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Heritability and Correlation Analysis for Agronomic and Morphological Traits in Cotton Collection (*Gossypium Hirsutum* L.) in Benin

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Abstract – This study was undertaken to estimate genetic variability and heritability of some morphological and agronomic parameters to discriminate some cotton genotypes in collection in field. The experiment was carried out in randomized complete block design with three replications at site of experiment of Cotton and Fibres Center for Agricultural Research at Cana located in south of Benin during 2010-2012.Analysis of variance showed highly significant ($p<0.0001$)differences among 14 cotton genotypes for agronomic parameters. The production of bolls on vegetative branches (BVB) ranged from 2.4±0.2 (Irma 772) to 11.6±0.5 (A 24). Mean values for number of bolls on fruiting branches (BFB) ranged from18.1±1.1 (chaco520) to 25.8±0.8 (A 24) and mean values of retention rate in first position of fruiting branches (RP1) ranged from 52.4±0,4 (Irma Z 856 ; Nta 88-6 ; H 279-1) to 68,6±0,4 (CR 92-534). High heritability values were obtained for three discriminant agronomic parameters (BVB:0.986; BFB:0.950; RP1:0.987). Genetic advance was ranged from 7.99% (BVB and BFB) to 15.72 (RP1). Highly significant positive correlation was observed between agronomic traits (number of bolls on vegetative branches, number of bolls on fruiting branches) and morphological traits (length of vegetative branch, length of fruiting branch, plant height to first fruiting branch and plant height). Results also indicated that length of vegetative branch, length of fruiting branch, plant height to first fruiting branch and plant height were good predictors of boll production. The observed extensive variation and high heritability provided with relevant information for further improvement programs.

Keywords – *Gossypium hirsutum,* Agronomic Traits, Morphological Traits, Variability, Heritability

I. INTRODUCTION

The cotton sector is an essential pillar of the Beninese economy. This sector accounts for 45% of tax revenues and contributes, in terms of added value, 13% to the formation of the product Gross Inside. Average seed cotton production over the last ten years estimated at 350 000 tonnes, represents about 70 billion francs of foreign currency paid to more than 325,000 producers. Cotton provides a monetary income to nearly 3 million people in Benin [1].Despite this production performance, the breeders must continuously identify cotton plants more adapted to the effects of climatic change. According to Sekloka *et al.*[2], the reduction of effective rainfall amount affects the crop yield. The identification and development of elite cotton adapted to these conditions are very important. Now, cotton breeding is handicapped by a lack of information on genetic diversity [3]. Indeed, knowledge of genetic diversity of elite breeding materials has been successfully used for efficient germ plasm management, genotype selection for different plant breeding purpose, and the conservation of genetic resources [4]. Therefore, precise identification and characterization of the accessions is of great value for quantifying the extent of intraspecific diversity within accessions [5].Despite morphological and agronomic traits are often limited in their numbers and may be controlled by epistatic and pleitropic gene effects [6], they constituted the starting point of the characterization of genetic diversity and identification of the accessions elites. Morphological and agronomic characteristics are used by breeders in the development of improved cultivars and by managers for specific cultivar selection. For example, Meena*et al.* [7] and Khan *et al.*[8] studied the stability and adaptability of *Gossypium hirsutum* cultivars and observed varied values for different agronomic, morphological and yield related traits. Ahmad *et al.*[9] showed that boll weight; bolls per plant, number of sympodia and bolls per sympodia can be exploited in future breeding programs. According to these authors, these morphological and agronomic traits may be kept in mind during making selection as they were the major attributes of the seed cotton yield. Sekloka *et al.*[2] too studied morphological and agronomic traits for the estimation of genetic diversity and selection criteria for cotton breeding. They proposed three breeding strategies involved high 8 heritable criteria as plant height, height to node ratio, length of fruiting branches, number of vegetative branches, first flower opening date, or length of vegetative branches, effective flowering time and boll retention at the first fruiting branches position. The improvement of its components like the number of fruiting branches, the number of bolls on fruiting branches and vegetative branches, the boll weight and the height of plant contribute then to increase the level of the seed cotton yield. However, achievement of any crop improvement depends upon the presence of genetic variability, heritability, correlation as well as genetic gain in selection [10]. Heritability is a key of transmissibility of traits and as such partition the total variance into genetic and environmental components [11]. Correlations are important in determining the degree to which various yield contributing characters are associated [12]. Plant traits having satisfactory variability, high heritability and genetic advance would be an effective tool for crop improvement [13]. Additive genes are considered to control traits with high heritability and genetic advance and the phenotypic selection thus would be effective [13]. Developing high yielding varieties need critical evaluation of existing genetic variability, heritability and genetic advance ([14], [15], [16]).

