AMMI and Stability Analyses of Bunch Mass in Multilocal Testing of *Musa* Germplasm in Sub-Saharan Africa

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ABSTRACT. There is a genuine need within a plantain and banana (*Musa* spp.) breeding program to assess thoroughly the experimental materials through a sequence of trials. This will result in the selection of promising clones as potential new cultivars in the targeted agroecozone. Stability analyses and the additive main effects and multiplicative interaction (AMMI) model provide together a means for the identification of clones with 1) homeostatic responses to environmental changes, 2) a genotypic response to environmental changes, and 3) adaptation to specific niches. Fourteen polyploid clones (10 tetraploid hybrids and 4 triploid cultivars) were evaluated in a broad range of environments in sub-Saharan Africa to determine the value of stability and AMMI analyses in *Musa* trials. The interpretation of the results, especially those concerning the genotype $\times$ environment interaction, was facilitated by the combination of stability and AMMI analyses. Tetraploid hybrids combining heavy and stable bunch mass were identified. The results also suggested that a clone should be assessed in the ratoon cycle because plantain and banana are perennial crops. Likewise, high yielding clones with specific adaptation should be selected in environments showing the respective environmental or biotic stress.

Plantain and banana breeders are interested in the identification of clones which perform well over a wide range of environments. To identify such clones, yield trials are carried out over years of testing in the breeding station and at different locations. In *Musa* the bunch mass seems to be less affected by the genotype $\times$ cycle interaction than by the genotype $\times$ location interaction, even in the same agroecological zone (De Cauwer and Ortiz, 1998; De Cauwer et al., 1995).

Hybrids developed by the International Institute of Tropical Agriculture (IITA) (Vuylsteke et al., 1993, 1995), along with their parental landraces, and exotic cooking bananas have been evaluated across different agroecozones in sub-Saharan Africa (Ortiz and Vuylsteke, 1995a). The final aim of this set of multilocal trials was to select clones which combine black sigatoka resistance with stable high yield and other qualities desired by farmers and consumers (IITA, 1993).

In the presence of a significant genotype $\times$ environment interaction (GE), the stratification of environments, according to their agro-climatological similarities and the determination of stability parameters for genotypes across environments are important tools for the management of the GE. Eberhart and Russell (1966) developed the most popular stability parameters for comparing cultivar performance across environments. In their model the regression coefficient (b_i) measures the specific cultivar response to varying environments, while another stability parameter (s_{di}^2) measures the unexplainable deviations from the regression on the environmental index. Also, the coefficient of phenotypic variation (CPV) (Francis and Kannenberg, 1978) was considered a measurement of static stability, i.e., homeostasis. It measures the disper-

sion of the dataset: viz. smaller CPV values reflect data more closely clustered around the mean.

The additive main effects and multiplicative interaction (AMMI) model (for a review see Gauch, 1992) was developed to facilitate the interpretation of the GE and identify genotypes adapted to specific niches. AMMI uses the conventional analysis of variance (ANOVA) and the principal component analysis (PCA) to identify any pattern in the data. The AMMI analysis first fits the additive effects for genotypes (G) and environments (E) by the standard ANOVA procedure, and then fits multiplicative effects for GE by PCA (Crossa et al., 1990). The results of AMMI are shown in the form of an ANOVA table and a biplot to visualize any relationships between the eigenvalues for the PCA and the means of the genotypes and environments (Kempton, 1984).

The objective of this study was to assess the joint value of stability and AMMI analyses for the identification of stable high yielding genotypes, and for a better understanding of the GE affecting bunch mass of *Musa* genotypes in multilocal trials.

Materials and Methods

Fourteen polyploid genotypes (Table 1) were evaluated in a wide range of agroecological conditions in sub-Saharan Africa (Table 2). A complete randomized design with two replications of five plants was the experimental design for multilocal testing (Ortiz and Vuylsteke, 1995b). All experimental plots were surrounded by a black sigatoka susceptible cultivar. Crop management practices have been described elsewhere (Ortiz, 1995). Bunches were harvested from each plant when green fruits of the oldest hands started yellowing. Bunches of individual plants were weighed independently. Missing values for four clones (one per environment) were calculated according to Sokal and Rohlf (1981).

