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Evaluation and Participatory Selection of Promising Sweetpotato F_1 Genotypes in Uganda

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***Abstract*— *Most of the important sweetpotato (Ipomoea batatas (L.) Lam) traits are sensitive to environmental change. This necessitates evaluating new sweetpotato genotypes in different environments to identify those that are stable. To enhance adoption, the new sweetpotato genotypes should have farmer preferred traits thus the need for farmer involvement during selection. This study was conducted to: evaluate and select promising sweetpotato F_1 genotypes with wide and specific adaptation, in association with performance for farmer preferred traits. Twenty-one promising sweetpotato F_1 genotypes were evaluated at Namulonge, Serere and Kachwekano with Tanzania and NASPOT 1 as checks. The randomised complete block design with three replications was used. Scientists and farmers evaluated the agronomic performance and quality traits of the genotypes before and at harvest. Significantly ($P<0.05$) higher mean total storage root yield (TRY) of 25.5 t ha^{-1} was recorded at Namulonge than at Kachwekano and Serere. Genotypes G67, G13, G14, G24 and G29 were the most stable across the sites for TRY and therefore the most widely adapted for this trait, while G68, G60 and G58 were specifically adapted to Kachwekano and Serere. Very low severity levels of Sweetpotato virus disease (SPVD) were recorded with a mean score of 1.9 across sites with Namulonge having the highest mean score of 2.3. Genotypes G14, G16, G24, G29 and G49 were the most stable across the sites for low Alternaria blight severity and can therefore, be recommended for cultivation in both low and high disease pressure areas. In the participatory selection, before harvest and at harvest, Spearman's rank correlation ($r = 0.44$) of the scientists and farmers' mean ranking of the genotypes at each site was positive and significant. Thus scientists were capable of selecting for farmer preferred traits. In addition, the study identified and selected five superior genotypes including G13, G14, G24, G49 and G69 for further evaluation.*

Keywords*— *Promising F_1 genotypes, Alternaria blight, farmer preferred traits, agronomic performance, and selection.

I. INTRODUCTION

Plant breeders desire stable genotypes with good performance under all conditions within the target production regions. Stable genotypes with high yield potential can only be identified by testing them in a series of environments (Martin et al., 1988) and it is always important to test them in environments which reveal their maximum genetic potential in terms of the traits under consideration (Frey, 1964). The major objective of any crop improvement programme is the development of cultivars with high yield potential and other desirable traits, and the ability to withstand seasonal fluctuations over a wide range of environments (Kamalam et al., 1978; Lebot, 2009). Most of the important sweetpotato traits, including yield, are strongly affected by environmental conditions associated with sites and years (Ngeve, 1993; Niringiye et al., 2014). In most cases, high yielding

genotypes are not yield stable and those that are yield stable are low yielding (Ngeve, 1993; Manrique and Hermann, 2000; Mwanga et al., 2006). However, breeding sweetpotato for high yield and wide adaptation is possible (Grüneberg et al., 2005). In sweetpotato, attention needs to be paid to testing in low-yielding marginal environments if farmers working in such environments are the main beneficiaries of the new cultivars. Hence, yield testing in early stages of a sweetpotato breeding program should use at least one favourable environment and one less favourable environment (Grüneberg et al., 2005).

In Uganda, the National Sweetpotato Program released 22 sweetpotato cultivars between 1995 and 2013 and all these releases were made after conducting on-station, on-farm and standard multi-locational yield trials focusing mainly on high yield, high dry mass and resistance to pests and diseases (Mwanga et al., 2011; Ssemakula et al., 2013; Mwanga et al., 2016). In 2017, five new varieties namely NAROSPOT 1, NAROSPOT 2, NAROSPOT 3, NAROSPOT 4, NAROSPOT 5, were released (MAAIF, 2018) to bring the total of released varieties to 27. Of all these released cultivars, only one, NASPOT 11 had been bred through a participatory plant breeding process (Mwanga et al., 2011) but efforts were made to incorporate farmer preferred attributes in the other cultivars. Despite releasing all these cultivars, farmers still demand new ones to meet their ever changing preferences and some of the cultivars for example NASPOT 2, NASPOT 5 and Sowola 6 have not been well received (Abidin et al., 2002). For this reason, many farmers have continued to cultivate their landraces which underscores the need to involve them in participatory cultivar selection so that their preferences are considered. Participatory cultivar selection, and participatory plant breeding (PPB), are considered the most appropriate strategies to develop cultivars for marginal agricultural systems (Almekinders and Elings 2001; Ceccarelli and Grando, 2006; Dawson et al., 2007). This approach allows incorporation of farmers' knowledge, identification of farmers' selection criteria and priorities. Participation of farmers can allow for exploitation of specific adaptation effects within sites and facilitate seed supply to farmers (Ceccarelli et al., 2000).

Evaluation by farmers helps scientists to design, test and recommend new technologies in light of information about farmers' requirements and needs. It facilitates close interaction among farmers, researchers and other role players in crop genetic improvement, allowing researchers to respond more closely to the needs and preferences of resource-poor farmers and their market clients (Sperling et al., 2001). Farmers can be involved through introduction, evaluation and selection of materials grown on the research station and also collaborate by growing and selecting breeding materials in their own fields (Ceccarelli et al., 2000; Mcharo et al., 2001; Keith et al., 2004). The cultivars obtained from this process are developed more rapidly, are more diverse and have higher adoption rates (Witcombe et al., 2003). Consideration of farmers' concerns and conditions leads to varieties that become widely adapted and more productive hence leading to sustainable agricultural systems (Odendo et al., 2002). Among the preferred attributes that farmers select for during PPB for sweetpotato are good yield, sweet taste and dry texture (Laurie and Magoro, 2008; Marti, 2003; Kwach et al., 2010; Sseruwu et al., 2015).

Twenty one promising F_1 genotypes previously selected from early breeding trials were used in this study which was carried out to identify superior genotypes as possible candidates for advanced yield and on-farm trials. The main objective of this study was therefore to evaluate and identify genotypes with wide and specific stable performance over three sites for Alternaria leaf petiole and stem blight (commonly referred to as Alternaria blight) resistance, total storage root yield (TRY), Sweetpotato virus disease (SPVD) and other farmer preferred traits.

II. MATERIALS AND METHODS

Genotypes and sites

Twenty one F_1 genotypes and two checks Tanzania and NASPOT 1 were planted at three sites during the first rain season of 2015 (2015A). The first site was the National Crops Resources Research Institute (NaCRRI), at Namulonge (0°32' N, 32°35' E; 1150 metres above sea level (masl)). The second site was Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) (01°16'S, 29°57'E; 2200 masl) and the third site was at the National Semi-Arid Resources Research Institute at Serere (NaSARRI) (1°32'N, 33°27'E; 1140 masl). A randomized complete block design with three replications was used for the trial at the three sites with each plot measuring 5 m long with four ridges spaced 1 m apart. On each ridge, seventeen vine-tip cuttings were planted at a spacing of 0.3 m thus a total of 68 cuttings per plot. No artificial inoculation with

Alternaria pathogens or SPVD virus was done thus all disease infection was by natural spread.

Data Collection

Disease rating

Rating for Alternaria blight and SPVD was conducted at monthly intervals from one month after planting (MAP) until four data sets were obtained. Alternaria blight rating was done using a subjective visual scale of 0 to 5 modified after van Bruggen (1984), where: 0 = no disease; 1 = <1%; 2 = 1 to 10%; 3 = 11 to 25%; 4 = 26 to 50%; and 5 = > 50% foliar infection. The disease severity scores were expressed on a plot mean basis. Disease severity data was used to calculate the Area Under Disease Progress Curve (AUDPC) according to Shaner and Finney (1977).

Rating for SPVD was also done using the subjective 1 to 9 severity rating scale of Grüneberg et al. (2010), where: 1 indicated no virus symptoms; 2 = unclear virus symptoms; 3 = clear virus symptoms at < 5% of plants per plot; 4 = clear virus symptoms at 6 to 15% of plants per plot; 5 = clear virus symptoms at 16 to 33% of plants per plot; 6 = clear virus symptoms at 34 to 66% of plants per plot (more than 1/3, less than 2/3); 7 = clear virus symptoms at 67 to 99% of plants per plot (2/3 to almost all); 8 = clear virus symptoms at all plants per plot (not stunted); 9 = severe virus symptoms in all plants per plot (stunted).

