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Stability of Sweet Potato Cultivars to *Alternaria* Leaf and Stem Blight Disease

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Abstract

Alternaria leaf petiole and stem blight is an economically important disease of sweet potato (*Ipomoea batatus* L.) in tropical and sub-tropical environments. Published research on cultivar resistance to the sweet potato disease is limited. To evaluate cultivar reaction and stability to the disease, multi-location and replicated experiments were established in 12 environments in Uganda. Disease severity (area under disease progress curves – AUDPC), and cultivar root yield were also assessed. Significant differences ($P < 0.001$) in AUDPC were detected among cultivars. Mean AUDPC ranged from 46.3 (Araka Red) to 78.4 (New Kawogo) across locations and seasons and the genotypes Araka Red and Tanzania had the lowest disease values. The location and season effects accounted for 67.1% and 7.5% of the total variance of AUDPC recorded among cultivars. The ranking of cultivars based on predicted AUDPC from Additive Main Effect and Multiplicative Interactive model (AMMI) showed that the NASPOT 1, the susceptible check, and New Kawogo were most susceptible to the disease in 11 of the 12 environments. Low and stable disease was consistently recorded and predicted on NASPOT 3 and the landrace cultivars Tanzania, Dimbuca, and Araka Red across environments. These results suggest that landrace cultivars had relative stability to the disease and wide adaptation across environments. These results suggest that AMMI statistical model and other multivariate techniques can be utilized for prediction of *Alternaria* disease stability in these locations.

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Introduction

Sweetpotato is an important food crop grown in many tropical and sub-tropical regions of the world. In the lowland and highland tropics, the crop is grown under intensive, small-holder cultivation systems, with multiple cropping cycles per year and often intercropped (Anginyah et al., 2001; Osiru et al., 2007a). Although Uganda is the second largest producer of sweetpotato in the world and superseded by China, average root yield under the marginal land productivity characteristic of the region often ranges from 2.5 to 6 tons/ha. The utilization of sweetpotato as a food security crop and source of pro-vitamin A for malnourished children has greatly enhanced its production in diverse locations (Mwanga et al., 2001).

There are many plant diseases limiting the production potential of sweetpotato crop. Among the most common and destructive disease is *Alternaria* leaf petiole and stem blight disease caused by the fungal pathogen *Alternaria bataticola* (Lenne, 1991; Lopes and Boiteux, 1994; Anginyah et al., 2001; Osiru et al., 2007a). *Alternaria* leaf petiole and stem blight disease is prevalent and the most severe and destructive fungal disease of sweetpotato in East and Central Africa (Lenne, 1991; Carey, 1996; Anginyah et al., 2001; Mwanga et al., 2003; Ndirigue, 2005; Osiru et al., 2007a). The disease affects sweetpotato foliage and crop through stem and foliage infection as well as lesion expansion subsequently reducing photosynthetic capacity of the plant and translocation of nutrients and water. Extensive foliage and stem infections may result in defoliation of leaves and total plant destruction (Lenne, 1991).

The current management strategies for sweetpotato diseases rely on integrated control with emphasis on host resistance (Hakiza et al., 2000; Mwanga et al., 2003). However, there are limited quantitative data on the resistance and disease stability of tropical-adapted sweetpotato cultivars to *Alternaria* disease in diverse

environments. In addition to cultural measures, knowledge of cultivar resistance and disease stability would provide viable alternatives for disease management in the cropping systems of tropical Africa.

Sweetpotato cultivars have been previously shown to exhibit resistance to sweetpotato virus disease (SPVD) and other virus diseases in East and Central Africa (Aritua et al., 2000). Previous research has documented resistance to fungal diseases in some sweetpotato germplasm and accessions; however, limited deployment of cultivars for disease control has been reported (Lenne, 1991; Anginyah et al., 2001; Ndirigue, 2005). Research by other authors have documented that identification of superior crop cultivars for yield, disease and other agronomic traits may be confounded by genotype by environment interactions (G × E) (Crossa et al., 1991; Eberhart and Russell, 1996; Nakitandwe et al., 2005; Mulema et al., 2005, 2008). Crop genotypes grown in diverse environments frequently show significant fluctuations in various traits such as disease resistance and yield relative to other cultivars as a result of G × E (Dias and Krzanowski, 2003). Limited published data is available with regard to stability of sweetpotato cultivars to *Alternaria* leaf blight. The evaluation of interactions of sweetpotato cultivars with respect to *Alternaria* disease (G × E) may be crucial for documenting disease reaction and cultivar stability under diverse environmental conditions (Osiru et al., 2007a,b).

Owing to the widespread cultivation of sweetpotato and its utilization as a food security crop in tropical and sub-tropical regions, knowledge of disease reaction and cultivar stability are of significance. In this research, a multivariate technique known as the Additive Main Effects and Multiplicative Interaction Model (AMMI), which combines the analysis of variance of genotype by environment main effects, principal component analysis (PCA), and the interaction of G × E into a unified approach (Gauch and Zobel, 1990; Gauch, 1993) was used. Therefore, the objective of this research was to assess the stability of *Alternaria* leaf petiole and stem blight disease resistance of sweetpotato cultivars and their reaction in diverse locations of Uganda using the AMMI statistical model.