This study was undertaken to estimate genetic variability, heritability, genetic advance and phenotypic correlation among morphological and agronomic

parameters to discriminate some cotton genotypes in collection in field and this way find the interest for cotton variety improvement.

II. Materials And Methods

The experiment was conducted in Benin (West Africa) at site of experiment of Cotton and Fibres Center for Agricultural Research at Cana (2°5'E, 7°6'N) located in south of Benin at an altitude about 89 metres above sea level.

Fourteen cotton genotypes (*Gossypium hirsutum L.*) were compared based on morphological and agronomic characters in this experiment. It concerned H 279-1 which is a commercial variety in Benin and thirteen other cotton genotypes diverse in morphological traits, growth cycle and fibre quality traits. They were collected from Tchad (A24), Zambia (CD14), Mali (Nta 88-6), Cameroun (Irma 772, Irma Blt-pf, and Irma Z 856), Australia (Sicala 34, CS 189), Argentina (Guazuncho II, Chaco 520) and Costa-Rica (CR 92-498, CR 92-534).

The 14 cotton genotypes were sown in randomized complete block design (RCBD) with three replications in experimental field of Cotton and Fibres Center for Agricultural Research, during three years (2010, 2011and 2012).Plots were single sows, 10 m in length and 1 m apart with 0.50 m plant spacing. The seeds were grown at the end of June with one genotype per row. All the recommended agronomic practices and plant protection measures for cotton production were adopted to obtain healthy plants. The crop was also grown under uniform conditions to minimize environmental variability to the maximum possible extent.

Djaboutou *et al.*[17] showed positive genotypic and phenotypic correlation between the yield and the height of cotton plant, the height to first fruiting branch, the number of fruiting branches and the number of bolls. Ali *et al.*[18] also founded that morphological and agronomic characteristics are used by breeders in the development of improved cultivars and by managers for specific cultivar selection. Therefore, plant height to first fruiting branch (PHFFB),plant height (PH),length of vegetative branch (LVB), length of fruiting branch (LFB), number of bolls on vegetative branches (BVB), number of bolls on fruiting branches (BFB),retention rate of boll in first position of fruiting branches (RP1), number of vegetative branches (NVB), number of fruiting branches (NFB), sites in first position on fruiting branches (SP1) were described using the technique of plant mapping[19]. These characters were recorded on eight randomly selected plants from each genotype of each replication.

Univariate analyses of variance and Student-Newman-Keuls (SNK) tests were used to describe the 14 cotton genotypes based on agronomic traits and identify the discriminative descriptors. Then, Least Square Means of genotypes were estimated and a Canonical Discriminant Analysis (using the Mahalanobis distance) was performed to reveal the agronomic descriptors best discriminate cotton genotypes. Afterwards, the within and between genotypes variability was evaluated based on agronomic descriptors best discriminate cotton genotypes.

Genotypic variance, phenotypic variance, environmental variance, heritability and genetic advance were determined. Genotypic variance (σ^2_g), phenotypic variance(σ^2_p) and environmental variance (σ^2_e)were calculated using genotypic, phenotypic and error mean squares obtained from analysis of variance of genotypes based on agronomic characters as suggested by [20] and were used to calculate estimates of broad sense heritability of the characters. The mean squares from ANOVA were evaluated following [21] for variance components to compute broad sense heritability using the relation:

$$h_s^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

Where, h^2_S is heritability, σ^2_g is genotypic variance and σ^2_p is phenotypic variance

Expected genetic advance under selection (GA) was computed according to the formula given by [22].

$$GA(\%) = i.\sigma_p.h_s^2$$

Where, ''i'' is selection intensity; σ_p is phenotypic standard deviation and h^2_s is heritability of the trait expressed in fraction.

