

Full Length Research Paper

Genotypic variability estimates of agronomic traits in secondary triploid banana 'Matooke' (*Musa sp.*, AAA-EA) hybrids

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Effective selection of hybrids for a trait is based on the extent of variation and heritability. This study examined yield parameters of secondary triploid 'Matooke' hybrids and the extent of their genetic diversity based on the traits evaluated. Eleven genotypes, including nine 'Matooke' hybrids and two landraces were evaluated for 12 characters in a preliminary yield trial (PYT) over three crop cycles. Plant height, bunch weight, number of standing leaves at flowering and the youngest leaf spotted with black Sigatoka symptoms showed significant interaction between genotype and crop cycle. While characters such as pseudo stem girth, number of days for fruit filling, number of hands, number of fingers on the second hand and the fruit length showed stable differences amongst these genotypes. The genotypic coefficient of variation for the characters ranged from 7.6% (finger length) to 33.5% (bunch weight); with moderate heritability estimates varying from 13.5% (pseudostem girth) to 67% (plant height). Bunch weight showed strong positive correlation with number of hands, number of fingers on the second hand, the fruit length and pseudostem girth. These results imply that breeders could select for some of these variable and ratoon stable traits in a single cycle of early evaluation trial, subsequently reducing costs, time and space in field testing.

Key words: Genetic variation, heritability, expected genetic gain, selection, *Musa sp.*

INTRODUCTION

Banana (*Musa sp.*) is the eighth most important global food commodity after maize, wheat, rice, potato, cassava, soybean and barley (FAOSTAT, 2013). It is grown in more than 100 countries, with an annual production of around 150 million metric tonnes. More than 30 million people in the East African region depend on banana,

mainly grown by smallholder farmers. About 80% of bananas grown in the region are the east African highland banana (*Musa sp.*, AAA-EA) type, locally known as 'Matooke'. Annual 'matooke' production in Uganda is estimated to be 10 million tons valued at USD 534 million (Kalyebara et al., 2006; Nyombi, 2013). Many rural

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communities earn income from sale of bananas. Bananas are perennial, with broad leaves which provide soil cover and a broad root network which maintains soil structure. The banana cropping system, therefore, is also an important component of sustainable environmental management. It is generally tolerant to long dry spells and can grow in a wide range of environments and farming systems and saves on labour for opening land seasonally. Because of the importance of this crop, many of the regional countries have considered banana a high research and development priority. However, average productivity has remained low (<30% of attainable), due to a complex of production constraints, including banana weevil (*Cosmopolites sordidus*, (Germer)), nematodes (e. g. *Radopholus similis* (Cobb) Thorne), black Sigatoka (*Mycosphaerella fijiensis* (Morelet)), Fusarium wilt (*Fusarium oxysporum* f. sp. *Cubense* (E.F. Smith) Snyder & Hansen)), banana bacterial wilt (*Xanthomonas campestris* pv. *musacerum*) and more recently drought stress (Tushemereirwe et al., 2003, Viljoen, 2010). Farmers manage some constraints through cultural control, many of which are effective in keeping the pest and disease pressures below threshold levels. However, cultural control involves manipulation of environment of the plant host and the parasite. It is a continuous and tedious process for the farmers and can only work in the short run. Use of resistance is more effective and durable option for the management of banana problems (Jones, 2000).

Genetic improvement of bananas to produce cultivars with host plant resistance and other desirable agronomic traits is complicated by low genetic variability, polyploidy nature and the low levels of female and /or male fertility in most widely grown triploid clones (Rowe, 1984; Hilber, 1997; Tezenas du Montcel et al., 1996; Pillay et al., 2002; Ssebuliba et al. 2006). Currently 'Matooke' breeding requires many years of field-testing for several rounds of selection including evaluation for agronomic performance in early evaluation trials (EET) (based on individuals), selected hybrids are further evaluated for pest/disease response, yield and consumer acceptability in the preliminary yield trials (PYT). Promising hybrids from the PYTs are advanced for participatory on-farm evaluation and multi-location evaluation (Ssebuliba et al. 2006; Ssali et al., 2010). An evaluation of the components of variation and heritability among characters will facilitate improvement of this crop by plant breeders. Knowledge of the genetic variability available among and between genotypes of 'Matooke' hybrids is needed as a guide for breeders and other scientist working on the improvement of this crop. Therefore this study was undertaken to evaluate components of genetic variance and to estimate the heritability between the various yield components of 'Matooke' hybrids.