Materials and Methods

Site characterization

Field studies were conducted during four cropping seasons of 2001A, 2001B, 2002A, 2002B (where A and B are first and second seasons) at three distinct locations of Namulonge Agricultural and Animal Production Research Institute (NAARI), Serere Agricultural and Animal Production Research Institute (SAARI), and Kachwekano Agricultural Research and Development Center (KARDC). These locations represented the main agro-ecologies for sweetpotato production in Uganda. NAARI is located in Central Uganda [0°32′N, 32°35′E; 1150 m above mean sea level (m.a.s.l.)] and is situated in the warm, moist tall grasslands agro-ecological zone where SPVD is prevalent. SAARI lies in the warm, sub-humid short grasslands agro-ecological zone (33°27′E, 1°32′N; 1140 m.a.s.l.) and KARDC is located in the western and eastern high altitude zone (WEHAZ; 01°16′S, 29°57′E; 2200 m.a.s.l.). Temperature (C), rainfall (mm), and relative humidity (%) were obtained from the climatological weather stations located at the research sites where the experiments were conducted (Fig. 1).

Plot establishment and experimental design

At each location, 10 sweetpotato cultivars were evaluated (Table 1). Five genotypes released by the Uganda National Sweetpotato Programme (Mwanga et al., 2001, 2002, 2003) and selected on the basis of dry matter content, tolerance to viruses and high root yield; and five landrace varieties (farmer's varieties) selected from various parts of the country based on its widespread utilization from diagnostic survey (Osiru et al., 2007a). The cultivar NASPOT 1, which is susceptible to *Alternaria* pathogen was used as the susceptible control and cultivar Tanzania was used as the resistant control.

The experimental layout in each location was a randomized complete block design (RCBD) with four replications and conducted at several cropping seasons. At NAARI the first and second seasons of 2001 and 2002 were March–July and September–December, respectively. At SAARI the cropping seasons were March–August and September–December, respectively. At KARDC, the first and second cropping seasons of 2001 and 2002 were April–December and November–June. Owing to the cooler growing periods (time to maturity) for all genotypes at this location, experiments were staggered or planted sequentially. Soils at this location are dark brown, acidic and low in base and potential for erosion is high because of long steep slopes.

Disease assessments across seasons and locations

Assessments of *Alternaria* leaf petiole and stem blight disease commenced 4 weeks after planting or as soon as symptoms appeared and continued at 2-week intervals until harvest. Harvest occurred at approximately 4–6 months after planting (MAP) at NAARI and SAARI locations and at 8 MAP at KARDC. Two rows per plot were assessed for disease incidence and severity in each field. Disease incidence was assessed as the number of symptomatic plants/total number of plants multiplied by 100%. Disease severity was scored using a modified visual scale of van Bruggen (1984) where 0 = no disease, 1 = <1%, 2 = 1–10%, 3 = 11–25%, 4 = 26–50%, 5 = >50% foliar infection. Disease severity data for each cropping season and locations were used to compute area under disease progress curves (AUDPC – per cent of disease days; Campbell and Madden, 1990).

Root yield of sweetpotato cultivars

Root yield was assessed on two row plots of sweetpotato cultivars at each location and cropping seasons.

