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Research Article

Assessment of Morphological Variability, Heritability, Genetic Advances, Correlation and Stepwise Regression for Some Yield Component Traits in Four Inbred Lines of *Citrullus Mucosospermus* (Fursa)

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Abstract: This study was initiated to generate information about genetic variability, heritability and genetic advance of yield components in *Citrullus mucosospermus*. In this way, four inbred lines of *C. mucosospermus* were evaluated at Kononfla city in Western Côte d'Ivoire, using a randomized complete block design with three repetitions. The results of discriminant analysis indicated significant differences between four *C. mucosospermus* inbred lines what are *Bebu*, *Wlêwlê small seeds 1*, *Wlêwlê small seeds 2* and *Wlêwlê small seeds 3*. Mahalanobis distances varied significantly from 8.44 to 629.50 between theses inbred lines. All investigated traits recorded high genotypic and phenotypic coefficients of variation values except fruit maturity period and fruit diameter where, low values were recorded. Studied morphological traits exhibited high heritability (H^2> 80%) coupled with moderate to high genetic advance as percentage of mean. Stepwise regression analysis revealed mass of fresh seeds per fruit followed by mass of fruit, seed width, seed length and fruit maturity as traits contributing for linear increase in mass of dry seeds. These traits could be considered as key criteria for selecting high yielding line in *C. mucosospermus* breeding program at Côte d'Ivoire.

Keywords: *Citrullus mucosospermus*, correlation, heritability, inbred lines, morphological diversity, stepwise regression.

1. INTRODUCTION

Citrullus mucosospermus (Fursa) is one of the most important pistachio of Côte d'Ivoire. It is known to be cultivated for its oleaginous seeds (Zoro *et al.*, 2003). This species belongs to *Citrullus* genus of Cucurbitaceae family, and is native to West Africa where it was domesticated (Chomicki and Renner, 2015). *C. mucosospermus* is a multipurpose species whose main importance is its food use. Indeed, because of their high protein, lipid and carbohydrate content (N'Goran *et al.*, 2015; Guédé *et al.*, 2017), dried slightly toasted and ground seeds are eaten in sauce during prestigious popular festivities and traditional ceremonies (first day of the new year, weddings, births and religious ceremonies, yams feast). In addition, seeds have good market value in rural and urban markets (Zoro *et al.*, 2003). To this, must be added the importance of this species in agronomy (Achigan-Dako *et al.*, 2008, Ndukauba *et al.*, 2015) and medicine (Adewuyi *et al.*, 2013, Erhirhie and Ekene, 2013). However, this species characterized by high market, nutritional, medicinal and agronomic values, is still neglected and have been overlooked for relatively long time by research and development organizations (Zoro *et al.*, 2005; 2006; Achigan-Dako *et al.*, 2008). Moreover, its culture is still traditional with low yields (Goré *et al.*, 2011). In fact, seed yield of *C. mucosospermus* can vary from 208.66 to 370 kg per ha depending on the cultivar (Adjoumani *et al.*, 2012). Nevertheless, the genetic improvement of this specie and the valorization of its improved varieties could contribute food security and income generation insurance (Zoro *et al.*, 2005; 2006; Achigan-Dako *et al.*, 2008).

The success of any crop-breeding program largely depends on the nature and magnitude of genetic variability available in breeding material, the degree of character associations with yield, the extent to which