Clustering of cotton genotypes based on the discriminant agronomic characters was carried out using an agglomerative hierarchical clustering procedure with squared Euclidean distance as a measure of similarity. Dendrogram was constructed on the basis of fusion level to examine similarities in pattern of performance among genotypes and discriminant agronomic characters.

Pearson's correlation was performed between morphological and discriminant agronomic characters of different cotton genotypes to test multicollinearity. Afterwards, Principal component analysis (PCA) was performed to investigate the relationship between the morphological and discriminant agronomic characters like relationship between these characters and different cotton genotypes. PCA was conducted in the dimension of first two principal components (comp.1 and comp.2), using a singular-value decomposition procedure [23].

As the number of bolls is the principal trait of yield importance, we again carried out a linear regression to identify predictors of bolls production and test if the predicting power of the explanatory variables differs between cotton genotypes [24]. We built a linear regression for boll production with morphological traits studies (plant height to first fruiting branch, plant height, length of vegetative branch, length of fruiting branch). The models tested were:

BVB = $ß_0$+ $ß_1$ (plant height to first fruiting branch) +$ß_2$(plant height) + $ß_3$(length of vegetative branch) + $ß_4$(length of fruiting branch) + ε

BFB = $ß_0$+ $ß_1$ (plant height to first fruiting branch) +$ß_2$(plant height) +$ß_3$(length of vegetative branch) + $ß_4$(length of fruiting branch) + ε

$ß_0$indicated the intercept; $ß_1$, $ß_2$, $ß_3$and $ß_4$were the partial regression stops and ε is the unexplained error associated to the models.

Data were processed under STATISTICA software, version 6 (www.statsoft.com) and R (Version 3.1).

III. RESULTS

III.1. Cotton genotypes influence on agronomic characters

The results of inferential tests (table1) showed cotton genotypes influence on agronomic variables selected for the study. These results revealed that, for all of the variables, there are very highly significant differences (p <0.0001) among cotton genotypes. Thus, number of fruiting branches (NFB), number of vegetative branches (NVB), number of bolls on vegetative branches (BVB), number of bolls on fruiting branches (BFB), retention rate of boll in first position of fruiting branches (RP1) and sites in first position of fruiting branches (SP1) can be used to describe precisely enough capsules production of 14 genotypes identified from their characteristics. Similarly, these large differences deserve to be exploited in selection to improve the level of analyzed characters and in the direction that promotes the expression of a performance and high yield stability.

Table 1: Mean square deviations of the univariate test on genotypes

Source of variability	Dl	NFB	NVB	BVB	BFB	RP1	SP1
Blocks	1	11823,86	183,962	3154,339	19131,74	137520,3	11833,93
Genotypes	13	3,68**	0,786***	41,217***	15,31***	58,4***	3,69**
Erreur	28	1,08	0,1443		1,07	1,0	1,01

*RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; NVB= number of vegetative branches; NFB= number of fruiting branches,***, ***= Significant at $p<0.001$ and $p<0.0001$, respectively; N.S = Non-significant

III.2. Discrimination of cotton genotypes from the agronomic variables

The tables 2 and 3 presented the results of canonical discriminant analysis make to determine the most discriminating agronomic variables for comparing cotton genotypes. The results showed that the variables that best discriminate cotton (p <0.0001) are number of bolls on vegetative branches; number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches. It would therefore be possible to describe fairly accurate the cotton genotypes studied from these three agronomic variables.

