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Selection of cooking banana genotypes for yield and black Sigatoka resistance in different locations in Uganda

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It is imperative to systematically evaluate new banana genotypes in different locations before national release. This enables selection and recommendation of superior genotypes as new varieties for a wider range of environments. The objective of the present study was to select banana genotypes with stable and high performance for bunch yield and leaf black Sigatoka resistance. Eleven cooking banana genotypes developed by the Uganda National Agricultural Research Organization in collaboration with Bioversity International, and two check varieties were evaluated in multi-location preliminary yield trials in Uganda. Data collected were analyzed using Additive Main Effects and Multiplicative Interaction (AMMI) model, AMMI Stability Value, and Genotype Selection Index (GSI). Genotype × location interaction was significant for all the traits assessed. Most of the new genotypes had low interaction effects with locations for bunch yield (69.2%) and black Sigatoka (92.3%). The most stable genotypes for bunch yield were NABIO815, NABIO1117, NABIO216 and NABIO306 whereas for black Sigatoka resistance, were NABIO1011, NABIO815, NABIO1009 and NABIO216. Using the GSI that defines the most desirable genotypes as those that combine high agronomic performance and stability across environments, four genotypes (NABIO306, NABIO1011, NABIO808 and NABIO1009) were selected. These genotypes, in addition to their high performance for agronomic traits and stability, had soft and yellow fruit pulp on cooking, and will be advanced on farm for further evaluation.

Key words: Banana breeding, AMMI, AMMI stability value, genotype selection index.

INTRODUCTION

Banana, including plantains (*Musa* spp.) is an important food and income generating crop in most tropical and subtropical regions of the world. In the Eastern Africa region, banana plays a major role in the diet of millions of

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people, providing up to one fifth of total calorie consumption per capita. In Uganda, banana ranks first in terms of area occupied, total production and per capita consumption (FAOSTAT, 2012). The crop is grown by over 75% of smallholder farmers owing to its unique advantages of producing acceptable yields amidst erratic rainfall, and a perennial nature coupled with an all-year-round fruiting character (Tushemereirwe et al., 2015). These attributes characterize banana as an ideal crop for household food, nutrition and income security.

Despite these benefits, banana productivity in Uganda is as low as ~ 9.2 t/ha and severely declining (FAOSTAT, 2012), although it is known that it could reach ~ 60 t/ha. Severe decline in yields is aggravated by a number of factors, key of which are: declining soil fertility, pests (weevils and nematodes) and diseases, especially black Sigatoka. Black Sigatoka, a leaf spot disease caused by *Mycosphaerella fijiensis* Morelet, causes substantial yield loss in banana production (Arzanlou et al., 2007; Daniells, 2009). This occurs because the disease attacks the leaves causing a decrease in functional leaf area. The reduction in functional leaf area results in a decline in the quality and quantity of the fruit since the fruits of infected plants ripen prematurely before proper filling (Barekye, 2009). The disease is reported to cause a yield loss of 30 to 50% on bananas (Barekye et al., 2011). For improved banana yields and sustainable food security of smallholder farmers in Uganda that largely depend on bananas, there is a need to address black Sigatoka disease.

There are several potential technology-based interventions for increasing banana yields, however, host plant resistance is the most appropriate and cost effective intervention (Tushemereirwe et al., 2015). It, in addition, offers significant spill over benefits for human health and positive environmental impacts. As a result, the Uganda National Agricultural Research Organization (NARO) through its National Banana Research Program (NBRP) and research partners, especially the International Institute of Tropical Agriculture and Bioversity International are jointly breeding banana for improved yields.

The NBRP through its Banana Conventional Breeding Unit generates banana genotypes through controlled pollination (Tenkouano et al., 2011). The genotypes generated are taken through three key evaluation and selection stages before release as new varieties. The three evaluation and selection stages are:

1. Early evaluation trial (EET),
2. Preliminary yield trial (PYT)
3. On farm trial.

Early evaluation trial stage involves the evaluation and selection of single plant genotypes in non-replicated-single site trials. Each genotype under evaluation is considered a potential variety. Selection of individual genotypes for advancement to PYT is based on high heritability traits such as plant type, bunch orientation, fruit pulp colour on cooking, and reaction of genotypes to prevalent diseases, especially black Sigatoka. Preliminary yield trial stage involves the evaluation and selection of genotypes in single or multi-location replicated trials of the few selected genotypes from EETs. Selection of genotypes at this stage of evaluation is essentially based on low heritability traits such as bunch yield and plant height. Also, reaction of genotypes to black Sigatoka, nematodes and weevils is considered. On farm trial involves the evaluation and selection of genotypes in multi-location replicated trials of the few selected genotypes from PYT. Usually, 5 to 10 farmers at each location are selected to host such trials. Selection of genotypes at this stage focuses largely on fruit sensory traits that is to say, food taste, colour, texture, smell, and mouth feel. These are judged by farmers, with the guidance of a breeder. Genotypes that are superior in the overall food acceptability, which is based on sensory traits and yield performance are recommended for national release as new varieties.

This study presents and discusses results of secondary triploid (3x) cooking banana genotypes evaluated in multi-location PYTs. Multi-locational trials have been found to be essential in plant breeding for understanding cultivar stability and yield performance across environments (Ebdon and Gauch, 2002) due to the existence of genotype x environment interaction (GEI). Genotype x environment interaction presents limitations in the selection of superior genotypes, reducing the utility of analyses of means and of inferences that would otherwise be valid (Gauch, 2006).

Genotype x environment interaction results from changes in the magnitude of differences between genotypes in different environments or from changes in the relative ranking of the genotypes (Ebdon and Gauch, 2002). Genotypes with insignificant GEI are considered to be stable (Annicchiarico et al., 2010).

The additive main effects and multiplicative interaction (AMMI) analysis is one of the widely used methods for GEI assessment (Ebdon and Gauch, 2002; Gauch, 2006). The method has been shown to be effective because it captures a large portion of the GEI sum of squares (Ebdon and Gauch, 2002). It clearly separates main and interaction effects depending on their statistical significance and presents plant breeders with different kinds of selection opportunities based on stresses that prevail in target environments (Gauch, 2006). The main objective of this study, therefore, was to select stable and high yielding-black Sigatoka resistant cooking banana genotypes with consumer-preferred traits.

