

Inheritance of seed yield and its components in oleaginous gourd *Lagenaria siceraria* (Molina) Standl

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ABSTRACT: To study the nature and magnitude of inheritance of seed yield and its components in three crosses of *L. siceraria* (Molina) Standl accessions involving four diverse parents under two environments, generation mean analysis was used seed yield and its components. Generations developed six generations, (P₁, P₂, F₁, F₂, BC₁P₁ and BC₁P₂) were planted for evaluation in a randomized complete block design with three replications. The result showed that the additive-dominance model was adequate in explaining the inheritance of seed yield and its components. This was ascribed to a non significant estimate of A, B and C scaling tests. The results of the generation mean analysis indicated that the additive genetic effects (*d*) significantly accounted for a large proportion of variability observed for fruit weight, seed number and 100-seed weight in the crosses evaluated. An additive genetic effect suggests that selection among segregating population could provide an average improvement in the performance of seed yield and its components in subsequent generations. Broad and narrow-sense heritability was estimated to be high ($\geq 0,5$) for yield and its components at Abidjan and Manfla. That indicate a great genetic effect on these traits expression. Additive components played a major role in improving the yield component that shown strong heritability whatever environment. The number of quantitative factors revealed multigenic appearance. These results confirm the appropriateness of these yield components in improving plant efficiency. A recurrent selection scheme has proposed as an effective selection strategy for improving oleaginous gourd *Lagenaria siceraria*.

KEYWORDS: Accessions, Generation mean analysis, Scaling test, Segregating population, multigenic.

1 INTRODUCTION

Oleaginous gourd, *Lagenaria siceraria* (Molina) Standl, is a member of Cucurbitaceae family. It is a prostrate-growing, herbaceous and monoecious plant easily distinguished by its white flowers [1]. *L. siceraria* is believed to be of African and Asian origin [2]. This specie is well adapted to various cropping systems, characterised by minimal inputs [3]. Juvenile shoots and fruits of *L. siceraria* are sliced and cooked as vegetables throughout South Africa [4]. In Côte d'Ivoire, Oleaginous gourd is mainly cultivated for seed consumption. Mature seeds are roasted and crushed to a paste used to thicken stews, while seed oil extract is an ideal alternative for vegetable oil [5], [6]. *L. siceraria* shows great diversity on yield components [7]. Seed yield per plant varied from 12 to 56 g per plant [8]. These plants are cultivated at small scale by women for their oleaginous seeds that are a great importance in the sociocultural live of several people [8]. Its cultivation permits achievement of food security for family unit and represents a potential source of additional income for rural women, who are the main producers in West Africa [9]. Increased production and use of these cucurbits can result in addition of food security a diversify of small farmer's income. Despite several studies conducted on cucurbit edible seed [10], [11] their production are weak. Therefore, identification of yield components is a fundamental step in the work prior to the implementation of plant variety improvement programs [12]. Indeed, knowledge of yield components of a crop facilitates and guides the search for molecular markers that lighten and accelerate the work of variety creation [12, 13]. This is how work carried out by [8] allowed the determination of yield components which are traits strongly and directly linked to yield. These characteristics which are the fruit weight, of 100 seeds

weight and the number of seeds can be used as selection criteria for the establishment of a breeding program for the oil gourd *Lagenaria siceraria*. However, to know if a yield component can actually contribute to varietal improvement following conventional crosses, it is essential to have a precise knowledge of its genetic basis [14], [15]. Such data are useful in determining the breeding approach to adopt in order to identify the best genotypes and to predict the response of plants to selection [16, 17], [18]. The works carried out by [19] on the calabash type have shown showed that the seed weight, fruit weight and 100 seed weight exhibited high broad-sense heritability with a low number of genes. Thus the traits controlled by a low number of genes have high heritability values in early generations. Very little genetic knowledge is available on genetic components and genes interactions yield components of oleaginous type of *L. siceraria*. Among other methods to study the quantitative inheritance of traits, a design based on the measure of variance from six generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 , and BC_1P_2) can be used to estimate environmental, additive, dominance, and phenotypic variances [20], [21]. The objective of this study is to determine genetic basis of yield components of oleaginous form of *Lagenaria siceraria*. In particular, it involves determining the type of variation that these components express, the interactions between the allele genes that govern their expression, the influence of the environment and their heritability. The results of this study should make it possible to propose a selection strategy optimizing genetic gain.

2 MATERIAL AND METHOD

2.1 PLANT MATERIALS, SITES AND EXPERIMENTAL DESIGN

In the experiment, we used three families developed from three crosses of *Lagenaria siceraria* inbred cultivars or lines to estimates the heritability of fruit weight, seed weight, 100-seed weight. Each of the three high yielding cultivars NI283, NI354 and NI106 was crossed with the low yielding cultivar NI215. These accessions were sourced from the germplasm collection of the University of Nangui Abrogoua. In this way three families were developed; 'NI283 x NI215', 'NI354 x NI215' and 'NI106 x NI215'. For each family, we developed six related generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 , and BC_1P_2) on both sites, Abidjan and Manfla. At each site, all six generations of the same family were planted in the following number and order P_1 (20); P_2 (20); F_1 (40); F_2 (100); BC_1P_1 (30) and BC_1P_2 (30).

The first experimental site was located in Abidjan at University of Nangui Abrogoua, between 5°17'N-5°31' and longitudes 3°45'W-4°22'W. The second experimental was conducted in the village of Manfla, located in centre (latitudes 7°00N – 7°26N and longitudes 6°00W- 6°30W) during 400 km north Abidjan.

Three families were developed from three crosses of *L. siceraria* cultivars or lines (NI283, NI354, NI106 and NI215). These cultivars were sourced from the germplasm collection of the University of Nangui Abrogoua. These lines are obtained after three self pollinated generations. F_1 seeds were planted and each F_1 plant was allowed to self pollinate to produce F_2 seeds. Subsequent flower buds were backcrossed to parents to obtain the BC_1P_1 and BC_1P_2 .