Storage root yield

At harvest the total storage root yield (TRY) was recorded on a per plot basis then the mass per plot was converted to t ha^{-1} for analysis.

Participatory selection data collection

In addition to collecting disease and agronomic data, participatory selection of the F_1 genotypes was also performed at two of the three sites namely; Namulonge (NaCRRI) and Kachwekano (KAZARDI). The genotypes were separately evaluated before harvest and at harvest by a group of five scientists and a group of 10 farmers (five males and five females) at each site. The groups of scientists and farmers at both sites were different. The five scientists at NaCRRI, and five scientists at KAZARDI, had a minimum qualification of a Bachelor's Degree in Agricultural Sciences and were employed by the National Agricultural Research Organisation (NARO). The selected farmers were knowledgeable about sweetpotato production and consumer preferences. At each site, the evaluation before harvest was carried out two days before harvesting the trial and it was preceded by familiarising both groups at each site with the selection procedure and criteria. Both groups used the same evaluation criteria and the traits considered were: Alternaria blight and SPVD severity; growth habit (spreading, erect); leaf morphological traits (broad, small leaves, leaf colour); and general acceptability as a new cultivar (i.e. whether each participant considered the genotype suitable to become a cultivar). A rating scale of 1-5 was used for all the traits. For diseases, a severely infected genotype was scored 1 and a symptomless genotype, 5. For leaf morphology traits, leaf colour and size were used, and for growth habit, a genotype with poor growth habit was scored 1 and excellent growth habit was scored 5.

For selection at harvest, the two groups at each site separately listed the traits that they wanted to use in the evaluation process and ranked them in order of importance. On this basis, each group developed a list of top five traits for scoring the genotypes (Table 1).

Table 1 Attributes used by scientists and farmers at harvest for the participatory selection process at Namulonge and Kachwekano

Namulonge scientists		**Namulonge farmers**		**Kachwekano scientists**		**Kachwekano farmers**	
Attribute	**Rank**	**Attribute**	**Rank**	**Attribute**	**Rank**	**Attribute**	**Rank**
High root yield	1	High root yield	1	High root yield	1	High root yield	1
Root size (big roots)	2	No weevil damage	2	No weevil damage	2	Root size (big roots)	2
Root shape	3	Root size (big roots)	3	Root size (big roots)	3	Root shape	3

Root number	4	Skin colour (red/cream)	4	Shape of roots	4	Straight roots	4
Skin colour (red)	5	Long straight roots	5	Root skin colour	5	No cracking	5
No surface defects	6	Root flesh colour (white)	6	No cracking	6		
Root flesh colour	7	Sap content	7	Root flesh colour	7		
Sap content	8	No cracking	8				

For each trait, the participants individually scored each harvested plot in all three replications on a scale of 1-5 where 1= trait absent and 5 = the genotype expressed the trait at a satisfactory level. Then the mean score for each trait was separately determined for each of the two groups per site. Roots were sampled from each plot of each genotype, boiled, taste tested and then scored for the following attributes: appearance of the flesh after cooking, sweetness, dry mass (hardness), fibre content and acceptability as a new cultivar. The same rating scale of 1-5 was used as mentioned above.

Data analysis

AMMI analysis of the data for the three sites

The genotype x environment interaction (GEI) and associated stability of the genotypes across three sites for area under the disease progress curve (AUDPC) for Alternaria blight severity scores, SPVD severity scores and TRY were analysed using the additive main effects and multiplicative interaction (AMMI) procedure in GENSTAT version 14 (Payne et al., 2011) based on the standard AMMI model (Gauch and Zobel, 1996).

The AMMI analysis partitions the GEI sum of squares (SS) into IPCA axes. Only IPCA1 and IPCA2 were significant and the non-significant IPCA3 was considered as "statistical noise" and accounted for by the residual term. The interaction patterns of the genotypes and the environments were graphically represented in a biplot of the respective IPCA1 scores (y-axis) versus the genotype and environmental means or IPCA2 (x-axis). In the biplot, displacement in the horizontal plane reflects differences in the mean performance, while displacement in the vertical plane reflects differences in interaction effects (Zobel et al., 1988).

Analysis of participatory selection data

The scores for all traits for each genotype at each of the two sites for each group were analysed by ANOVA in GENSTAT version 14 to obtain the mean scores for each trait per genotype, evaluation group and site. Weights were assigned to each scored trait such that the trait ranked first by a group was assigned a weight of 5 and the one ranked fifth was assigned a weight of 1. For each genotype, the mean score for each trait was multiplied by the assigned weight then all five weighted scores were summed up to obtain an aggregate score for each genotype.

Aggregate weighting index used for the both the scientist and farmer groups:

$\sum ATW = (AT_1*W_5) + (AT_2*W_4) + (AT_3*W_3) + (AT_4*W_2) + (AT_5*W_1)$

Where: $AT_{1...5}$ = Attributes ranked 1…5; and $W_5 \ldots W_1$= assigned weight ranging from 5 to 1.

The aggregate scores of the genotypes at each site for each group were ranked to determine two separate rank orders (one per group) of the genotypes at each site. The ranks for each genotype per group were summed across the two sites (Kang, 1993) and the genotype with the lowest rank sum was the best over the two sites.

III. RESULTS

Genotype x environment interaction and stability of the genotypes

Alternaria blight

The genotypes, environments and genotype x environment interaction (GEI) mean squares (MS) were highly significant ($P<0.001$) for Alternaria blight AUDPC (Table 2). The genotypes, environments and GEI accounted for 16.4, 24.5

and 21.8% of the total SS for AUDPC. Only IPCA1 was significant and accounted for 72.0% of the GEI SS. The genotype G14 had the smallest IPCA1 score of 0.00525 and was therefore the most stable (in terms of the interaction pattern captured by IPCA1) for Alternaria blight (Table 3). Genotype G28 with an IPCA1 value of -3.41636 was the least stable. NASPOT 1 (susceptible check) with the highest mean Alternaria blight AUDPC value of 86.7 across the three sites was more susceptible than all the F_1 genotypes evaluated. Tanzania (resistant check) was more resistant than any of the F_1 genotypes with the lowest mean Alternaria blight AUDPC value of 46.1 across the three sites. Across the sites, G49, G13, G67, G14 and G65 had the lowest Alternaria blight AUDPC values of 46.6, 48.7, 48.7, 49.1 and 51.1, respectively. Genotype G58 had the highest mean Alternaria blight AUDPC value of 79.8 among the genotypes. Of the three sites, genotypes at Kachwekano recorded the highest Alternaria blight severity with an average AUDPC value of 76.6 (Table 3).