MATERIALS AND METHODS

Trial sites

Trials were conducted from January, 2013 to September, 2015 at Kawanda, Mbarara, Bulindi and Nakabango agricultural research

Table 1. Properties of soil determined at planting at four experimental sites: Kawanda, Mbarara, Bulindi and Nakabango.

Variable	Soil chemical elements						
	pH	OM	N	P	Ca	Mg	K
Location	-	%	-	ppm			
Kawanda	5.1	3.8	0.21	5.7	1978.6	436.1	114.3
Mbarara	4.8	3.7	0.20	4.1	253.7	113.6	367.5
Bulindi	5.8	7.8	0.36	5.4	2302.3	904.5	305.8
Nakabango	5.7	8.0	0.35	6.6	3095.7	573.4	261.7

OM= organic matter; N= nitrogen; P= phosphorus; Ca= calcium; Mg = magnesium; K= potassium.

Table 2. Thirteen banana genotypes evaluated at four sites: Kawanda, Mbarara, Bulindi and Nakabango.

Genotype name	Pedigree	Category
NABIO1009	376K-7 x 304	Test genotype
NABIO1011	660K-1 x 1345K-1	Test genotype
NABIO1117	917k-2 x SH3362	Test genotype
NABIO216	660K-1 x 1345K-1	Test genotype
NABIO306	660K x 8075-7	Test genotype
NABIO318	4302 x 3702	Test genotype
NABIO614	917k-2 x SH3362	Test genotype
NABIO617	660K-1 x TMB2X8075-7	Test genotype
NABIO808	660K-1 x 1345K-1	Test genotype
NABIO815	376K-7 x TMB2X8075-7	Test genotype
NABIO817	222K-1 x 1345K-1	Test genotype
Kabana 6H	1201K-1 X SH3217	Check variety (hybrid)
Mbwazirume	N/A	Check variety (landrace)

stations. Kawanda is located in central Uganda at 32°36′E and 0°25′N, 1210 m above sea level (m.a.s.l.). During the trial period, mean annual rainfall and temperature were 1390 mm and 12.5°C, respectively. Nakabango is located in eastern Uganda at 33°12′E and 00°31′N, 1178 m.a.s.l. During the trial period, mean annual rainfall at the site was 1400 mm and mean temperature was 13.6°C. Bulindi is located in North western Uganda at 33°28′E and 0°28′N, 1230 m a.s.l. During the trial period, mean annual rainfall was 1150 mm and mean temperature range was 14.9°C. Mbarara is located in south western Uganda at 36°20'S and 30°37′E, 1430 m a.s.l. During the experimental period, mean annual rainfall was 1219 mm and mean temperature was 15.1°C. Soil properties for each site at planting were recorded (Table 1).

Plant germplasm

Three hundred fifty cooking banana genotypes developed by the NBRP through crossing parents of desired traits as described by Tenkouano et al. (2011), were first evaluated in an EET for three years from 2009 to 2012. Eleven genotypes selected from the EET (Table 2) were multiplied *in vitro* to generate enough plantlets for establishing replicated multi-location PYTs whose results are presented in this study. Tissue culture plantlets of Mbwazirume (landrace) and Kabana 6H (commercial hybrid variety) that were used as check cultivars were sourced locally.

Trial design

Experiments at each location were laid out in a randomized complete block design with two replications. Banana tissue culture plantlets, three months old were planted in holes (0.4 m deep and 0.6 m wide) at a spacing of 3 × 3 m, giving a plant population density of 1111 plants/ha. Before planting, 10 kg of well decomposed cow dung manure were applied in each hole. Plantlets of each genotype were established in line plots of 10 plants per line. Each replication/block was surrounded by Mbwazirume, a black Sigatoka susceptible cultivar. Two months after planting, the trials were mulched to about 0.2 m high from ground using dry grass. De-suckering was done at flowering of the mother plants to maintain the plant density and ensure that the number of bunch bearing plants was maintained at a level that reduces competition for water, light and nutrients; that is, three plants (mother, daughter and granddaughter) were maintained. The trials were regularly hand weeded and no supplemental irrigation was applied.

Data collection

At flowering, the genotypes' response to black Sigatoka infection was assessed using youngest leaf spotted (YLS) methods as described by Vakili (1968) and Carlier et al. (2002). Increasing YLS values indicate the presence of more healthy leaves on the plant, hence, greater resistance to black Sigatoka (Tenkouano et al.,

2003). At harvest, data were collected on bunch mass (kg), number of hands and fruit finger circumference. Fruit finger circumference was determined by measuring the length around the middle finger of each hand on a bunch and the average circumference calculated. Bunch yield (t/ha) was estimated from the bunch mass as follows:

$$\text{Bunch yield (t/ha)} = \frac{\text{Bunch mass(kg/plant)} \times \text{Number of plants/ha}}{1000}$$

Data analysis

The data analysed were collected for two crop cycles: 2 and 3. The two crop cycle data sets for each location were first analysed separately and found non-significantly different. Thus, combined AMMI analysis of variance (ANOVA) was conducted across locations using Genstat, version 14 (Payne et al., 2011). The AMMI ANOVA was performed using the following model:

$$Y_{ij} = \mu + g_i + e_j + \sum_{N=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + \rho_{ge} + \varepsilon_{ij}$$

Where: Y_{ij} = observed yield of genotypes; μ = grand mean; g_i = genotypic main effect; e_j = environmental main effect; N = number of PCA axes considered; λ_n = singular value of the n^{th} PCA axis; α_{in} = scores for the *i*th genotype on the n^{th} axis; and γ_{jn} = scores for the j^{th} environment on the n^{th} axis; ρ_{ge} = residual for IPCAs not fitted; ε_{ij} = error term.

Interaction patterns of the genotypes and locations were graphically represented in a biplot of the respective IPCA1 scores versus the genotype and location means for the traits assessed. In biplots, displacement in the horizontal plane reflects differences in the mean performance, whereas displacement in the vertical plane reflects differences in interaction effects (Zobel et al., 1988).