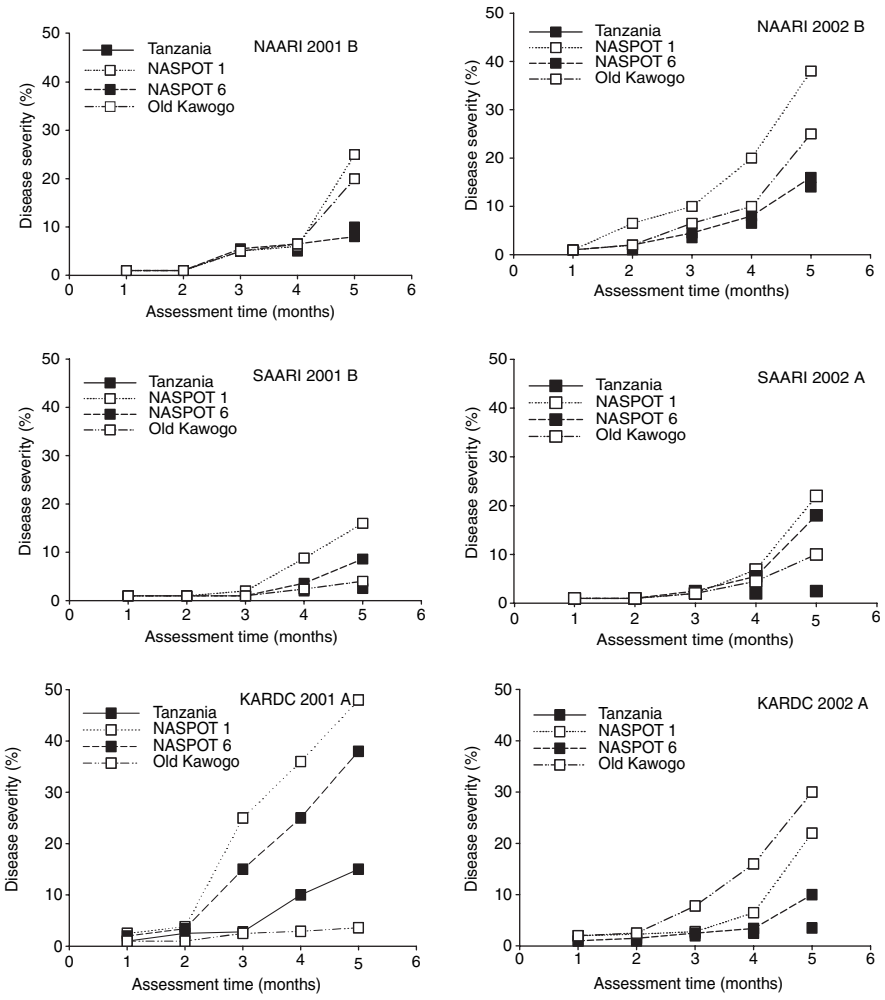

Fig. 1 Severity of *Alternaria* leaf petiole and stem blight disease (disease severity %) on sweetpotato genotypes Araka Red, Tanzania (resistant), New Kawogo, and NASPOT1 (susceptible). Disease was initiated from natural infections and assessed at Namulonge, Serere, and Kachwekano locations (NAARI, SAARI, KARDC, respectively)

Sweetpotato root yield were harvested after 162, 168, and 224 days in 2001A; 184, 186, and 257 days in 2001B; 153, 156, and 228 days in 2002A and 173, 177, and 243 days in 2002B after planting at NAARI, SAARI, and KARDC, respectively.

Data analysis

AUDPC data and root yield for each cultivar at each environment were subjected to analysis of variance (ANOVA) to compute means, standard errors (SE), standard errors of difference (SED) as well as coefficients of variation (Gomez and Gomez, 1984; Steel et al., 1997). Rank correlations were used to categorize relative cultivar susceptibility/resistance to disease. The effects of *Alternaria* leaf petiole and stem blight disease on cultivar reaction across seasons and locations were computed by ANOVA [Proc GLM of Genstat (Genstat 5 Release 3.22; Lawes Agricultural Trust, Rothamsted Experimental Station, UK] and IRRISTAT for Windows Version 5.0 (IRRI, 2005) to compare cultivar susceptibility or resistance across locations and cropping seasons. In this model, genotypes were considered fixed effects, while locations, cropping seasons, and replications were designated as random effects. Disease progress across time of assessments (months) was plotted for two susceptible and two resistant cultivars.

Stability of cultivars to *Alternaria* disease

Data on disease severity were additionally subjected to $G \times E$ analysis using the AMMI statistical model (Gauch, 1993; IRRISTAT-International Rice Research Institute (IRRI), 2005). A graphical illustration (AMMI biplot) was drawn by plotting the mean AUDPC of genotypes averaged across seasons on the *x*-axis and 1PCA values on the *y*-axis. Similarly, mean AUDPC for environment (*x*-axis) were plotted against 1PCA values on the *y*-axis. To compare resistance or susceptibility of sweetpotato cultivars to *Alternaria* disease, the data was subjected to Proc GLM resulting in variances from the analysis.

Results

Site characterization

Weather variables (rainfall, temperature, relative humidity) at the locations used for the evaluation of sweetpotato genotypes varied across locations and seasons. Rainfall patterns varied at the different testing locations in which the highest average monthly rainfall amount (179 mm) was recorded during 2002B season at NAARI followed by SAARI location (140 mm) during the same period. Highest yearly total rainfall was noted in NAARI in 2002 (1534 mm) followed by 1443 mm at SAARI during 2001, while the lowest

Table 1
Morphological and agronomic characteristics of ten sweetpotato genotypes evaluated for resistance to *Alternaria* leaf petiole and stem blight disease in 12 environments during four consecutive cropping seasons (2001A, 2001B, 2002A, 2002B)[a]

Genotypes	Year of cultivar release	Clones/names	Source/ origin	Root yield (tons/ha)	Skin colour (root)	Flesh colour (root)	Growth habit	Maturity Period (months)	Dry matter content (%)[a]	Reaction to SPVD	Reaction to *Alternaria*	Weevil reaction
NASPOT 1	1999	NIS/91/52	NARO	7–45	Cream	Pale yellow	Spreading	4	31	MR	S	S
NASPOT 2	1999	NIS/91/178	NARO	7–33	Mod purple	Red	Spreading	4	28	R	S	S
NASPOT 3	1999	NIS/91/218	NARO	5–29	Brown orange	Cream	Spreading	5	38	R	R	MR
NASPOT 6	1999	NIS/91/324	NARO	7–28	Cream	White	Spreading	5	32	MR	R	MR
New Kawogo	1995	CIP 441743	NARO	6–45	Red	White	Spreading	3–5	32	R	S	S
Tanzania	1995/farmer's cultivar	KEMB 10 SPN/O Simama Osukut	Wakiso	5–58	Cream	Pale yellow	Semi-erect to spreading	3–5	32	S	R	S
Dimbuca	Farmer's cultivar	———	Wakiso	——	Cream	White	Spreading	——	——	S	——	——
Silk	Farmer's cultivar	———	Wakiso	——	Purple	White	Semi-erect	——	——	——	——	——
Araka Red	Farmer's cultivar	———	Soroti/									
Kumi	5–15	Red	White	Erect	——	——	R	——	MR			
Old Kawogo	Farmer's cultivar	———	Kabale	——	Cream	White	Spreading	——	——	R	S	——