Stability analysis was performed for bunch mass (kg/plant). The stability model used to describe the performance of a clone across the 10 environments was that defined by Eberhart and Russell (1966). The most important stability parameters in this model are the regression coefficient (b_i) and the deviation from the regression model (s_{di}^2), which was estimated by s_b (Ortiz and Izquierdo, 1994). The statistics s_b was recommended as an estimate

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Table 1. Clones tested in multilocal trials in sub-Saharan Africa.

Genotype	Genome or parentage	Black sigatoka response
Triploid landrace and cultivars (2n = 33)		
Bluggoe	ABB cooking banana cultivar	Less susceptible
Bobby Tannap	AAB French plantain landrace	Susceptible
Cardaba	ABB cooking banana cultivar	Less susceptible
Valery	AAA export dessert banana cultivar	Susceptible
Tetraploid hybrids (2n = 44)		
[AAB x AA] hybrids		
TMPx 548-4	Obino 1' Ewai (OL) x 'Calcutta 4' (C4)	Partially resistant
TMPx 582-4	Bobby Tannap (BT) x C4	Partially resistant
TMPx 1621-1	OL x C4	Less susceptible
TMPx 1658-4	OL x Pisang lili (PI)	Less susceptible
TMPx 2481	OL x TMB2x 366-8	Partially resistant
TMPx 2637-49	OL x C4	Partially resistant
TMPx 2796-5	BT x PI	Partially resistant
TMPx 5511-2	OL x C4	Partially resistant
TMPx 6930-1	OL x C4	Partially resistant
[ABB x AA] hybrid		
TMBx 612-74-OT	Bluggoe x C4	Highly resistant

of the stability parameter instead of s_{di}^2 , since it has an easy biological interpretation because s_b shares the same unit system as b_i . A stable genotype performs comparably in different environments and should have a regression coefficient (b) equal to 1 and a very small deviation from the regression model, i.e., $s_b = 0$. The reliability of the datasets for the regression analyses was assessed by the Durbin-Watson test of residuals (Sokal and Rohlf, 1981).

The coefficient of phenotypic variation (CPV, %) was calculated as $CPV = (s_i / x_i) \times 100$, where s_i and x_i are a measurement of phenotypic dispersion and the genotypic mean for each clone, respectively (Francis and Kanneberg, 1978). The smaller the CPV, the closer the results around the mean and therefore, the more stable performance across environments. Correlations were determined among all the stability parameters (Table 3) to determine their degree of association.

Based on the covariance matrix of genotype $\times$ environmental effects, the residual multiplicative GE of the additive linear model was analyzed by PCA, while the main effects were analyzed following the mixed model of the ANOVA. Environments were considered as random variables while clones were fixed in this

model. The resulting interaction PCA scores (IPCA) for clones and environments were used to construct the AMMI biplots following the model (Zobel et al., 1988): $Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}$, where Y_{ge} is the bunch mass of the clone g in the environment e, μ is the grand mean, α_g are the genotype deviations, i.e., genotype mean minus grand means, β_e are the environmental deviations; λ_n is the eigenvalue for PCA axis n, n is the number of PCA axis retained in the model, γ_{gn} and δ_{en} are the genotype and environment PCA scores for PCA axis, and ρ_{ge} is the residual in the AMMI model when all axes are not used. The degrees of freedom for the AMMI model were calculated as $g + e - 1 - 2n$ (Gollob, 1968).

An AMMI analysis generates models depending of the number of axis retained (Hill et al., 1998). For example, AMMI0 fits only the additive main effects of the genotypes and environments, whereas AMMI1 fits the additive effects of AMMI0 plus GE interactions associated to IPCA1. Furthermore, the amount of information obtained from the AMMI analysis may be enhanced by using the biplot technique, i.e., a graphical representation of the additive main effects versus the interaction pattern defined by the IPCA1 (AMMI1 model), or the interaction patterns alone as

Table 2. Range of agroecological characteristics of the testing sites in multilocal trials of *Musa* clones in sub-Saharan Africa.