Table 2 AMMI analysis for Alternaria blight severity, sweetpotato virus disease severity score and total storage root yield for 23 sweetpotato genotypes evaluated at Namulonge, Kachwekano and Serere

	Alternaria AUDPC					SPVD				Total storage root yield (t ha^{-1})			
Source of variation	**df**	**SS**	**MS**	**% Total SS**	**% G x E SS**	**SS**	**MS**	**% Total SS**	**% G x E SS**	**SS**	**MS**	**% Total SS**	**% G x E SS**
Total	206	126650	615			262.1	1.27			13574	65.9		
Treatments	68	79424	1168***	62.7		107.4	1.58*	41.0		10535	154.9***	77.6	
Genotypes	22	20809	946***	16.4		27.6	1.26	10.5		1312	59.7***	9.7	
Environments	2	31049	15525***	24.5		20.9	10.45***	8.0		6489	3244.7***	47.8	
Interaction	44	27566	626**	21.8		58.9	1.34	22.5		2734	62.1***	20.1	
IPCA1	23	19857	863***		72.0	39.9	1.73		67.8	1716	74.6***		62.8
IPCA2	21	7709	367		28.0	19.0	0.90		32.2	1018	48.5***		37.2
Error	132	46789	354			148.2	1.12			2701	20.5		

* = significant at 0.05; ** = significant at P<0.01; *** = significant at P<0.001; AUDPC = area under disease progress curve for Alternaria blight severity; SPVD = sweetpotato virus disease severity scores (scores 1-9 used; 1 = no SPVD and 9 = SPVD causing stunted growth); df = degrees of freedom; SS = sum of squares; MS = mean square; % Total SS = percentage of total sum of squares; % G x E SS = percentage of genotype x site sum of squares

Table 3 Mean AMMI performance estimates and ranking of the genotypes for Alternaria blight severity at Namulonge, Kachwekano and Serere

Genotype	Overall mean AUDPC	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	67.1	-0.39336	1.83402	48.3	8	90.1	18	63.0	20
G13	48.7	2.46564	-1.92151	56.3	18	45.5	1	44.3	9
G14	49.1	0.00525	-1.71079	51.0	10	63.7	7	32.7	1
G16	58.7	-0.18533	-1.51633	59.1	20	74.9	13	42.0	8
G21	67.8	-2.50861	-0.17353	56.4	19	102.6	19	44.3	10
G24	58.8	0.77041	1.21857	45.6	5	72.6	10	58.3	18
G28	63.3	-3.41636	-0.77916	53.7	16	103.6	20	32.7	1
G29	51.8	0.50558	-1.29120	52.2	13	63.5	6	39.7	5
G30	56.4	-1.43335	0.07224	45.6	6	84.0	16	39.7	5
G38	60.1	2.02679	0.42608	53.7	17	63.7	8	63.0	20
G49	46.6	-0.92678	1.82993	26.8	1	73.3	12	39.7	5
G53	57.7	-1.88434	-0.80294	51.0	11	87.1	17	35.0	3
G58	79.8	-2.32293	-2.78913	83.4	23	109.2	22	46.7	12
G59	57.7	-0.94515	1.41543	40.3	4	83.9	15	49.0	13
G60	63.6	1.79363	-1.85431	69.6	22	65.3	9	56.0	16
G61	54.4	2.31667	-0.01823	51.0	12	55.2	4	57.0	17
G65	51.1	3.15645	0.61656	45.6	7	46.9	2	60.7	19
G67	48.7	1.31573	1.03116	37.6	2	58.3	5	50.3	14
G68	68.8	2.33462	2.15257	53.2	14	72.9	11	80.3	23
G69	55.6	-0.32871	1.71497	37.6	3	77.9	14	51.3	15
G79	66.2	-2.99241	0.82728	48.3	9	106.0	21	44.3	11
NASPOT 1	86.7	-1.16207	1.79274	66.7	21	115.0	23	78.3	22
Tanzania	46.1	1.80864	-2.07441	53.3	15	47.3	3	37.7	4
Mean	**59.3**			**51.6**		**76.6**		**49.8**	

AUDPC = area under disease progress curve for Alternaria blight severity; IPCA = Interaction principal component axes

In the AMMI biplot of IPCA1 versus AUDPC mean values for genotypes and environments (Figure 1), genotypes on the right hand side of the vertical line were the most susceptible to Alternaria blight and those on the left were the most resistant. Genotypes closest to the horizontal line were more stable for the expression of Alternaria blight across the three sites. Genotypes G8 and NASPOT 1 were stable for the disease but they had above average AUDPC values. Genotypes G14, G16, G24, G29, G49, G59 and G69 were stable for the disease with below average AUDPC values. None of the sites was very stable for

Alternaria blight severity but Namulonge was more stable than Serere and had several genotypes specifically adapted to it (Figure1). Kachwekano was a high disease pressure site and the least stable with high interaction with the genotypes.

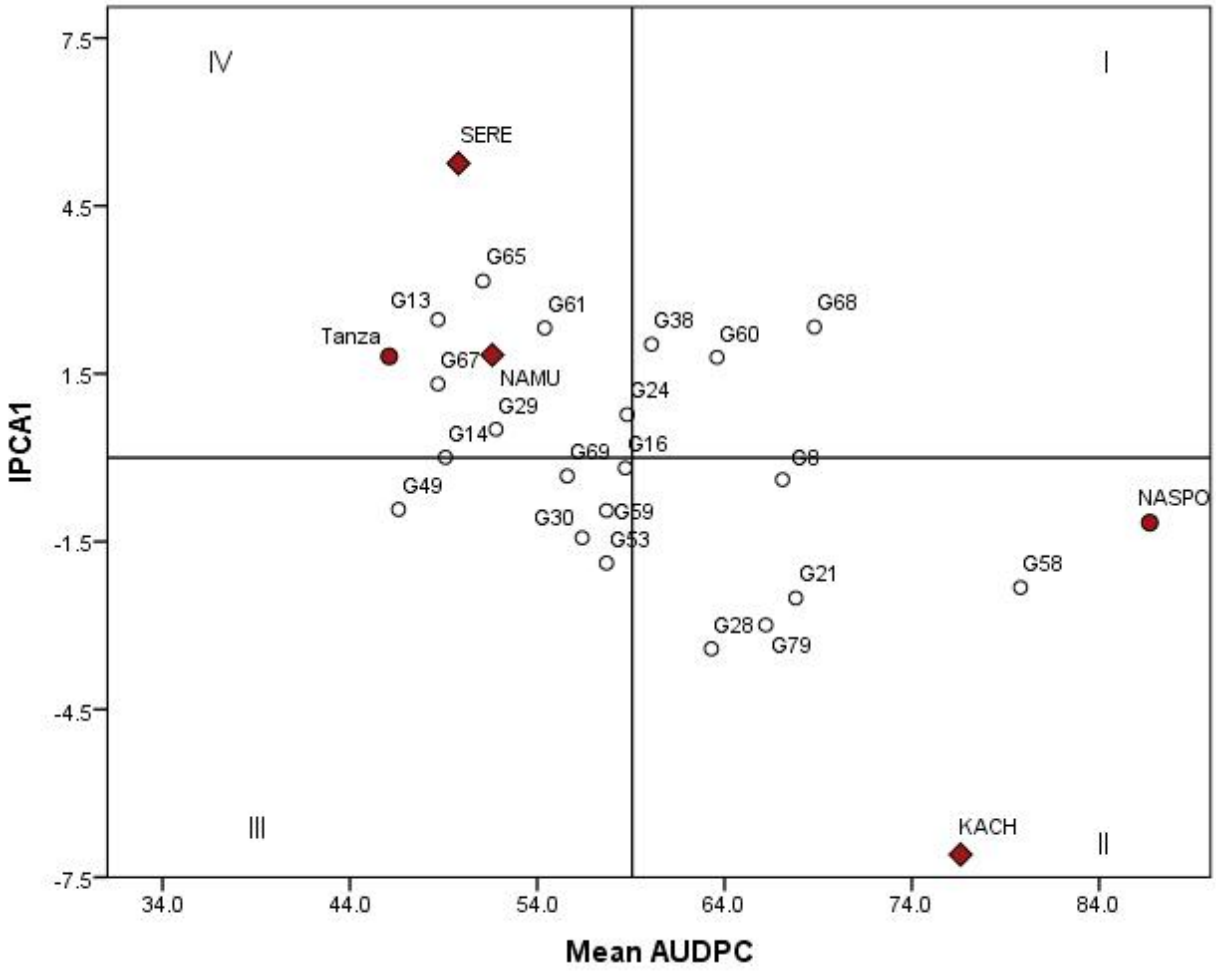

Fig.1: Biplot of IPCA1 scores versus genotype and environment Alternaria blight AUDPC means

Key

- ● Check genotypes: NASPO = NASPOT 1; Tanza = Tanzania
- O F_1 test genotypes: G8, G13, G14, G16, G21, G24, G28, G29, G30, G38, G49,G53, G58, G59, G60, G61, G65, G67, G68, G69 and G79
- ◆ Sites: NAMU = Namulonge; KACH = Kachwekano; SERE = Serere

Sweetpotato virus disease

The MS for the environments were highly significant (P<0.001) for SPVD and not significant (P>0.05) for the genotypes and GEI (Table 2). Very low severity levels of SPVD were recorded for these genotypes with a mean score of 1.9 across sites (Table 4). Serere recorded the highest SPVD severity with a mean score of 2.3 while Namulonge had the lowest mean severity score of 1.6.