[a]Source: Mwanga et al. (2001, 2003).
NARO, National Agricultural Research Organization, Uganda; Kabale, Kumi, Soroti, and Wakiso are districts in Uganda; SPVD, sweetpotato virus disease; HS, highly susceptible; S, susceptible; MR, moderately resistant; R, resistant; HR, highly resistant; ———, no data.

total yearly rainfall was observed in KARDC (936 mm) during the second rainy season of 2002. Average yearly relative humidity (%) was highest at NAARI (86%) in 2001 followed by KARDC (80%) in 2001. Average temperatures during the period of study were highest in SAARI (24.4) and lowest at KARDC (17.8). The morphological characteristics of sweetpotato cultivars as well as agronomic, storage root yield, and disease reaction are presented in Table 1.

Disease development across seasons and locations

The epidemics of *Alternaria* leaf blight occurred at the three locations during the cropping seasons, but corresponding disease levels differed significantly ($P < 0.001$) among locations and seasons (Table 2). Across locations, AUDPC (% disease days) ranged from 45.59 to 78.38 (Table 3). Disease levels were highest at KARDC location (66.11) for all genotypes, followed by NAARI (53.17) and SAARI (46.69). Overall, the highest mean AUDPC was recorded on the cultivar New Kawogo (78.38), followed by the susceptible check cultivar NASPOT 1 (75.14; Table 3). Similarly, across the cropping seasons, the highest mean disease values were recorded at KARDC where the cultivars New Kawogo and NASPOT 1 had AUDPC of 117.1 and 105.4, respectively. The lowest mean AUDPC value (42.00) was recorded on a landrace cultivar, Araka Red, at SAARI location.

Disease progress curves were almost linear to exponential across the assessment period at all locations (Fig. 1). At NAARI and SAARI, disease levels were significantly greater during the 2002 than the 2001 cropping years. At NAARI (2001B, 2002B) and at KARDC (2002A), the susceptible cultivars (Old Kawogo, NASPOT 1) had higher disease levels than the resistant cultivars (Tanzania, NASPOT 6), particularly at the last assessment period (Fig. 2). In general,

Table 2
Analysis of variance on the effect of sweetpotato genotypes on root yield (tons/ha) at three locations and four cropping seasons in 2001 and 2002

Source of variation	*df*	AUDPC (% disease days) *F*-value	AUDPC (% disease days) P > *F*	Yield (tons/ha) P > *F*
Locations (Loc)[a]	2	173.87	0.001**	0.001**
Seasons[b]	3	172.08	0.001**	0.001**
Loc × seasons	6	197.65	0.001**	0.001**
Reps (seasons × loc)	36	1.14	0.2756ns	0.4965ns
Genotypes[c]	9	77.28	0.0001**	0.001**
Loc × genotypes	18	27.83	0.001**	0.001**
Seasons × genotypes	27	1.04	0.4156ns	0.0112*
Genotypes × seasons × loc	54	2.11	0.001**	0.007**

*Significant at 5%.
**Significant at 1%.
[a]Experimental locations consist of Kachwekano Agricultural Research & Development Center (KARDC), Namulonge Agricultural Research Station (NAARI), and Serere Animal Agricultural Research Station (SAARI).
[b]Seasons consist of 2001A, 2001B, 2002A, and 2002B.
[c]Genotypes consist of NASPOT 1, NASPOT 2, NASPOT 3, NASPOT 6, Tanzania, Dimbuca, Silk, New Kawogo, Old Kawogo, and Araka Red.
AUDPC, mean area under disease progress curves; ns, non significant at 5%.