AMMI Stability Value (ASV) (Purchase et al., 2000) and Genotype Selection Index (GSI) (Farshadfar, 2008) were used to identify genotypes combining high stability and mean performance for the traits assessed. Genotype selection index for each genotype was calculated as the sum of the corresponding rankings for mean performance and ASV. AMMI stability value is a measure of the stability of a genotype (the lower the value the greater the stability) based on weighted IPCA1 and IPCA2 scores (Purchase et al., 2000). The ASV was calculated as follows:

$$\text{ASV} = \sqrt{\frac{\text{IPCA1SS}}{\text{IPCA2SS}}(\text{IPCA1score}) + (\text{IPCA2score})^2}$$

Where: ASV= AMMI stability value, IPCA1 and IPCA2: interaction principal component axes one and two, respectively and SS= sum of squares.

In selection of superior genotypes across environments, stability *per se* is not the only parameter for selection since the most stable genotypes would not necessarily give the best performance for the trait of interest. In view of that, the GSI, which combines agronomic performance across environments and stability, was used to select the most desirable genotypes. The GSI for each genotype was calculated as follows:

$$GSI_i = RY_i + RASV_i$$

Where: GSI_i = genotype selection index for the i^{th} genotype across locations for each trait;

RY_i = rank of the i^{th} genotype based on mean performance across locations; *RASV*= rank for AMMI stability value

A genotype with lowest GSI was considered to be the most stable and highest performing for that particular trait. To determine the overall best genotype that combined stability and good performance, the sum of GSI for all traits assessed was calculated. A genotype with the lowest GSI rank sum was the best in terms of the four traits assessed.

RESULTS

Variation in traits in response to genotypes and locations

Genotypes and locations in the combined AMMI ANOVA were highly significant (P < 0.001) for all the traits assessed (Table 3). Genotype × location interaction was highly significant (P < 0·001) for the number of hands, fruit finger circumference and youngest leaf spotted, and significant (P < 0·05) for bunch yield. IPCA1 was highly significant (P < 0.001) for all the traits except bunch yield (P < 0.01), and IPCA2 was highly significant (P < 0.001) for the number of hands and significant (P < 0.05) for the rest of the traits. The % treatment SS attributed to genotype for bunch yield was higher than that attributed to location or to GEI. That is, 45.3% of the treatment SS for bunch yield was attributed to genotype, 22.8% to location and 31.9% to GEI. The %treatment SS attributed to location for youngest leaf spotted was higher than that attributed to genotype or to GEI whereas for the number of hands and fruit finger circumference, the % treatment SS attributed to GEI were higher than those attributed to genotype or location.

Mean performance and genotype x location interaction for traits across locations

Bunch yield

Genotypes in quadrants II and III yielded above average (25.6 t/ha) and those in quadrants I and IV yielded below average (Figure 1). Kabana 6H, a check variety and an officially released commercial banana hybrid in Uganda had highest bunch yield (29.3 t/ha) followed closely by test genotypes *viz.* NABIO1117 (29.1 t/ha), NABIO1011 (27.3 t/ha), NABIO808 (27.2 t/ha) and NABIO617 (27.0 t/ha; Table 4). Mbwazirume, a local check variety was the worst performer for bunch yield (17.0 t/h). Genotypes NABIO815, NABIO1117, NABIO216 and NABIO306 had low IPCA1 scores for bunch yield and were accordingly the most stable genotypes for this trait. The least stable genotypes for the trait shown by high IPCA1 scores were NABIO318 and Mbwazirume. The stability of the genotypes was confirmed by the ASV (Table 4). The lower the ASV, the more stable the genotype is. Ranking

Table 3. AMMI analysis of 13 banana genotypes evaluated across four locations in Uganda for bunch yield, number of hands, fruit finger circumference and youngest leaf spotted.

Source of variation	Mean squares				
	DF	BY	NH	FC	YLS
Treatments	51	41.3***	1.59***	1.87***	7.91***
Genotypes (G)	12	79.4***	2.25***	1.67***	4.51***
Locations (E)	3	160.0***	3.89***	11.28***	89.14***
GxE Interactions	36	18.6*	1.18***	1.16***	2.28***
IPCA 1	14	24.4**	2.13***	1.56***	5.11***
IPCA 2	12	21.1*	0.74***	1.03*	0.54*
Residuals	10	7.6	0.37***	0.74	0.4
Error	48	9.6	0.04	0.37	0.5
		Sum of squares			
Source of variation	DF	BY	NH	FC	YLS
Treatments	51	2104.1	81.0	95.4	403.5
Genotypes (G)	12	953.1	27.0	20.0	54.2
Locations (E)	3	480.0	11.7	33.8	267.4
GxE Interactions	36	671.1	42.4	41.6	81.9
IPCA 1	14	342.0	29.8	21.8	71.5
IPCA 2	12	252.6	8.9	12.3	6.4
Residuals	10	76.4	3.7	7.4	4.0
Error	48	458.6	1.9	17.9	24.2
% Treatment SS due to G	12	45.3	33.3	21.0	13.4
% Treatment SS due to E	3	22.8	14.4	35.4	66.3
% Treatment SS due to GEI	36	31.9	52.3	43.6	20.3
% GEI due to IPCA1	14	51.0	70.3	52.4	87.3
% GEI SS due to IPCA2	12	37.6	21.0	29.6	7.8
% Residuals	10	11.4	8.7	17.8	4.9

DF; degrees of freedom; BY= bunch yield (t/ha); NH= number of hands; FC= fruit finger circumference (cm); YLS= youngest leaf spotted, IPCA1 and IPCA2: interaction principal component axes one and two, respectively; SS: sum of squares; ∗, ∗∗, ∗∗∗ significant at the 0.05, 0.01, and 0.001 probability level, respectively.

of genotypes based on GSI that incorporates both the mean performance and ASV rankings identified NABIO1117, NABIO306, NABIO216, Kabana 6H and NABIO808 as the genotypes combining high bunch yield and stability. Considering IPCA1, 69.2% of the genotypes had scores of less than one, implying that most of the new genotypes were stable for bunch yield. Nakabango and Mbarara had low interaction effects for bunch yield with genotypes, indicated by negligible IPCA1 scores, and were thus, stable for the trait. Kawanda and Bulindi on the other hand, had high contrasting interaction effects for the trait with genotypes and were therefore, the most unstable sites. Mbarara in general was the most yield stable site with above average performance for bunch yield.

