54 ^{abcde}
Backcrosses						
OWODExNGAE-96-012-1 x OWODE	205.00 ^{pqrs}	133.67 ^{op}	15.30 ^{defghijk}	11.43 ^a	20.79 ^{abc}	5647.91 ^{op}
NGAE-96-012-1 x OWODE x NGAE-96-012-1	230.13 ^w	166.56 ^{tu}	20.10 ^{kl}	11.87 ^a	21.00 ^{abc}	7504.00 ^{tuw}
NGAE-96-0067 x OWODE x NGAE-96-0067	227.96 ^{uv}	154.70 ^t	17.90 ^{ghijkl}	11.43 ^a	21.57 ^{bc}	6986.84 st
NGAE-96-012-1 x OJA-OBA4 x NGAE-96-012-1	228.13 ^w	164.00 ^{stu}	20.13 ^{kl}	11.50 ^a	21.81 ^c	7790.18 ^{stuv}
OJA-OBA4 x NGAE-96-012-1 x OJA-OBA4	162.23 ⁿ	111.17 ^{lm}	13.77 ^{cd}	10.83 ^a	19.71 ^{abc}	4792.82 ^{mn}
NG/SA/07/0516 x NGB/06/080 x NG/SA/07/0516	160.73 ^{mn}	52.13 ^{de}	8.53 ^{abc}	11.90 ^a	17.94 ^{abc}	2697.02 ^{abcde}
NGB/06/080 x NG/SA/07/0516 x NGB/06/080	137.60 ^{defghijk}	71.13 ^{hij}	11.73 ^{abcde}	11.20 ^a	17.00 ^{abc}	3544.89 ^{fghij}
NG/SA/07/0522 x NG/SA/07/0516 x NG/SA/07/0522	141.17 ^{efghijkl}	68.30 ^{ghi}	11.20 ^{abcde}	11.77 ^a	17.41 ^{abc}	3446.63 ^{efghi}
NG/SA/07/0528 x NGB/06/080 x NG/SA/07/0528	122.87 ^{cd}	56.20 ^{def}	9.03 ^{abcd}	11.70 ^a	18.63 ^{abc}	2987.67 ^{bcd}
NGB/06/080 x NG/SA/07/0528 x NGB/06/080	142.87 ^{ghijkl}	74.77 ^{hij}	13.33 ^{cd}	11.13 ^a	17.51 ^{abc}	4149.48 ^{ijklm}
NGAE-96-012-1 x NGB/06/080 x NGAE-96-012-1	225.53 ^{uv}	167.33 ^{tu}	20.70 ^{kl}	11.73 ^a	20.28 ^{abc}	7448.90 ^{stuv}
NGB/06/080 x NGAE-96-012-1 x NGB/06/080	140.60 ^{efghijkl}	70.20 ^{ghij}	12.20 ^{bcd}	11.13 ^a	19.85 ^{abc}	4279.81 ^{ijklm}
NGAE-96-0067 x NG/SA/07/0516 x NGAE-96-0067	221.43 ^{stuv}	162.93 ^{tu}	19.13 ^{kl}	11.47 ^a	20.79 ^{abc}	7047.64 st
NG/SA/07/0516 x NGAE-96-0067 x NG/SA/07/0516	123.43 ^{cd}	67.13 ^{fghi}	8.50 ^{abc}	12.13 ^a	20.84 ^{abc}	3138.78 ^{defgh}

Within the a column means with the same superscript are the same, while means with different superscript are not the same at 5% probability.

Table 2: Additive genetic effects ($\frac{1}{2}D$), dominances ($\frac{1}{4}H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for plant height in eight intra-specific crosses of *A. caillei*

Crosses	$\frac{1}{2}D$	$\frac{1}{4}H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	604.646	246.675	165.124	0.595
NGAE-96-012-1 x OWODE	872.873	202.328	93.544	0.747
OWODE x NGAE-96-0067	674.130	249.963	177.452	0.612
NGAE-96-0067 x OWODE	913.370	200.370	101.406	0.752
NGAE-96-012-1 x OJA-OBA-4	770.620	205.050	119.066	0.703
OJA-OBA-4 x NGAE-96-012-1	587.897	309.790	172.309	0.549

Table 3: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for plant height in six intra crosses of *A. esculentus*

