Characterization of Ugandan Sweetpotato Germplasm Using Fluorescent Labeled Simple Sequence Repeat Markers

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Abstract. The genetic relationships among 192 superior, high-yielding, and disease-resistant sweetpotato [*Ipomoea batatas* (L.) Lam] accessions from the Ugandan germplasm collection were analyzed using 10 fluorescent labeled simple sequence repeat (SSR) markers. Relatedness among the genotypes was estimated using the Nei and Li genetic distance coefficient, cluster analysis and principle component analysis methods of NTSYS-pc software. The polymorphic information content of the SSR markers used in this study ranged from 0.23 to 0.76 for loci IB-S07 and IB-R12, respectively, with a mean value of 0.62. The number of polymorphic alleles detected per locus ranged from two to six with a mean of four, a confirmation of the effectiveness of microsatellite detection on an automated ABI 3730 sequencer. The mean pairwise genetic distance among the 192 genotypes was 0.57, an indication of moderately high genetic diversity. Cluster analysis divided the accessions into four major groups with no relationship to the district of origin. Two sets of duplicates were identified through SSR genotyping in this study. Up to 190 distinct accessions for use as potential parental genotypes in hybridization schemes for cultivar development in the region were identified.

Successful conservation and genetic improvement of sweetpotato is to a great extent dependent on the level of knowledge accumulated by scientists regarding germplasm genetic diversity. Sweetpotato ($2n = 6x = 90$), the world's seventh most important food crop after wheat, rice, maize, potato, barley, and cassava (FAOSTAT, 2007), is widely cultivated in Uganda and sub-Saharan Africa

(SSA) as a food security crop (Aritua and Gibson, 2002; Diaz et al., 1996). Uganda ranks third in global sweetpotato production after China and Nigeria (FAOSTAT, 2007), and SSA is a secondary center of diversity for the crop (Huamán and Zhang, 1997). The ultimate goal of sweetpotato breeding in Uganda is to generate improved cultivars for a combination of traits with broad or specific adaptation to overcome constraints in different agroecologies (Mwanga et al., 2003). New cultivars released from breeding programs are often more vulnerable to pests, pathogens, and environmental stresses (He et al., 2006). Therefore, identification of parental genotypes with high sweetpotato virus disease (SPVD), *Alternaria* blight disease and pest resistance, yield, and dry matter content for breeding is critical in Uganda.

The National Crops Resources Research Institute (NaCRRI), Namulonge, holds 1303 accessions of sweetpotato germplasm collected from 21 districts of Uganda, from which 946 morphologically distinct accessions were identified (Yada et al., 2010). To date, morphological characterization (Huamán, 1992) has been predominantly used for the analysis of diversity in sweetpotato germplasm collections (Abidin and Carey, 2001; Gichuru et al., 2006; Huamán et al., 1999; Veasey et al., 2007). Limited success has been achieved with morphological diversity analysis alone in the selection of parental genotypes for hybridization schemes because of phenotypic plasticity (Price et al., 2003) and the environmental impact on morphological traits.

Molecular markers have become an important genetic diversity analysis tool for enhancing sweetpotato breeding efficiency. Many molecular techniques have been used in sweetpotato genetic diversity studies, including random amplified polymorphic DNAs (Connolly et al., 1994; He et al., 2006; Zhang et al., 1998), amplified fragment length polymorphisms (Elameen et al., 2008; Zhang et al., 2000b), intersimple sequence repeats (Hu et al., 2003), DNA amplification fingerprinting (He et al., 1995), selective amplification of microsatellite polymorphic loci (SAMPL) (Tseng et al., 2002), and simple sequence repeat markers (SSRs) (Gichuru et al., 2006). Microsatellites developed for genotyping sweetpotato (Buteler et al., 1999; Hu et al., 2004) have been widely used for diversity analysis (Hwang et al., 2002; McGregor et al., 2001). With the fluorescently labeled microsatellite primers and sequencing on automated sequencers such as the ABI 3730 (Applied Biosystems, Foster City, CA), multiplexing of many polymerase chain reaction (PCR) products and accuracy in allele sizing and data collection can be achieved (Coburn et al., 2002). This technology is potentially useful for a detailed understanding of sweetpotato genetic diversity. The objective of this research project was to characterize diversity among selected superior sweetpotato accessions from the Ugandan collection using fluorescent labeled SSR markers for conservation and use in breeding.

Materials and Methods

Plant material and DNA extraction. A total of 192 superior sweetpotato genotypes was selected from the evaluation of the morphologically distinct accessions of the Ugandan germplasm collection being clonally maintained at NaCRRI (Table 1). The superior genotypes were high-yielding and SPVD- and *Alternaria* blight-resistant, whereas others had high dry matter content and could be useful as parental genotypes for hybridization.

Genomic DNA was isolated from tender fresh leaf samples using CIP's molecular biology laboratory protocols modified from the CTAB method (Doyle and Doyle, 1990). For each genotype, 100 mg of fresh leaf

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Table 1. List of 192 superior sweetpotato landrace accessions selected and genotyped.

