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Variability, correlation and heritability studies in West African okra (*Abelmoschus caillei*)

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Nine (9) varieties of *Abelmoschus caillei* were evaluated for yield and yield components in a randomized complete block design replicated three times at the Michael Okpara University of Agriculture, Umudike. F₁ hybrids were raised through crosses between parents. Backcross₁, Backcross₂ and F₂ plants were raised from F₁. The total variance was partitioned into genetic and environmental variances and showed that large heritable variations existed among the varieties. High genotypic coefficient of variation, high broad sense heritability (82.42 – 94.03) estimates and high genetic advance (32.49 -40.47) with moderate to high narrow sense heritability (0.500 – 0.810) for plant height, number of leaves/plant, number of pods/plant and their high correlation coefficients, with fresh pod yield confirmed that vast potentials exist for *A. caillei* improvement through selection of desirable characters such as plant height, number of leaves/plant and number of pods/plant. Selection from crosses between these genotypes: NGAE-96-012-1x OWOE, NGAE-96-0067 x OWOE and NGAE-96-0067 x NCRI-02 with very high narrow sense heritability estimates could be made during early segregating generations.

Key words: *Abelmoschus caillei*, yield, correlation studies, phenotypic variation, heritability.

INTRODUCTION

West African okra (*A. caillei* (A. Chev) is an important vegetable crop of tropical and subtropical world. A short day plant with green stem (Adeniji et al., 2007) which has slight traces of red pigmentation in some accessions (Adeniji, 2003), and is cultivated for fresh pods, leaves and seeds. Siemonsma (1982) reported that *A. caillei* contained 194 diploid chromosomes against 130 of *A. esculentus*, indicating that *A. caillei* constitutes a new okra species. Its high yield and hardiness have made it a major source of okra pods in Nigeria and cultivation is progressively replacing *A. esculentus* (Kehinde, 1999). It has potential for industrial, nutritional and biomedical uses in developing countries, but is under-utilized in sub-Saharan Africa (Adeniji et al., 2007). *A. caillei* is photoperiod sensitive (Kehinde, 2001; Adeniji and Kehinde, 2004). Okra contains moderate levels of some

essential mineral and vitamins which are important for body metabolic processes that utilize carbohydrates, proteins and fats (FAO, 2008). The immature fruits are eaten either fresh or prepared by boiling or frying, and used in soup and stews. Pods and seeds are rich in phenolic compounds and hydroxycinnamic derivatives (Arapitsas, 2008). Dietary portfolio studies have indicated that eating plant based diets (rich in viscous fibres) may be an effective strategy of reducing low - density lipoprotein cholesterol in humans. Fortunately, okra and eggplant are the most important vegetable sources of viscous fibre (Kendall and Jenkins, 2004). Genetic improvement using available germplasm within the genus *Abelmoschus* is highly desirable to improve its yield, since unavailability of improved and early maturing varieties are the major constraints in the cultivation of *A. caillei* (Kehinde, 1999). Improvement of any crop depends on the magnitude of genetic variability, heritability and genetic advance of yield related traits (Nwofia and Adikibe, 2012; Chinatu and Ukpaka, 2016).

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Heritability is the proportion of observed variability, which is due to heredity (Uguru, 2000). Estimation of heritability in a population depends on partitioning of observed variation into genetic and environmental components (Abdelmageed, 2010a). Heritability can be expressed in broad or narrow sense. Broad sense heritability indicates whether there is sufficient genetic variation present in a population (Walter, 1987), while narrow sense heritability measures the relative importance of additive portion of genetic variance that can be transmitted to the next generation of offspring. This is particularly important when heritability is used to predict gain expected from selection for a character (Walter, 1987; Fehr, 1987; Eid, 2007).

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 (Mohammadi et al., 2003; Kashiani et al., 2010). Direct selection for yield is deceptive as it is highly influenced by fluctuating environment and large genotype by environmental interactions (Talebi et al., 2007; Kashiani and Saleh, 2010). Thus, it is necessary to select plants based on characters that have positive relationships with yield, since it often lead to changes in other components due to the polygenic nature of yield (Ariyo, 1995). Correlation studies enable the breeder to know the strength of relationships between various characters as well as the magnitude and direction of changes expected during selection (Ariyo, 1995; Nakawuka and Adipala, 1999). The correlation coefficient analysis is useful in the selection of several traits that influence yield simultaneously (Yasin and Singh, 2010; Menkir, 2008). The objectives of this study were to ascertain the level of variations within the *A. caillei* varieties, determine heritability estimates, genetic gain and relationships between okra pod yield and other agronomic traits studied.