Variable	Range
Latitude	0°31' N (Namulonge) to 7°26' N (Ibadan)
Longitude	3° W (Akure) to 32°27' E (Namulonge)
Agroecological zone	
Lowland humids	Assin-Fosu (Ghana), Benin, Bori and Onne ² (Nigeria), Mbalmayo (Cameroon)
Derived coastal savanna	Ibadan (Nigeria)
Mid-altitude woodland savanna	Namulonge (Uganda)
Vegetation	Marsh/swamp (Benin, Onne), mild/hot farmland (Bori) regrowing wood/crop/grass (Ibadan), tropical forest (Mbalmayo), grass/crop/wood (Namulonge)
Soil type	Dystric Nitisols (Benin, Bori), Ferric Luvisols (Ibadan), Orthic Ferrasols (Mbalmayo, Namulonge), Thionic Fluvisols (Onne)
Altitude	10 (Onne) to 1190 (Namulonge) masl
Rainfall	1253 (Ibadan) to 2502 (Onne) mm·year ⁻¹ ; either unimodal or bimodal
Radiation	5060 (Onne) to 5816 (Namulonge) MJ·m ⁻² ·year ⁻¹
Temperature	
Minimum	14–17 °C (Namulonge) to 22–24 °C (Bori and Onne)
Maximum	25–28 °C (Namulonge) to 28–34 °C (Ibadan)

²Ortiz et al. (1997) provide more specific details about this location.

Table 3. Percentage of variation for bunch mass (kg/plant) accounted by respective significant source in multilocal testing of 14 *Musa* genotypes grown in 10 African environments.

Source of variation ^a	df	Percentage of variation accounted for	P (F test)
Environment (E)	9	58.2	<0.001
Genotype (G)	13	8.4	<0.05
G × E	113	33.4	<0.01
IPCA1	21	43.2	<0.001
IPCA2	19	22.0	<0.01
Residual	73	34.8	

^aThe total sum of squares was 2879.09 for this multilocal testing experiment.

defined by plotting the IPCA1 versus the IPCA 2 (AMMI2 model). Hence, the AMMI analysis may provide means to select stable high yielding clones (AMMI1 model) and to identify clones with a specific environmental adaptation (AMMI2 model). The accuracy of these models depends on the percentage of the sum of squares explained by the respective source of variation.

Results and Discussion

There were significant differences between environments and clones (Table 3). Also bunch mass was significantly affected by the GE. Environments accounted for 58.2% and the clones for

8.4% of the sum of squares for bunch mass whereas the GE accounted for the remaining 33.4%.

YIELD STABILITY: HOMEOSTASIS AND RESPONSE TO ENVIRONMENTAL CHANGE. Table 4 shows the stability parameters for bunch mass of 14 polyploid clones. The data followed a normal distribution as shown by their nonsignificant ($P > 0.05$) skewness and kurtosis.

On average, plantain hybrids and cooking banana cultivars had higher yields across environments than the local plantain landrace 'Bobby Tannap' (Table 4). Based on the stability parameters for homeostasis and their response to environmental change TMPx 5511-2, TMPx 6930-1, and TMPx 2637-49 should be regarded as stable high yielding black sigatoka resistant hybrids for sub-Saharan Africa. Also the cooking banana 'Cardaba' showed stable heavy bunches in these locations. The identification of these stable high yielding clones, except 'Cardaba', was supported by reliable databases as shown by the nonsignificant Durbin-Watson test of residuals for serially correlated data (Table 4).

Correlation analysis between bunch mass and its stability parameters (Table 5) reveals that the bunch mass of some high yielding cultivars were insensitive to environmental change; i.e., no correlation ($P = 0.906$) between bunch mass and cpv. However, b_i was significantly correlated with cpv ($r = 0.781$; $P < 0.001$) and bunch mass ($r = 0.573$; $P = 0.031$). This indicates that some genes controlling phenotypic response to environmental change may also help to buffer the homeostatic phenotypic response.

Most of the low yielding phenotypes in poor environments (i.e., low a value in regression equation) had a poor homeostatic stability

Table 4. Stability parameters^a for bunch mass of 14 clones tested in multilocal trials in 10 environments.