Number of hands

Genotypes in quadrants II and III performed above average (9.1 hands) and those in quadrants I and IV performed below average (Figure 2). The first four genotypes with above average number of hands were all new hybrids *viz.* NABIO1117, NABIO817, NABIO617 and NABIO1011. These four genotypes were followed by Kabana 6H, a commercial check hybrid released by NARO in 2010. NABIO1009 and NABIO216 had the worst performance for number of hands. NABIO1117, NABIO808, NABIO306, Kabana 6H, NABIO817 and NABIO815 had low IPCA1 scores for the number of hand and were accordingly the most stable genotypes for the trait. The stability status of the genotypes indicated by the biplot (Figure 2) was confirmed by ASV (Table 5). Examination of genotypes based on GSI identified NABIO1117 followed by Kabana 6H, NABIO817 and NABIO808 as best genotypes combining high number of hands and stability. Nakabango and Mbarara had low interaction effects for number of hands with genotypes, indicated by negligible IPCA1 scores. Kawanda and

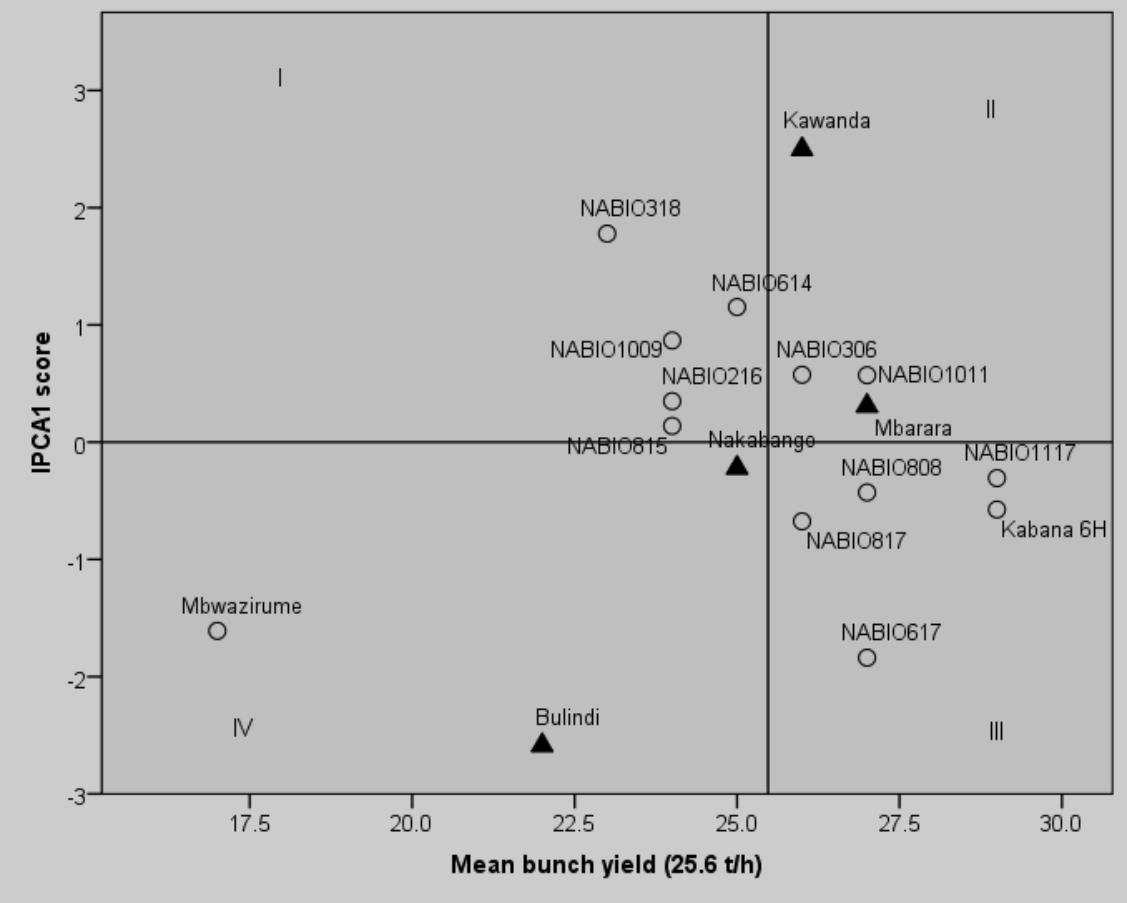

Figure 1. Biplot of mean bunch yield and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Bulindi had high contrasting interaction effects for the number of hands with genotypes, and were therefore the most unstable sites. Although unstable, Bulindi had highest performance for the number of hands.

Fruit finger circumference

The most stable genotypes with above average performance for fruit finger circumference were NABIO306, NABIO318, NABIO617 and NABIO808. The least stable genotype with above average performance for the trait was NABIO616 (Figure 3). Mbarara and Nakabango had high contrasting interaction effects for the trait with genotypes and were therefore, the most unstable sites although heir performance was above average. The most stable sites for fruit finger circumference as indicated by very low IPCA1 scores were Kawanda and Bulindi. Ranking of genotypes based on GSI that incorporated mean performance and ASV identified NABIO306 followed by NABIO808 as the best genotypes (Table 6).