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these characters are heritable as well as the extent of environment influence on them (Ndukauba *et al.*, 2015). Genetic diversity is the variability among different genotypes of species. In any genetic diversity studies, morphological characterization is recommended as the first step to be taken before both biochemical and molecular analysis are used (Bello *et al*., 2015). Genetic diversity studies are major breakthrough in understanding intra-species crop performance leading to crop improvement. In fact, knowledge of crop performance in diverse population reveals not only the differences in the genetic materials used, but also identifies parental combinations exploitable to create segregation progenies with maximum genetic potential for further selection (Djè *et al.,* 2000; Aremu, 2012). The heritability assessment of yield components is essential for formulating effective breeding strategies aiming yield improvement. However, information about heritability alone may not help in identifying characters for enforcing selection; heritability estimates must be coupled with these of genetic advance (Fayeun and Odiyi, 2015). Indeed, heritability provides information on the magnitude of character inheritance from parent to offspring, while genetic advance provides information on the actual gain expected under selection (Ogbonna and Obi, 2010; Khan *et al.*, 2016). According to Gupta *et al.*, (2015), Meena and Bahadur (2015), selection for yield based on multiple traits is always better than selection based on yield alone. Thus, knowledge about the magnitude and degree of association between yield components has a great importance to breeders. In fact, correlation provides information about the association between two characters (Khan *et al.*, 2016). Using this information permit to know yield components, which could be improved simultaneously in the breeding program (Gupta *et al.*, 2015; Meena and Bahadur, 2015). Stepwise regression allows accessing the relative contribution of yield components to yield. This method is used to estimate the value of quantitative variable regarding its relation with one or other quantitative variables. This relation is such that it is possible to predict other changes using one variable (Nasri *et al.*, 2014). Even if stepwise regression was largely used in many species (Ahmadizadeh *et al.*, 2011; Hannachi *et al.*, 2013; Nasri *et al.*, 2014; Yao *et al.*, 2015) it is not the case for *C. mucosospermus*, since stepwise regression studies have not been reported in the literature. Therefore, the present investigation was initiated to assess genetic variability, heritability, correlation among yield components and their relative contribution on seeds yield in *C. mucosospermus*.

2. MATERIALS AND METHODS

2.1. Experimental Site

This study was conducted in peasant area at Kononfla city in West-Center of Côte d'Ivoire with geographic coordinates, latitude 6° 37′ 18″ N, longitudes 5° 54′ 37″ W and altitude 243 m above sea level. Soil type in the area is ferralitic form and average temperature varies from 25 to 30 °C with rainfall comprised between 1500 and 2000 mm per annual.

2.2. Plant Materials

Three inbred lines of *Wlêwlê small seeds* (*Wss1, Wss2 and Wss3*) and one inbred line of *Bebu* (*B*) constituted plant material of this study. These inbred lines were developed in *C. mucosospermus* gene bank of the university of Nangui Abrogoua from original accessions coming from Korhogo in the North (Bebu accession), Béoumi in the Center (*Wlêwlê small seeds 1* accession coded *Wss1*), Gohitafla in the West Center (*Wlêwlê small seeds 2*) accession *coded Wss2*) and Tanda in the East (*Wlêwlê small seeds 3* accession *coded Wss3*) of Côte d'Ivoire.

To initiate the development of the four *C. mucosospermus* inbred lines, purification of different original accessions was carried out through four cycles of cropping over period from May 2014 to August 2015, during which self-pollinations (B x B, *Wss1* x *Wss1, Wss2* x *Wss2 and Wss3* x *Wss3)* were realized. Each self-fertilization trial was carried out on a plot of 180 m² (15 m × 12 m) with 4 equidistant lines of 5 m. Each line had 5 sowing points spaced 3 m apart. Only one accession has been sown per line. Direct sowing was carried out using 2 to 3 seeds per hole and at emergence, seeding were separated to keep only one vigorous plant per seedbed. At flowering, the self-pollinations were carried out following the controlled pollination method described in detail by Adjoumani *et al.*, (2013).

2.3. METHODS

2.3.1. Experimental Design

The four inbred lines of *C. mucosospermus* were evaluted in the same environment using a Randomized Complete Block Design (RCBD) with three repetitions in cropping saison from September to December 2015. The experimental field divided into 3 blocks, had an area of 648 m^2 (27 m × 24 m). In one block, each inbred line was sowed on one line with 10 sowing points at a spacing of 3 m × 2 m between plants. Two to three seeds were sown per hole and a separating was made 3 weeks after planting to leave only the most vigorous plant per sowing point. Regular weeding was done during the vegetative stage of the plants.

2.3.2. Yield Component Traits Measured

Data were collected on all plants, giving a total of 30 plants per inbred line. Yield component traits related to fruits and seeds were evaluated on three mature fruits randomly selected on each of the 30 plants by inbred line except, the number of fruits where all the fruits of one plant are counted. The measurements were done on a total of 11 traits that are fruit maturity period (FMp), number of fruits per plant (NFr), mass of fruit (MFr), fruit diameter (DFr), fruit volume (VFr), mass of fresh seeds per fruit (MfS), mass of dry seeds per fruit (MdS), mass of 100 seeds (M100), percentage of seed

integuments (PSi), seed length (SL) and seed width (SW).