MATERIALS AND METHODS

The experiments were carried out at the Western Farm of the Michael Okpara University of Agriculture, Umudike from 2009 to 2011. The planting materials collected from National Biotechnology centre, Ibadan were nine (9) varieties of *Abelmoschus caillei* (A. Chev) Stevels which were as follows: NGAE-96-012-1, NGAE-96-0062 -2, OJA - OBA 4, CEN - 012, NGAE - 96 - 0067, NGAE - 96 - 0061, NGAE - 96 - 0068, OWODE, and NCRI - 02. After hybridization, some F₁ hybrids were backcrossed with parents to raise backcross1 (BC₁) and backcross2 (BC₂) seeds while others were selfed to raise F₂ seeds. Zero level of success was recorded for crosses involving NGAE-96-0068, NGAE-96-0062 and CEN-012. Comparison blocks were established to evaluate the traits of parents, F₁, F₂, BC₁ and BC₂. The treatments

consisted of 54 genotypes made up of 8 parents, 16F₁, 10F₂, 11BC₁ and 9BC₂, planted in a randomized complete block design replicated three times. Data were collected on the following: plant height plant⁻¹, number of leaves plant⁻¹, number of lateral branches plant⁻¹, number of flowers plant⁻¹, number of pods plant⁻¹, length of pods, weight of pods and fresh pod yield plant⁻¹. Mean, range and standard error were obtained in respect of data generated. Data were analyzed by one way analysis of variance, (ANOVA). The least significant differences (0.05) were calculated (Snedeco and Cochran, 1989). The gross variability was partitioned into genetic and non - genetic components. Phenotypic, genotypic and error variances were estimated using the formulae by Wrikke and Weber (1986), where

$$\sigma^2 P = \frac{MSG}{r}, \sigma^2 G = \frac{MSG - MSE}{r}, \sigma^2 E = \frac{MSE}{r} \quad MSG,$$

MSE and r are the mean squares genotypes, mean square error and number of replication respectively.

$$PCV = \frac{\sigma P}{\text{mean}} \times \frac{100}{1}, \quad GCV = \frac{\sigma G}{\text{mean}} \times \frac{100}{1}. \quad PCV, \quad GCV$$

and ECV are phenotypic, genotypic and environmental coefficients σ_{Ph} , σ_g and σ_e were phenotypic, genotypic and environmental standard deviations respectively, while P CV, GCV, ECV and X were phenotypic, genotypic, environmental coefficients of variations and grand mean, respectively. Broad sense heritability (h^2_B) was expressed as the ratio of genotypic (VG) to the phenotypic (VP) variances as described by Allard (1991). The additive component (1/2D) of the genetic variation was obtained as; $1/2D = 2VF_2 - (VBC_1 + VBC_2)$ (Hanson et al., 1956). Where, VF_2 = second filial generation variances: VBC_1 = Backcross 1 variance and VBC_2 = Backcross -2 variances. Environmental variance (VE) was obtained as

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

where VP_1 , VP_2 , and VF_1 were parent-1, parent-2 and F₁ variances respectively, (Hanson et al., 1956). Dominance (1/2H) was obtained as $1/2H = VBC_1 + VBC_2 - (1/2D + 2VE)$. Narrow sense heritability was obtained as;

$$\frac{1/2D}{1/2D + 1/4H + VE} \quad (\text{Hanson et al., 1956}).$$

Correlation analysis was done using SPSS to determine the effect of yield attributes on pod yield.

RESULTS AND DISCUSSION

Evaluation studies showed that the 6 okra varieties (parents) were highly significantly different ($P < 0.001$) with respect to plant height, number of leaves, number of

Table 1. Phenotypic, environmental, genotypic variances and heritability estimates of 6 agronomic characters of 6 okra genotypes (parents) in Umudike.

| CHARACTERS | Phenotypic variances(σ^2_{ph}) | Environmental variances(σ^2_e) | Genotypic variances (σ^2_g) |
|------------------|---|---|--------------------------------------|
| Plant height | 2218.56 | 340.94 | 1877.66 |
| Number of leaves | 2020.64 | 197.69 | 1822.95 |
| Number of pods | 23.52 | 3.89 | 19.63 |
| Length of pods | 0.22 | 0.21 | 0.01 |
| Weight of pods | 2.93 | 0.51 | 2.41 |
| Fresh pod yield | 5161.84 | 257.81 | 4853.93 |