Table 4 Mean AMMI performance estimates and ranking of the genotypes for sweetpotato virus disease score at Namulonge, Kachwekano and Serere

Genotype	Mean SPVD	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	1.3	-0.01957	-0.12729	1.3	4	1.3	2	1.7	6
G13	2.0	-0.63277	-0.39805	2.3	20	2.3	20	1.3	1
G14	1.9	-0.14939	0.29899	2.0	18	1.3	2	2.3	10
G16	2.2	0.47151	0.05500	1.3	4	2.0	15	3.3	20
G21	1.7	-0.38595	-0.39269	1.7	11	2.0	15	1.3	1
G24	1.7	0.35452	-0.37663	0.7	1	2.0	15	2.3	10
G28	2.1	0.10256	-0.03882	1.7	11	2.0	15	2.7	17
G29	1.7	-0.13913	-0.38734	1.3	4	2.0	15	1.7	6
G30	2.4	0.58851	0.48664	1.7	11	1.7	11	4.0	21
G38	2.0	0.35452	-0.37663	1.0	2	2.3	20	2.7	17
G49	1.7	0.22726	-0.12194	1.0	2	1.7	11	2.3	10
G53	1.6	-0.64304	0.28829	2.3	20	1.0	1	1.3	1
G58	1.8	-0.02470	0.21588	1.7	11	1.3	2	2.3	10
G59	2.1	0.11026	-0.55357	1.3	4	2.7	22	2.3	10
G60	2.9	0.84560	-0.19435	1.3	4	3.0	23	4.3	23
G61	2.1	-0.64561	0.45987	3.0	23	1.3	2	2.0	8
G65	1.7	-0.14683	0.12741	1.7	11	1.3	2	2.0	8
G67	1.9	0.22469	0.04965	1.3	4	1.7	11	2.7	17
G68	1.4	-0.39108	-0.04953	1.7	11	1.3	2	1.3	1
G69	1.6	-0.51578	0.03359	2.0	18	1.3	2	1.3	1
G79	1.9	-0.02213	0.04430	1.7	11	1.7	11	2.3	10
NASPOT 1	1.7	0.10000	0.13276	1.3	4	1.3	2	2.3	10
Tanzania	2.6	0.33655	0.82445	2.3	20	1.3	2	4.0	21
Mean	**1.9**			**1.6**		**1.7**		**2.3**	

SPVD = sweetpotato virus disease; IPCA = interaction principal component axes

Total storage root yield

The genotypes, environments and GEI MS were highly significant (P<0.001) for TRY (Table 2). The genotypes, environments and GEI SS accounted for 9.7, 47.8 and 20.1% of the total SS for TRY, respectively. Both IPCA1 and IPCA2 were significant and accounted for 62.8 and 37.2% of the GEI SS. Genotypes G14 and G13 were the most stable for TRY across the sites with IPCA1 scores of 0.08633 and 0.18901, respectively (Table 5). Genotypes G58 and G60 were the least stable with IPCA1 values of 2.2542 and -1.74938, respectively. Across sites, G67, G24, G13, G53 and G65 had the highest TRY of 21.6, 21.4, 20.8, 19.9 and 19.4 t ha^{-1}, respectively while genotypes G68, G60, G58, G29 and G21 had the lowest TRY of 12.9, 13.5, 14.0, 14.0 and

15.3 t ha^{-1}, respectively across sites. The mean TRY across genotypes of 25.5 t ha^{-1} recorded at Namulonge was the highest of the three sites while the 12.3 t ha^{-1} recorded at Serere was the lowest. The most outstanding genotypes at Namulonge were G30, G69 and G16 with yields of 34.0, 31.3 and 30.6 t ha^{-1}, respectively. There was no consistency in the ranking of the genotypes in that highly ranked genotypes at one site ranked poorly at the other sites.

Table 5 Mean AMMI performance estimates and ranking of the genotypes for total storage root yield (t ha^{-1}) at Namulonge, Kachwekano and Serere

Genotype	Overall Mean TRY t ha^{-1}	IPCA1	IPCA2	Namulonge		Kachwekano		Serere	
				Mean	Rank	Mean	Rank	Mean	Rank
G8	20.5	0.49816	0.02743	30.2	4	17.2	8	14.1	7
G13	20.8	0.18901	-0.29646	29.1	7	17.4	7	16.0	4
G14	18.9	0.08633	1.44211	27.7	11	20.5	3	8.6	20
G16	19.0	0.92707	0.52908	30.6	3	16.0	13	10.4	15
G21	15.3	1.03024	-1.23778	26.4	14	7.2	23	12.3	11
G24	21.4	0.13619	-0.90956	29.2	6	16.4	11	18.7	2
G28	17.1	1.05036	-1.81533	28.0	10	7.4	22	15.9	5
G29	14.0	-0.26961	0.32112	20.8	19	13.4	18	7.9	22
G30	19.4	1.69363	0.54536	34.0	1	14.5	14	9.6	18
G38	17.8	-0.65650	0.38515	23.1	18	18.4	5	12.0	12
G49	17.7	0.49669	-0.40570	27.1	13	13.2	19	12.7	10
G53	20.0	-0.13348	-1.50316	26.3	15	14.0	17	19.5	1
G58	14.0	-2.25420	-1.11901	12.2	23	14.4	15	15.5	6
G59	17.7	0.88763	-0.14469	28.8	9	13.0	20	11.3	13
G60	13.5	-1.74938	0.12783	14.4	22	16.1	12	10.2	16
G61	18.6	-0.95907	1.59782	23.3	16	23.3	1	9.3	19
G65	19.4	0.64465	0.87561	30.1	5	18.1	6	10.1	17
G67	21.6	-0.22108	1.00442	28.9	8	22.7	2	13.1	9
G68	12.9	-1.08135	0.27452	16.4	21	14.2	16	8.0	21
G69	18.4	1.17342	1.16814	31.3	2	16.5	10	7.3	23
G79	16.0	0.99172	-0.44067	27.3	12	10.2	21	10.4	14
NASPOT 1	20.2	-1.13006	-0.19483	23.3	17	20.3	4	17.0	3
Tanzania	16.4	-1.35035	-0.23140	18.7	20	17.0	9	13.7	8
Mean	**17.9**			**25.5**		**15.7**		**12.3**	

IPCA = Interaction principal component axes

In the AMMI biplot of the two significant axes IPCA1 vs IPCA2 for TRY (Figure 2), the genotypes and the three environments generally dispersed around the origin (centre) of the biplot (the sites more so than the genotypes) indicating strong interactions between the genotypes and environments in response to the abiotic or biotic factors underlying or driving the IPCA1 & 2 scores. Genotypes G13, G8, G49 and G29 were positioned close to the origin indicating minimal interaction of these genotypes with the

environments. The remaining 17 genotypes and checks (Tanzania and NASPOT 1) were positioned further away from the origin and therefore had strong interactions with some of the environments.