2.3.3. Data Analysis

Discriminant Analysis (DA) based on Mahalanobis distances was performed with STATISTICA software version 7.1 (StatSoft, 2005), in order to appreciate the divergence among different inbred lines of *Citrullus mucosospermus*.

Analysis of variance (ANOVA) was performed with GENES software package (Cruz, 2013) using the Generalized Linear Model (GLM) procedures for randomized complete block design. Estimation of selective accuracy (SA) was used to evaluate the experimental precision of each trait (Resende and Duarte, 2007):

$$SA = \sqrt{1 - \frac{1}{F}}$$

Where **F** is the value obtained for genotypes effect by ANOVA.

Phenotypic variation for each trait was partitioned into genetic and non-genetic factors and were estimated through formulas proposed by Prasad *et al*., (1981):

Ve = MSe/r; Vg = (MSg – Mse)/r; Vp = Vg + Ve

With **Ve**, **Vg** and **Vp** designating environmental, genotypic and phenotypic variances respectively, and **MSe**, **MSg** and **r** being the mean square of experimental error, mean square of genotypes and number of replications respectively.

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were estimated according to the method suggested by Sharma (1988)**:**

$$CVP = \frac{\sqrt{Vp}}{\bar{X}} \times 100$$

$$CVG = \frac{\sqrt{Vg}}{\bar{X}} \times 100$$

$$ECV = \frac{\sqrt{Ve}}{\bar{X}} \times 100$$

Where, **X** is the general mean for each evaluated trait.

Broad sense heritability (H^2) was calculated by the method of Allard (1960):

$$H^2 = \frac{\sqrt{Vg}}{Vp} \times 100$$

Genetic advance as the percentage of mean (GAM) was computed according to Johnson *et al.* (1955):

$$GAM = \frac{GA}{\bar{X}} \times 100$$

where $$GA = \frac{K\sqrt{Vg + Vp}}{Vp}$$

K is equal to 2.06 and represents selection differential expressed in phenotypic standard deviations.

The mutual association between two traits was evaluated through estimation of phenotypic and genotypic correlation coefficients using the standard procedure as described by Miller *et al.*, (1958):

$$r_g = \frac{G_{cov}X.Y}{\sqrt{Vg(x) \times Vg(y)}}$$

$$r_p = \frac{P_{cov}X.Y}{\sqrt{Vp(x) \times Vp(y)}}$$

Where $\mathbf{r_g}$ is genotypic correlation coefficient between traits x and y, $\mathbf{r_p}$ is the phenotypic correlation coefficient between traits x and y, $\mathbf{G_{cov}X.Y}$ is the genotypic covariance between traits **x** and **y**, $\mathbf{P_{cov}X.Y}$ is the phenotypic covariance between traits x and y, **Vg(x)** and **Vg(y)** are genotypic variances of traits x and y respectively, **Vp(x)** and **Vp(y)** are phenotypic variances of traits x and y, respectively.

Stepwise regression was performed with GENES software package (Cruz, 2013) in order to evaluate the relative contribution of each yield component toward seed mass per fruit.

3. RESULTS AND DISCUSSION

3.1. Morphological Divergence Among Inbred Lines and Variability of Yield Component Traits

The lambda significance test of Wilks revealed the variables that make it possible to discriminate the four inbred lines (*B*, *Wss1*, *Wss2* and *Wss3*). Thus, characters that discriminate well these four inbred lines are fruit maturity period (FMp), fruit mass (MFr), fruit diameter (DFr), fruit volume (VFr), mass of 100 seeds (P100), percentage of seed integuments (PSi), seed length (SL) and seed width (SW) (**Table 1**). The projection of the individuals in the plane (1- 2) shows 4 distinct groups (**Figure 1**). In fact, the first group is only composed by individuals of *Bebu* cultivar while, the second group is constituted by all individuals of *Wlêwle small seeds* 3 (*Wss3*). In the third group, all individuals of *Wlêwlê small seeds* 1 (*Wss1*) are only observed. The fourth group is only composed of individuals from *Wlêwlê small seeds* 2 (*Wss2*). These results confirm the genetic variability that exists between these four inbred lines, especially between *Wlêwlê small seeds* inbred lines. Thus, the inbred line

of *Wlêwlê small seeds* would be composed of three distinct morphotypes (**Figure 2**). Our results corroborate those of Zoro Bi *et al.*, (2003, 2005, 2006), Adjoumani *et al.*, (2012) and Gbotto *et al.*, (2016).