MATERIALS AND METHODS

The experiment was established in October 2010 at National

Table 1. Origin of the genotypes evaluated at the National Agricultural Research Laboratories at Kawanda.

Genotype	Pedigree	
	Female	Male
12468S1	917K-2	SH3217
3123K2	246K-1	TMB2X7197-2
12748S1	660K-1	TMB2X8075-7
3192K2	917K-2	TMB2x8075-7
3637K13	222K-1	TMB2X7197-2
4360K3	222K-1	Calcutta 4
3626K1	401k-2	SH3217
3068K1	376K-7	Calcutta 4
3639K2	917K-2	TMB2X8075-7
Km 5		Landrace
Mbwazirume		Landrace

Agricultural Research Laboratories, NARL. NARL is located at 0°25'N, 32°32'E, 1190 m above sea level, 13 km north of Kampala. Mean annual rainfall is about 1190 mm per year with bimodal distribution, the two rainy seasons span from March to June and September to December. Average daily temperatures are 16°C minimum and 29°C maximum. These conditions are generally representative of major banana growing areas of Central Uganda region.

Eleven cultivars were assigned in a randomised complete block design for the experiment. The test materials included nine 'Matooke' hybrids developed by the National Banana research Programme, NARO and two control varieties ('Yangambi Km-5' and 'Mbwazirume'). Details on the hybrids and parents are presented in Table 1. Forty eight (48) tissue culture plants for each genotype were planted in four replicates for 3 cropping cycles. The plants were spaced at 3m x 3m and organic manure was applied at planting and regular banana management was followed (Tushemereirwe et al., 2003).

Data was collected on the flowering dates used to compute days to flowering (DTF) and number of standing leaves at flowering (NSL). Harvest date was used to compute Days from flowering to harvest (DFF), number of leaves at harvest, bunch weight (Bwt, kg⁻¹), number of clusters (HDS), number of fingers on the 2nd cluster (FHND2), finger length (FL), finger circumference (FC), youngest leaf spotted at flowering (YLS), plant height at flowering (HT), and girth at 100 cm (G) and the number of leaves at harvest (Lhar). The crop cycling index (CCI=HTS/PHT) was computed from the height of the tallest sucker and the height of the mother plant at flowering.

Statistical analysis

The statistical analysis was performed using the SAS package (SAS Institute Inc., 2004). The generalised linear model (GLM) was used for the analysis of variance. Let Y_i be the average of the measure of a given character of the i th genotype for $i = 1, \dots, 11$ from the experimental group. The linear model for Y_i is:

$$Y_{ij} = \mu + \alpha_i + c_j + \epsilon_{ij} \quad 1$$

Where μ is the grand mean, α_i is the genetic effect of the i th genotype expressed as deviation from the mean, c_j is the crop cycle and ϵ_{ij} is the environmental error for the i th genotype and the j th crop cycle.

The observed variance or phenotypic variance (V_p) of a character

Table 2. Analysis of variance- mean squares for analysis of characters in triploid 'Matooke' hybrids.

Trait	Mean squares			
	Genotype	Cycle	Genotype × Cycle	Error
Plant height (cm)	29047.73*	236098.09*	2663.42*	1083.81
Pseudostem girth at 100 cm (cm)	906.86*	6702.06*	321.91	313.03
Crop cycling index	0.11	0.22	0.06	0.07
Days to fruit filling	2698.49*	3037.42*	570.36	453.19
Bunch weight (Kg)	203.77*	364.43*	26.22*	16.17
No. Hands	7.31*	10.43*	1.24	1.41
No. of fingers on the 2nd hand	37.24*	107.13*	7.13	7.53
Finger length (cm)	23.78*	110.05*	4.98	4.84
Finger circumferences (cm)	20.99	1.09	53.83	140.44
Number of standing leaves	25.07*	24.05*	6.97*	2.51
Youngest leaf spotted	43.50*	17.21	13.30*	7.81
number of leaves at harvest	2.83	0.52	1.16	1.84