No.	Code	District	No.	Code	District	No.	Code	District	No.	Code	District
1	MLE191	Mbale	49	RAK791	Rakai	97	MSK1020	Masaka	145	LUW1254	Luweero
2	PAL102	Pallisa	50	RAK829	Rakai	98	MSK1040	Masaka	146	LUW1243	Luweero
3	LIR279	Lira	51	RAK831	Rakai	99	MPG1118	Mpigi	147	MPG1146	Mpigi
4	MLE183	Mbale	52	RAK835	Rakai	100	MKN1173	Mukono	148	IGA1003	Iganga
5	PAL133	Pallisa	53	PAL1303	Pallisa	101	MKN1200	Mukono	149	MSK1094	Masaka
6	PAL148	Pallisa	54	KBL648	Kabale	102	MKN1180	Mukono	150	KML943	Kamuli
7	PAL94	Pallisa	55	KML932	Kamuli	103	MPG1151	Mpigi	151	HMA484	Hoima
8	PAL134	Pallisa	56	KML940	Kamuli	104	MKN1186	Mukono	152	KML960	Kamuli
9	SRT45	Soroti	57	KML924	Kamuli	105	LUW1238	Luweero	153	BSH761	Bushenyi
10	SRT1	Soroti	58	RAK846	Rakai	106	MKN1210	Mukono	154	BSH764	Bushenyi
11	BSH747	Bushenyi	59	KML915	Kamuli	107	MKN1212	Mukono	155	KBL616	Kabale
12	MLE171	Mbale	60	APA354	Apac	108	MKN1224	Mukono	156	IGA971	Iganga
13	PAL115	Pallisa	61	MBR535	Mbarara	109	LUW1250	Luweero	157	MPG1103	Mpigi
14	KMI83	Kumi	62	HMA490	Hoima	110	LUW1280	Luweero	158	KML916	Kamuli
15	KMI76	Kumi	63	HMA496	Hoima	111	LUW1286	Luweero	159	IGA982	Iganga
16	BSH740	Bushenyi	64	MBR530	Mbarara	112	LUW1285	Luweero	160	IGA983	Iganga
17	BSH748	Bushenyi	65	KSR659	Kisoro	113	LUW1302	Luweero	161	MPG1148	Mpigi
18	LIR276	Lira	66	BSH751	Bushenyi	114	KBL650	Kabale	162	MSK1026	Masaka
19	SRT24	Soroti	67	LUW1300	Luweero	115	KSR 663	Kisoro	163	MSK1045	Masaka
20	SRT47	Soroti	68	LUW1257	Luweero	116	KRE713	Kabarole	164	MPG1158	Mpigi
21	SRT32	Soroti	69	LUW1230	Luweero	117	KRE724	Kabarole	165	KML945	Kamuli
22	ARA222	Arua	70	MKN1188	Mukono	118	KRE734	Kabarole	166	KBL617	Kabale
23	MLE170	Mbale	71	MPG1150	Mpigi	119	BSH777	Bushenyi	167	SRT27	Soroti
24	KRE725	Kabarole	72	MPG1122	Mpigi	120	RAK815	Rakai	168	SRT41	Soroti
25	KRE693	Kabarole	73	IGA985	Iganga	121	RAK805	Rakai	169	MLE172	Mbale
26	RAK801	Rakai	74	MSK1072	Masaka	122	KML877	Kamuli	170	PAL153	Pallisa
27	MSD382	Masindi	75	KML944	Kamuli	123	KML875	Kamuli	171	KMI80	Kumi
28	ARA224	Arua	76	IGA972	Iganga	124	KSR661	Kisoro	172	KMI69	Kumi
29	MLE163	Mbale	77	IGA995	Iganga	125	ARA232	Arua	173	APA379	Apac
30	PAL120	Pallisa	78	MPG1128	Mpigi	126	ARA237	Arua	174	PAL158	Pallisa
31	SRT12	Soroti	79	MKN1168	Mukono	127	ARA 236	Arua	175	MBR609	Mbarara
32	MSD380	Masindi	80	MKN1195	Mukono	128	LIR265	Lira	176	APA352	Apac
33	ARA212	Arua	81	LUW1237	Luweero	129	LIR303	Lira	177	APA345	Apac
34	KML900	Kamuli	82	LUW1274	Luweero	130	MSD432	Masindi	178	APA373	Apac
35	RAK808	Rakai	83	MSK1079	Masaka	131	APA 349	Apac	179	MSD429	Masindi
36	KML882	Kamuli	84	MKN1169	Mukono	132	MBR509	Mbarara	180	KMI68	Kumi
37	RAK841	Rakai	85	IGA975	Iganga	133	MBR605	Mbarara	181	MBR546	Mbarara
38	RAK836	Rakai	86	KML956	Kamuli	134	MBR577	Mbarara	182	LIR295	Lira
39	RAK817	Rakai	87	KML941	Kamuli	135	MBR531	Mbarara	183	BSH754	Bushenyi
40	KML881	Kamuli	88	IGA978	Iganga	136	HMA512	Hoima	184	RAK796	Rakai
41	RAK819	Rakai	89	KML961	Kamuli	137	HMA495	Hoima	185	RAK811	Rakai
42	RAK821	Rakai	90	KML942	Kamuli	138	PAL159	Pallisa	186	MKN1219	Mukono
43	RAK786	Rakai	91	IGA963	Iganga	139	MLE201	Mbale	187	KML950	Kamuli
44	RAK787	Rakai	92	IGA998	Iganga	140	PAL125	Pallisa	188	SRT333	Soroti
45	KBL631	Kabale	93	MPG1112	Mpigi	141	PAL98	Pallisa	189	LUW1239	Luweero
46	KML876	Kamuli	94	HMA494	Hoima	142	SRT26	Soroti	190	MKN1215	Mukono
47	KML872	Kamuli	95	MPG1149	Mpigi	143	KMI86	Kumi	191	LUW1290	Luweero
48	KSR676	Kisoro	96	MPG1117	Mpigi	144	SRT35	Soroti	192	LUW1242	Luweero