Table 1: Center-reduced coefficients of discriminating canonical functions and discriminant analysis based on fruit and seed traits of *C. mucosospermus*

Traits (SI unit)	Center-reduced coefficients		λ-Wilk	F (3,106)	p	Tolerance	1-Tolerance (R^2)
	First factor	Second factor					
FMp	0.232	-0.436	0.0022	11.038	<0.001	0.929	0.071
NFr	0.213	-0.145	0.0018	2.359	0.076	0.930	0.070
MFr (g)	0.692	-0.417	0.0019	6.227	<0.001	0.205	0.795
DFr (cm)	-1.475	-2.673	0.0020	6.719	<0.001	0.020	0.980
VFr (cm^3)	1.033	2.640	0.0019	5.211	<0.002	0.019	0.981
MfS (g)	-0.495	0.311	0.0018	2.630	0.054	0.210	0.790
MdS (g)	0.195	-0.357	0.0017	1.311	0.275	0.182	0.818
M_{100} (g)	-0.551	0.116	0.0023	13.640	<0.001	0.658	0.342
PSi (%)	-0.318	-0.319	0.0021	10.160	<0.001	0.810	0.190
SL (mm)	0.047	1.117	0.0035	40.598	<0.001	0.466	0.534
SW (mm)	-0.635	-0.572	0.0038	47.016	<0.001	0.707	0.293

FMp: fruit maturity period; **NFr**: number of fruits per plant; **MFr**: mass of fruit; **DFr**: fruit diameter; **VFr**: fruit volume; **MfS**: mass of fresh seeds per fruit; **MdS**: mass of dry seeds per fruit; **M100**: mass of 100 seeds; **Psi**: percentage of seed integuments; **SL**: seed length; **SW**: seed width; **p**: probability values; **SI**: international system.

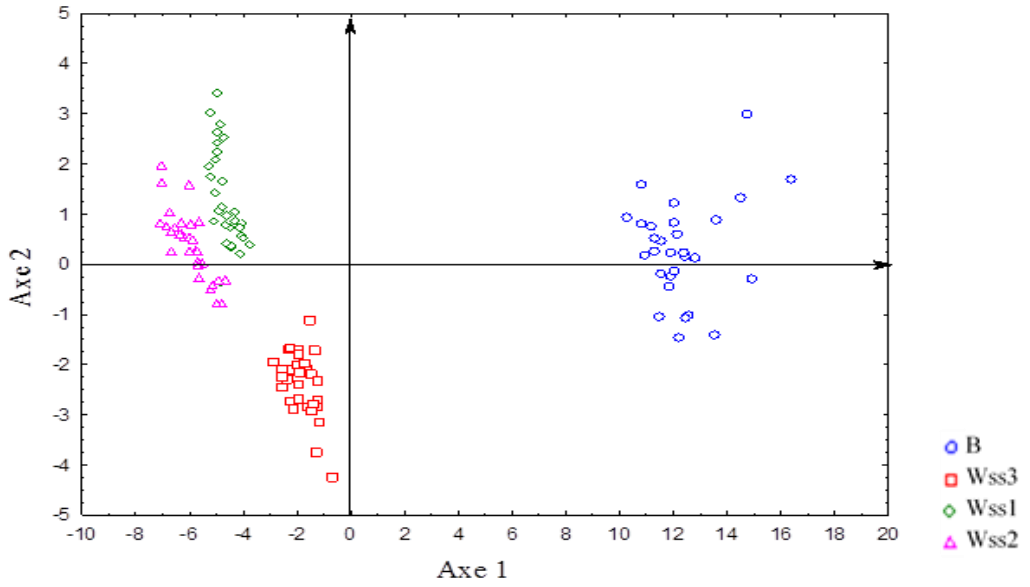

Figure 1: Projection of individuals from four inbred lines of *C. mucosospermus* in the plane formed by the main discriminating factors of discriminant analysis

B = *Bebu*; **Wss1** = *Wlêwlê small seeds 1*; **Wss2** = *Wlêwlê small seeds 2*; Wss**3** = *Wlêwlê small seeds 3*.