Field evaluation of the parental P_1 , P_2 , F_1 , F_2 and BC_1 was carried out at the University of Nangui Abrogoua. The experimental layout was a randomized completed block design with some replications. Planting was done according to a completely randomized block design with three replications. Each plot was 96 x 30 m. The holes at depth of 3 cm and they were arranged in rows at spacing of 3 m between and within rows. Two or three seeds of each generation were planted per hole, with intra row spacing of 3 m. The plots were hoe weeded regularly to prevent any interaction between plant materials and weed load. Disease and pest control was carried out using a carbamate-based insecticide applied when necessary. The field was harvested when more than 90% of the fruit were ripe.

2.2 DATA ANALYSIS

We tested the F_2 data for homogeneity of variances using Bartlett's method.

The individual scaling tests of [25] were employed to test the adequacy of additive-dominance model for seed yield and its components in each case i.e.:

$$A=2\times\mu(BC_1P_1)-\mu(F_1)-\mu(P_1)$$

$$B=2\times\mu((BC_1P_2))-\mu(F_1)-\mu(P_2)$$

$$C=4\times\mu(F_2)-2\times\mu(F_1)-\mu(P_1)-\mu(P_2)$$

The generation mean analysis was conducted under the assumptions that observed variation was due to additive and dominance effects, with no epistasis or linkage using the method of [22] where M is midpoint, d is the additive genetic effects, h is the dominance genetic equations:

$$M = \mu (F_2)$$

$$d = \mu (BC_1P_1) - \mu (BC_1P_2)$$

$$h = 2 \times \mu (BC_1P_1) + 2 \times \mu (BC_1P_2) - 4 \times \mu (F_2) + \mu (F_1) - \frac{1}{2} \times \mu (P_1) - \frac{1}{2} \times \mu (P_2)$$

$$i = 2 \times \mu (BC_1P_1) + 2 \times \mu (BC_1P_2) - 4 \times \mu (F_2)$$

$$j = 2 \times \mu (BC_1P_1) - 2 \times \mu (BC_1P_2) - \mu (P_1) + \mu (P_2)$$

$$l = \mu (P_1) + \mu (P_2) + 4 \times \mu (F_2) - 4 \times \mu (BC_1P_1) - 4 \times \mu (BC_1P_2)$$

P_1 is the parent with a high mean value, while P_2 is the parent with a lower mean value. BC_1P_1 and BC_1P_2 are corresponding backcrosses to parent P_1 and parent P_2 , respectively.

ESTIMATE OF VARIANCE

The variance components E , D , A , P and G representing the environmental variance, additive variance, dominance variance, phenotypic and genotypic variance respectively were calculated as specified by the method of [27], [28], [29] as follows:

$$\sigma^2 (A) = 4 (\sigma^2 (BC_1P_1) + \sigma^2 (BC_1P_2) - \sigma^2 (F_1) - \sigma^2 (E))$$

$$\sigma^2 (D) = 2 \times \sigma^2 (F_2) - (\sigma^2 (BC_1P_1) + \sigma^2 (BC_1P_2))$$

$$\sigma^2 (E) = \frac{\sigma^2 (P_1) + \sigma^2 (P_2) + [2 \times \sigma^2 (F_1)]}{4}$$

$$\sigma^2 (P) = \sigma^2 (F_2)$$

$$\sigma^2 (G) = \sigma^2 (P) - \sigma^2 (E)$$

Where $\sigma^2 (P)$; $\sigma^2 (F_1)$; $\sigma^2 (F_2)$; $\sigma^2 (BC_1P_1)$; $\sigma^2 (BC_1P_2)$ are the variances of parental, F_1 , F_2 and Backcross generation respectively. Approximate variations of these variances were estimated.

ESTIMATION OF HERITABILITY

Broad (H^2) and narrow (h^2) sense heritability were estimated based on the formula:

Broad-sense heritability:

$$(H^2) = \frac{\sigma^2 (G)}{\sigma^2 (P)}$$

Narrow-sense heritability:

$$(h_n^2) = \frac{\sigma^2 (A)}{\sigma^2 (P)}$$

Negative estimates should be considered equal to zero [23] but should be reported" in order to contribute to the accumulation of knowledge, which may, in the future, be properly interpreted [24].

Number of quantitative factor:

The number (N) of factors actually involved in the expression of a given quantitative traits was estimated using the means (μ) of the different generations according to the following formula.

$$N = \frac{D^2}{8(\sigma^2(F_2) - \sigma^2(F_1))}$$

With D which represents the numerical value of the difference between the Means of the two parental lines.

$$D = (\mu_{P2} - \mu_{P1})$$

3 RESULTS

3.1 EFFECT OF THE ENVIRONMENT AND FAMILIES

Multivariate analysis of variance indicates that site study has a significant effect on the performance of families (table1). Indeed, various parameters evaluated vary significantly from one site to another ($P < 0.001$). Likewise, the performances of generations differ from each other within the same locality regardless of the trait studied ($P < 0.001$). Analysis of the study site-family interaction shows that the study site does not influence the variability between generations for all the traits studied ($P > 0.05$). Whatever the environment, wide variability can be observed between parental generations and F_1 , F_2 and BC_1 hybrids.