Youngest leaf spotted due to black Sigatoka

The genotypes' response to black Sigatoka infection was assessed using YLS. Genotypes in quadrants II and III were above average performance (8.3) for resistance to black Sigatoka whereas those in quadrants I and IV were below average performance (Figure 4). The top eight genotypes for black Sigatoka resistance were test genotypes *viz.* NABIO1009, NABIO1011, NABIO808, NABIO617, NABIO614, NABIO318, NABIO815 and NABIO1117. As expected, Mbwazirume, a susceptible check cultivar was the worst performer for black Sigatoka resistance (Table 7). NABIO1011, NABIO815, Kabana 6H, NABIO1009 and NABIO216 had low IPCA1 score for YLS and were accordingly the most stable genotypes for the trait. The stability of these genotypes was confirmed by ASV. The least stable genotype for the trait as indicated by high IPCA1 scores was Mbwazirume. Categorizing genotypes based on GSI identified NABIO1011 followed by NABIO 1009, NABIO815, NABIO216, NABIO306 and Kabana 6H as the best genotypes combining high resistance to black Sigatoka

Table 4. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for bunch yield evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV rank	GSI	GSI rank
NABIO1009	24.2	11	1.2	5	16	9
NABIO1011	27.3	3	1.2	5	8	2
NABIO1117	29.1	2	0.4	2	4	1
NABIO216	24.7	9	0.5	3	12	7
NABIO306	26.7	6	0.9	4	10	3
NABIO318	23.2	12	2.4	11	23	12
NABIO614	25.5	8	1.6	8	16	9
NABIO617	27.0	5	2.5	12	17	11
NABIO808	27.2	4	1.8	9	13	5
NABIO815	24.6	10	0.3	1	11	4
NABIO817	26.3	7	1.5	7	14	8
Kabana 6H	29.3	1	2.5	12	13	5
Mbwazirume	17.0	13	2.2	10	23	2
Mean	25.6	7.0	1.5	7	13.8	6.0
$LSD_{0.05}$	3.3	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

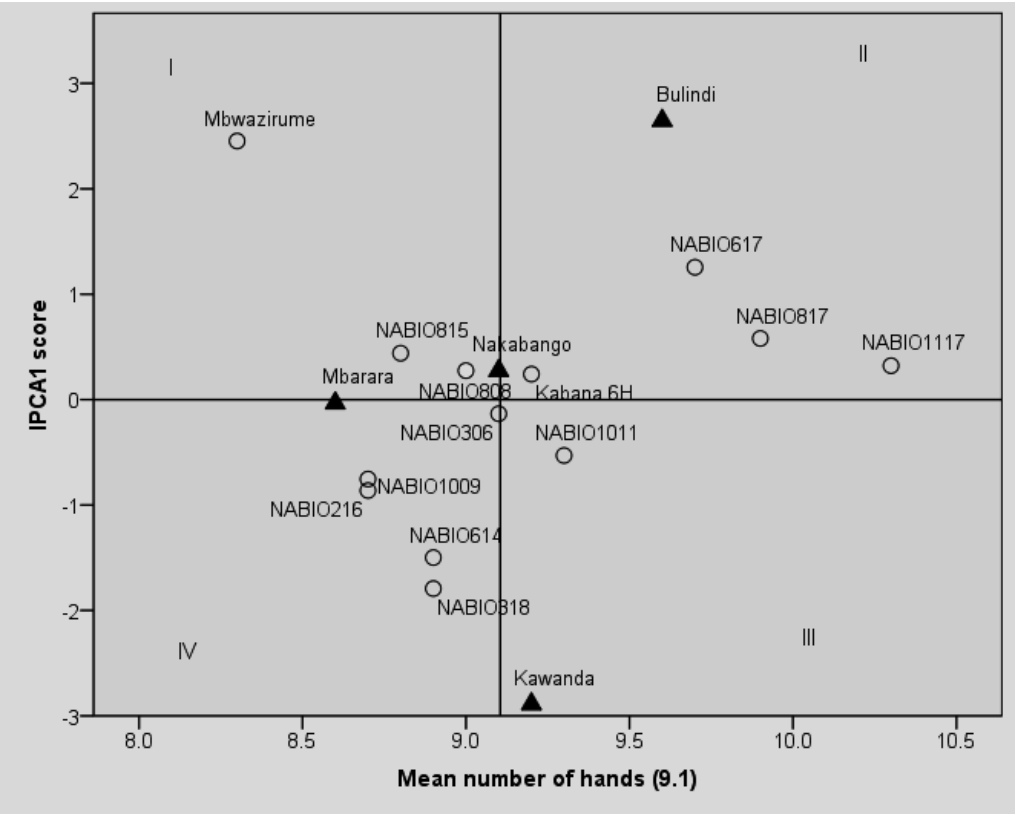

Figure 2. Biplot of mean number of hands and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

and stability. According to IPCA1 scores, all the genotypes except Mbwazirume had IPCA1 scores of less than one, implying that most of the genotypes (92.3%) were stable for black Sigatoka resistance. Kawanda and

Table 5. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for number of hands evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	8.7	11	1.3	8	19	9
NABIO1011	9.3	4	1.1	6	10	4
NABIO1117	10.3	1	0.5	2	3	1
NABIO216	8.7	11	1.4	9	20	11
NABIO306	9.1	6	0.7	4	10	4
NABIO318	8.9	8	3.0	12	20	11
NABIO614	8.9	8	2.5	11	19	9
NABIO617	9.7	3	2.2	10	13	7
NABIO808	9.0	7	0.6	3	10	4
NABIO815	8.8	10	1.1	6	16	8
NABIO817	9.9	2	1.0	5	7	3
Kabana 6H	9.2	5	0.4	1	6	2
Mbwazirume	8.3	13	4.1	13	26	13
Mean	9.1	7	1.5	7	13.8	7
$LSD_{0.05}$	0.2	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