Figure 2: Fruits (a) and seeds (b) of four *C. mucosospermus* inbred lines showing their variabilities

B = *Bebu*; **Wss1** = *Wlêwlê small seeds* 1; **Wss2** = *Wlêwlê small seeds* 2; **Wss3** = *Wlêwlê small seeds* 3.

Results given in **Table 3** show that the greatest genetic distance (507.18 unit of Mahalanobis) is observed between *B* and *Wss2* while, the smallest distance (6.77 unit of Mahalanobis) is recorded between *Wss1* and *Wss2*. The genetic distance that separates *B* from *Wss3* is smaller than these separating *B* from *Wss3*. *Wss1* and *Wss2* are more or less equidistant genetically from *Wss3*. The large genetic distance

separating *B* cultivar from *Wss* morphotypes offers great opportunities for improving *C. mucosospermus*. Indeed, according to Banerjee and Kole (2009), hybrids resulting from crossing of two genetically distant parents' express strong hybrid vigor. However, expression of high heterosis level in hybrid for a given trait indicates its ability to produce transgressive segregants, which may be selected for creation of the superior genotypes (Mohammadi *et al.*, 2010; Aremu, 2012; Wannows *et al.*, 2015).

Table 3: Mahalanobis distance between four inbred lines of *C. mucosospermus*

	B	***Wss1***	***Wss2***	***Wss3***
B	-	437.34**	505.18**	349.40**
Wss1		-	6.77**	31.39**
Wss2			-	34.00**
Wss3				-

** Significant at 1% level of significance. **B** = *Bebu*; **Wss1** = *Wlêwlê small seeds 1;* **Wss2** = *Wlêwlê small seeds 2*; **Wss3** = *Wlêwlê small seeds 3.*

Table **4** presents results of analysis of variances, minimum and maximum observed values, mean and standard deviations and estimations of selective accuracy for each evaluated traits.

Analysis of variances showed a high significant difference ($p \leq 0.001$) between different inbred lines of *C. mucosospermus* for all studied traits, which indicates variability among these inbred lines (**Figure 2**). The estimations of the selective accuracy (SA) indicates a high experimental precision with regard to the criteria of Resende and Duarte (2007).

Table 4: Analysis of variances, observed minimum and maximum values, means and standard deviations (SE) and estimate of selective accuracy (SA) of assessed traits.

Traits (SI unit)	Blocks	Inbred lines	error	Range	Means ± SE	SA
FMp	0.83	220.55**	1.34	82.00-110.00	96.42±8.47	0.996
NFr	0.56	10.27**	0.35	1.00-10.00	5.41±2.31	0.982
MFr (g)	7247.45	115840.55**	1342.31	466.67-1600.00	822.41±230.37	0.994
DFr (cm)	0.19	2.57**	0.04	9.63-14.62	11.62±1.03	0.991
VFr (cm^3)	8783.41	129624.57**	2170.33	468.09-1749.42	862.78±255.29	0.991
MfS (g)	24.86	1042.82**	21.67	16.45-91.00	44.44±18.21	0.989
MdS (g)	6.58	212.75**	7.60	10.21-47.12	21.49±8.94	0.982
M_{100} (g)	0.14	117.09**	0.13	3.67-24.26	7.78±5.53	0.999
PSi (%)	0.73	229.51**	0.09	14.32-43.38	23.08±7.88	0.999
SL (mm)	0.02	31.11**	0.15	9.10-20.65	12.12±2.93	0.997
SW (mm)	0.01	24.53**	0.03	3.04-11.84	5.98±2.53	0.999
df	2	3	6			

** Significant at 1% level of significance respectively; **df**: degree of freedom; **FMp**: fruit maturity period; **NFr**: number of fruits per plant; **MFr**: mass of fruit; **DFr**: fruit diameter; **VFr**: fruit volume; **MfS**: mass of fresh seeds per fruit; **MdS**: mass of dry seeds per fruit; **M100**: mass of 100 seeds; **Psi**: percentage of seed integuments; **SL**: seed length; **SW**: seed width.