Table 1. Effect of environment, inter-family variability and study site-family interaction on yield components

| Traits | Sites | Family | Interaction |
|-----------------|----------|----------|-------------|
| Fruit weight | 6,64*** | 43,81*** | 25,05*** |
| 100-Seed Weight | 11,36*** | 23,93*** | 9,79*** |
| Number of seed | 24,25*** | 41,25*** | 20,88*** |
| See weight | 2,43*** | 46,97*** | 24,24*** |

Value of test statistic test (Frequency followed by Probability in asterisk) ***Very significant

3.2 GENERATION MEAN

The mean values of seed yield and those of its components were subjected to individual tests or scaling test [21]. The results of these tests showed that the parameters A, B, C are not significantly different from zero (Table 2). This information reveals that only the model of additivity and dominance could explain the mode of action of genes in the transmission of traits. The six-parameter model was therefore used to determine the type and extent of action of the genes that govern the transmission of the characteristics studied (Table 2). Fruit weight (FW) showed a positive additive effect (d) at crosses. For C1 cross at Manfla, although a positive value is observed, it is not significant. As for dominance, negative values are recorded for cross C1 at both sites and for cross C3 at Manfla. In addition, the other crossings presented positive values on the sites. The same trend is observed for the interaction components (i). On the other hand, additivity x dominance (j) values obtained are all negative, except in the C3 cross made at Manfla. Finally, with regard to dominance x dominance (l), only crosses C1 in Abidjan and C2 in Manfla are positive. All other recorded values are negative. 100 seed weight (100-SW) showed a positive additive effect (d) in all the crosses made. Only the C1 cross in Abidjan showed a significant additivity effect. For the dominance (h), negative values were obtained in the C1 cross in Abidjan and in the Manfla crosses. The same trends were observed for the parameter additivity x additivity (i). As for the additivity x dominance interaction effect, non-significant negative values were observed in crosses C2 and C3 in Abidjan and C1 and C3 in Manfla. For the parameter dominance x dominance (l) non-significant positive values were recorded only in the crossings C2 in Abidjan and C3 in Manfla. Regarding the number of seeds (NS), positive values were observed in the media except for the C3 cross in Abidjan which presented a negative value. A positive and significant effect of additivity was observed in the C2 crosses of both sites.

Table 2. Effect of genes through Hayman's six-parameter model for yield components of *Lagenaria siceraria* in Abidjan and Manfla

| | | Model of six parameters | | | | | |
|---------|---------------|---------------------------|-----------------------|----------------------|------------------------------------|-----------------------------------|----------------------------------|
| | | <i>M</i> (Mean of F_2) | <i>d</i> (additivity) | <i>h</i> (dominance) | <i>i</i> (additivity x additivity) | <i>j</i> (additivity x dominance) | <i>l</i> (dominance x dominance) |
| ABIDJAN | | | | | | | |
| FW | | | | | | | |
| C1 | 659.72±210.5 | 148.33±26.04* | -276.37±1216.72 | -52.65±1199.32 | -291.23±691.02 | 430.67±1618.13 | |
| C2 | 588.51±217.91 | 370.83±27.11* | 29.24±1035.48 | 226.95±1026.53 | -23.32±640.62 | -144.74±1456.31 | |
| C3 | 557.39±193.35 | 241.17±18.39* | 234.65±120.46 | 328.10±856.39 | -364.65±441.18 | -1151.40±1114.61 | |
| 100-SW | | | | | | | |
| C1 | 14.72±3.31 | 2.91±0.28* | -1.96±14.61 | -0.62±14.36 | 1.33±6.70 | -5.06±18.28 | |
| C2 | 12.28±2.75 | 0.77±3.90 | 3.97±13.63 | 2.89±13.50 | -0.42±8.34 | 2.23±19.63 | |
| C3 | 12.44±2.42 | 0.25±2.82 | 6.33±18.12 | 7.09±11.19 | -1.73±6.46 | -11.98±15.92 | |
| NS | | | | | | | |
| C1 | 165.50±52.83 | 4.00±59.75 | 14.99±247.95 | 25.98±242.76 | -66.18±142.69 | -50.77±342.47 | |
| C2 | 156.12±55.13 | 96.80±6.36* | 63.83±259.58 | 74.04±254.56 | 27.21±144.97 | -104.09±357.65 | |
| C3 | 138.50±43.03 | -3.50±71.04 | 188.21±61.98 | 191.28±223.19 | -8.38±148.98 | -490.23±342.65 | |
| SY | | | | | | | |
| C1 | 21.12±8.45 | 3.02±10.31 | 5.85±40.45 | 9.55±39.60 | -8.96±24.17 | -13.63±57.05 | |
| C2 | 22.99±9.80 | 14.11±1.15* | -0.43±46.08 | -0.05±45.40 | 2.71±26.10 | 4.49±63.50 | |
| C3 | 17.47±6.57 | 1.82±13.38 | 37.58±22.67 | 38.70±37.49 | -4.91±27.92 | -88.64±61.16 | |
| MANFLA | | | | | | | |
| FW | | | | | | | |
| C1 | 686.70±332.97 | 27.67±222.77 | -839.77±1426.00 | -718.80±1404.41 | -293.00±596.33 | -4287.41±1705.79 | |
| C2 | 638.26±318.37 | 238.83±30.68* | 197.28±1822.17 | 35.44±1413.58 | -632.86±626.46 | 217.54±1429.54 | |
| C3 | 628.36±181.87 | 296.33±18.50* | -286.69±1080.12 | -186.76±816.15 | 99.94±417.99 | -110.19±1080.12 | |
| 100-SW | | | | | | | |
| C1 | 17.16±4.09 | 1.16±3.54 | -7.48±18.29 | -8.16±17.82 | -1.29±8.53 | -126.62±23.29 | |
| C2 | 14.53±2.99 | 0.04±2.62 | -1.38±16.99 | -2.62±13.04 | 5.42±6.05 | -0.97±13.32 | |
| C3 | 15.73±2.27 | 0.15±3.00 | -8.20±16.13 | -8.81±10.89 | -1.68±6.49 | 12.53±16.13 | |
| NS | | | | | | | |
| C1 | 144.34±60.00 | 40.40±72.11 | -90.00±286.50 | -81.89±279.99 | 2.61±162.40 | -1030.70±396.99 | |
| C2 | 128.70±44.03 | 21.03±4.37* | 63.95±267.30 | -41.05±196.66 | -76.19±99.28 | 27.03±201.73 | |
| C3 | 129.56±45.45 | 14.10±52.28 | -72.37±287.80 | -67.65±209.72 | 1.02±111.52 | 49.80±287.80 | |
| SY | | | | | | | |
| C1 | 24.82±12.63 | 7.48±11.75 | -21.20±57.21 | -21.24±55.71 | -1.62±28.43 | -166.72±74.37 | |
| C2 | 18.21±10.12 | 3.62±8.24 | 10.70±56.18 | -9.71±43.70 | -3.77±18.65 | 4.88±44.73 | |
| C3 | 17.46±8.09 | 2.11±0.77* | -9.42±47.05 | -9.13±35.86 | -2.16±16.84 | 12.28±47.05 | |