*Significant at 5% probability level.

comprises the genotypic variance (V_g) and the environment variance (V_e). This relationship could be expressed symbolically as:

$$V_p = V_g + V_e \quad 2$$

These components of variance V_g = genotypic variance, V_p = phenotypic variance and V_e = environmental variance were estimated using the following formula (Wricke and Weber, 1986):

$$V_g = (MSG - MSE / r) \quad 3$$

$$V_p = (MSG / r)$$

$$V_e = (MSE / r)$$

Where MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replication, respectively (Baye, 2002). Broad sense heritability (h^2) was estimated as a ratio of genetic variance (V_g) and phenotypic variance (V_p) specified by Singh and Chaudhary (1985):

$$h^2 = (V_g / V_p) \times 100 \quad 4$$

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested by Johnson et al. (1955).

$$GCV = (\text{Genotypic variance} / \text{mean value of the trait}) \times 100 \quad 5$$

$$PCV = (\text{Phenotypic variance} / \text{mean value of the trait}) \times 100 \quad 6$$

Genotypic correlation coefficients among the traits of 11 banana genotypes were computed using the Proc Corr procedure in SAS.

RESULTS AND DISCUSSION

Mean squares in the combined analysis of variance for 12 traits were significant for nine of the traits including plant height (HT), bunch weight (Bwt), number of standing leaves at flowering (NSL), the youngest leaf spotted with black Sigatoka symptoms (YLS), pseudo stem girth (G), number of days for fruit filling (DFF), number of fingers on the second hand (FHDS2), number

of hands (HDS) and fruit length (FL) (Table 2). Genotypic variance indicates that selection can be successfully applied in this population (Allard, 1960) in terms of these characters. The most important variance components for defining adaptation strategy and yield stability targets are those relating to genotypic and genotype-environment effects (Annicchiarico, 2002). Plant height (HT), bunch weight (Bwt), number of standing leaves at flowering (NSL) and the youngest leaf spotted with black Sigatoka symptoms (YLS) show significant interaction between genotype and crop cycle. While pseudo stem girth (G), number of days for fruit filling (DFF), number of hands (HDS), number of fingers on the second hand (FHDS2) and the fruit length (FL) showed no significant interaction between genotype x crop cycle. Therefore the variable traits under study in 'Matooke' hybrids can be categorised into (a) ratoon unstable agronomic traits-which lack stability of the average effects over crop cycles and (b) ratoon stable agronomic traits-showing stable differences amongst genotypes across the crop cycles.

Difficulties in breeding bananas due to the long generation of the crop (about 18 months to establish from seed to seed), the high cost and space requirements (9 m² per mat), it is plausible to select for characters showing stable differences amongst genotypes (Rowe, 1984; Hilber, 1997; Pillay et al., 2002). However, variability is the addition of total hereditary effects from expressed genes as well as the environment. Therefore, the variability is grouped into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability (h^2 %) and the expected genetic gain (ega%). These genetic parameters help in the selection of the genotypes for genetic improvement of the crop.

Genetic analysis was made for the nine variable

Table 3. Phenotypic and genotypic components of variability for the agronomic characters of 'Matooke' hybrids.

Trait	Mean	Range	Variance					
			Genotypic	Phenotypic	GCV (%)	PCV (%)	h^2 (%)	Ega (%)
Pseudostem girth (cm)	44.9	38.9-52.9	48.7	361.8	15.6	42.4	13.5	11.8
Days to fruit filling	149.1	113.9-161.3	177.3	630.5	8.9	16.8	28.1	9.8
No. Hands	7.0	5.9-8.6	0.5	1.9	10.1	19.7	26.5	10.7
No. of fingers(2nd hand)	17.7	15.3-22.2	2.5	10.0	8.9	17.9	25.0	9.2
Finger length (cm)	16.4	14.9-20.6	1.6	6.4	7.6	15.4	24.5	7.8
Plant height (cm)	258.0	227.6 -309.0	2198.7	3282.5	18.2	22.2	67.0	30.6
Bunch weight (Kg)	11.5	5.9-19.9	14.8	31.0	33.5	48.4	47.8	47.6
No. of standing leaves	9.7	8.5-10.8	1.5	4.0	12.6	20.6	37.5	15.9
Youngest leaf spotted	7.9	6.3-9.2	2.5	10.3	20.0	40.6	24.4	20.4