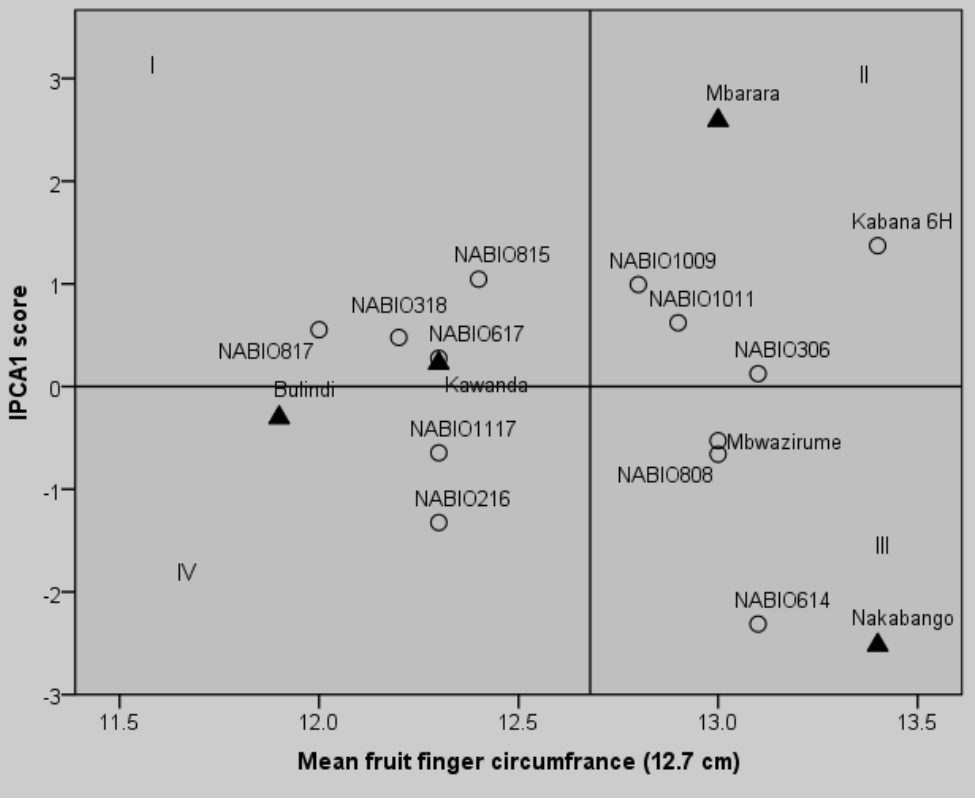

Figure 3. Biplot of mean fruit finger circumference and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Nakabango had low interaction effects for YLS with genotypes indicated by negligible IPCA1 scores, and were therefore, stable for the trait. Mbarara and Bulindi on the other hand, had high contrasting interaction effects

Table 6. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection index for fruit finger circumference evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	12.8	7	0.9	8	15	8
NABIO1011	12.9	6	0.9	10	16	10
NABIO1117	12.3	9	0.6	4	13	6
NABIO216	12.3	9	1.3	12	21	13
NABIO306	13.1	2	0.1	1	3	1
NABIO318	12.2	12	0.4	2	14	7
NABIO614	13.1	2	2.2	13	15	8
NABIO617	12.3	9	0.4	2	11	3
NABIO808	13.0	4	0.6	4	8	2
NABIO815	12.4	8	0.9	8	16	10
NABIO817	12.0	13	0.6	4	17	12
Kabana 6H	13.4	1	1.2	11	12	5
Mbwazirume	13.0	4	0.7	7	11	3
Mean	12.7	7	0.8	7	13.2	7
$LSD_{0.05}$	0.6	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

for the trait with genotypes and were therefore the most unstable sites.

Selection of genotypes

Genotype selection index that incorporates the rank of ASV (as an indicator of stability) and the rank of the overall trait mean values (as an indicator of performance) of genotypes in a single selection criterion, was employed to identify the desirable genotypes for all traits (Table 8). A genotype with lowest overall GSI was considered most desirable since it had a combination of overall high stability and agronomic performance for all traits. Accordingly, other than the check genotypes (Kabana 6H and Mbwazirume), four new genotypes that is, NABIO306, NABIO1011, NABIO808 and NABIO1009 were selected for advancement to on farm trials because in addition to having best performance for stability and agronomic performance for the traits assessed, they had soft and yellow fruit pulp on cooking (results not presented). Soft and yellow fruit pulp of cooking bananas are most preferred by consumers. Although NABIO1117 and NABIO815 were ranked 2nd and ^{6th} respectively, they were not selected because their fruits were seeded. The two genotypes would, however, be incorporated in the breeding program as parental germplasm. Irrespective of food sensory attributes, NABIO306, NABIO1117, NABIO1011, NABIO808, NABIO815, NABIO1009 and NABIO617 were the most stable and best performers for all traits across all environments.

DISCUSSION

Genotypes, locations and genotype x location interaction were significantly different for the four traits assessed (bunch yield, number of hands, fruit finger circumference and YLS due to black Sigatoka). Significant differences observed among genotypes for these traits indicated that significant progress would be achieved in selecting for the traits assesed. On the other hand, significant differences observed among locations for all the traits underlined the need to conduct multi-location PYTs in banana breeding in order to identify generally and specifically adapted genotypes with good performance for the traits of interest before release. Significant location effects for bunch yield, number of hands and fruit finger circumference were similarly reported by Ortiz and Cauwer (1999). Significant genotype x location interaction for the four traits assessed implied that the genotypes had different patterns of response to change in locations and should be selected at each test site.

In the AMMI ANOVA, 45.3% of the treatment SS for bunch yield was attributed to genotype, 22.8% to location and 31.9% to GEI, indicating the predominance of genetic variation among genotypes over variation among the locations or GEI for the trait. On the other hand, the contribution of GEI to treatment SS for number of hands and fruit finger circumference was higher than that of genotype and location, indicative of substantial differences in the genotype responses across locations for these traits. Therefore, selection for these traits should be done at each location to maximize potential