FW: Fruit weight; 100-SW: 100-seed weight; SY: Seed yield; NS: Number of seed;; C1: NI215 (P_1) x NI283 (P_2); C2: NI215 (P_1) x NI354 (P_2); C3: NI215 (P_1) x NI106 (P_2);

*Significant at 5% level of probability, M: Mean

Positive values of dominance (*h*) were also observed in Abidjan and negative values in Manfla with the exception of crossing C2 which gave a positive value. On the other hand, the additivity x additivity (*i*) parameter showed positive values in Abidjan and negative values at Manfla in the three crossings. At the level of the additivity x dominance (*j*) parameter, negative values were observed in crosses C1 and C3 in Abidjan. However at Manfla, the values obtained were all positive. For the dominance x dominance (*l*) parameter, negative values were observed in Abidjan while only the C1 cross showed a negative value in Manfla. Seed yield gave positive values in crosses at both sites at additivity (*d*). For this parameter, significant effects were noted in crossings C2 in Abidjan and C3 at Manfla. The additivity x additivity (*i*) component presented negative values only at Manfla. However, the C1 and C3 crosses in Abidjan showed positive values in Abidjan. The additivity x dominance (*j*) interaction effect showed negative values at both sites with the exception of crossing C2 in Abidjan. The dominance x dominance (*l*) interaction effect showed negative values in crosses C1 and C3 in Abidjan and C1 at Manfla. The values observed for the other crosses were positive.

3.3 ESTIMATE OF VARIANCES

Overall, the variances of F_2 are greater than the parental variances for the yield and its components. The mean variances of parents NI283, NI354 and NI106 are higher than that of parent NI215: 8733.26 respectively against 5877.70 for total weight of fruits; 4.12 versus 2.43 for 100-seed weight; 839.04 against 593.34 for the number of seeds, finally 26.04 against 12.76 for the seed yield (Table 3).

The values of variances observed in F_2 for fruit weigh, number of seed and total weight of seeds are high by locality. For fruit weight, number of seeds and yield, the highest values for the variance in F_2 are observed in Abidjan.

There was no difference in backcross variance, BC_1P_1 and BC_1P_2 for 100 seed weight (100-SW). But differences were observed across the results in backcross variances for total number of seeds (NS) within crosses and sites. The variance in BC_1P_1 observed for this trait varies from 2136.45 in the C1 cross at Manfla to 3726.21 in the C1 cross at Abidjan (Table 3). The variance observed in BC_1P_2 for this trait varies from 2054.25 in C1 cross in Manfla to 3678.76 in the C3 cross in Abidjan. The backcross variance observed with the first parent (BC_1P_1) ranges from 33,164.26 to 51549.45 with C3 crosses in Manfla and C1 in Abidjan (Table 4). The backcross variances observed with the second parent vary from 29,031.16 to 48,477.04 for the respective crosses C3 in Manfla and C1 in Abidjan (Table 3). In the results observed for yield and its components, the estimated environmental variance, $\sigma^2(E)$ is lower than that of the genetic variance, $\sigma^2(G)$ (Table 4). Positive values of the additive variance were recorded in all crosses. The overall mean of the observed genetic variance is greater than that of the additive variance in yield and its components. The results of the analysis of the genetic components, shown in table 4, revealed that the additive effect is greater than the effect of the dominant genes for the different characters studied in the different crosses made. This result was observed for the fruit weight and 100-seed weight in crosses C1 and C3 in Abidjan and only for 100-seed weight in the three crosses at Manfla.

Table 3. Variances by generation for genotypes of *Lagenaria siceraria* for Fruit weight, of seeds weight, 100-seed weight and Number of seed in Abidjan and Manfla