Table 2: Canonical analysis of agronomic data

Variables	Wilk (Lambda)	Partiel (Lambda)	F	p
NFB	0,000035	0,559432	1,39332	0,235NS
NVB	0,000043	0,451800	2,14673	0,052NS
BVB	0,000281	0,069719	23,60738	0,000***
BFB	0,000112	0,174683	8,35898	0,000***
RP1	0,000349	0,056089	29,77407	0,000***
SP1	0,000031	0,636525	1,01029	0,473NS

*RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; NVB= number of vegetative branches; NFB= number of fruiting branche ,****= Significant at $p<0.001$; N.S = Non-significant

Table 3: Discriminant analysis on agronomic variables

Variables	Valeur propres	R canonique	Lambda	Chi²	dl	p
BVB	50,17922	0,990182	0,000020	336,0530	78	0,000***
RP1	37,82635	0,987038	0,001003	214,0577	60	0,000***
BFB	9,17185	0,949573	0,038930	100,6256	44	0,000***
NVB	0,97303	0,702258	0,395991	28,7173	30	0,532NS
NFB	0,27950	0,467382	0,781304	7,6505	18	0,983NS
SP1	0,00032	0,017899	0,999680	0,0099	8	1,000NS

*RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; NVB= number of vegetative branches; NFB= number of fruiting branche ,****= Significant at $p<0.001$; N.S = Non-significant

III.3. Variability of discriminate agronomic variables per cotton genotypes

Mean comparisons, genotypic variance, phenotypic variance, environmental variance, genotypic variation coefficient and phenotypic variation coefficient ofthree discriminate characters retained in production of bolls, estimated for 14 cotton genotypes, are displayed in Table 4.

Results showed highly significant variations (p<0.001)among cotton geno types for production of boll son vegetative branches. The production of bolls on vegetative branches varied from 2.4±0.2 (Irma 772) to 11.6±0.5 (A 24).Variability measured by the coefficients of phenotypic and genotypic variation (74.61%; 75.11%) is very high. Moreover, the difference between the CVg and CVp is low (0.50%), suggesting that the effect of the environment is relatively less on the genotype expression.

The analysis of variance for number of bolls on fruiting branches showed highly significant differences (p<0.001)

among cotton genotypes. Mean values for number of bolls on fruiting branches ranged from18.1±1.1 (chaco520) to 25.8±0.8 (A 24) with an average of 19.7±0.4. Coefficients of phenotypic and genotypic variation, respectively 19.13and 18.65, were average. The difference between the CVg and CVp is low(0.38%).

Highly significant difference (p<0.0001)for retention rate in first position of fruiting branches was observed among cotton genotypes. Mean values of the data rangedfrom52.4±0.4 (Irma Z 856 ; Nta 88-6 ; H 279-1) to 68.6±0.4 (CR 92-534). Environmental variance was 1.04, phenotypic variance was 59.80and genetic variance was 59.02. Genetic variance was greater than environmental variance indicating that the character was controlled genetically. The study revealed high genotypic and phenotypic coefficients of variation. Datawere103.15 and 104.5, respectively.

Genotypic coefficient of variation does not give an exact idea on total variation that is heritable. Thus, a perusal heritability (h^2s) estimates indicated that all the discriminate characters under study showed high heritability in all genotypes. Heritability was 0.986 for number of bolls on vegetative branches, 0.950 for number of bolls on fruiting branches and 0.987 for retention rate of boll in first position of fruiting branches. Genetic advance ranged from 7.99% (BVB and BFB) to 15.72 (RP1). These data confirm the advance awaited theoretically selection based on number of bolls on vegetative branches, number of bolls on fruiting branches and of retention rate of boll in first position of fruiting branches.

Table 4: Variability, heritability and genetic advance based on agronomic characters measured on the 14 cotton genotypes