3.2. Variance Components and Coefficients of Variation

The study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits, but also very useful to estimate the scope for improvement by selection (Bello *et al.*, 2012). Results given in table **5** depicted that phenotypic variances (Vp) and PCV are slightly greater than genotypic variances (Vg) and GCV for all studied traits, indicating the least environmental influence in these character expressions. These results are confirmed by lower values of environmental variances (Ve) and environmental coefficient of variation (ECV). GCV values range from 7.89 to 80.26% while those of PCV range from 7.95 to 80.30%. According to Khan *et al.*, (2016), GCV and PCV values above 20% are considered high, those between 10 and 20% are moderate and values less than 10% are low. Thus in this study, all traits recorded high GCV and PCV values except fruit maturity period and fruit diameter, which recorded low values of GCV and PCV. High GCV and PCV values for traits indicate the existence of a large genetic variability that could be exploitable in breeding for the genetic improvement of these traits as emphasized by Ahsan *et al.*, (2015), Bello *et al.*, (2015) and Ndukauba *et al.*, (2015).

Table 5: Genetic variability parameters of yield component traits of *C. mucosospermus*

Traits (SI unit)	Vp	Vg	Ve	GCV	PCV	ECV	H^2	GAM
FMp	73.52	73.07	0.45	8.86	8.89	0.70	99.39	18.23
NFr	3.42	3.32	0.12	33.61	34.17	6.13	96.78	68.22
MFr (g)	38613.52	38166.08	447.44	23.75	23.89	2.57	98.84	48.72
DFr (cm)	0.85	0.84	0.01	7.89	7.95	0.86	98.83	16.21
VFr (cm^3)	43208.19	42484.75	723.44	23.89	24.09	3.12	98.33	48.87
MfS (g)	347.60	340.38	7.22	41.51	41.95	6.05	97.92	84.75
MdS (g)	70.91	68.38	2.53	38.47	39.19	7.40	96.43	77.96
M_{100} (g)	39.03	38.99	0.04	80.26	80.30	2.57	99.90	165.48
PSi (%)	76.50	76.47	0.03	37.89	37.90	0.75	99.96	78.15
SL (mm)	10.37	10.32	0.05	26.51	26.57	1.84	99.52	54.55
SW (mm)	8.18	8.17	0.01	47.79	47.82	1.67	99.88	98.53

Vp : Phenotypic variance; Vg : genotypic variance; Ve : environmental variance ; GCV : genotypic coefficient of variation; PCV: phenotypic coefficient of variation; ECV: environmental coefficient of variation; H^2: broad sense heritability; GAM: Genetic advance as the percentage of mean; FMp: fruit maturity period; NFr: number of fruits per plant; MFr: mass of fruit; DFr: fruit diameter; VFr: fruit volume; MfS: mass of fresh seeds per fruit; MdS: mass of dry seeds per fruit; M100: mass of 100 seeds; Psi: percentage of seed integuments; SL: seed length; SW: seed width.

3.3. Heritability and Genetic Advance of Yield Component Traits

One character can be improved only if it is highly heritable (Rana and Pandit, 2011). Broad sense heritability was estimated in order to determinate the total genetic variation proportion and results are recorded in Table **5**. According to Singh (2000), heritability values above 80% are very high, those between 60 and 79% are high when values ranging from 40 to 59% are assumed to be moderate and those less than 40% are low. Based on this ranking, all studied traits had a high heritability (H^2> 80%). Our results are in accordance with those obtained by Ogbonna and Obi, (2010) and Adjoumani *et al.*, (2016a, 2016b). A high heritability of one trait indicates not only low environmental influence in the observed variation of this trait (Ndukauba *et al.*, 2015; Sánchez *et al.*, 2019) but also, indicates the great opportunity for genetic improvement of this trait through selection (Ogbonna and Obi, 2010). The genetic advance as a percentage of mean (GAM) vary from 16.21 to 165.48% (**Table 5**). Johnson *et al.*, (1955) classified GAM values above 20%, ranging from 10 to 20% and those less than 10% as high, medium, and low respectively. Thus, fruit maturity period and fruit diameter recorded medium values of GAM while the remaining traits obtained high GMA values. Johnson *et al.*, (1955) also suggested that heritability and GAM values must be considered simultaneously to define an effective strategy for the genetic improvement of a trait. Based on this recommendation, high heritability accompanied with moderate to high GAM were observed for traits under study. These results indicate that traits under study are predominantly controlled by additive gene effects and thus, can effectively be genetically improved through selection as pointed by Ndukauba *et al.*, (2015) and Khan *et al.*, (2016).