| Crosses | $\sigma^2 (P_2)$ | $\sigma^2 (P_1)$ | $\sigma^2 (F_1)$ | $\sigma^2 (F_2)$ | $\sigma^2 (BC_1P_1)$ | $\sigma^2 (BC_1P_2)$ |
|---------------------------------|------------------|------------------|------------------|------------------|----------------------|----------------------|
| Fruit weight (FW) | | | | | | |
| Abidjan | | | | | | |
| C1 | 9785.85 | 5363.84 | 21960.78 | 80734.14 | 51549.45 | 48477.04 |
| C2 | 7035.74 | 5179.91 | 30162.95 | 70483.60 | 45093.94 | 44411.61 |
| C3 | 9054.52 | 6440.49 | 20038.51 | 57383.05 | 41096.55 | 39123.59 |
| Mean | 8625.37 | 5661.41 | 24054.08 | 69533.60 | 45913.31 | 44004.08 |
| Manfla | | | | | | |
| C1 | 8045.42 | 5628.45 | 21251.08 | 60202.26 | 42879.38 | 37652.15 |
| C2 | 9451.35 | 6132.24 | 21749.31 | 45234.15 | 37546.43 | 34542.27 |
| C3 | 9026.65 | 6521.25 | 23745.62 | 44271.36 | 33164.26 | 29031.16 |
| Mean | 8841.14 | 6093.98 | 22248.67 | 49902.59 | 37863.36 | 33741.86 |
| Overall mean | 8733.26 | 5877.70 | 23151.38 | 59718.09 | 41888.34 | 38872.97 |
| 100-Seed weight (100-SW) | | | | | | |
| Abidjan | | | | | | |
| C1 | 5.15 | 3.34 | 4.61 | 8.87 | 7.22 | 6.41 |
| C2 | 4.54 | 2.12 | 2.56 | 7.04 | 5.34 | 4.87 |
| C3 | 2.21 | 2.65 | 3.25 | 8.77 | 6.28 | 5.43 |
| Mean | 3.97 | 2.70 | 3.47 | 8.23 | 6.28 | 5.57 |
| Manfla | | | | | | |
| C1 | 5.21 | 2.13 | 3.46 | 12.24 | 10.21 | 6.23 |
| C2 | 4.31 | 2.08 | 5.43 | 12.32 | 9.23 | 8.58 |
| C3 | 3.28 | 2.26 | 3.98 | 11.25 | 9.35 | 8.24 |
| Mean | 4.27 | 2.16 | 4.29 | 11.94 | 9.60 | 7.68 |
| Overall mean | 4.12 | 2.43 | 3.88 | 10.08 | 7.94 | 6.63 |
| Number of seeds (NS) | | | | | | |
| Abidjan | | | | | | |
| C1 | 980.12 | 659.34 | 2815.21 | 5090.94 | 3726.21 | 3475.94 |
| C2 | 857.23 | 584.06 | 2027.46 | 5539.19 | 3635.26 | 3404.31 |
| C3 | 914.28 | 600.02 | 2276.27 | 4834.24 | 3454.35 | 3678.76 |
| Mean | 917.21 | 614.47 | 2372.98 | 5154.79 | 3605.27 | 3519.67 |
| Manfla | | | | | | |
| C1 | 870.21 | 676.78 | 1598.17 | 2654.27 | 2136.45 | 2054.25 |
| C2 | 648.26 | 466.48 | 1205.43 | 3201.65 | 2457.86 | 2365.12 |
| C3 | 764.12 | 573.36 | 1068.32 | 3054.49 | 2341.37 | 2221.78 |
| Mean | 760.86 | 572.21 | 1290.64 | 2970.14 | 2311.89 | 2213.72 |
| Overall mean | 839.04 | 593.34 | 1831.81 | 4062.46 | 2958.58 | 2866.69 |
| Seed Weight (SY) | | | | | | |
| Abidjan | | | | | | |
| C1 | 26.75 | 10.99 | 31.56 | 75.44 | 52.31 | 49.38 |
| C2 | 25.28 | 11.48 | 33.24 | 54.65 | 44.65 | 39.25 |
| C3 | 27.23 | 13.06 | 43.25 | 68.25 | 62.14 | 42.31 |
| Mean | 26.42 | 11.84 | 36.02 | 66.11 | 53.03 | 43.65 |
| Manfla | | | | | | |
| C1 | 25.15 | 10.54 | 36.36 | 60.44 | 48.34 | 43.36 |
| C2 | 24.38 | 11.22 | 37.45 | 55.65 | 45.21 | 39.25 |
| C3 | 27.44 | 19.25 | 39.69 | 70.25 | 57.14 | 50.76 |
| Mean | 25.66 | 13.67 | 37.83 | 62.11 | 50.23 | 44.46 |
| Overall mean | 26.04 | 12.76 | 36.93 | 64.11 | 51.63 | 44.05 |

C1: NI215 (P₁) x NI283 (P₂); C2: NI215 (P₁) x NI354 (P₂); C3: NI215 (P₁) x NI106 (P₂)

The same result was also observed at the level of seed yield only in C1 cross in Abidjan and in the three crosses in Manfla. Regarding the number of seeds, the trend was noted in crosses C1 and C2 at Abidjan and C2 at Manfla.

3.4 HERITABILITY

Broad-sense heritability for fruit weight in Abidjan and Manfla, estimated (H^2) is high, respectively 0.77 and 0.69. 100-seed weight also showed high broad-sense heritability in Abidjan and Manfla, which are respectively 0.59 and 0.69 with an average value of 0.64 (Table 4). Broad-sense heritability for the number of seeds per fruit are also high in Abidjan and Manfla, ie 0.69 and 0.66 with an average of 0.68. high level of broad-sense heritability were recorded for seed yield in Abidjan and Manfla, ie 0.58 and 0.54 with an average of 0.56 (Table 4)

Narrow-sense heritability (h^2), obtained during this work presented high values in the sites. The values observed for each of the yield components in Abidjan and Manfla are presented respectively as follows: for fruit weigh 0.70 and 0.63; for 100 seed-weight 0.56 and 0.55; for the number of seeds 0.61 and 0.54; finally for the yield 0.53 and 0.48. The overall means of narrow-sense heritability are 0.63; 0.55; 0.54 and 0.50 respectively for the FW, 100-SW, NS, and SY (Table 4).

Overall broad and narrow-sense heritability are all high at both sites. However, those observed in broad-sense for the yield and its components were all higher than those observed in the narrow-sense

3.5 ESTIMATE OF GENETIC GAIN FROM SELECTION

Estimates of the different average genetic gains for fruit weight is 315.67; 268.54 and 237.94 g for the respective selection intensities of 5, 10 and 20% (Table 5). The mean values of expected genetic gains for seed yield are 8.30; 7.06 and 6.26 g respectively for the selection intensities of 5, 10, and 20%. The means expected genetic gains are respectively 3.63 g; 3.09 g and 2.74 g for 100-seed weight according to the selection intensities of 5; 10 and 20%. Finally, the averages of the expected gains for the number of seeds are respectively 71.44; 60.77 and 53.85 for the respective selection intensities of 5, 10 and 20% (Table 5). Overall, for each trait, the best gains are obtained with a selection intensity of 5%. From this selection intensity, which is both strong and rigorous, it is possible to have individuals with strong performance in crosses because it only takes into account the 5 best individuals in the population.