CROSSES	$1/2D$	$1/4H$	VE	h^2_{ns}
NG/SA/07/0516 x NGB/06/080	112.233	154.660	60.667	0.344
NGB/06/080 x NG/SA/07/0516	162.213	139.836	42.422	0.471
NG/SA/07/0516 x NG/SA/07/0522	220.020	208.994	109.826	0.407
NG/SA/07/0522 x NG/SA/07/0516	249.014	184.254	107.699	0.460
NG/SA/07/0528 x NGB/06/080	118.023	194.958	105.966	0.282
NGB/06/080 x NG/SA/07/0528	196.093	123.470	102.675	0.464

Table 4: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for plant-height in six inter-specific crosses between *A. caillei* and *A. esculentus*.

CROSSES	$1/2D$	$1/4H$	VE	h^2_{ns}
NGAE-96-012-1 x NGB/06/080	470.427	131.626	81.400	0.688
NGB/06/080 x NGAE-96-012-1	325.793	202.01	123.525	0.500
NGEA-96-0067 x NG/SA/07/0516	543.300	170.586	102.970	0.665
NG/SA/07/0516 x NGEA-96-0067	464.503	255.543	99.890	0.568
NGAE-96-0067 x NG/SA/07/0522	455.734	124.332	70.490	0.701
NG/SA/07/0522 x NGAE-96-0067	330.414	219.820	106.906	0.488

Table 5: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for Number of leaves/ plant in eight intra-specific crosses of *A. caillei*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	263.540	179.894	92.283	0.511
NGAE-96-012-1 x OWODE	373.380	100.790	54.615	0.706
OWODE x NGAE-96-0067	271.963	134.739	76.649	0.523
NGAE-96-0067 x OWODE	307.323	93.609	59.939	0.667
NGAE-96-012-1 x OJA-OBA-4	274.993	90.400	67.530	0.635
OJA-OBA-4 x NGAE-96-012-1	230.547	104.064	82.921	0.552

Table 6: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number leaves/ plant in six intra-specific crosses of *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NG/SA/07/0516 x NGB/06/080	116.883	164.352	55.634	0.346
NGB/06/080 x NG/SA/07/0516	160.283	116.732	48.244	0.480
NG/SA/0516 x NG/SA/07/0522	131.273	108.721	50.320	0.452
NG/SA/07/0522 x NG/SA/07/0516	139.240	89.848	55.699	0.489
NG/SA/07/0528 x NGB/06/080	97.907	117.259	60.020	0.356
NGB/06/080 x NG/SA/07/0528	124.794	94.790	57.811	0.464

Table 7: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number of leaves/plant in six inter-specific cross between *A. caillei* and *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NGAE-96-012-1 x NGB/06/080	288.560	61.278	45.854	0.729
NGB/06/080 x NGAE-96-012-1	210.984	100.698	64.977	0.560
NGEA-96-0067 x NG/SA/07/0516	311.180	99.909	61.067	0.659
NG/SA/07/0516 x NGEA-96-0067	235.180	140.322	74.079	0.514
NGAE-96-0061 x NG/SA/07/0519	202.613	64.120	43.020	0.654
NG/SA/07/0519 x NGAE-96-0061	158.633	92.794	50.673	0.525

Environmental variance was smallest for both intra and inter specific crosses in *A. caillei* and *A. esculentus* indicating that length pods was determined by genetic factor (Tables 14 to 16). In the intra-specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability values ranged from 0.444 to 0.620 (moderate). In intra specific crosses in *A. caillei* and inter-specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently higher than dominance, narrow sense heritability ranged from 0.565 (moderate) to 0.0.808 (high) and 0.446 (moderate) to 0.742 (high)

values, respectively. Additive gene effect was more pronounced in inter specific crosses between *A. caillei* and *A. esculentus* and intra specific crosses in *A. caillei* than in intra specific crosses in *A. esculentus*. This implies that the heritable trait (number of pods plant⁻¹) can be transferred faster through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties than intra specific crosses in *A. esculentus*. Alake et al., (2012) had reported that okra yield improvement is highly feasible through intra specific crosses due to high genetic variation among the varieties.