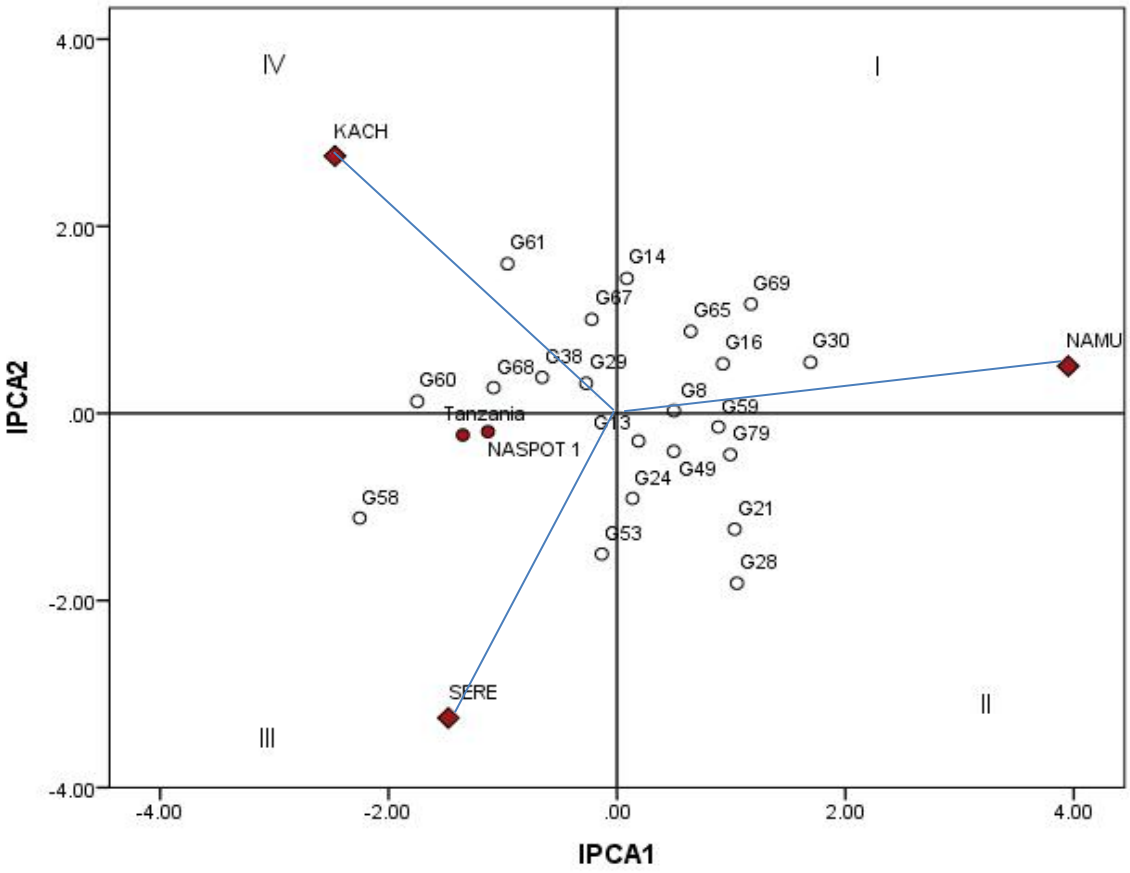

Fig. 2: Biplot of IPCA1 scores versus IPCA2 scores for genotype and environment mean total storage root yield (t ha^{-1})

Key

- Check genotypes: NASPOT 1; Tanzania
- O F_1 test genotypes: G8, G13, G14, G16, G21, G24, G28, G29, G30, G38, G49,G53, G58, G59, G60, G61, G65, G67, G68, G69 and G79
- Site: NAMU = Namulonge; KACH = Kachwekano; SERE = Serere

Participatory genotype selection

Genotype evaluation before harvest

For the evaluation done before harvest, the scientists and farmers at both sites selected different genotypes (Table 6). Based on the selection index, the scientists at Namulonge ranked NASPOT 1, G58, G79, G69 and G2 and those at Kachwekano ranked G60, G67, NASPOT 1, G49 and G16 as their most preferred genotypes. Similarly, the farmers at Namulonge ranked G58, G59, NASPOT 1, G21 and G29 and at Kachwekano G14, G29, NASPOT 1, G60 and G16 as their most preferred genotypes. NASPOT 1, G21, G53, G58 and 65 were ranked as the best across the groups and sites. The Spearman's correlation between scientists and farmers' rankings before harvest at Namulonge was significant ($P<0.05$) and positive ($r = 0.324$). Similarly, the Spearman's correlation between scientists and farmers' rankings at Kachwekano was also significant ($P<0.05$) and positive ($r = 0.282$) (Table 7).

Table 6 Scientists and farmers' selection and ranking of genotypes before harvest at Namulonge and Kachwekano

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers			
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Rank sum	Overall rank
G8	36	10	27	8	23	22	16	9	49	14
G13	37	5	28	4	23	22	15	11	42	9
G14	20	23	24	12	29	10	30	1	46	11
G16	24	21	20	18	34	5	21	5	49	15
G21	38	5	28	4	29	10	21	5	24	2
G24	32	13	17	21	29	10	13	17	61	20
G28	23	22	25	11	30	9	12	21	63	21
G29	27	19	28	4	29	10	29	2	35	6
G30	37	5	21	17	29	10	13	17	49	16
G38	32	13	27	8	25	20	14	13	54	18
G49	31	16	22	15	35	4	18	8	43	10
G53	37	5	28	4	29	10	16	9	28	3
G58	47	2	32	1	28	17	14	13	33	4
G59	31	16	32	1	26	18	12	21	56	19
G60	33	12	16	22	42	1	24	3	38	8
G61	34	11	18	19	24	21	13	17	68	22
G65	38	4	27	8	34	5	13	17	34	5
G67	27	19	22	15	39	2	14	13	49	17
G68	31	16	16	22	29	10	12	21	69	23
G69	45	3	24	12	31	7	14	13	35	7
G79	45	3	23	14	26	18	15	11	46	12
NASPOT 1	50	1	30	3	39	2	24	3	9	1
Tanzania	32	15	18	19	31	7	21	5	46	13

Aggregate = sum of the weighted attributes for each genotype per group; Rank sum = sum of the genotype rank across the four groups

Table 7 Spearman's rank correlations between the scientists and farmers' genotype rankings before harvest at Namulonge and Kachwekano

NS	-			
NF	**0.342***	-		
KS	-0.153	**-0.305***	-	
KF	-0.04	0.103	**0.283***	-
	NS	NF	KS	KF

NS = Namulonge scientists; NF = Namulonge farmers; KS = Kachwekano scientists; KF = Kachwekano farmers;
* = Significant at P<0.05

Genotype evaluation at harvest

For the evaluation at harvest, each group listed their own set of traits that they considered important for desirable sweetpotato genotypes and they ranked these attributes (7). Storage root yield was the most important trait ranked first by all four groups followed by root size, weevil resistance, root shape and skin colour.

At harvest, on the basis of the selection index, the ranked order of the scientists' selected genotypes at Namulonge was: G30, G28, G49, G67 and G24; and at Kachwekano was: G29, G49, G30, NASPOT 1 and G14 (Table 8). The ranked order of the farmers' selections at Namulonge was: G8, G30, G53, G29 and G49; and at Kachwekano was: G21, G24, G30, G29 and G14.

At harvest, the Spearman's correlation between scientists and farmers' rankings at Namulonge was highly significant (P<0.01) and positive (r = 0.412) and that between scientists and farmers at Kachwekano was also highly significant (P<0.01) and positive (r = 0.440) (Table 9). The other rank correlations were non-significant.