Table 4. Estimated variances and heritability in *Lagenaria siceraria* crosses for yield and Seed yield components in Abidjan and Manfla

| Pedigree | $\sigma^2 (P)$ | $\sigma^2 (G)$ | $\sigma^2 (E)$ | $\sigma^2 (A)$ | H^2 | h^2 |
|-------------------------|----------------|----------------|----------------|----------------|-------|-------|
| Fruit weight | | | | | | |
| Abidjan | | | | | | |
| C1 | 80734.14 | 65966.33 | 14767.81 | 61441.79 | 0.82 | 0.76 |
| C2 | 70483.60 | 52348.21 | 18135.39 | 51461.65 | 0.74 | 0.73 |
| C3 | 57383.05 | 43490.04 | 13893.01 | 34545.96 | 0.76 | 0.60 |
| Mean | 69533.60 | 53934.86 | 15598.74 | 49149.80 | 0.77 | 0.70 |
| Manfla | | | | | | |
| C1 | 60202.26 | 46158.25 | 14044.01 | 39872.99 | 0.77 | 0.66 |
| C2 | 45234.15 | 30463.60 | 14770.55 | 18379.60 | 0.67 | 0.41 |
| C3 | 44271.36 | 28511.58 | 15759.79 | 26347.30 | 0.64 | 0.60 |
| Mean | 49902.59 | 35044.48 | 14858.12 | 28199.96 | 0.69 | 0.55 |
| Overall meane | 59718.09 | 44489.67 | 15228.43 | 38674.88 | 0.73 | 0.63 |
| 100-Seed weight | | | | | | |
| Abidjan | | | | | | |
| C1 | 8.87 | 4.44 | 4.43 | 4.11 | 0.50 | 0.46 |
| C2 | 7.04 | 4.10 | 2.95 | 3.87 | 0.58 | 0.55 |
| C3 | 8.77 | 5.93 | 2.84 | 5.83 | 0.68 | 0.66 |
| Mean | 8.23 | 4.82 | 3.40 | 4.60 | 0.59 | 0.56 |
| Manfla | | | | | | |
| C1 | 12.24 | 8.68 | 3.57 | 8.04 | 0.71 | 0.66 |
| C2 | 12.32 | 8.01 | 4.31 | 6.83 | 0.65 | 0.55 |
| C3 | 11.25 | 7.88 | 3.38 | 4.91 | 0.70 | 0.44 |
| Mean | 11.94 | 8.19 | 3.75 | 6.59 | 0.69 | 0.55 |
| Overall meane | 10.08 | 6.50 | 3.58 | 5.60 | 0.64 | 0.55 |
| Number of seed | | | | | | |
| Abidjan | | | | | | |
| C1 | 5090.94 | 3273.47 | 1817.47 | 2979.73 | 0.64 | 0.59 |
| C2 | 5539.19 | 4165.14 | 1374.05 | 4038.81 | 0.75 | 0.73 |
| C3 | 4834.24 | 3317.53 | 1516.71 | 2535.37 | 0.69 | 0.52 |
| Mean | 5154.79 | 3585.38 | 1569.41 | 3184.64 | 0.69 | 0.61 |
| Manfla | | | | | | |
| C1 | 2654.27 | 1468.44 | 1185.83 | 1117.84 | 0.55 | 0.42 |
| C2 | 3201.65 | 2320.25 | 881.40 | 1580.32 | 0.72 | 0.49 |
| C3 | 3054.49 | 2185.96 | 868.53 | 1545.83 | 0.72 | 0.51 |
| Mean | 2970.14 | 1991.55 | 978.59 | 1414.66 | 0.66 | 0.47 |
| Overall mean | 4062.46 | 2788.46 | 1274.00 | 2299.65 | 0.68 | 0.54 |
| Seed Weight (SY) | | | | | | |
| Abidjan | | | | | | |
| C1 | 75.44 | 50.23 | 25.22 | 49.19 | 0.67 | 0.65 |
| C2 | 54.65 | 28.84 | 25.81 | 25.40 | 0.53 | 0.46 |
| C3 | 68.25 | 36.55 | 31.70 | 32.05 | 0.54 | 0.47 |
| Mean | 66.11 | 38.54 | 27.57 | 35.55 | 0.58 | 0.53 |
| Manfla | | | | | | |
| C1 | 60.44 | 33.34 | 27.10 | 29.18 | 0.55 | 0.48 |
| C2 | 55.65 | 28.03 | 27.63 | 26.84 | 0.50 | 0.48 |
| C3 | 70.25 | 38.73 | 31.52 | 32.60 | 0.55 | 0.46 |
| Mean | 62.11 | 33.37 | 28.75 | 29.54 | 0.54 | 0.48 |
| Overall mean | 64.11 | 35.95 | 28.16 | 32.54 | 0.56 | 0.50 |

C1: NI215 (P₁) x NI283 (P₂); C2: NI215 (P₁) x NI354 (P₂); C3: NI215 (P₁) x NI106 (P₂)

Table 5. Gain and selection intensity of 5, 10 and 20% of the Yield and its components in Abidjan and Manfla.