Table 3
Mean area under disease progress curves (AUDPC) for *Alternaria* leaf petiole and stem blight disease and root yield of 10 sweetpotato cultivars grown at three locations averaged across four cropping seasons[a] in Uganda in 2001 and 2002

	AUDPC (% disease days)				Yield (tons/ha)			
Genotypes	NAARI[b]	SAARI[b]	KARDC[b]	Means	NAARI	SAARI	KARDC	Means
Dimbuca	53.87	42.17	43.16	46.4	21.85	20.28	49.94	29.41
Tanzania	51.41	42.29	43.07	45.59	17.47	12.58	40.74	22.45
NASPOT 1	58.49	61.50	105.4	75.14	28.01	15.32	48.52	29.42
NASPOT 2	48.89	43.93	53.44	48.75	18.26	28.61	31.67	25.82
Silk	49.58	42.03	53.80	48.47	17.11	14.55	48.78	25.35
New Kawogo	59.63	58.39	117.1	78.38	12.22	6.07	36.78	17.13
NASPOT 3	50.09	43.61	57.47	50.39	13.57	9.33	43.13	20.60
NASPOT 6	51.12	43.12	53.83	49.36	11.37	12.13	47.31	22.03
Araka Red	52.69	42.00	44.30	46.33	7.11	18.21	38.12	20.02
Old Kawogo	55.93	47.85	89.49	64.42	21.62	10.44	30.74	20.28
Site means	53.17	46.69	66.11	55.32	16.86	14.75	41.57	23.25
$LSD_{0.05}$[c]	10.84	4.45	10.79	——	7.46	7.28	31.03	———

[a]Seasons consist of 2001A, 2001B, 2002A, and 2002B.
[b]Experimental locations consist of Kachwekano Agricultural Research and Development Center (KARDC), Namulonge Agricultural Research Station (NAARI), and Serere Animal Agricultural Research Station (SAARI).
[c]Means are significantly different based on Fisher's least significant difference (LSD) statistics.
AUDPC, mean area under disease progress curves; ———, no data.

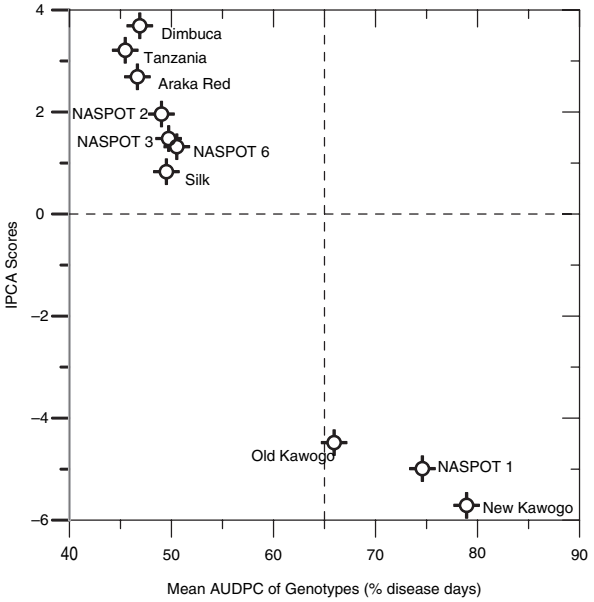

Fig. 2 Plot of mean *Alternaria* disease levels (AUDPC) and combined additive, multiplicative interaction (AMMI) with principal component (IPCA1) scores for 10 sweetpotato genotypes evaluated in 12 environments. The average AUDPC means for genotypes from 40 to 80 are plotted on the *x*-axis, while the IPCA1 scores from –6 to 4 are plotted on the *y*-axis. The variable along the *x*-axis reflect differences in main effects, and the values along the *y*-axis represent differences in interaction effects. The genotypes to the right side of the mid-point of the graph are classified as those with high disease potential, and those to the left side as having low disease potential

highest disease levels were recorded at KARDC than at other locations and disease severity did not exceed 50% across all locations (Fig. 2).The analyses of variance for *Alternaria* disease (AUDPC) resulted in significant differences ($P < 0.001$) on cultivar effects and interactions of cultivar × locations (Table 4). Similarly, interactions of seasons × locations was significant ($P < 0.001$).

Table 4
Combined additive, multiplicative interaction (AMMI) and analysis of variance for cultivar disease levels (*Alternaria* AUDPC) of 10 sweetpotato genotypes assessed at three locations and four cropping seasons

Source of variation	*df*	SS	MS
Treatments	119	269 867	2268*
Genotype (G)[a]	9	52 787	5866*
Environment (E)[b]	11	168 785	15 344*
Blocks	24	2240	93ns
G × E	99	48 296	488*
AMMI 1	19	41 350	2176*
AMMI 2	17	4583	270ns
AMMI 3	15	1604	107ns
Residual	63	759	
Error	216	18 495	

*Significant at 5%.
[a]Genotypes consist of NASPOT 1, NASPOT 2, NASPOT 3, NASPOT 6, Tanzania, Dimbuca, Silk, New Kawogo, Old Kawogo, and Araka Red.
[b]Environment consists of three locations × four cropping seasons.
AUDPC, mean area under disease progress curves; SS, sum of squares; MS, mean of squares; ns, non significant.

Root yield of sweetpotato cultivars

Significant differences ($P < 0.01$) in sweetpotato root yield were recorded among locations, cropping seasons as well as the interactions of locations and seasons (Table 2). The root yield averaged across locations and seasons also varied significantly. Similarly, the genotype effects and associated interactions were also significant. The yield of genotypes averaged across locations and cropping seasons ranged from 17.12 on New Kawogo cultivar to 29.42 on the cultivar NASPOT1 (Table 3). High variability in root yield was detected among cropping seasons, locations, and sweetpotato genotypes. The total root yield at each location showed large variances and were significant among the testing locations of KARDC, NAARI, and SAARI respectively (data not shown).