Source of variability	BVB	BFB	RP1
A 24	11.6±0.5 a	25.8±0.8 a	60±3 bc
CD 14	4.2±1.1 def	19.5±0.5 ef	59.7±0.3 bc
Chaco 520	3.4±0.3 ef	18.1±1.1 f	60.8±0.2 b
CR 92-498	4.6±0.6b cde	19.2±0.1 ef	55.9±0.7 de
CR 92-534	6.4±0.4 b	24±1.5 ab	68.6±0.4 a
CS 189	5.6±0.5 bcd	20.5±0.5 cdef	57.4±0.4 bcd
Dp 90	4.5±0.3 cde	20.4±0.3 cdef	57.9±1.2 cd
Guazuncho II	3.3±0.2 ef	22.7±0.3 bcd	59.3±1 bc
H 279-1	5.4±0.3 bcd	23.2±0.8 abc	52.4±0.4 f
Irma 772	2.4±0.2 f	21.9±0.9 bcde	55.7±0.7 ef
Irma Blt-pf	3.4±0.2 ef	23±1.5 abc	53.5±1 ef
Irma Z 856	3±0.2 ef	19.7±0.4 def	52.4±0.4 f
Nta 88-6	6.3±0.7 bc	18.6±0.4 f	52.4±0.6 f
Sicala 34	6.1±1b c	22.2±0.2 bcde	55.1±0.1 def
P	0.001**	0.001**	0.000***
$б^2$g	15.26	15.84	59.02
$б^2$e	0.365	1.07	1.04
$б^2$p	15.47	16.67	59.80
CVg (%)	74.61	18.65	103.15
CVp (%)	75.11	19.13	104.5
CVp-CVg	0.50	0.38	0.35
H^2s	0.986	0.950	0.987
GA	7.99	7.99	15.72

BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches;***= Significant at *p<0.001*; N.S = Non-significant

III.4. Hierarchical cluster analysis

The dendrogram based on discriminate agronomic characters results grouped the cotton genotypes into three clusters (figure 1). The first cluster contained two genotypes (A24 and CR 92-534), the second seven (CD14, Chaco 520, CR 92-498, CS 189, DP 90, Guazuncho II and Irma 772)and the third five genotypes (Irma Z 856, Nta 88-6,Sicala 34, H 279-1 and Irma Blt-pf). It is also interesting to note that cophenetic correlation of cluster ranged from 0.99 (G3) to 1.567(G1), indicating a good fit of the cluster to the original data. All the three clusters had a low square sum (G1= 4.913, G2=5.639, G3= 3.595), suggesting therefore that they are compact.

The results obtained from analysis of variance (table 5), indicated very high significant difference among clusters (<0.0001).The cotton genotypes of the first cluster (A24 and CR 92-534) had greater number of bolls on fruiting branches, number of bolls on vegetative branches and retention rate of boll in first position of fruiting branches. However the genotypes of second cluster retained more boll in first position of fruiting branches (58.10±0.54) than the third cluster's genotypes (53.27±0.68) which presented more number of bolls on fruiting branches and number of bolls on vegetative branches than them.

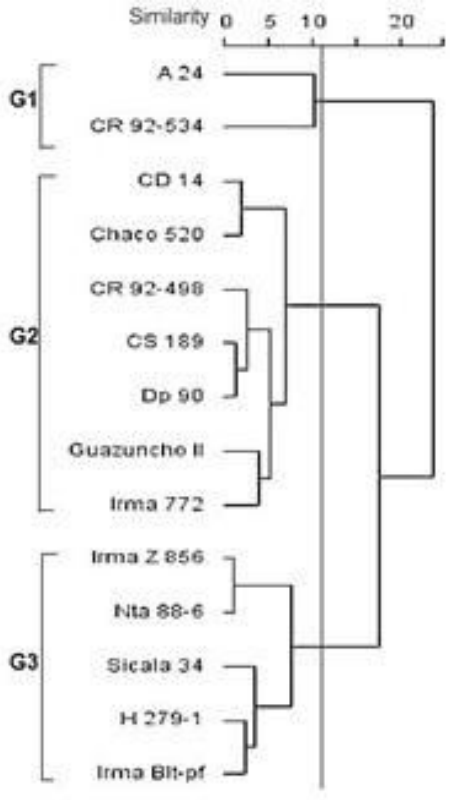

Figure 1: UPGMA cluster of

Table5: Mean performance of the groups for fourteen cotton genotypes

	G1	G2	G3	Pr(>F)
Groups component	2	7	5	-

BVB	9±0.61 c	4±0.32 a	5.7±0.41b	<0.0001***
BFB	24.9± 0.72b	20.32±0.38a	21±0.49a	<0.0001***
RP1	64.30±1.01c	58.10±0.54b	53.27±0.68a	<0.0001***

BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches;***= Significant at *p<0.0001*

III.5. Correlation between morphological variables and discriminant agronomic variables