3.4. Genotypic and Phenotypic Correlations

Yield is a character with complex heredity and is strongly affected by environment (Gupta *et al.*, 2015; Hannachi *et al.*, 2017). It is composed by several single traits with simple heredity (Rana and Pandit, 2011) and is genetically improved through its different components (Hannachi *et al.*, 2017). Knowledge about mutual association between different yield components is essential in selection criteria establishment (Singh *et al.*, 2017) permitting direct or indirect selection of genotypes for yield improvement (Ndukauba *et al.*, 2015; Singh *et al.*, 2017). Results of genotypic and phenotypic correlations between different studied traits are summarized in **Table 6**. For each studied trait, the estimate of genotypic correlation coefficient was higher than phenotypic correlation coefficient, which can be interpreted as a strong inherent genotypic relationship between these characters, through their phenotypic expression was impeded by environmental influence (Meena and Bahadur, 2015; Khan *et al.*, 2016). Fruit maturity period (FMp) had a highly significant positive phenotypic correlation with number of fruits per plant (NFr) and had a significant negative genotypic and phenotypic correlation with M_{100} and SL. NFr exhibited significant and negative correlation with all studied seed characters at phenotypic level and with MfS, MdS, PSi and SW. MFr showed significant positive phenotypic correlations with DFr, VFr, MfS, MdS, M100, PSi and SW while, at genotypic level it is positively correlated with , MdS, M100, PSi and SW. DFr and VFr was significantly and positively correlated with VFr, MfS, MdS, PSi and SW at genotypic and phenotypic level. However, VFr had a positive significant genotypic correlation with M100. significant and positive phenotypic correlation was observed between MfS and MdS. These two characters exhibited significant and positive phenotypic association with M100, PSi and SW. However, a significant and positive association was observed between MfS and M100 at genotypic level. M100 showed positive significant genotypic and phenotypic correlations with PSi, SL and SW while, PSi had a positive significant association with SW at genotypic and phenotypic at level. Significant and positive correlation between two characters suggests that these characters can be improved simultaneously in selection programs

because, it shows mutual relationship among characters and selection for one will translate to selection and improvement of the other (Ndukauba *et al.,* 2015; Singh *et al.,* 2017). On the contrary, a significant and negative correlation between two characters indicates that it would be difficult to make a simultaneous selection of these two characters (Meena and Bahadur 2015). Some values of genotypic correlation were greater than or equal to 1 instead of covered the whole range values from -1 to +1. According to Kersay and Pooni (1996), the estimate of genotypic correlation sometimes take values that fall outside the limit of -1 to +1.

Table 6: Genotypic and phenotypic correlation coefficients between yield component traits

Traits		NFr	MFr	DFr	VFr	MfS	MdS	M100	PSi	SL	SW
FMp	Rp	0.989**	-0.845	-0.812	-0.831	-0.893	-0.906	-0.962*	-0.917	-0.986*	-0.899
	Rg	1.021	-0.851	-0.818	-0.838	-0.902	-0.924	-0.966*	-0.919	-0.993**	-0.900
NFr	Rp		-0.915	-0.890	-0.904	-0.950*	-0.958*	-0.991**	-0.966*	-0.984*	-0.952*
	Rg		-0.944	-0.919	-0.931	-0.981*	-0.996**	-1.007	-0.984*	-1.000	-0.975*
MFr (g)	Rp			0.998**	0.999**	0.993**	0.988**	0.952*	0.987**	0.858	0.983*
	Rg			1.002	1.004	1.000	0.996**	0.959*	0.993**	0.862	0.988**
DFr (cm)	Rp				0.999**	0.987*	0.980*	0.935	0.977*	0.832	0.977*
	Rg				0.999**	0.995**	0.994**	0.945	0.984*	0.841	0.977*
VFr (cm^3)	Rp					0.991**	0.986*	0.946	0.983*	0.849	0.983*
	Rg					0.999**	0.998**	0.957*	0.991**	0.859	0.991**
MfS (g)	Rp						0.999**	0.980*	0.998**	0.911	0.997**
	Rg						1.002	0.992*	1.008	0.922	1.007
MdS (g)	Rp							0.986*	0.999**	0.926	0.999**
	Rg							1.005	1.016	0.942	1.017
M_{100} (g)	Rp								0.988**	0.974*	0.984*
	Rg								0.990**	0.975*	0.986*
PSi (%)	Rp									0.928	0.994**
	Rg									0.932	0.995**
SL (mm)	Rp										0.927
	Rg										0.931