Table 8 Scientists and farmers' selection and ranking of genotypes at harvest at Namulonge and Kachwekano

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers		Across four groups	
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Rank Sum	Final rank
G8	52.0	16	71.3	1	36.7	18	23.6	22	57	16
G13	41.6	23	60.3	22	38.3	14	34.0	13	72	23
G14	52.7	14	64.7	16	49.6	5	42.7	5	40	7
G16	47.0	22	64.3	18	44.3	9	37.7	10	59	18
G21	48.7	19	64.7	15	34.3	23	50.0	1	58	17
G24	61.3	5	65.3	12	47.7	6	49.0	2	25	4
G28	67.4	2	66.3	8	40.3	11	40.0	7	28	5
G29	56.4	12	67.7	4	56.0	1	44.7	4	21	2
G30	70.0	1	68.7	2	52.7	3	47.0	3	9	1
G38	47.7	20	64.3	19	39.0	12	30.0	19	70	22
G49	66.7	3	67.3	5	55.4	2	36.7	11	21	3
G53	57.4	10	67.7	3	35.0	20	21.0	23	56	13
G58	58.6	6	56.3	23	35.0	20	31.0	16	65	20
G59	57.7	8	65.3	10	35.7	19	40.6	6	43	8
G60	47.3	21	65.3	11	45.4	7	40.0	7	46	9
G61	57.0	11	67.0	6	34.6	22	32.3	15	54	11
G65	52.3	15	62.6	20	37.3	15	35.0	12	62	19
G67	62.7	4	67.0	7	37.0	16	30.0	19	46	10
G68	50.0	18	65.7	9	38.7	13	31.0	16	56	14
G69	58.6	7	64.7	17	41.7	10	27.0	21	55	12
G79	51.0	17	65.0	14	37.0	16	30.7	18	65	21
NASPOT1	57.7	8	65.2	13	52.1	4	39.6	9	34	6
Tanzania	53.4	13	60.4	21	44.5	8	32.9	14	56	15

Aggregate score based on weighted selection index

Table 9 Spearman's rank correlation between the scientists and farmers' genotype rankings at Namulonge and Kachwekano at harvest

NS	-			
NF	**0.412****	-		
KS	0.206	0.093	-	
KF	0.115	0.028	**0.440****	-
	NS	NF	KS	KF

NS = Namulonge scientists; NF = Namulonge farmers; KS = Kachwekano scientists; KF = Kachwekano farmers;

** = significant at P<0.01

The quality traits (mostly organoleptic) of the genotypes that were evaluated at harvest included sweetness (taste), root firmness (hardness), root fibre content, appearance and general acceptability based on taste and appearance. At Namulonge, scientists ranked G24, NASPOT 1, Tanzania, G38 and G28 as the best and at Kachwekano G68, NASPOT1, G14, G60 and G29 were ranked as the best genotypes. Farmers at Namulonge ranked NASPOT 1, G28, G38, G68 and Tanzania as the best genotypes, and at Kachwekano G14, G29, G68, G60 and NASPOT 1 were ranked as the best. Genotypes NASPOT 1, G68, G24, G60 and G53 were the best ranked across the groups (Table 10). The positive Spearman's correlation (r = 0.605) between scientists and farmers' rankings at Namulonge and rank correlation (r = 0.552) between scientists and farmers' ranking at Kachwekano were highly significant (P<0.01) (Table 11).

Table 10 Scientists and farmers' selection and ranking of quality traits of genotypes at harvest at Namulonge and Kachwekano

Genotype	Namulonge scientists		Namulonge farmers		Kachwekano scientists		Kachwekano farmers		Rank sum	Overall rank
	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank	Aggregate	Rank		
G8	47.0	13	39.5	18	41.0	18	39.5	18	67	19
G13	42.0	20	35.0	21	40.5	19	45.5	11	71	21
G14	39.5	21	43.0	12	55.5	3	56.5	1	37	6
G16	37.5	23	42.5	13	45.0	16	43.0	15	67	20
G21	45.0	16	32.0	23	35.5	23	33.0	21	83	23
G24	61.5	1	50.0	6	48.5	10	44.5	12	29	3
G28	54.5	5	55.5	2	38.0	21	42.0	16	44	9
G29	43.5	17	42.5	14	55.0	5	55.0	2	38	7
G30	51.0	7	48.5	8	50.5	8	31.5	22	45	12
G38	55.0	4	53.5	3	46.0	14	30.5	23	44	10
G49	43.5	18	39.0	19	47.0	12	41.5	17	66	18
G53	47.5	11	49.5	7	50.5	9	49.5	7	34	5
G58	46.5	15	47.5	10	38.5	20	51.5	6	51	14
G59	43.5	19	48.5	9	45.5	15	47.5	9	52	15
G60	48.5	9	40.0	16	55.5	4	53.5	4	33	4
G61	48.5	10	46.0	11	51.0	7	44.0	14	42	8
G65	49.0	8	41.5	15	48.5	11	37.0	19	53	17
G67	53.5	6	40.0	17	46.5	13	48.5	8	44	11
G68	47.5	12	52.5	4	62.0	1	54.0	3	20	2
G69	38.0	22	36.5	20	36.0	22	44.0	13	77	22

G79	47.0	14	34.0	22	51.5	6	46.0	10	52	16
NASPOT 1	58.5	2	57.0	1	56.0	2	53.0	5	10	1
Tanzania	58.0	3	51.0	5	43.5	17	36.5	20	45	13

Aggregate score based on weighted selection index (sweetness (taste), root firmness (hardness), root fibre content, appearance and general acceptability).

Table 11 Spearman's rank correlation between scientist and farmers' genotype rankings for quality traits at harvest at Namulonge and Kachwekano

NS	-			
NF	0.605**	-		
KS	0.217	0.275*	-	
KF	-0.229	0.058	0.552**	-
	NS	NF	KS	KF

KF = Kachwekano farmers; KS = Kachwekano scientists; NF = Namulonge farmers; NS = Namulonge scientists;

** = significant at P<0.01; * = significant at P <0.05

Discussion

The objectives of this study were to evaluate and identify F_1genotypes with wide and specific stable performance over three sites for Alternaria blight resistance, SPVD, TRY and other farmer preferred traits. Additionally, the ranking of the genotypes by two different groups of scientists and farmers at two of the sites for selected traits were compared using Spearman's rank correlations.

Performance and stability of the genotypes

The severity of Alternaria blight was higher at Kachwekano than at the other two sites (Table 3). The AMMI analysis revealed that the Alternaria blight was influenced more by environmental effects, than by the GEI effects and least by genotypes effects. During the season, Kachwekano did not receive as much rainfall as Namulonge but the disease was more severe at this site. This is consistent with what was reported by Sseruwu et al. (2015) where some farmers in Luwero district reported the disease to be more severe during the dry season than during the wet season. It is possible that the disease infected the crop during the first month after planting when there was sufficient moisture and the symptoms became visible later on when the crop was stressed due to insufficient moisture. Mwanga et al. (2007b) described Serere as a low pressure area for Alternaria blight. However, this study has provided an indication that the effect of Alternaria blight under natural infestation in Serere is increasing since the severity was not significantly less than that of Namulonge. However, this can only be confirmed after obtaining data for several seasons. Should the trend be confirmed, farmers at Serere will require Alternaria blight resistant genotypes and this would necessitate evaluation of all the popular sweetpotato genotypes in the area for resistance to the disease in order to identify those with good levels of resistance.

Resistance of the genotypes across sites to Alternaria blight was not consistent, with some genotypes having lower Alternaria blight AUDPC values at one site and higher values at another site. However, some genotypes maintained lower Alternaria blight AUDPC values across sites and if these genotypes can maintain this consistency in subsequent evaluations (particularly over more seasons) and also meet the required performance levels for other important traits then they will be recommended to the farmers for cultivation in all the tested and similar sites/environments. Those that have consistent, good performance at particular sites will be recommended for those sites. Genotypes G49, G67, G69, 59 and G24 were the best genotypes at Namulonge. Genotypes G13 and G65 performed better than the check, Tanzania at Kachwekano. Similarly, G14, G28 and G53 were also better than the Tanzania at Serere. Thus these genotypes are well adapted to those sites. Genotypes G49, G13, G67 and G14 recorded lower mean AUDPC values across sites and should be further evaluated for even wider adaptation.

The AMMI biplot provided an indication of the stability of the different genotypes for Alternaria blight. In this context, stability means a genotype that maintains the same level of disease severity, either high or low across sites. Genotypes that are stable for low Alternaria blight severity and good yields are desired for this programme. Stability of genotypes G14, G16, G24, G29, G49, G59 and G69 for low Alternaria blight severity implies that these genotypes can be grown in all of the test sites and maintain low disease severities. They can also be used as sources of resistance in breeding for Alternaria blight resistance. Genotypes NASPOT 1 and G8 expressed stable but above average AUDPC values. This implies that these genotypes can only be grown in areas of low Alternaria blight pressure or may need fungicide protection when grown in high disease pressure areas. Kachwekano is a high Alternaria blight pressure site; therefore, it is ideal for evaluating the resistance of germplasm to the disease while Namulonge and Serere are ideal for germplasm multiplication.