Table 2. Mean, Range, Phenotypic and Genotypic co-efficient of variation, broad sense heritability and genetic gain for 6 economically important characters of 6 okra genotypes (parents) in Umudike.

| Plant attribute | Mean | Range | PCV | GCV | H ² _{bs} | GA |
|------------------|---------|-----------------|-------|-------|------------------------------|-------|
| Plant height | 163.32 | 48.53-267.20 | 36.86 | 33.90 | 84.63 | 40.04 |
| Number of leaves | 106.17 | 22,20 -176.50 | 42.34 | 40.22 | 90.22 | 40.47 |
| Number of pods | 13.79 | 4.00-21.17 | 35.18 | 32.14 | 83.46 | 32.49 |
| Length of pods | 11.18 | 8.50 -12.80 | 4.23 | 00.94 | 05.00 | 01.85 |
| Weight of pods | 19.46 | 15.85-22.07 | 8.79 | 07.98 | 82.42 | 06.40 |
| Fresh pod yield | 4845.07 | 1270.93-7944.72 | 47.12 | 45.71 | 94.03 | 32.58 |

Table 3. Correlation coefficient (r) between fresh pod yield/ha and other agronomic parameters in Parent of okra.

| | PH | NL | NP | LP | WP | FPY |
|-----|-------|------------------------|----------|---------|----------|----------|
| PH | 1.000 | 0.958*** ⁸⁴ | *** | - 0.309 | 0.075 | 0.971*** |
| NL | | 1.000 | 0.957*** | - 0.252 | 0.202 | 0.960*** |
| NP | | | 1.000 | - 0.318 | 0.029 | 0.959*** |
| LP | | | | 1.000 | 0.675*** | - 0.144 |
| WP | | | | | 1.000 | 0.265 |
| FPY | | | | | | 1.000 |

** Implies highly significant difference ($p < 0.01$), ***Impliesvery highly significant difference ($p < 0.001$),

*Implies significant difference ($p < 0.05$)

Symbol: Connotation

PH = Plant height; LP = Length of pod; NP = Number of pods/ plant; NF = Number of flowers/ plant, NLB = Number of lateral branches/plant; NL = Number of leaves/plant; WP = Weight of pods
FPY = Fresh pod yield

pods, weight of pods and fresh pod yield. Phenotypic, genotypic and environmental variances were calculated (Table 1). Genotypic variance was consistently higher than environmental variance, indicating that genotypic component contributed more to total variance, which implied that heritable variations exist among the traits except length of pods. Phenotypic coefficient of variation (PCV), genotypic coefficient (GCV) of variations, heritability (h^2_{ns}) estimates and genetic advance (GA) were computed (Table 2). The PCV was higher than the GCV for all the characters, suggesting that the environment had effect on expression of the traits. But GCV was consistently far higher than ECV for all the traits except pod length, indicating that genes in these genotypes influenced the inheritance of these traits more than the environment. The same trend was reported by Baye (2002) in *V. galamensis*, Nwofia and Adikibe (2012) in *Ocimum gratissimum* and Chinatu and Ukpaka (2016)

in *Piper guineense*. Partitioning of the total phenotypic variance of each character into heritable and non-heritable components is useful in determining the proportion of heritable variations that could be explored during selection for superior individuals (Chinatu and Okocha, 2006). The high genotypic variance showed that the genes contributed more to the characters of study than environmental variance. Broad sense heritability estimates obtained were high except in pod length (Table 2). This showed that large proportions of exploitable variations are existing within these genotypes. From Table 2, Genetic advance was high in all the traits with the exception of pod-length and weight of pod. This implied that these large variations within these genotypes can be transferred to their progenies, since these traits are expected to be under the control of additive gene action. From Tables 3, 4, 5, 6 and 7, correlation studies revealed positive and highly significant ($P < 0.01$)

Table 4. Correlation coefficient (r) between fresh pod yield/ha and other agronomic parameters in F₁ hybrids of okra.