Table 5
Ranking of genotypes based on combined additive, multiplicative interaction (AMMI) estimates and observed means (in parentheses) for areas under disease progress curves (AUDPC) of 10 sweetpotato genotypes grown in 12 environments (location by season combinations)

Genotypes[b]	NAARI[a] 2001A[c]	NAARI 2001B	NAARI 2002A	NAARI 2002B	SAARI 2001A	SAARI 2001B	SAARI 2002A	SAARI 2002B	KARDC 2001A	KARDC 2001B	KARDC 2002A	KARDC 2002B
Dimbuca	10 (8)	9 (10)	10 (10)	9 (10)	2 (10)	4 (10)	1 (10)	4 (10)	4 (10)	4 (4)	5 (9)	7 (4)
Tanzania	9 (9)	8 (8)	8 (9)	8 (9)	7 (5)	10 (8)	2 (5)	8 (8)	7 (4)	10 (5)	9 (1)	9 (7)
NASPOT 1	1 (1)	3 (2)	3 (2)	3 (2)	3 (1)	1 (1)	5 (1)	1 (2)	1 (2)	1 (1)	1 (3)	2 (1)
NASPOT 2	8 (7)	6 (4)	6 (6)	6 (5)	4 (7)	9 (3)	6 (7)	10 (5)	8 (6)	9 (10)	10 (6)	5 (10)
Silk	4 (5)	7 (5)	7 (4)	7 (4)	10 (8)	7 (6)	9 (8)	6 (3)	10 (8)	7 (8)	6 (8)	8 (9)
New Kawogo	2 (6)	1 (6)	1 (5)	1 (6)	1 (9)	2 (5)	4 (9)	2 (6)	2 (9)	2 (7)	2 (2)	1 (6)
NASPOT 3	6 (2)	5 (1)	5 (1)	5 (1)	6 (2)	8 (2)	8 (3)	9 (1)	9 (1)	8 (2)	8 (4)	6 (2)
NASPOT 6	5 (3)	4 (3)	4 (3)	4 (3)	5 (3)	6 (4)	7 (2)	7 (4)	6 (3)	6 (3)	7 (10)	4 (3)
Araka Red	7 (4)	10 (7)	9 (7)	10 (7)	8 (4)	5 (9)	3 (6)	5 (9)	5 (7)	5 (9)	4 (7)	10 (8)
Old Kawogo	3 (10)	2 (9)	2 (8)	2 (8)	9 (6)	3 (7)	10 (4)	3 (7)	3 (5)	3 (6)	3 (5)	3 (5)

[a]The locations refer to: NAARI, Namulonge; SAARI, Serere; and KARDC, Kachwekano.
[b]Genotypes consist of NASPOT1, NASPOT2, NASPOT3, NASPOT6, Tanzania, Dimbuca, Silk, New Kawogo, Old Kawoho, Araka Red.
[c]2001A and 2002A correspond to first rainy season (March–July) of 2001 and 2002, respectively; 2001B and 2002B refer to second rainy season (September–December) of 2001 and 2002.
The numbers 1–10 indicate the ranking of genotypes for AUDPC levels relative to the 10 genotypes evaluated for disease levels. 1 refers to highest disease and 10 refers to lowest disease levels.

Stability of *Alternaria* leaf petiole and stem blight disease

The analysis of variance for the AMMI statistical model showed that the G × E interaction was significant. The environmental variation and G × E interaction explained 21% and 33.5% of the total variation, respectively (Table 4). The genotype showed the highest fraction of variation (45.5%), followed by the G × E interaction (33.2%). Only the first principal component axis (AMMI Component 1) showed significant effects.

The ranking of genotypes based on disease levels (AUDPC) predicted by AMMI model indicated that NASPOT 1 was the most susceptible genotype in 6 of the 12 environments (Table 5). Similarly, the genotype New Kawogo was ranked as the most susceptible cultivar in the five environments (NAARI 2001B, 2002A and 2002B; SAARI2001 and KARDC 2002B). On the other hand, a landrace cultivar, Dimbuca, was recorded as the most susceptible in only one environment (SAARI, 2002A).

The plot of mean *Alternaria* disease levels (AUDPC) of genotypes and 1PCA1 scores revealed large differences in the IPCA1 scores among genotypes (Fig. 2) and environments (Fig. 3). The genotypes Dimbuca, Tanzania, NASPOT 2, Silk, NASPOT 3, NASPOT 6, and Araka Red all revealed positive PCA1 scores and clustering, while the genotypes Old Kawogo, NASPOT 1, and New Kawogo had negative IPCA scores. The genotypes NASPOT 6, NASPOT 3, and Silk resulted in PCA scores in close proximity to 0. The genotypes Dimbuca, Tanzania, NASPOT12, Silk, and Araka Red showed negative PCA1 scores at KARDC location.