* And ** significant at 5% and 1% level of significance respectively. FMp: fruit maturity period; NFr: number of fruits per plant; MFr: mass of fruit; DFr: fruit diameter; VFr: fruit volume; MfS: mass of fresh seeds per fruit; MdS: mass of dry seeds per fruit; M100: mass of 100 seeds; Psi: percentage of seed integuments; SL: seed length; SW: seed width; Rp: phenotypic coefficient of correlation; Rg: genotypic coefficient of correlation.

3.5. Stepwise Regression

Stepwise regression has been used to evaluate the relative contributions of each yield component to yield (Yao *et al.,* 2015) through the remove effect of non-effective characteristics in regression model on yield (Hannachi *et al.,* 2013). It permits to identify the best subset of predictors through the order in which variables were included in the regression equation (Ndukauba *et al.,* 2015). Result of stepwise regression analysis showed that mass of fresh seeds per fruit followed by mass of fruit, seed width, seed length and fruit maturity period explain 93.5% of variation in mass of dry seeds per fruit (R^2 = 0.935) (**Table 7**). Existence of significant R^2 in a successful regression equation indicates the effectiveness of the traits to increase dry seeds per fruit. Although SL and DCv are not correlated with MdS, they are involved in its prediction model. Our results are similar to those of Hannachi *et al.,* (2013) who found that the harvest index was part of the yield equation, although it did not correlate with it. According to Ahmadizadeh *et al.* (2011), in stepwise regression, effective factors were use directly on grain yield. Our results suggest that these characters are the major contributors to mass of dry seed per plant variance and should therefore greatly considered in *C. mucosospermus* breeding programs.

Table 7: Stepwise regression for mass of dry seeds per fruit and other traits

Traits	B	t	Sig.	Const.	R^2	Final model
MfS	0.478	18.238	0.000	-17.404	0.935	PdS = -17.404 + 0.478**MfS** + 0.005**MFr** -1.074**SW** + 0.813**SL** + 0.102**FMp**
MFr	0.005	3.334	0.001			
SW	-1.074	-4.444	0.001			
SL	0.813	4.344	0.001			
FMp	0.102	2.212	0.027			

B = Step-wise regression coefficient; **R^2** = coefficient of determination. Sig.: significance; Const: constant; MfS: mass of fresh seeds per fruit; MFr: mass of fruit; SW: seed width; SL: seed length; FMp: fruit maturity period

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4. CONCLUSION

From the present study, it can be conclued the existence of significant differences between the four *C. mucosospermus* inbred lines *Bebu*, *Wlêwlê small seeds 1*, *Wlêwlê small seeds 2* and *Wlêwlê small seeds 3*. Mahalanobis distances varied significantly from 8.44 to 629.50 between theses inbred lines. All investigated

traits recorded high genotypic coefficient of variation and phenotypic coefficient of variation values except fruit maturity period and fruit diameter where, low values were recorded. Studied traits had high heritability accompanied with moderate to high genetic advance as percentage of mean under Kononfla environmental conditions. Stepwise regression analysis revealed mass of fresh seeds per fruit followed by mass of fruit, seed width, seed length and fruit maturity as traits contributing for linear increase in mass of dry seeds. These traits could be considered as key criteria for selecting high yielding line in *C. mucosospermus* breeding program at Côte d'Ivoire.

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