^{GCV} Genotypic coefficient of variation; ^{PCV} Phenotypic coefficient of variation; h^2 Broad sense heritability; ^{ega} expected genetic advance at 5% selection.

characters between genotypes (Table 3). Phenotypic coefficient of variation (PCV%) was found superior than the genotypic coefficient of variation (GCV%) for all the characters indicating environmental effect on all characters. The phenotypic coefficient of variation ranged from 15.40% (fruit length) to 48.4% (bunch weight). Similarly, genotypic coefficient of variation (GCV%) varied from 7.6% (Finger length) to 33.5% (bunch weight). Heritability (h^2 %) estimates were low to moderate, ranging from 13.5% (pseudostem girth) to 67% (plant height). The heritability estimates were moderate for plant height (67%), bunch weight (47.8%) and the number of standing leaves at flowering (37.5%); all of which are ratoon unstable agronomic traits. This means that the potential for genetic improvement was greater in the ratoon unstable agronomic characters than ratoon stable agronomic characters like pseudo stem girth (G), number of days for fruit filling (DFF), number of hands (HDS), number of fingers on the second hand (FHDS2) and the fruit length (FL). Moderate heritability estimates suggested that selection should be delayed to more advance generations for these characters (Teich, 1984; Chaturvedi and Gupta, 1995).

Selection efficiency is related to both the magnitude of heritability and genetic advance (Johnson et al., 1955). The expected genetic advance (ega%) was estimated considering 5% selection from the parent population by the method of Falconer (1976) and Singh and Choudhry (1985). Genetic advance as percent of the mean was moderate to very low for the agronomic traits, highest in bunch weight (47.6%) and lowest in finger length (7.8%). Low genetic advance indicates slight changes of improvement of traits in subsequent generations (Teich, 1984; Chaturvedi and Gupta, 1995). Bunch weight is one of the most preferred yield aspect of bananas; it is directly related to food security and economic returns for banana growing households. Large bunch size, good taste and crop maturation time are some of the key selection attributes by banana farmers in Uganda (Gold

et al., 2002, Akankwasa et al., 2013). Despite the importance of the large bunch size to banana farmers, our results show that selection for bunch weight in 'Matooke' hybrids would be difficult due to the lack of stability of the average effects over crop cycles.

Correlation estimates are helpful in determining the components of a complex trait, such as yield, being the complex outcome of different characters; they do not provide an exact picture of the relative importance of direct and indirect influences of each of the components characters towards this trait (Bhatt, 1973). Correlation between traits was done to determine whether selection for one trait will have an effect on another. Simple correlation coefficient for the nine variable characters is shown in Table 4. Bunch weight showed strong positive correlation with number of hands (HDS), number of fingers on the second hand (FHD2), the fruit length (FL), pseudostem girth (G), plant height (Ht) and the number of standing leaves at flowering (NSL). Therefore, selection for these characters may increase bunch weight as a correlated response. This enables early selection of superior genotypes with respect to bunch weight. Fruit maturity period (DFF) had negative correlation with the bunch weight and its components. This implies that selection for early maturity is expected to increase banana yields. A high range of variability, heritability, genetic advance and positive correlation coefficient among traits are an excellent tool for improving or selection of genotypes (Akbar et al., 2003). 'Matooke' hybrids '12468S1' and '3123K2' have been selected from the mean separation of the stable traits. These genotypes have significantly more hands (HDS), number of fingers on the second cluster (FHD2), longer fingers (FL) than the local landrace variety 'Mbwazirume'. In addition these genotypes have a comparable Girth (G) to 'Mbwazirume' unlike other genotypes which had either more hands (HDS), number of fingers on the second cluster (FHD2) or longer fingers (FL) but with significantly smaller pseudo stem girth than 'Mbwazirume' (Table 5). It should

Table 4. Simple correlation coefficients among nine traits in 'Matooke' hybrids.