The plot of *Alternaria* disease (mean AUDPC) of genotypes and PCA scores (1PCA1) revealed large differences in scores among genotypes (Fig. 3) and environments (Fig. 4). The genotypes Dimbuca, Tanzania, NASPOT 2, Silk, NASPOT 3, NASPOT 6, and Araka Red had positive 1PCA1 scores and clustering, while the genotypes Old Kawogo, NASPOT 1, and New Kawogo had negative 1PCA scores. The genotypes

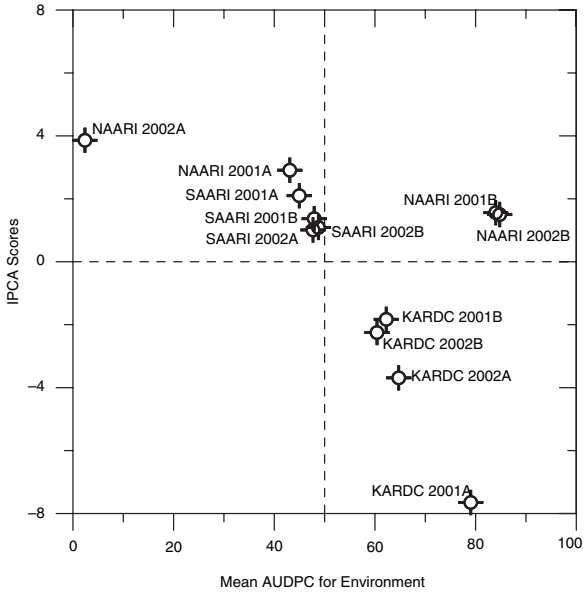

Fig. 3 Plot of mean *Alternaria* disease (AUDPC) and combined additive, multiplicative interaction (AMMI) with principal component (IPCA1) scores averaged across 10 sweetpotato genotypes for each environment in which disease was evaluated. The designations for the environment means (locations × seasons) are represented by: NAARI, Namulonge; SAARI, Serere; KARDC, Kachwekano; 2001A and 2002A correspond to the first rainy season (March–July); 2001B and 2002B to the second rainy season (September–December). The environments with PCA scores near zero represent little variation in disease levels (high stability), while those to the right of the mid-points represent unstable environments

NASPOT 6, NASPOT 3, and Silk had PCA scores in close proximity to 0. Similarly, the genotypes Dimbuca, Tanzania, NASPOT 2, Silk, and Araka Red showed negative PCA1 scores at KARDC location.

The plot of disease data (mean AUDPC) for environment revealed high variation in 1PCA1 scores and very low interactions (Fig. 4). Although KARDC exhibited the highest root yield, the PCA1 scores were also negative. The SAARI and NAARI locations showed positive

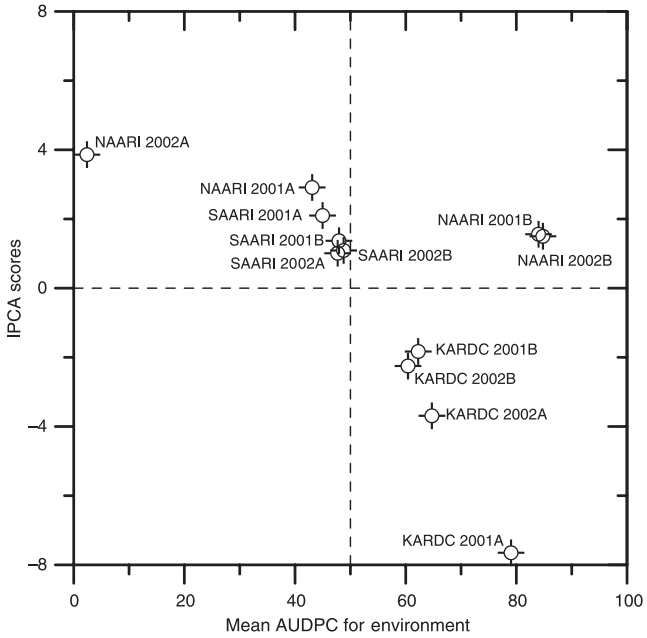

Fig. 4 Plot of mean *Alternaria* disease (AUDPC) and AMMI interaction (IPCA1) with scores averaged across 10 sweetpotato genotypes for each environment in which disease was evaluated. The designations for the environment means (locations × seasons) are represented by: NAARI - Namulonge; SAARI - Serere; KARDC - Kachwekano; 2001A and 2002A correspond to first rainy season (March–July); 2001B and 2002B to second rainy season (September–December). The environments with principal component scores near zero represent little variation in disease levels (high stability), while those to the right of mid-points represent unstable environments

PCA1 scores for AUDPC means of that environment. In general, the genotypes with low AUDPC scores (Dimbuca, Tanzania, Araka Red, NASPOT 6, Silk, NASPOT 3) showed negative PCA1 values, while those with high AUDPC scores (NASPOT 1, New Kawogo, Old Kawogo) showed positive values. The differences in the additive main effect for environments were found to be larger than that for genotype effects.