Table 6 indicated morphological variables and discriminant agronomic variables correlation coefficients. Data regarding number of bolls on vegetative branches showed highly significant positive phenotypic relationship with number of bolls on fruiting branches (0.472), length of vegetative branch (0.656)and length of fruiting (0.729).Otherwise, highly significant positive phenotypic correlation for number of bolls on fruiting branches was recorded with length of vegetative branch (0.469)and length of fruiting (0.699).Significant positive phenotypic correlation for plant height to first fruiting branch was observed with plant height (0.783) and length of vegetative branch (0.489). Similarly, plant height showed highly significant positive phenotypic correlation with length of vegetative branch (0.75)and length of fruiting (0.524).Negatively non-significant phenotypic correlation for retention rate of boll in first position of fruiting branches was observed with all the morphological variables. Overall, these results are suggesting that if plant height increases then yield, number of bolls on vegetative branches, number of bolls on fruiting branches, length of vegetative branch and length of fruiting branch also increase. Number of bolls on vegetative branches and number of bolls on fruiting branches can be predicted by morphological variables (PHFFB, PH, LVB and LFB).

The Principal Component Analysis performed on morphological traits and agronomic variables discriminant showed that the first two axes explained 76.77% of the total variation. Table7 and figure 2 show the correlation between the axes and the variables. The first axis was found significantly and positively correlated with number of bolls on fruiting branches, number of bolls on vegetative branches, plant height, length of vegetative branch, length of fruiting branch and three genotypes (A24; Irma Blt-pf and H 279-1).The first axis was found also significantly and negatively correlated with five genotypes (CD24, CR-926498, CS 189, Dp 90 and Guazuncho II). The second axis was mostly influenced positively by retention rate of boll in first position of fruiting branches and genotype Sicala 34. The second axis was also negatively influenced by plant height to first fruiting branch and two genotypes (Irma Z 856 and Nta 88-6). The other relationships were not significant. Overall, it can be deduced that the genotypes (A24; Irma Blt-pf and H 279-1) generally had greater number of bolls on fruiting branches, number of bolls on vegetative branches, plant height, length of vegetative branch and length of fruiting branch. Likewise, genotypes (Irma Z 856 and Nta 88-6) had greater plant height to first fruiting branch.

Table 6: Morphological and discriminant agronomic variables correlation coefficients for all cotton genotypes studied

	BVB	BFB	RP1	PHFFB	PH
BFB	0.472 **				
RP1	0.149 ns	0.273 ns			
PHFFB	0.156 ns	-'0.092 ns	-'0.206 ns		
PH	0.136 ns	0.263 ns	-'0.274 ns	0.783***	
LVB	0.656***	0.469**	-'0.233 ns	0.489**	0.75***
LFB	0.729***	0.699***	-'0.118 ns	0.159 ns	0.524***

RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; PHFFB=plant height to first fruiting branch; PH=plant height; LVB=length of vegetative branch; LFB= length of fruiting branch;,***= Significant at *p<0.001*; N.S = Non-significant

Table 7: Correlations variables ; genotypes and composants

		Comp.1	Comp.2
Discriminate agronomic variables	RP1	-0.1781217	0.6300990
	BFB	0.6175590	0.6159526
	BVB	0.6918305	0.4380632
morphologic Variables	PH	0.7658930	-0.5195432
	PHFFB	0.5023916	-0.7231028
	LFB	0.9231872	0.2913325
	LVB	0.9683419	-0.0815594
Genotypes	A 24	0.7358438	0.23663741
	CD 14	-0.1882530	-0.28602619
	Chaco 520	-0.94459720	0.00521902
	CR 92-498	-0.77550536	-0.05251229
	CR 92-534	0.02120681	0.19259428
	CS 189	-0.55096787	0.20376927
	Dp 90	-0.82826358	0.04076091
	Guazuncho II	-0.57159929	0.28178295
	H 279-1	0.41104561	-0.00007416
	Irma 772	0.08458267	-0.21766875
	Irma Blt-pf	0.37329562	-0.31720983
	Irma Z 856	0.05535597	-0.66261274
	Nta 88-6	0.24272842	-0.65075589
	Sicala 34	-0.09703298	0.38312150

RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; PHFFB=plant height to first fruiting branch; PH=plant height; LVB=length of vegetative branch; LFB= length of fruiting branch;,

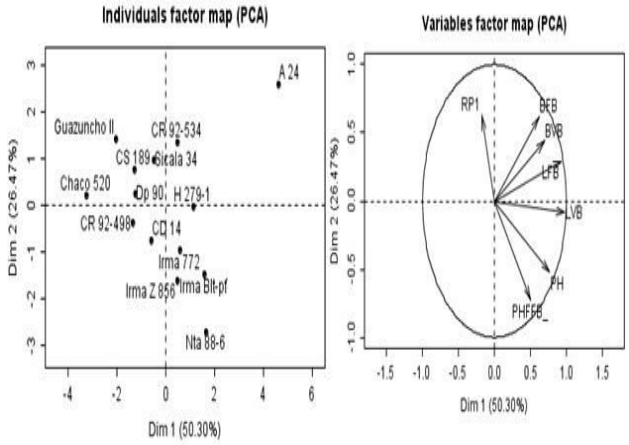

Figure 2: Principal Component Analysis (PCA) performed on morphological and discriminant agronomic variables
RP1= retention rate of boll in first position of fruiting branches; SP1 = sites in first position of fruiting branches; BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches;
PHFFB=plant height to first fruiting branch; PH=plant height; LVB=length of vegetative branch; LFB= length of fruiting branch

III.6. Modelling number of bolls on vegetative branches and number of bolls on fruiting branches based on morphological variables

Regression equations were used to build predictive model for number of bolls on vegetative branches and number of bolls on fruiting branches based on morphological variables studied (PHFFB, PH,LVB and LFB). The independent variables are BVB and BFB. There were highly significant and strong relationships between number of bolls on vegetative branches and four morphological traits (R^2= 0.862; p<0.0001) (table8). However, length of vegetative branch and length of fruiting branch were a strong predictor of number of bolls on fruiting branches (R^2= 0.532; p<0.0001). Thus, further use of the obtained models should be made with respect to the morphological traits considered.

Table8: Linear regression model for number of bolls on vegetative branches and number of bolls on fruiting branches

Regression equations	R^2(%)	R^2(%) (ajust)	R^2(%) (prev)	P
BVB = - 4.69 + 0.526 PHFFB – 0.161 PH + 0.0993 LVB + 0.227 LFB	89.2	88.0	86.25	***
BFB = 15.1 – 0.143 LVB + 0.359 LFB	58.8	56.7	53.20	***

BVB=number of bolls on vegetative branches; BFB=number of bolls on fruiting branches; PHFFB=plant height to first fruiting branch; PH=plant height; LVB=length of vegetative branch; LFB= length of fruiting branch;***= Significant at *p<0.001*; N.S = Non-significant

IV. DISCUSSION

This study focused on the variability of six agronomic characters and estimated the heritability as well as the genetic advance of these characters in14 cotton genotypes from which H 279-1 is one of commercial varieties in Benin. The thirteen other cotton genotypes (A24, CD14, Nta 88-6, Irma 772, Irma Blt-pf, Irma Z 856,Sicala 34, CS 189, Guazuncho II, Chaco 520, CR 92-498, CR 92-534) were collected. The study also describes the relationship between agronomic characters and morphological characters. Results showed that the variables which best discriminate cotton geno types are number of bolls on vegetative branches; number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches. The analysis of variance based on discriminate traits, revealed high level and significant variation among the cotton genotypes and indicated that the genotypes groups can be separated based on studies traits. This extensive variability among genotypes is probably attributed to genetic differences as well as the environment in which they were regenerated [25]. However, all the discriminate characters under study showed high heritability and genetic advance in all genotypes. Moreover, the difference between genotypic and phenotypic coefficients of variation is low. These results suggested that the effect of the environment is relatively less on the genotype expression for number of bolls on vegetative branches, number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches.High variation in these agronomic traits among cotton genotypes was genetically fixable, thus of additive nature. Therefore, the early selection of the off springs inside the cotton genotypes studied based on these agronomic characters would be possible and effective. It would therefore be possible to describe fairly accurate the cotton genotypes studied from these three agronomic variables. Similarly, the number of bolls on vegetative branches, number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches can be used to describe precisely enough capsules production of 14 genotypes identified from their characteristics. According to Fellahi *et al.*[26], high heritability coupled with high genetic advance, suggest the possibility of selecting within the populations in order to develop new genotypes presenting of the desirable characteristics, because the genetic effects of such characters are of additive nature and thus are fixable at the offspring. Agronomic characters variation for the cotton genotypes can be also explained based on the diverse geographic origins of these genotypes [27].