| Crosses | Selection gain | | |
|-------------------------|----------------|--------|--------|
| | 5 % | 10 % | 20 % |
| Fruit weight | | | |
| Abidjan | | | |
| C1 | 446.10 | 379.50 | 336.25 |
| C2 | 399.89 | 340.19 | 301.42 |
| C3 | 297.51 | 253.09 | 224.25 |
| Mean | 379.56 | 322.89 | 286.10 |
| Manfla | | | |
| C1 | 335.25 | 285.20 | 252.70 |
| C2 | 178.28 | 151.66 | 134.38 |
| C3 | 258.33 | 219.76 | 194.72 |
| Mean | 255.58 | 217.43 | 192.65 |
| Overall mean | 315.67 | 268.54 | 237.94 |
| 100-seed weight | | | |
| Abidjan | | | |
| C1 | 2.85 | 2.42 | 2.15 |
| C2 | 3.01 | 2.56 | 2.27 |
| C3 | 4.06 | 3.45 | 3.06 |
| Mean | 3.31 | 2.82 | 2.49 |
| Manfla | | | |
| C1 | 4.74 | 4.03 | 3.57 |
| C2 | 4.01 | 3.42 | 3.03 |
| C3 | 3.02 | 2.57 | 2.28 |
| Mean | 3.91 | 3.33 | 2.95 |
| Overall mean | 3.63 | 3.09 | 2.74 |
| Number of seed | | | |
| Abidjan | | | |
| C1 | 86.15 | 73.29 | 64.94 |
| C2 | 111.95 | 95.24 | 84.38 |
| C3 | 75.23 | 64.00 | 56.70 |
| Mean | 90.79 | 77.24 | 68.43 |
| Manfla | | | |
| C1 | 44.76 | 38.08 | 33.74 |
| C2 | 57.62 | 49.02 | 43.43 |
| C3 | 57.70 | 49.09 | 43.49 |
| Mean | 53.25 | 45.30 | 40.14 |
| Overall mean | 71.44 | 60.77 | 53.85 |
| Seed weight (SY) | | | |
| Abidjan | | | |
| C1 | 11.68 | 9.94 | 8.81 |
| C2 | 7.09 | 6.03 | 5.34 |
| C3 | 8.00 | 6.81 | 6.03 |
| Mean | 8.87 | 7.55 | 6.69 |
| Manfla | | | |
| C1 | 7.74 | 6.59 | 5.84 |
| C2 | 7.42 | 6.31 | 5.59 |
| C3 | 8.02 | 6.83 | 6.05 |
| Mean | 7.75 | 6.59 | 5.84 |
| Overall mean | 8.30 | 7.06 | 6.26 |

C1: NI215 (P₁) x NI283 (P₂); C2: NI215 (P₁) x NI354 (P₂); C3: NI215 (P₁) x NI106 (P₂)

3.6 NUMBER OF QUANTITATIVE FACTORS

The results showed that the average number of polygenic factors which control fruit weight, yield and 100-seed weight is 2 and 4 for the number of seeds (Table 6). While the highest number of quantitative factors (8.67) was recorded for the number of seeds per fruit from the data of C1 cross at Manfla.

Table 6. Estimate of number of quantitative or polygenic factors of yield and its components in Abidjan and Manfla

| Characters | Number of quantitative or poligenic factors (N) | | | | | | | | | | | |
|------------|---|------|------|------|------|------|--------|------|------|------|------|------|
| | FW | | | SY | | | 100-SW | | | NS | | |
| Crosses | C1 | C2 | C3 | C1 | C2 | C3 | C1 | C2 | C3 | C1 | C2 | C3 |
| Abidjan | 1.64 | 1.93 | 0.19 | 1.47 | 4.16 | 0.16 | 1.12 | 1.13 | 0.79 | 5.69 | 4.01 | 0.12 |
| Manfla | 1.32 | 0.88 | 0.94 | 0.42 | 4.77 | 0.04 | 1.18 | 1.81 | 0.76 | 8.67 | 0.47 | 0.09 |
| Mean | 1.06 | | | 1.02 | | | 1.10 | | | 3.18 | | |
| N | 2 | | | 2 | | | 2 | | | 4 | | |

FW: Fruit weight; SY: Seed Yield 100-SW: 100-seed weight; NS: Number of seed; C1: NI215 (P₁) x NI283 (P₂); C2: NI215 (P₁) x NI354 (P₂); C3: NI215 (P₁) x NI106 (P₂)

N: Number of quantitative factors

4 DISCUSSION

According to [27] the hypothesis of the effect of additive genes in the transmission of traits is accepted when the mean expected in F₁ is between the mean values of the crossed parents. However, a heterosis effect was observed for fruit weight and number of seeds in C3 cross. Indeed, average value of the F₁ population is greater than that of the two parents for fruit weight. This result is consistent with the work of [30] who observed a heterosis effect in the cucurbit *Citrullus lanatus* in terms of fruit weight. These results also confirm the genetic distance of the crossed parents.

Scaling tests performed [21] are not significantly different from zero for all characters. Such results could suggest that the mode of action of genes is not under the control of non-allelic genes. In fact, this result reveals a situation of additivity and dominance in the transmission of genes that govern traits. The significant effect of additivity (*d*) for the characteristics fruit weight, 100-seed weight and number of seeds in different crosses highlights the action of additive genes in the transmission of these traits. This study is the first of its kind on the oilseed form of *Lagenaria siceraria*, so there is no benchmark against which to conduct a meaningful discussion of results. Nevertheless, it should be noted that similar results were obtained by [28], [29] then [30] on okra in West Africa and by [31] on maize. These authors showed that effect of additive genes is significantly greater than the effect of dominant genes on seed yield, precocity and 100-seed weight in okra and the number of seeds in corn. The importance of the additivity effect suggests that there is an effective possibility of obtaining, by self-fertilization and selection in each generation, genotypes with better phenotypic values.