Genotype	Bunch mass	CPV					R ²	H ₀		Residuals
	(kg/plant)	(%)	b _i	s _b	a	(%)	MSE	b _i = 1	b _i = 0	D-W (r = 0)
[AAB x AA] hybrids										
TMPx 548-4	11.2	45	1.3	0.2	-3.3	83	4.8	NS	***	2.35 ^{NS}
TMPx 582-4	10.6	52	1.1	0.4	-1.9	53	15.7	NS	*	2.96 [?]
TMPx 1621-1	9.6	37	0.7	0.3	1.9	45	8.0	NS	*	0.49 ⁺
TMPx 1658-4	13.6	42	1.4	0.2	-2.4	80	7.6	NS	***	1.57 ^{NS}
TMPx 2481	10.4	32	0.7	0.2	2.4	56	5.6	NS	*	0.67 ⁺
TMPx 2637-49	11.6	34	0.8	0.3	2.9	48	9.1	NS	*	2.40 ^{NS}
TMPx 2796-5	11.4	42	1.1	0.2	-1.0	82	3.9	NS	***	2.72 [?]
TMPx 5511-2	13.0	37	1.0	0.3	1.3	60	10.4	NS	**	1.33 ^{NS}
TMPx 6930-1	12.7	39	1.3	0.1	-2.0	92	2.2	NS	***	1.62 ^{NS}
[ABB x AA] hybrid										
TMBx 612-74 OT	9.3	31	0.6	0.2	2.2	59	3.9	NS	**	2.82 [?]
AAB plantain landrace										
B. Tannap	9.7	47	1.0	0.3	-1.1	57	10.2	NS	*	1.16 [?]
ABB cooking banana cultivars										
Blugoe	11.4	30	0.7	0.2	3.8	58	5.7	NS	*	2.58 ^{NS}
Cardaba	12.1	28	0.7	0.2	4.0	54	5.9	NS	*	1.14 [?]
AAA dessert banana cultivar										
Valery	12.0	55	1.6	0.3	-6.4	81	9.4	NS	***	0.94 ⁺
LSD _{0.05}	2.6									
CV (%)	25.8									
Mean	11.3									
Skewness	0.1433 (<i>P</i> = 0.2458, NS)									
Kurtosis	-0.6677 (<i>P</i> = 0.0540, NS)									

^aCPV = coefficient of phenotypic variation; b_i = slope of regression line; s_b = standard error of b_i ; a = intercept of regression line; R^2 = coefficient of determination of the regression model; MSE = mean square error of deviations; D-W = Durbin-Watson statistics. Environmental mean (kg/plant) (based on above genotypes): Onne (PC), 10.7; Onne (RC), 14.5; Mbalmayo (PC), 16.4; Mbalmayo (RC), 14.6; Bori (PC), 5.5; Ibadan (PC), 9.4; Benin City (PC), 8.4; Assin-Fosu (PC), 7.2; Namulonge (PC), 13.4; Namulonge (PC-nematodes), 12.6; LSD_{0.05} = 2.2; PC = plant crop and RC = ratoon crop.

NS, *, **, *** Nonsignificant, and significant at $P = 0.05$, 0.01, or 0.001, respectively; (?) and (+) indicate inconclusive and positive (i.e., autocorrelation) test of residuals.

Table 5. Correlations (r) between stability parameters in *Musa* germplasm ($n = 14$).

Trait ^a	CPV	b_i	s_b	a	R^2	MSE	D-W
Bunch mass	0.035	0.573*	0.054	-0.250	0.521	-0.067	0.022
CPV		0.781***	0.321	-0.907***	0.403	0.508	0.019
b_i			0.050	-0.936***	0.798***	0.121	-0.016
s_b				-0.040	-0.515	0.912***	-0.032
a					-0.717**	-0.170	0.035
R^2						-0.471	0.109
MSE							0.010

^aBunch mass = kg/plant; CPV = coefficient of phenotypic variation; b_i = slope of regression line; s_b = standard error of b_i ; a = intercept of regression line; R^2 = coefficient of determination; MSE = mean square error of deviations; D-W = Durbin-Watson statistics.

*, **, ***Significant at $P = 0.05, 0.01$, or 0.001 , respectively.

($r = -0.907$; $P < 0.001$) but a high response to environmental change ($r = -0.936$; $P < 0.001$); i.e., they may exhibit high bunch mass in rich environments. Moreover, clones exhibiting a high bunch mass response to the environmental change and low yields in poor environment fit very well to their regression equation as shown by the significant associations between b_i and R^2 ($r = 0.798$; $P = 0.001$) and a and R^2 ($r = -0.717$; $P = 0.003$). The use of s_b as a stability parameter was supported by its significant association with the mean square error (MSE) for the deviations from the linear regression model (Table 5).

ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION (AMMI) MODEL. A biplot was constructed with genotypes and environment main effects on the abscissa and the interaction PCA score 1 for bunch mass (IPCA1) on the ordinate (Fig. 1). This AMMI1 for bunch mass explained 81% of the variation in this set of multilocal trials. The IPCA1 alone captured 43.2% of the interaction variance for bunch mass.

The AMMI1 model revealed that TMPx 6930-1 was the most stable high yielding hybrid in this set of multilocal trials, and that Mbalmayo (plant crop) and Onne (ratoon crop) were high yielding environments showing low GE. This was based on their relative position in the AMMI biplot; i.e., points near the center express stable performance across environments. The results from the ratoon crop at Mbalmayo showed a higher GE than in the plant crop. This interaction pattern could be explained by the occurrence

of severe wind damage and high incidence of virus-like symptoms in most of the plants growing in the ratoon at this location. Average yielding clones such as TMPx 2796-5 and 'Bluggoe' showed stable bunch mass across environments. While two of the low yielding clones ('Bobby Tannap', TMPx 1621-1) had unstable bunch mass across environments. Also low yielding environments such as Bori and Assin-Fosu had a significant GE.

The IPCA1 for bunch mass was plotted on the abscissa against the interaction PCA score 2 (IPCA2) for bunch mass (on the ordinate) in the AMMI2 biplot (Fig. 2). The AMMI 2 model accounted for almost 2/3 of the total GE for bunch mass (i.e., 22% more than AMMI1). The IPCA3 accounted for a smaller fraction of the GE sum of squares than the IPCA2. Hence, IPCA3 was excluded for consideration in this analysis.

The AMMI2 (Fig. 2) served to study in detail the interaction patterns. The most stable genotype (close to the center of the graph) was TMPx 6930-1, followed by the average yielders 'Bluggoe' and TMPx 2796-5. The GE patterns differed across cycles within the same location (e.g., plant and ratoon crop at Mbalmayo) or between clean and infested-nematode plots at Namulonge. This result suggests that the performance of a clone should be assessed in the ratoon cycle since plantain and banana are perennial crops. Also high-yielding clones with specific adaptation should be selected in environments showing the respective environmental or biotic stress. This selection may be facilitated by the identification of genotypes and environments sharing the same quadrant in the AMMI biplot. For example, TMPx 548-4 and TMPx 1658-4 may have enhanced bunch mass at Onne, where they were selected. The

Fig. 1. AMMI 1 for bunch mass (kg/plant). PC = plant crop and RC = ratoon crop. Vertical line indicates the bunch mass grand mean ($\bar{m}$) while the horizontal line indicate zero IPCA score. Displacements along the abscissa indicate differences in main (additive) effects, while displacements along the ordinate show differences in interaction effects.

Fig. 2. AMMI 2 for bunch mass (kg/plant). PC = plant crop and RC = ratoon crop. Points similar to each other have similar interaction patterns. Conversely, points distant from each other have completely different values for interaction effects.

high yielding TMPx 5511-2 may exhibit high yielding bunches even in poor environments such as Assin-Fosu or Bori. The performance of TMPx 5511-2 could be explained by its average response to environmental change (i.e., $b_1 = 1$) and relatively high yield in tested poor environments.

The polyploid genotypes had either 33 (plantain landrace and banana cultivars) or 44 (hybrids) chromosomes. However, some triploid cultivars (e.g., 'Cardaba') were among the top yielders in this experiment, which suggest that bunch mass was not always affected by ploidy. Likewise, the results suggest that adaptation and stability depended on the genotype and not on either ploidy or origin (hybrids versus landrace or cultivars).

This combined analysis of the GE have provided means to identify *Musa* genotypes with an homeostatic response across environments (through cvp); other genotypes which have a response to environmental change (through the regression analysis), and those genotypes adapted to specific environments (through AMMI analysis). This information will facilitate the recommendation of genotypes with broad adaptation; or fitting genotypes to specific environments and further testing, before their release to farmers in the targeted region.

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