The high significance (P<0.001) of the effects of genotypes, environments and GEI for TRY implied that all these factors are important in determining the expression of this trait. However, environmental effects were more important

than genotypes and GEI effects. Namulonge was the highest yielding site with a mean TRY of 25.5 t ha^{-1} and Serere was the lowest yielding site with a mean of 12.3 t ha^{-1}. The cause of such high variation in yield was in all likelihood the amount of rainfall received during the season. At Kachwekano and Serere, the crops received reasonable amounts of rainfall only during the first month after planting but very little in the subsequent months unlike Namulonge which had good rainfall for the first three months after planting (Appendix 1).The yield recorded at Namulonge which ranged between 12.2 (G58) and 34.0 t ha^{-1} (G30) is an indication of the high yield potential of this set of genotypes. However, the full genotype yield potential was not realised at the other two sites possibly due to moisture stress. However, the best genotypes for TRY across the three sites were G67 (21.6 t ha^{-1}) and G24 (21.4 t ha^{-1}).

The AMMI biplot provided an indication of the stability of the genotypes for TRY. Genotypes G53, G67, G14, G13, G29 and G24 were very close to the horizontal line and therefore the most stable. These genotypes are widely adapted and can be grown at any of the three test sites and should give good yields. Provided the necessary agronomic requirements are available, they can be recommended to farmers at all three sites. Genotypes G68, G60 and G58 were low yielding and specifically adapted to the low yield potential sites of Kachwekano and Serere hence may not perform well outside these sites.

Participatory Clonal selection

At the two selection stages, before harvest and at harvest, the scientists and farmers at the two sites ranked some of the genotypes similarly and in other instances differently. The significant ($P<0.05$), positive Spearman's rank correlation between scientists and farmers at each site ($r = 0.342$ for Namulonge, $r = 0.283$ for Kachwekano) before harvest indicated that the two groups ranked many genotypes in the same way before harvest. Therefore, at each site the scientists in this study were capable of selecting genotypes that had farmer preferred traits. The groups of scientists at the two sites selected different genotypes and so did the farmers. Since they based their selection on crop vigour, the cause of the difference in genotype selection was likely to be the differences in the performances of the genotypes across the sites due to the poor weather conditions at Kachwekano, which did not receive enough rainfall during the trial (Appendix 1). Ranking of genotypes before harvest may be influenced by the amount of aboveground foliage produced particularly the leaves which at that stage are the economic yield component of the crop. On the other hand, farmers may prefer genotypes with more upright growth habit than prostrate growth habit with spreading vines. However, the aboveground characteristics of any genotype may not always be a good indicator of belowground performance.

At harvest, most of the attributes identified by the scientists and farmers were similar but the ranking of the genotypes differed. Just as in any formal selection system where yield is considered as a major criterion (Joshi et al., 1997), yield was ranked the number one trait by the groups. Scientists and farmers at both sites preferred high-yielding genotypes with big storage roots which implied the converse that high yielding genotypes that produce small storage roots are not preferred. This is certainly the case where the farmers are market oriented. The buyers select and pay only for the large storage roots and leave the small ones or take them at no cost. Abidin et al. (2002) in north-eastern Uganda, also reported that farmers prefer genotypes that produce numerous, large storage roots, which tend to also have large overall yields. Similarly, Ndirigwe et al. (2005) in Rwanda reported that farmers rejected one cultivar which was high yielding because it had small size storage roots. In addition to storage root size, shape of the storage root was identified as an important trait by all groups except farmers at Namulonge. Grooved roots are not preferred because they are difficult to peel and will not be bought in the market unless they are the only ones available. Skin colour was important to all groups except the Kachwekano farmers. Red skin colour was mostly preferred by the groups and this is also the market preference. That skin colour was not identified as an important trait by the Kachwekano farmers, probably because most of them produce for home consumption. In previous studies by Abidin et al. (2002) in north-eastern Uganda, the preferred skin colour was white/tan and flesh colour was yellow. Therefore, the importance of skin colour depends on the region where the evaluation is carried out. According to Ndirigwe et al. (2005), in Rwanda the reddish skin was also preferred by both the farm household and the market.

At harvest, the significant ($P<0.01$), positive Spearman's rank correlation coefficient between scientists and farmers at Namulonge ($r = 0.412$) and between scientists and farmers at Kachwekano ($r = 0.440$), indicated that it is

possible for the evaluation to be carried out by scientists only and successfully identify farmer preferred traits. This would obviously enable considerable savings for research budgets and will facilitate quicker selection processes.

For the cooking qualities of the genotypes, the farmers also represented the consumer since they also consume sweetpotato and they interact frequently with other consumers. The highly significant ($P<0.01$), positive Spearman's rank correlations between the rankings of scientists and farmers at Namulonge ($r = 0.605$) and scientists and farmers at Kachwekano ($r = 0.552$) for cooking quality traits indicates that the scientists at each site are capable of selecting for the same cooking qualities preferred by farmers. Therefore, it is not necessary to use site specific groups in the selection process. NASPOT 1, which is a popular cultivar, emerged as the best genotype across the groups for cooking quality traits with G68 and G24 ranking second and third respectively. Since NASPOT 1, which is already a very popular cultivar in Uganda, was ranked as the best by the groups this provides some validation of the outcome of the current study.

IV. CONCLUSION

Some of the F_1 genotypes selected from the crosses conducted in this breeding programme are highly adaptable and have farmer preferred attributes. Genotypes that exhibited stability for resistance to Alternaria blight as well as stability for high storage root yield were G14, G16, G24, G49 and G59. These genotypes can be recommended to farmers on a trial basis at the three test sites and other associated sites. However, a full investigation of the stability of these genotypes across a representative range of environments will have to be performed. Stability for the scientist and farmer evaluated traits will be the basis upon which any genotype will be advanced.

The good correlations between scientist and farmer rankings of genotypes at each of the two sites in this study demonstrated that the identification of selection criteria and application thereof by scientists and farmers was not that different. The practical implication of this study is that selection within sites can be generally carried out by experienced scientists who have a good understanding of the production requirements of sweetpotato and consumer preferences. Importantly, the selection has to be conducted by site specific sets of scientists.

Overall, genotype G49 was ranked well both for stability by GEI analysis and for scientist and farmer preferred traits by the participatory selection process. In the participatory process it was ranked tenth before harvest and third at harvest. It is an above average yielder with good yield stability, and is stable for Alternaria blight with below average Alternaria blight AUDPC value. This genotype will be recommended for cultivation by selected farmers on a trial basis, as further evaluations are done at more sites.

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REFERENCES

[1] Abidin, P.E., F.A. van Eeuwijik, P. Stam, Struik.P.C, D.P. Zhang, M. Hermann and E.E. Carey. 2002. Evaluation of sweepotato (*Ipomoea batatas* (L.) Lam.) germplasm from North-eastern Uganda through a Farmer Participatory Approach. In: Ames, T., editor, Proceedings of the First InternationalSymposium on Sweetpotato. Acta Horticulturae 583, ISHS. p. 61-68.

[2] Almekinders CJM, Elings A. 2001. Collaboration of farmers and breeders: participatory crop improvement in perspective. Euphytica 122: 423–424.

[3] Ceccarelli S, Grando S. 2006. Decentralized-participatory breeding: an example of demand driven research. Euphytica 155:349–360.

[4] Ceccarelli, S., S. Grando, R. Tutwiler, J. Baha, A.M. Martini, H. Salahieh and A. Goodchild. 2000. A methodological study on participatory barley breeding.I. Selection phase. Euphytica 111: 91-104.

[5] Dawson J.C, Murphy K.M, Jones S.S. 2007. Decentralized selection and participatory approaches in plant breeding for low-input systems. Euphytica 160: 143–154.