	HT	G	YLS	DFF	BWT	HDS	FHD2	FL
G	0.3878*							
YLS	-0.0001	0.0247						
DFF	-0.1964*	-0.2211*	0.0296					
BWT	0.51847*	0.5379*	0.0346	-0.1188*				
HDS	0.3093*	0.2583*	-0.0168	0.0180	0.6461*			
FHD2	0.3898*	0.3625*	0.0266	-0.0096	0.6172*	0.4933*		
FL	0.5045**	0.5444*	0.0822	-0.1530*	0.7105*	0.3937*	0.4955*	
NSL	0.0943*	0.1219*	0.5571*	0.0976	0.2309*	0.1280*	0.1467*	0.2565*

*Significant at 5% probability level.

Table 5. Means (\pm Standard error) of agronomic performance of 'Matooke' hybrids for ratoon stable characters.

Genotype	Girth (cm)	DFF (days)	HDS	FHND2	FL(cm)
12468S1	51.4 \pm 1.2	148.43 \pm 5.6*	8.23 \pm 0.3*	18.27 \pm 0.9*	20.55 \pm 0.7*
12748S1	48.32 \pm 6.6	156.56 \pm 3.8*	7.90 \pm 0.2*	17.90 \pm 0.4*	16.59 \pm 0.4
3068K1	40.83 \pm 1.0*	158.21 \pm 4.9*	7.44 \pm 0.2*	16.97 \pm 0.4	15.61 \pm 0.3
3123K2	52.87 \pm 1.0	133.94 \pm 2.6*	8.58 \pm 0.2*	22.21 \pm 0.4*	18.41 \pm 0.4*
3192K2	40.31 \pm 1.0*	156.66 \pm 4.4*	5.90 \pm 0.2	18.21 \pm 0.5*	15.86 \pm 0.5
3626K1	42.79 \pm 5.6	161.27 \pm 3.4*	6.19 \pm 0.2	17.52 \pm 0.6*	15.87 \pm 0.3
3637K13	45.74 \pm 0.9	142.09 \pm 3.1*	7.11 \pm 0.3*	17.97 \pm 0.6*	16.21 \pm 0.5
3639K2	43.06 \pm 1.3	156.33 \pm 6.4*	6.10 \pm 0.3	17.40 \pm 0.5*	15.00 \pm 0.6*
4360K3	38.88 \pm 1.0*	155.35 \pm 2.7*	6.74 \pm 0.1	15.78 \pm 0.4	14.90 \pm 0.4*
Km5	42.10 \pm 0.8*	157.22 \pm 3.0*	6.41 \pm 0.2	18.25 \pm 0.6*	15.17 \pm 0.5*
Mbwazirume	49.29 \pm 0.8	113.90 \pm 3.2	6.06 \pm 0.1	15.29 \pm 0.3	17.23 \pm 0.4

*Within the same column indicates significant different at 5% probability level from landrace-'Mbwazirume' by Dunnett's test.

be noted that all the genotypes take a significantly longer time to mature than the local landrace 'Mbwazirume'.

Bunch weight in 'Matooke' hybrids is moderately heritable and correlated with traits that are least influenced by environment over the cropping cycles like pseudostem girth (G), number of days for fruit filling (DFF), number of hands (HDS), number of fingers on the second hand (FHDS2) and the fruit length (FL). We conclude that the genetic improvement of 'Matooke' for yield could be achieved by selecting for these ratoon-stable traits in early evaluation trials. This implies that by selecting for ratoon-stable agronomic traits, 'Matooke' hybrids can be evaluated in a single cycle in early evaluation trails, subsequently reducing costs, time and space in field testing. Furthermore, these ratoon-stable traits in 'Matooke' can be combined with high density genetic markers to develop genomic selection models for improving 'Matooke' (Ortiz and Swennen, 2014).

Conflict of interests

The authors hereby declare that no conflict of interest exists among them.

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