Table 8: Additive genetic effects ($_{1/2}D$), dominances ($_{1/4}H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number of pods/ plant in eight intra-specific crosses of *A. caillei*

CROSSES	$_{1/2}D$	$_{1/4}H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	7.125	4.422	1.063	0.565
NGAE-96-012-1 x OWODE	7.997	2.382	1.147	0.693
OWODE x NGAE-96-0067	6.487	3.952	1.007	0.567
NGAE-96-0067 x OWODE	8.337	0.858	1.129	0.808
NGAE-96-012-1 x OJA-OBA-4	11.980	3.405	2.003	0.684
OJA-OBA-4 x NGAE-96-012-1	09.607	5.076	2.174	0.570

Table 9: Additive genetic effects ($_{1/2}D$), dominances ($_{1/4}H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number of pods/plant in six intra-specific crosses of *A. esculentus*

Crosses	$_{1/2}D$	$_{1/4}H$	VE	h^2_{ns}
NG/SA/07/0516 x NGB/06/080	2.480	1.744	1.361	0.444
NGB/06/080 x NG/SA/07/0516	3.370	1.866	0.607	0.577
NG/SA/0516 x NG/SA/07/0522	2.151	1.616	1.215	0.450
NG/SA/07/0522 x NG/SA/07/0516	2.570	1.229	0.999	0.536
NG/SA/07/0528 x NGB/06/080	2.080	1.360	1.060	0.462
NGB/06/080 x NG/SA/07/0528	2.814	1.016	0.708	0.620

Table 10: Additive genetic effects ($_{1/2}D$), dominances ($_{1/4}H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number of pods/plant in six inter-specific crosses between *A. caillei* and *A. esculentus*

Crosses	$_{1/2}D$	$_{1/4}H$	VE	h^2_{ns}
NGAE-96-012-1 x <i>Clemson spineless</i>	6.574	2.506	1.226	0.606
<i>Clemson spineless</i> x NGAE-96-012-1	4.660	4.322	1.475	0.446
NGEA-96-0067 x NG/SA/07/0516	7.413	3.352	1.134	0.623
NG/SA/07/0516 x NGEA-96-0067	5.647	3.589	1.535	0.524
NGAE-96-0061 x NG/SA/07/0519	7.490	1.605	1.003	0.742
NG/SA/07/0519 x NGAE-96-0061	6.130	2.435	1.369	0.617

Table 11: Additive genetic effects ($_{1/2}D$), dominances ($_{1/4}H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for pod- length in eight intra crosses in of *A. caillei*

Crosses	$_{1/2}D$	$_{1/4}H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	1.470	1.763	0.589	0.385
NGAE-96-012-1 x OWODE	0.884	1.676	0.488	0.290
OWODE x NGAE-96-0067	1.490	1.559	0.493	0.421
NGAE-96-0067 x OWODE	1.097	1.714	0.595	0.322
NGAE-96-012-1 x OJA-OBA-4	1.220	1.565	0.717	0.349
OJA-OBA-4 x NGAE-96-012-1	1.520	1.402	0.779	0.411

Tables 17 to 19 showed that environmental variance was smallest for both intra and inter specific crosses in *A. caillei* and *A. esculentus* indicating that pod yield h^{a-1} was influenced by genes more than the environment. In the intra- specific crosses in *A. esculentus* varieties, dominant variation was at par with additive genetic variation, hence, narrow sense heritability ranged from 0.328 (low) to 0.479 (moderate) values. In intra specific crosses in *A. caillei* and inter- specific crosses between *A. caillei* and *A. esculentus*, additive genetic variance was consistently higher than dominance, narrow sense heritability values ranged from 0.469 (moderate) to 0.759 (high) and from 0.0.499 (moderate) to 0.778 (high) values respectively. Additive gene effect was more pronounced in inter specific crosses between *A. caillei* and *A. esculentus* and intra specific crosses in *A. caillei* than in intra specific crosses in *A. esculentus*. This implies that pod yield h^{a-1} can be transferred faster through intra

specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties than intra specific crosses in *A. esculentus*.