[6] Frey, K.J. 1964. Adaptation reaction of oats strains selected under stress and non-stress environmental conditions. Crop Science 4: 55-58.
[7] Gauch, H.G. and R.W. Zobel. 1996. AMMI analysis of yield trials. In: Kanga, M. S. and H. G. Gauch, editors, Genotype by Environment Interaction. CRS, Boca Raton, Florida, USA. p. 85-122.
[8] Gibson, R.W., E. Byamukama, I. Mpembe, J. Kayongo and R.O.M. Mwanga. 2008. Working with farmer groups in Uganda to develop new sweetpotato cultivars: Decentralisation and building on traditional approaches. Euphytica 159: 217-228.
[9] Grüneberg, W.J., K. Manrique, D. Zhang and M. Hermann. 2005. Genotype x environment interactions for a diverse set of sweetpotato clones evaluated across varying ecogeographic conditions in Peru. Crop Science 451: 2160-2171.
[10] Joshi, K., M. Subedi, R. Rana, K. Kadayat and B. Sthapit. 1997. Enhancing on farm varietal diversity through participatory varietal selection: a case for Chaite rice in Nepal. Experimental Agriculture 33: 335-344
[11] Kamalam, p., R.S. Biradar and N. Hrishi. 1978. Stability parameters in sweetpotato (*Ipomoea batatas* (L.) Lam.). Journal of Root Crops 4: 35-39.
[12] Kang, M.S. 1993. Simultaneous selection for yield and stability in crop performance trials. Consequences for growers. Agronomy Journal 85: 754-757.
[13] Keith, T., Rwiza, E., Nyango, A., Amuor, R., Ngendello, K.R., Jolliffe, D.F. (2004). The use of sensory evolution and consumer preference for the selection of sweetpotato cultivars in East Africa. Journal of the Science of Food and Agriculture 84(8): 791-799.
[14] Kwach, J. K., Odhiambo, G. O., Dida, M. M. and Gichuki, S. T. 2010. Participatory consumer evaluation of twelve sweetpotato varieties in Kenya. African Journal of Biotechnology. 9(11): 1600-1609
[15] Laurie S.M and Magoro M.D. 2008. Evaluation and release of new sweetpotato varieties through farmer participatory selection. African Journal of Agricultural Research 3 (10): 672-676
[16] Lebot V. 2009. Tropical root and tuber crops: cassava, sweetpotato, yams and aroids. Wallingford: CABI Publishing.
[17] MAAIF. 2018. Ministry of Agriculture Anima Industry and Fisheries. 2018. Performance Report. Kampala, Uganda. p.15
[18] Manrique, K. and M. Hermann. 2000. Effect of Genotype x Environment interactions on root yield and beta-carotene concentration of selected sweetpotato (*Ipomoea batatas* (L.) Lam.) varieties and breeding clones. International Potato Centre. Program report 1999-2000, Lima, Peru. p. 281-287.
[19] Marti, R.H. (2003). Estimation of sample size in skin and flesh colour measurements of dry flesh sweet potato (Ipomoea batata (L) Lam). Scientia Horticulturae 98:331-336.
[20] Martin, W.F., A.N. Flores and G.S. Carmer. 1988. Identification of a key environment for determination of yield stability in sweetpotato. Tropical Agriculture (Trinidad) 65: 313-316.
[21] Mcharo, M., Carey, E.E., Gichuki, S.T. (2001). Performance of selected sweetpotato varieties in Kenya. African Crop Science Journal 9: 49-59.
[22] Mwanga, R., Lemaga, B., Nsumba, J., Ndolo, P., Agili, S., Marandu, E.2006. Evaluation of stability performance of orange-fleshed sweetpotato clones in East African regional trials. In: Book of Abstracts of the 14th Symposium of the International Society for Tropical Root Crops, 20–26 November 2006, Thiruvananthapuram, India. pp 62–63.
[23] Mwanga R.O.M., G. Kyalo., G. N. Ssemakula., C. Niringiye., B. Yada., M. A. Otema., J. Namakula., A. Alajo., B. Kigozi., R.N.M. Makumbi., A. Ball., W.J. Greuneberg., J.W. Low and G.C. Yencho. 2016. 'NASPOT 12 O'and 'NASPOT 13 O'Sweetpotato. HortScience.51(3): 291–295.
[24] Mwanga, R.O.M., B. Odongo, A.Alajo, B. Kigozi, N. Niringiye, R. Kapinga, S. Tumwegamire, R.M. , E. Lugwana, J. Namakula, B. Lemaga, J. Nsumba and C. Yencho. 2007. Submission to the Variety Release Committee for the release of sweetpotato varieties. National Agricultural Research Organisation (NARO)/National Crops Resources Research Institute (NaCRRI), Kampala, Uganda.
[25] Mwanga, R.O.M., B. Odongo, C. Niringiye, R. Kapinga, S. Tumwegamire, P.E. Abidin, E.E. Carey, B. Lemaga, J. Nsumba and D. Zhang. 2007. Sweetpotato selection releases: lessons learnt from Uganda. African Crop Science Journal 15: 11- 23.
[26] Mwanga, R.O.M., C. Niringiye, A. Alajo, J. Namakula, I. Mpembe, S. Tumwgamire, R.W. Gibson and G.C. Yencho. 2011. 'NASPOT 11', a sweetpotato cultivar bred by a participatory plant breeding approach in Uganda. HortScience 46: 317-321.
[27] Ndirigwe, J., S. Muyango, R. Kapinga and S.Tumwegamire. 2005. Participatory on-farm selection of sweetpotato varieties in some provinces of Rwanda. African Crop Science Conference Proceedings. 7: 1205-1209.
[28] Ngeve, J.M. 1993. Regression analysis of genotype x environment interaction in sweetpotato. Euphytica 71: 231-238.
[29] Niringiye, C.S., Ssemakula, G.N., Namakula, J., Kigozi, C.B., Alajo, A., Mpembe, I and Mwanga R.O.M. 2014. Evaluation of promising sweetpotato clones in selected agro-ecological zones of Uganda. Time Journals of Agriculture and Veterinary Sciences 2(3):81-88.
[30] Odendo, M., H.D. Groote, O. Odongo and P. Oucho. 2002. Participatory Rural Appraisal of Farmers' Criteria for Selection of Maize Varieties and Constraints to Maize Production in Moist-Midaltitude Zone of Western Kenya. A

case study of Butere-Mumias, Busia and Homa Bay Districts. Final Technical Report. CIMMYT, Nairobi, Kenya. pp. 17.

[31] Payne, R.W., S.A. Harding, D.A. Murray, D.M. Soutar, D.B. Baird, A.I. Glaser, S.J. Whelham, A.R. Gilmour, R. Thompson and R. Webstar. 2011. The guide to Genstat release 14, Part 2: Statistics. VSN International, Hemel Hempstead, UK.

[32] Sperling, L., J.A. Ashby, M.E. Smith, E. Weltzien and S. Mcguire. 2001. A framework for analysing participatory plant breeding approaches and results. Euphytica 122: 439-450.

[33] Ssemakula, G., C. Niringiye, B. Yada, M. Otema, G. Kyalo, J. Namakula, A. Alajo, B. Kigozi, R. Makumbi, G.C. Yencho, and R.O.M. Mwanga. 2013. Submission to the variety release Committee for the release of sweetpotato varieties. National Agricultural Research Organization (NARO)/National Crops Resources Research Institute (NaCRRI), Kampala, Uganda.

[34] Sseruwu G., P. Shanahan, R. Melis, G. Ssemakula. 2015. Farmers' awareness and perceptions of Alternaria leaf petiole and stem blight and their preferred sweetpotato traits in Uganda. Journal of Plant breeding and Genetics. 3:1-13

[35] Witcombe, J.R., A. Joshi and S.N. Goyal. 2003. Participatory plant breeding in maize for low-input systems. A case from Gujarat, India. Euphytica 130: 413-422.

[36] Zobel, R.W., M.J. Wright and H.G.Gauch. 1988. Statistical analysis of yield trials. Agronomy Journal 80:388-393.

Appendix 1.Rainfall (mm) received at each site from planting to harvesting

Location	**2015A**				
	March	**April**	**May**	**June**	**July**
Namulonge	150.4	226.0	104.1	87.73.4	33.0
Kachwekano	161.3	69.9	54.7	22.8	00
Serere	152.2	56.6	37.1	1.5	0.0