| | PH | NL | NP | LP | WP | FPY |
|-----|-------|----------------------|----------------------|--------------------|---------------------|----------------------|
| PH | 1.000 | 0.932 ^{***} | 0.848 ^{***} | 0.316 [*] | 0.658 ^{**} | 0.452 ^{**} |
| NL | | 1.000 | 0.888 ^{***} | 0.298 [*] | 0.742 ^{**} | 0.542 ^{**} |
| NP | | | 1.000 | 0.283 [*] | 0.745 ^{**} | 0.282 [*] |
| LP | | | | 1.000 | 0.433 ^{**} | 0.395 ^{**} |
| WP | | | | | 1.000 | 0.864 ^{***} |
| FPY | | | | | | 1.000 |

Table 5. Correlation coefficient (r) between fresh pod yield/ha and other agronomic parameters in F₂ of okra.

| | PH | NL | NP | LP | WP | FPY |
|-----|-------|----------------------|----------------------|-------|----------------------|----------------------|
| PH | 1.000 | 0.965 ^{***} | 0.955 ^{***} | 0.145 | 0.527 ^{**} | 0.955 ^{***} |
| NL | | 1.000 | 0.956 ^{***} | 0.110 | 0.586 ^{***} | 0.968 ^{***} |
| NP | | | 1.000 | 0.114 | 0.443 [*] | 0.980 ^{***} |
| LP | | | | 1.000 | -0.111 | -0.144 |
| WP | | | | | 1.000 | 0.597 ^{***} |
| FPY | | | | | | 1.000 |

Table 6. Correlation coefficient (r) between fresh pod yield/ha and other agronomic parameters in backcross1 generation of okra.

| | PH | NL | NP | LP | WP | FPY |
|-----|-------|----------------------|----------------------|--------|----------------------|----------------------|
| PH | 1.000 | 0.953 ^{***} | 0.948 ^{***} | 0.031 | 0.625 ^{**} | 0.946 ^{**} |
| NL | | 1.000 | 0.947 ^{***} | -0.089 | 0.741 ^{***} | 0.967 ^{***} |
| NP | | | 1.000 | -0.028 | 0.600 ^{**} | 0.980 ^{***} |
| LP | | | | 1.000 | -0.271 [*] | -0.083 |
| WP | | | | | 1.000 | 0.741 ^{***} |
| FPY | | | | | | 1.000 |

Table 7. Correlation coefficient (r) between fresh pod yield/ha and other agronomic parameters in backcross2 generation of okra.

| | PH | NL | NP | LP | WP | FPY |
|-----|-------|----------------------|----------------------|---------------------|---------------------|----------------------|
| PH | 1.000 | 0.921 ^{***} | 0.880 ^{**} | 0.143 | 0.531 ^{**} | 0.911 ^{***} |
| NL | | 1.000 | 0.858 ^{***} | 0.364 [*] | 0.557 ^{**} | 0.902 ^{***} |
| NP | | | 1.000 | 0.448 ^{**} | 0.294 [*] | 0.949 ^{***} |
| LP | | | | 1.000 | -0.017 | 0.495 ^{**} |
| WP | | | | | 1.000 | 0.491 ^{**} |
| FPY | | | | | | 1.000 |

^x ^{xx} Implies highly significant difference (p<0.01), ^{xxx} Implies very highly significant difference (p<0.001).

^{*} Implies significant difference (p<0.05).

Symbol: Connotation

PH = Plant height; LP = Length of pod; NP = Number of pods/ plant; NF = Number of flowers/ plant.

NLB = Number of lateral branches/plant; NL = Number of leaves/plant;

WP = Weight of pods.

FPY = Fresh pod yield.

association between plant height, number of leaves, number of pods, weight of pods and fresh pod yield/ha in parents, F₁, F₂, BC₁ and BC₂. This implied that these traits affected pod yield ha⁻¹ significantly. Their direct

selection in okra breeding improvement programme may lead to genetic improvement of okra. Positive and highly significant association between plant height, number of leaves, number of pods, weight of pods and fresh pod

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

| Crosses | $1/2D$ | $1/4H$ | 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 |
| NCRI-02 x NGAE-96-0067 | 650.176 | 253.544 | 63.934 | 0.672 |
| NGAE-96-0067 x NCRI-02 | 798.470 | 194.211 | 54.218 | 0.763 |
| 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 9. 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 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 |
| NCRI-02 x NGAE-96-0067 | 244.270 | 140.396 | 62.235 | 0.547 |
| NGAE-96-0067 x NCRI-02 | 321.510 | 83.905 | 30.743 | 0.725 |
| 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 10. Additive gene effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2_{ns}) for number of pods/ plant in eight crosses of *A. caillei*.

| CROSSES | $1/2D$ | $1/4H$ | 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 |
| NCRI-02 x NGAE-96-0067 | 10.683 | 5.736 | 2.097 | 0.578 |
| NGAE-96-0067 x NCRI-02 | 11.980 | 4.007 | 1.747 | 0.675 |
| 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 |

yield/ha have also been reported by Adeniji and Aremu (2007) and Chinatu et al. (2014).