Table 12: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for pod-length in six intra-specific crosses of *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NG/SA/07/0516 x NGB/06/080	0.483	1.044	0.318	0.262
NGB/06/080 x NG/SA/07/0516	0.763	0.694	0.352	0.421
NG/SA/0516 x NG/SA/07/0522	0.556	0.634	0.306	0.373
NG/SA/07/0522 x NG/SA/07/0516	0.880	0.653	0.317	0.476
NG/SA/07/0528 x NGB/06/080	0.554	0.954	0.179	0.328
NGB/06/080 x NG/SA/07/0528	0.700	0.774	0.194	0.420

Table 13: Additive genetic effects ($1/2D$), dominance ($1/4H$) environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for pod-length in eight inter crosses between *A. caillei* and *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NGAE-96-012-1 x <i>Clemson spineless</i>	1.041	0.890	0.376	0.451
<i>Clemson spineless</i> x NGAE-96-012-1	0.537	1.152	0.397	0.257
NGEA-96-0067 x NG/SA/07/0516	1.278	1.092	0.229	0.492
NG/SA/07/0516 x NGEA-96-0067	1.072	1.044	0.355	0.433
NGAE-96-0061 x NG/SA/07/0519	1.420	1.242	0.262	0.486
NG/SA/07/0519 x NGAE-96-0061	1.014	1.688	0.242	0.344

Table 14: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for weight of pods in eight intra-specific crosses of *A. caillei*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	2.153	1.322	0.755	0.509
NGAE-96-012-1 x OWODE	2.840	0.793	0.476	0.660
OWODE x NGAE-96-0067	1.992	1.590	0.565	0.480
NGAE-96-0067 x OWODE	2.510	0.784	0.709	0.627
NGAE-96-012-1 x OJA-OBA-4	5.168	1.164	1.063	0.699
OJA-OBA-4 x NGAE-96-012-1	3.802	1.732	1.562	0.534

Table 15: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for weight of pods in six intra-specific crosses of *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NG/SA/07/0516 x NGB/06/080	1.154	2.092	0.363	0.320
NGB/06/080 x NG/SA/07/0516	1.580	1.572	0.410	0.444
NG/SA/0516 x NG/SA/07/0522	1.414	2.278	0.413	0.345
NG/SA/07/0522 x NG/SA/07/0516	1.928	2.058	0.284	0.452
NG/SA/07/0528 x NGB/06/080	1.728	1.806	0.268	0.454
NGB/06/080 x NG/SA/07/0528	2.168	1.320	0.291	0.570

Table 16: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for weight of pods/plant in eight inter-specific crosses between *A. caillei* and *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NGAE-96-012-1 x <i>Clemson spineless</i>	3.002	1.162	0.407	0.657
<i>Clemson spineless</i> x NGAE-96-012-1	2.326	1.503	0.770	0.506
NGEA-96-0067 x NG/SA/07/0516	3.101	2.022	0.209	0.582
NG/SA/07/0516 x NGEA-96-0067	2.687	1.704	0.236	0.581
NGAE-96-0061 x NG/SA/07/0519	3.79	1.300	0.340	0.698
NG/SA/07/0519 x NGAE-96-0061	2.556	2.466	0.374	0.474

Table 17: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for fresh pod yield per hectare in eight intra-specific crosses of *A. caillei*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
OWODE x NGAE-96-012-1	5,125.190	2,708.520	1,052.960	0.577
NGAE-96-012-1 x OWODE	6,801.820	2,509.560	591.472	0.686
OWODE x NGAE-96-0067	6,189.801	4,902.053	1,719.615	0.483
NGAE-96-0067 x OWODE	7,995.508	3,754.126	909.760	0.624
NGAE-96-012-1 x OJA-OBA-4	8,114.245	1,385.736	1,192.918	0.759
OJA-OBA-4 x NGAE-96-012-1	5,404.828	3,937.689	2,187.971	0.469

Table 18: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for fresh pod yield/hectare in six intra-specific crosses of *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	H^2_{ns}
NG/SA/07/0516 x NGB/06/080	6,971.909	11,464.607	2,805.603	0.328
NGB/06/080 x NG/SA/07/0516	1,129.114	883.863	382.607	0.471
NG/SA/0516 x NG/SA/07/0522	6,355.610	9,337.722	1,515.150	0.369
NG/SA/07/0522 x NG/SA/07/0516	1,464.319	856.185	2001.570	0.339
NG/SA/07/0528 x NGB/06/080	1,163.011	1,115.374	609.234	0.403
NGB/06/080 x NG/SA/07/0528	1,103.491	795.426	313.211	0.479

Table 19: Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for fresh pod yield/plant¹ in six inter-specific crosses between *A. caillei* and *A. esculentus*