Discussion

The differences in disease levels among locations and cropping seasons may be attributed to climatic factors or pathogen inoculum. The KARDC location is situated at 2200 m.a.s.l., and had comparatively lower temperatures and higher relative humidities throughout the four cropping seasons compared with the other two locations (NAARI and SAARI). Therefore, the variation in disease levels among locations and seasons may be explained by the differences in temperature and relative humidity conditions. In previous research, it has been documented that most epidemics incited by *Alternaria* spp. have been associated with extended periods of wet weather and high humidity (Strider, 1963; Rotem et al., 1989; Rotem, 1994). Therefore, cooler temperatures and higher relative humidities may have contributed to longer durations of moisture availability thereby enhancing pathogen infection. Our results are supported by published research which documented that correlation between disease intensity and decreased temperature in the *Alternaria* pathosystem is associated with moisture, rather than temperature *per se* (Holley et al., 1985).

The temporal variation of *Alternaria* leaf petiole and stem blight disease also was detected in this study. Disease levels were more severe during the second season (B) of 2001 and 2002 than in the first season (A) at SAARI and KARDC locations. This may be attributed to varying temperature, humidity, and rainfall conditions resulting in temporal variation of infection and disease development. Humidity or moisture and low temperatures are required for pathogen infection (Rotem, 1994).

The differences in *Alternaria* disease levels among the three locations may also be explained in terms of duration of genotype growth at respective climatic conditions. At KARDC, sweetpotato genotypes have longer duration of physiological growth and maturity periods than the same cultivars at lower altitude locations (NAARI and SAARI) leading to prolonged growth. The longer duration of growth period may have contributed to a greater potential period for pathogen infection and subsequent disease progression and increased susceptibility of the crop to *Alternaria* pathogen owing to the presence of older vines. The age-related (vine senescense and crop maturity) susceptibility of crops to *Alternaria* pathogen has been previously documented in various pathosystems (Prabhu and Prasada, 1966; Droby et al., 1984; Mohit and Shukla, 1986; Rotem, 1994).

Variation in disease levels was detected among sweetpotato genotypes across testing locations and there were significant interactions of genotypes × locations. The significance of genotypes × locations imply the differential response of genotypes across environments. Although the highest AUDPC values were recorded on variety NASPOT 1, variation in the disease levels was detected among sweetpotato genotypes. The differential reaction of the genotypes may indicate the relative susceptibility or resistance to this disease. Although the variation in disease levels may also be a consequence of inoculum variability, quantification of pathogen inoculum load at the various locations was not done. However, the trend of disease progress across all locations and cropping seasons is still indicative of the relative cultivar susceptibility or resistance to this disease. No previous publication on G × E interaction effects of *Altenaria* disease on sweetpotato has been published.

The ranking of genotypes based on AUDPC estimates from the AMMI analysis indicated that genotype NASPOT 1 (the susceptible control) and New Kawogo were the most susceptible varieties to the *Alternaria* disease in 11 of the 12 environments tested. These cultivars (NASPOT 1 and New Kawogo) were predicted by the AMMI model as having the worst disease reactions. This suggests that the two genotypes would not perform well under *Alternaria* disease pressure and may have limited utility. On the other hand, Dimbuca, a landrace cultivar was predicted as a

cultivar with good disease stability. Therefore, this model was useful in prediction of reaction of cultivars to *Alternaria* disease. This finding is supported by pervious research which indicates that AMMI analysis increased the accuracy of disease or yield predictions in various environments (Gauch and Zobel, 1990; Mulema et al., 2005, 2008).

The PCA1 scores for genotypes were useful in explaining disease stability across environments. The genotypes with positive PCA1 scores suggest that they will have less disease in an environment than would be expected from the main effects. Therefore, the cultivars Dimbuca, Tanzania, Araka Red, NASPOT 2, NASPOT 3, NASPOT 6, and Silk with positive PCA1 scores performed better and had low disease levels (less susceptible) under *Alternaria* disease pressure. Similarly, the genotypes with high and negative PCA1 scores such as New Kawogo, NASPOT 1, and Old Kawogo would be expected to have high disease levels than would be expected and were therefore unstable. The correlation of main effects and PCA scores can then be used in making predictions of disease reactions. Similarly, the environments with positive PCA scores and close proximity to zero indicate that *Alternaria* disease levels are low and stable. Therefore, NAARI 2001A SAARI 2001A, SAARI 2001B, SAARI 2002A, SAARI 2002B, NAARI 2001B, and NAARI 2002B locations could be effectively used for cultivar resistance screening. On the other hand, the environments with negative and high PCA scores such as KARDC 2001B, KARDC 2002B, KARDC 2002A, and KARDC 2001A imply potentially high disease pressure; therefore, potentially not very suitable for maximizing sweetpotato production.

The findings showed that genotypes performed differently in the different environments as a result of $G \times E$ interactions. Disease pressure at various environments and disease stability of genotypes can be predicted from AMMI models and utilized effectively for improved yield performance.

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