Cluster analysis obtained from agglomerative hierarchical clustering procedure with squared Euclidean distance grouped cotton genotypes nearly similar to number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches. However, the cotton genotypes of the first cluster (A24 and CR 92-534) were characterized by highest number of bolls on fruiting branches, number of bolls on vegetative branches and retention rate of boll in first position of fruiting branches.

Breeding populations can be produced from A24 and CR 92-534 using recurrent selection by recombining yield with number of bolls on fruiting branches, number of bolls on vegetative branches and retention rate of boll in first position of fruiting branches. From these populations could be developed high new recombinant varieties with the intermediate to high combination of NFB, NVB and RP1 that will be resistant against the stress of climate change in Republic of Benin. This can help cotton hybridization programs which are in progress in Benin.

The results showed also high significant positive correlations between morphological traits (plant height to first fruiting branch, plant height, length of vegetative branch and length of fruiting branch) and two of three discriminant agronomic traits (number of bolls on vegetative branches and number of bolls on fruiting branches). They indicated highly significant positive phenotypic relationship between number of bolls on vegetative branches, number of bolls on fruiting branches, length of vegetative branch, length of fruiting branch, plant height to first fruiting branch and plant height. These results are suggesting that if plant height increases, number of bolls on vegetative branches, number of bolls on fruiting branches, length of vegetative branch and length of fruiting also increase. A24, Irma Blt-pf and H 279-1 had greater number of bolls on fruiting branches, number of bolls on vegetative branches, plant height, length of vegetative branch and length of fruiting branch. The relatively strong relationships between number of bolls on vegetative branches, number of bolls on fruiting branches, length of vegetative branch, length of fruiting branch, plant height to first fruiting branch and plant height obtained by the predictive models confirm the advance awaited theoretically selection based on these characters. According to Ahmad *et al.*[28], morphological traits like sympodial, plays an important role in cotton crop and those fruiting branches which bear cotton bolls also manage the bolls number and seed cotton yield in cotton plant. Godoy [29] observed that plant height was one of the most efficient criteria to identify the early maturing cotton cultivars. The cotton breeders have succeeded in developing early maturing genotypes with short fruiting branches and also rated cultivars with short fruiting branches as early maturing ones ([30]; [31]; [32]).Several other breeders have also reported strong relationship between lower sympodial branch and the early maturity in cotton i.e. mostly positively correlation between morphological and agronomic traits ([33]; [34]; [35]; [36]).Use of morphological markers may accelerate the time-consuming procedure of progeny screening resulting from the offspring juvenility phase as a biological barrier and decreased the high expenses caused by a long period of time for nursery field occupation and relative laborious management [37], still to separate the genetic and environmental variations [38].Therefore, these traits can be used as valid and efficient criteria for screening of progenies for earliness during the juvenile phase in breeding programs. However, molecular markers could be useful if one wishes to accumulate various characters in the same genotype.

V. Conclusion

This study revealed high level and significant variation among the cotton genotypes based on agronomic traits like number of bolls on vegetative branches, number of bolls on fruiting branches and retention rate of boll in first position of fruiting branches. All the characters under study showed high heritability and genetic advance in all genotypes. The results showed also highly significant positive relationship between number of bolls on vegetative branches, number of bolls on fruiting branches, length of vegetative branch, length of fruiting branch, plant height to first fruiting branch and plant height. A24, Irma Blt-pf and H 279-1 had greater number of bolls on fruiting branches, number of bolls on vegetative branches, plant height, length of vegetative branch and length of fruiting branch. These large differences deserve to be exploited for selection to improve the level of the analyzed characters and in the direction that promotes the expression of a performance and high yield stability.

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