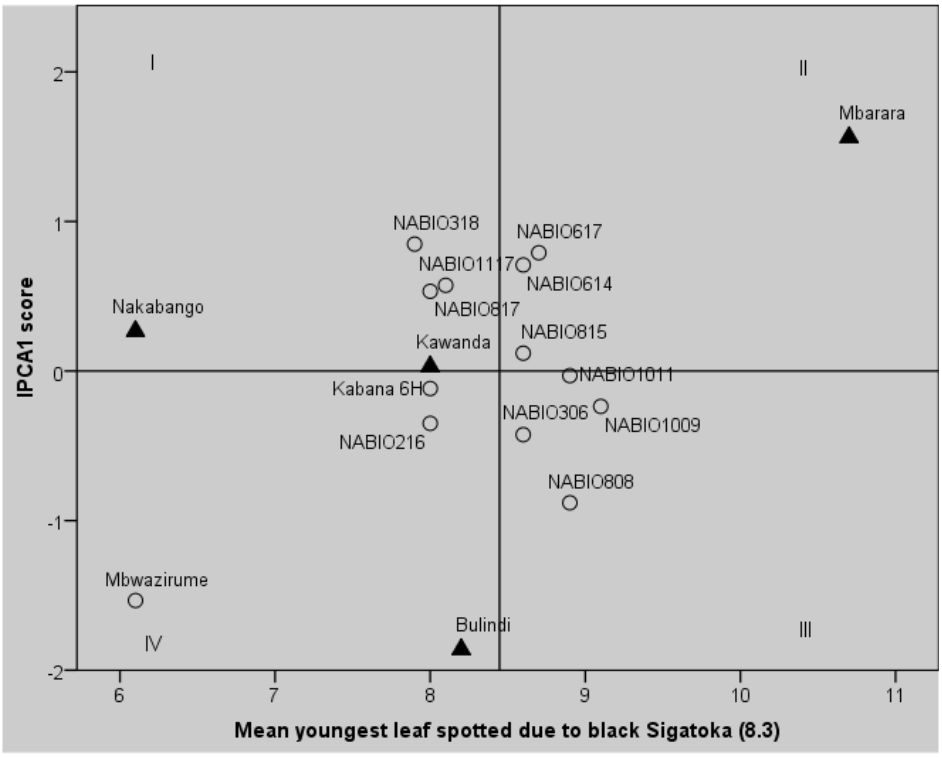

Figure 4. Biplot of mean youngest leaf spotted due to black Sigatoka and IPCA1 scores for 13 banana genotypes evaluated across two cycles at four locations in Uganda**.**

Table 7. Ranking of 13 banana genotypes by mean performance, AMMI stability value and genotype selection for youngest leaf spotted evaluated across two crop cycles and four locations in Uganda.

Genotype	Mean	Mean rank	ASV	ASV Rank	GSI	GSI rank
NABIO1009	9.1	1	2.7	4	5	2
NABIO1011	8.9	2	0.6	1	3	1
NABIO1117	8.1	8	6.4	8	16	10
NABIO216	8.0	9	3.9	5	14	4
NABIO306	8.6	5	4.8	6	11	4
NABIO318	7.9	12	9.5	11	23	12
NABIO614	8.6	5	7.9	9	14	6
NABIO617	8.7	4	8.8	10	14	6
NABIO808	8.9	2	9.8	12	14	6
NABIO815	8.6	5	1.3	2	7	3
NABIO817	8.0	9	6.0	7	16	10
Kabana 6H	8.0	9	1.3	2	11	4
Mbwazirume	6.1	13	17.1	13	26	13
Mean	8.3	7	6.1	7	13.4	7
$LSD_{0.05}$	0.7	-	-	-	-	-
P-value	< 0.001	-	-	-	-	-

GSI: genotype selection index; ASV= AMMI stability value.

gain.

IPCA1 was significant for all traits and IPCA2 for bunch yield, number of hands and YLS, whilst further IPCAs were not significant and captured mostly noise, thus being less helpful. This in agreement with Gauch (2006) who stated that IPCA1 and higher components in AMMI capture interaction exclusively in a monotonic sequence that decreases from the first and largest component to

Table 8. Overall ranking and selection of 13 banana genotypes by genotype selection index for bunch yield, number of hands, fruit finger circumference and youngest leaf spotted evaluated across two cycles and four locations in Uganda.

Genotype	BY		NH		FC		YLS		GSI Sum	Overall Rank	Remark[§]
	GSI	Rank	GSI	Rank	FC	Rank	YLS	Rank			
NABIO1009	16	9	19	9	15	8	5	2	55	7	S
NABIO1011	8	2	10	4	16	10	3	1	37	3	S
NABIO1117	4	1	3	1	13	6	16	10	36	2	NS
NABIO216	12	7	20	11	21	13	14	4	67	11	NS
NABIO306	10	3	10	4	3	1	11	4	34	1	S
NABIO318	23	12	20	11	14	7	23	12	80	12	NS
NABIO614	16	9	19	9	15	8	14	6	64	10	NS
NABIO617	17	11	13	7	11	3	14	6	55	7	NS
NABIO808	13	5	10	4	8	2	14	6	45	5	S
NABIO815	11	4	16	8	16	10	7	3	50	6	NS
NABIO817	14	8	7	3	17	12	16	10	54	9	NS
Kabana 6H	13	5	6	2	12	5	11	4	42	4	CV
Mbwazirume	23	2	26	13	11	3	26	13	86	13	CV

CV = check variety; S = selected, NS = not selected; BY = bunch yield (t/ha); NH = number of hands; FC = finger circumference (cm); YLS= youngest leaf spotted; and GSI = genotype selection index; Remark[§]= selection puts into consideration sensory evaluation results not presented in this paper.

the last and smallest component. Accordingly, Fikere et al. (2009) revealed that the interaction of genotypes in the field is best explained by the first two interaction principal component axes. Nevertheless, sometimes the first two IPCAs tend to rank genotypes differently giving negative and positive values. The use of ASV was therefore advocated (Farshadfar, 2008) since it gives a balanced measure between the first two IPCAs.

Based on AMMI biplots and associated IPCA1 scores, NABIO genotypes and Kabana 6H were most responsive to location effects. They represented either the best or the poorest performers in locations, corresponding to their displacement nearer to or farther from the IPCA1 origin. Nevertheless, different genotypes emerged as the best in different locations. For example, the most stable genotypes for bunch yield were: NABIO815, NABIO1117, NABIO216 and NABIO306; for number of hands: NABIO1117, NABIO808, NABIO306 and Kabana 6H; for fruit finger circumference: NABIO306, NABIO318, NABIO617 and NABIO808; and for YLS: NABIO1011, NABIO815, Kabana 6H and NABIO1009. Mbarara was the overall best site for the bunch yield due low pressure for black Sigatoka. Nakabango, on the other hand, was the second best site for bunch yield due to relatively higher soil fertility.