In the situation where the mode of action of genes is governed by the effect of additive genes, early selection within the segregating population would be possible. Similar results have been reported by [32] who also showed that the effects of additive genes play an important role in the transmission of fruit weight in tomatoes. Insignificant interactions of the parameters *i* (additivity x additivity), *j* (additivity x dominance) and *l* (dominance x dominance) for yield and its components (FW; 100-SW and NS) do not indicate any evidence of interaction between genes non-allelic. This could reflect the additivity of genes in the transmission of these traits. This result is consistent with the result of individual tests A, B and C by [21]. Indeed, these individual tests are not significant. Effects of additive genes were greater than effects of dominant genes and environmental variation. This result is observed for the fruit weight in crosses C1 in Abidjan and C3 in Manfla and for the weight of seeds in cross C1 in Abidjan. The same is true for 100-seed weight in crosses C1 and C3 in Abidjan and in the three crosses in Manfla, then for the number of seeds (C1, C2 in Abidjan and C2 in Manfla). These results could be attributed to the preponderance of the effects of additive genes in the transmission of these traits. In addition, the genetic strengths of these traits can be retained in a single line. Which could be ideal in the creation of pure line. The different trends observed in these traits at the two sites could be linked to environmental variation.

In the study of variance components, estimation of genetic heritability was used to assess the possibilities for improvement by selection. Analysis of results showed that the genetic and additive variances are significantly greater than the environmental variances at both sites. A selection according to the yield components would therefore be beneficial for the continuation of work to improve the plant. These results suggest a weak influence of the environment on the genotype for seed yield and its

various components. However, these results show that the heritability assessed is a function of the environment and the character as observed by [33], [34].

Broad-sense heritability (H^2) ranges from 0.64 to 0.82 for the total fruit weight (FW). This trait revealed an overall mean heritability of 0.73. Similar values of heritability for total fruit weight in Cucurbitaceae *Citrullus lanatus* have been reported by [20], [35] and [19] on the calabash. This value of heritability ($H^2 = 0.73$) explains that 73% of the variation in fruit weight is due to genetic variation. The remaining 27% is thought to be mainly due to environmental factors and probably to other experimental causes. According to Bernard et al. (2002), the environment plays an important role in broad heritability in the expression of the phenotype. High values of broad heritability are recorded for seed yield. This result is similar to those of [19] on calabash, [36] on peanuts and [37] on rapeseed, which reported a high value for broad heritability in yield. These results also indicate that for the most part, variation in yield is influenced by genotype. The 100 seed weight also has high values of broad heritability in Abidjan and Manfla. These results are similar to those of [19] on calabash, [38] on melon, Singh [39] on chickpea and [40] on field beans, who found high values of heritability (H^2) for this character. The number of seeds per fruit also showed a high value for heritability (H^2). These results agree quite well with those of [38] then of [41] for the number of seeds trait respectively in melon and chickpeas. Similar results have been reported by [42] and [43]. The values of heritability in the strict sense (h^2) are also high for the fruit weight, the yield, 100-seed weight and the number of seeds. These heritability values are high and also indicate, that these traits can all be considered as good selection criteria for plant improvement. The reference [20] also found high values for heritability for fruit weight in melon. Data from this study indicate that additive components could play a major role in improving these traits. Also, high heritability values obtained indicate that the selection of these yield components may be effective for improvement of *L. siceraria*. Expected genetic gains in selection depend on the family or cross and the site of experimentation. Based on results obtained in the two sites, it should be possible to improve the production of *L. siceraria* in a few generations of selection through fruit weight, 100-seed weight and the number of seeds, with changes more important for the high selection intensities ($k = 5\%$). That is to say, select from the F_2 populations of C1 cross (NI215 x NI283) which have a wide distribution, the best individuals with low numbers and cross them in order to have significantly improved offspring. However, because of the risk of genetic erosion and the uncertainty of the contribution of the female parent in the genotype at the level of the parent chosen in F_2 , it would be more interesting to orient the selection at a selection intensity of 10% at the level of BC_1P_2 or in the crossing C1 (NI215 x NI 283) x NI283. Breeding programs that might allow a high rate of recombination can help all of efficient factors needed to obtain the desired genotype, and break down unfavorable links. In addition, due to a relatively low number of quantitative or polygenic factors which appear to regulate fruit weight, seed weight fixation can be achieved within a few generations under high selection intensity. Variations observed in the parameter, number of quantitative factors may be due to the size of the population or to the calculation method adopted. This number of quantitative factors was calculated from variance estimates and may not be very precise. These results show that the yield and its components are quantitative traits controlled by at least two quantitative factors which could be major genes. They are therefore multigenic characters. Variation in environment and the high heritability observed for these traits may require progeny testing using self-pollination of half-sibling families in several settings. This study demonstrated that plant breeders can modify or improve seed yield by focusing on yield components within *L. siceraria* populations through efficient breeding methods. Possible biases could be introduced into this experiment because a large number of plants produced only two fruits. Therefore, it is desirable to perform several crosses for a better estimate of the variability in order to better assess the heritability of the yield components. It should also be noted that the drop of many female flowers during the experiment must have influenced the yield per plant in this work. However, the proposal of a recurrent selection scheme with cyclic intercrosses between families selected on the basis of yield components, would best suit a strategy for effective improvement of *L. siceraria* populations. This technique of improvement by recurrent selection must be applied for an improvement of the productivity of the plant through each of the yield components.

5 CONCLUSION

All of the results obtained showed genetic variability in yield and its components. One of the important results obtained is the fact that all the F_1 averages are between the averages of the two crossed parents. The implications of this result were shown through the scaling test which revealed that the transmission of genes is not under the control of non-allelic genes. However, the significant effect of additivity (d) observed for the yield components revealed that gene transmission is under the control of the action of additive genes. The broad and narrow heritability values of yield components are high. These results clearly demonstrate the relevance of the choice of weight of fruit, weight of 100 seeds and number of seeds as good selection criteria for improvement of the plant. Observation of the number of quantitative factors showed that the yield and its components are multigenic traits. Expected genetic gain in selection for each trait is greater when the selection intensity is high (5%). However, recurrent selection for population improvement should be an efficient selection method, although the smallest gains are obtained from the lower intensity of selection (20%).

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