Crosses	$1/2D$	$1/4H$	VE	h^2_{ns}
NGAE-96-012-1 x <i>Clemson spineless</i>	5,000.060	1158.636	271.661	0.778
<i>Clemson spineless</i> X NGAE-96-012-1	4773.544	3002.558	503.982	0.577
NGEA-96-0067 X NG/SA/07/0516	7169.589	3231.533	761.756	0.642
NG/SA/07/0516 X NGEA-96-0067	4956.625	2790.637	1208.402	0.553
NGAE-96-0061 X NG/SA/07/0519	5092.435	1411.704	408.751	0.737
NG/SA/07/0519 X NGAE-96-0061	3378.528	2853.924	544.595	0.499

Table 20: Linear correlation matrix between eight agronomic characters and fresh pod yield of nine genotypes of *A. caillei* (okra) under Umudike conditions in 2010 cropping season

	PH	NL	NLB	NF	NP	LP	WP	FPY
PH	1.000							
NL	0.963***	1.000						
NLB	0.963***	0.947***	1.000					
NF	0.855***	0.813**	0.867***	1.000				
NP	0.949***	0.818**	0.935***	0.941***	1.000			
LP	0.367	0.356	0.349	0.304	0.310	1.000		
WP	0.707**	0.786**	0.738**	0.555*	0.671*	0.626*	1.000	
FPY	0.926***	0.951***	0.946***	0.846***	0.944***	0.322	0.800**	1.000

*** = highly significant difference ($p < 0.01$), ** = highly significant difference ($p < 0.01$), * = significant difference ($p < 0.05$). Symbol: Meaning: PH = Plant height, LP = Length of pod, NP = Number of pods/plant¹, NLB = Number of branches/plant¹, NL = Number of leaves/plant¹, WP = Weight of pods, NF = Number of flowers/plant¹, SW = Seed Weight, FPY = Fresh pod yield

The correlation analysis (Table 20) showed that okra pod yield had positive and very highly significant ($P < 0.001$) coefficient with okra height (0.926), number of leaves per plant (0.951), number of pods plant⁻¹ (0.944) and weight of pods (0.800). This implies that increase in these traits would lead to increase in pod yield (Table 19). Eid (2007) and Ariyo (1995) obtained similar results in wheat and okra respectively. Exploitable variations exist within *A. caillei* varieties, *A. esculentus* varieties and between *A. caillei* and *A. esculentus* varieties. These variations are heritable and can be transferred from parents to offspring through intra specific crosses in *A. caillei* or *A. esculentus* and inter specific crosses between *A. caillei* and *A. esculentus*. Higher heritable variations were expressed as high narrow sense heritability values in specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus*. In all their crosses the non-heritable variations (dominant and environmental variations) were smaller than heritable components, thereby confirming that okra height, number of leaves/plant⁻¹, number of pods/plant⁻¹, weight of pods and fresh pod yield ha⁻¹ were mostly under additive genes influence. This implies that selections for yield improvement can be made during early segregating generations of genotypes raised through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* varieties. Since the non-heritable components were higher than additive genetic variation in genotypes raised

through intra crosses in *A. esculentus*, the traits involved were mostly influenced by dominant and environmental genetic effects. Selection of traits for crop improvement could be done at later stages of segregating generations. Based on their positive and highly significant coefficient of correlation with yield, the traits that could be selected in the breeding programme for pod yield improvement include: okra height, number of leaves plant⁻¹, number of podsplant⁻¹, and weight of pod. Genes transfer from parents to offspring through hybridization would be faster through specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A. esculentus* than specific crosses in *A. esculentus*.

CONCLUSION

Genetic variance in okra that could be transmitted to the next generation of offspring was larger in intra specific crosses in *A. caillei* and inter specific crosses between *A.caillei* and *A.esculentus*, than intra specific crosses in *A. esculentus*. Okra pod yield improvement would be faster through intra specific crosses in *A. caillei* and inter specific crosses between *A. caillei* and *A.esculentus* than intra specific crosses in *A. esculentus*. This shows that *A. esculentus* improvement using *A. caillei* germplasm is a viable option in okra breeding programme. The characters to select for such pod yield improvement program include, height, number of leaves plant⁻¹, number of podsp lant⁻¹ and weight of pods.

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