Farmers generally are more interested in genotypes that perform consistently better across sites, indicating preference for widely adapted genotypes (Zhang et al., 2006), and likewise, breeders would like to consider both yield and stability of performance simultaneously to reduce the effect of GEI and to make selection of genotypes more precise and refined. Although more resources may be required in breeding for specific environments, the merits of genotypes with local adaptation should also be recognized. In this study, none of the genotypes evaluated was ranked best for stability in all the four traits assessed, but widely adapted genotypes for specific traits were identified. A number of other genotypes with high trait mean values, but specifically adapted to particular environments for specific traits were also identified.

Genotype selection index helped selection of superior genotypes combining best mean performance and stability across environments since the most stable genotypes would not necessarily give the best performance for the trait of interest. In view of that, the best four genotypes selected for advancement to on farm trials were: NABIO306, NABIO1011, NABIO808 and NABIO1009. These genotypes, in addition to having better performance for all the traits assessed as well as stability, had soft and yellow fruit pulp on cooking as attributes most preferred by cooking banana consumers.

Conclusion

Genotype x location interaction was significant for all the four traits assessed, implying that the genotypes had significantly different patterns of response to change in locations and could be selected at each test site. Results suggested that it is possible to make progress in selecting high yielding banana genotypes with resistance to black sigatoka. However, the presence of significant GEI for all the traits assessed will complicate selection for these traits. The top four genotypes in terms of bunch yield, stability and preferred fruit quality traits were

selected (NABIO306, NABIO1011, NABIO808 and NABIO1009) and multiplied *in vitro* for advancement to multi-location on farm trials. Selected genotypes from farmers' fields will be recommended for national release. Multi-location preliminary yield trials are recommended in banana breeding to ensure a sound selection process that considers the effects of GEI.

Conflict of Interests

The authors have not declared any conflict of interests.

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REFERENCES

Annicchiarico P, Chiapparino E, Perenzin M (2010). Response of common wheat varieties to organic and conventional production systems across Italian locations, and implications for selection. Field Crops Res. 116:230-238.

Arzanlou M, Abeln ECA, Kema GHJ, Waalwijk C, Carlier J, De Vries I (2007). Molecular diagnostics for the Sigatoka disease complex of banana. Phytopathology 97:1112-1118.

Barekye A (2009). Breeding investigations for black Sigatoka resistance and associated traits in diploids, tetraploids and the triploid progenies of bananas in Uganda. PhD.Thesis, University of KwaZulu-Natal, Pietermaritzburg, South Africa, P 210.

Barekye A, Tongoona P, Derera J, Laing MD, Tushemereirwe WK (2011). Appraisal of methods for assessing black Sigatoka resistance in diploid banana populations. Afr. J. Plant Sci. 5:901-908.

Carlier J, De Waele D, Escalant JV (2002). Global evaluation of Musa germplasm for resistance to *Fusarium* wilt, *Mycosphaerella* leaf spot diseases and nematodes. (Vézina A, Picq C (Eds). INIBAP Technical Guidelines 6. The International Network for the Improvement of Banana and Plantain, Montpellier, France.

Daniells JW (2009). Global banana disease management: Getting serious with sustainability and food security. Acta Hortic. 828:411-416.

Ebdon JS, Gauch HG (2002). Additive main effects and multiplicative interaction analysis of national turfgrass performance trials. Crop Sci. 42:497-506.

FAOSTAT (2012*)*. Food and Agriculture Organisation statistical database for agriculture. Crops and products domain. http://faostat.fao.org/ (Accessed 15, July 2015).

Farshadfar E (2008). Incorporation of AMMI stability value and grain yield in a single non parametric index (GSI) in bread wheat. Pak. J. Biol. Sci. 11:1791-1796.

Fikere M, Fikiru E, Tadesse T, Legesse T (2009). Parametric stability analysis in field peas (*Pisum sativum* L.) under South Eastern Ethiopian condition. World J. Agric. Sci. 5:146-151.

Gauch HG (2006). Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46:1488-1500.

Ortiz R, De Cauwer L (1999). Genotype-by-environment interaction and testing environments for plantain and banana (*Musa* spp. L.) breeding in West Africa. Tropicultura 17:97-102.

Payne RW, Harding SA, Murray DA, Soutar DM, Baird DB, Glaser AI, Welham SJ, Gilmour AR, Thompson R, Webster R (2011). The guide to Genstat release 14, part 2: statistics. VSN International, Hemel Hempstead, UK.

Purchase JL, Hatting H, Van Deventer SC (2000). Genotype x environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South Afr. J. Plant Soil 17:101-107.

Tenkouano A, Pilly A, Ortiz R (2011). Breeding Techniques. In: Tenkouano A, Pilly (eds.), Banana breeding progress and challenges. Taylor and Francis Group, pp.181-202.

Tenkouano A, Vuylskeke D, Okoro J, Makumbi D, Swennen R, Ortiz R (2003). Diploid banana hybrids TMB2x5105-1 and TMB2x 9128-3 with good combining ability, resistance to black Sigatoka and nematodes. HortScience 38:468-472.

Tushemereirwe W, Batte M, Nyine M, Tumuhimbise R, Barekye A, Tendo S, Talengera D, Kubiriba J, Lorenzen J, Swennen R, Uwimana B (2015). Performance of NARITA banana hybrids in the preliminary yield trial for three cycles in Uganda. Banana Technical Report, pp. 35 Available at :www.musalit.org/seeMore.php?id=15482

Vakili NG (1968). Responses of Musa acuminata species and edible cultivars to infection by *Mycosphaerella musicola*. Trop. Agric. (Trinidad) 45:13-22.

Zhang Y, He Z, Zhang A, Van Ginkel M, Ye G (2006). Pattern analysis on grain yield of Chinese and CIMMYT spring wheat cultivars grown in China and CIMMYT. Euphytica 147:409-420.

Zobel RW, Wright MJ, Gauch HG (1988). Statistical analysis of yield trials. Agron. J. 80:388-393.