From Tables 8 to 13, the additive ($1/2D$) component of genetic variability was consistently higher than non additive ($1/4H$) and environmental (VE) components in plant height, number of leaves, number of pods, and weight of pods. This confirms that plant height, number of leaves/plant, number of pods/plant and weight of pods/plant were under additive gene effects. This agreed with the findings of Abdelmageed, (2010b), and implied

that these traits are highly heritable. Plant height, number of leaves/plant, number of pods/ plant and fresh pod yield are most heritable in the genotypes NGAE-96-012-1x OWODE, NGAE-96-0067 x OWODE, NGAE-96-0067 x NCRI-02 and NGAE-96-012-1 x OJA-OBA-4. Since plant height, number of leaves/plant, number of pods/ plant and fresh pod yield/ha, have high correlation coefficient with yield, high genetic heritability estimates and genetic advance, early generation selection among the segregating populations of these genotypes is

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

| CROSSES | $1/2D$ | $1/4H$ | VE | H^2ns |
|---------------------------|--------|--------|-------|---------|
| 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 |
| NCRI-02 x NGAE-96-0067 | 0.788 | 0.762 | 0.503 | 0.384 |
| NGAE-96-0067 x NCRI-02 | 0.528 | 1.186 | 0.421 | 0.247 |
| 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 |

Table 12. Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2ns) for weight of pods in eight crosses of *A.caillei*.

| CROSSES | $1/2D$ | $1/4H$ | VE | H^2ns |
|---------------------------|--------|--------|-------|---------|
| 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 |
| NCRI-02 x NGAE-96-0067 | 2.480 | 1.324 | 0.697 | 0.551 |
| NGAE-96-0067 x NCRI-02 | 2.962 | 1.070 | 0.583 | 0.642 |
| 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 13. Additive genetic effects ($1/2D$), dominances ($1/4H$), environmental variances (VE) and narrow sense heritability estimates (h^2ns) for fresh pod yield/ha in eight of *A. caillei*.

| CROSSES | $1/2D$ | $1/4H$ | VE | H^2ns |
|---------------------------|-----------|-----------|-----------|---------|
| 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 |
| NCRI-02 x NGAE-96-0067 | 5,070.102 | 2,501.201 | 1,875.044 | 0.536 |
| NGAE-96-0067 x NCRI-02 | 5760.926 | 1,733.609 | 1,475.403 | 0.642 |
| NGAE-96-012-1 x OJA-OBA-4 | 8,114.245 | 1,385.736 | 1,192.918 | 0.759 |
| OJA-OBA-4 xNGAE-96-012-1 | 5,404.828 | 3,937.689 | 2,187.971 | 0.469 |

worthwhile, while genotypes with traits that have moderate narrow sense heritability estimates and moderate genetic advance could be selected during the later generations. This is consistent with the findings of Kehinde (2001) and Adeniji *et al.*, (2007) for pod yield in *A. caillei*.

Conclusions

This study has shown that large genetic (heritable) variations exist within West African okra, which can be exploited for improvement of *A. caillei* through breeding. The high significant correlation coefficients between plant height, number of leaves /plant, number of pods/plant, weight of pods and fresh pod yield showed that these

traits moderated fresh pod yield ha^{-1} . The high genetic variance, high genotypic coefficient of variation, high broad sense heritability estimates, high genetic advance and moderate to high narrow sense heritability for plant height, number of leaves/ plant, number of pods/plant and weight of pods showed that selection of these traits would lead to improvement in fresh pod yield of *A. caillei*. Selection from crosses between the varieties: NGAE-96-012-1x OWODE, NGAE-96-0067 x OWODE NGAE-96-0067 x NCRI-02 and NGAE-96-012-1 x OJA-OBA-4 with very high narrow sense heritability could be made during early segregating generations. Genotypes (OWODE x NGAE-96-012-1, OWODE x NGAE-96-0067, OJA-OBA-4 x NGAE-96-012-1) with traits that have moderate narrow sense heritability estimates and high genetic variability could be selected during later generations for genetic

improvement of fresh pod yield of *A. caillei*.

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