material from the screen house was ground to powder in a prechilled mortar in liquid nitrogen and transferred to 1.5-mL Eppendorf tubes. Thereafter, 700 μ L of fresh extraction buffer (2% CTAB buffer and 2% β -mercaptoethanol) was added to the powder, vortexed, and the homogenate was incubated for 45 min at 65 °C in a water bath. The samples were cooled to room temperature for 2 min. Then, 700 μ L of chloroform:isoamyl alcohol (24:1) was added to each tube and vortexed briefly, and the tubes were inverted several times. The homogenates were centrifuged for 5 min at 14,000 rpm in a microcentrifuge. The aqueous phases were removed and carefully transferred into new-labeled Eppendorf tubes. Fifty microliters of 10% CTAB (in 0.7 M NaCl) was added to the samples and vortexed gently. Again 700 μ L of chloroform:isoamyl alcohol (24:1) was added to each tube and vortexed briefly, and the tubes were inverted several times. The homogenates were centrifuged for 5 min at

14,000 rpm. The aqueous phases were removed and carefully transferred into new-labeled Eppendorf tubes. To each tube was added 400 to 500 μ L of isopropanol. The tubes were inverted several times and allowed to sit at 4 °C for 30 min. The tubes were spun at 14,000 rpm for 20 min, and the supernatants in each tube were poured off and the tubes were inverted and air-dried. The DNA pellets were washed in 1.0 mL of 70% ethanol for 3 min and centrifuged at 14,000 rpm for 30 min. The ethanol was carefully poured off and the pellets were washed in 1.0 mL of 90% ethanol and centrifuged at 14,000 rpm for 30 min. The ethanol was poured off and the pellets were dried overnight. The DNA samples were dissolved in 150 μ L of T10E buffer. To the DNA samples 2.0 μ L of DNase-free RNaseA was added then incubated at 37 °C for 1 h. The purified samples were stored at 4 °C. The DNA concentration and purity (A260/A280 ratios) was determined using a NanoDrop ND-1000 spectro-

photometer (NanoDrop Technologies, Wilmington, DE).

Simple sequence repeat amplification and polymerase chain reaction conditions. Ten polymorphic SSR markers with forward primers labeled at the 5' end using fluorescent dyes, PET (red), 6FAM (blue), VIC (green), and NED (yellow) [International Potato Center (CIP), Lima, Peru] (Table 2) were used in this study. The PCR was performed in a total reaction volume of 10 μ L using the Accupower PCR premix tube containing lyophilized 1 U top Taq DNA polymerase, 250 μ M dNTPs, 10 mM Tris-HCl (pH 9.0), 30 mM KCl, 1.5 mM MgCl₂, and a tracking and stabilizing dye (Bioneer, Daejeon, North Korea). To the premix was added 2.5 μ L of 1.0 pmol of primers, 5.0 μ L of 1.0 ng DNA template, and 2.5 μ L of double-distilled water. The PCR program consisted of an initial denaturation at 94 °C for 4 min followed by 35 cycles of 94 °C for 1 min, 1 min annealing at 58 °C, and 72 °C for 1 min. This was followed by

a final extension step of 20 min at 72 °C and a hold at 4 °C. All the PCRs were run in a GeneAmp PCR system 9700 thermocycler (Applied Biosystems).

Pooling of polymerase chain reaction products and simple sequence repeat fragment analysis. PCR products were pooled by combining 5.0 µL of each amplified product diluted with double-distilled water. Dilution was based on the relative intensities of amplification resolved on a 2% TBE agarose gel and the relative fluorescence unit on the ABI 3730 sequencer. The capillary electrophoresis runs were post-PCR-coloaded in three sets on the basis of dye color and fragment size (Table 2). A standard cocktail mix for fragment analysis was prepared by thoroughly mixing 12.0 µL of 500 LIZ size standard and 1000 µL Hi-Di Formamide. Then 1.0 µL of each pooled PCR product was mixed with 9.0 µL of the cocktail mix in a 96-well PCR plate, gently vortexed, and spun down at 3000 rpm for 2 min. The mix was denatured at 95 °C for 3 min and quickly chilled on ice for 5 min and then loaded into the ABI 3730 sequencer for fragment analysis. SSR fragment sizing was done using the Genemapper v3.7 software (Applied Biosystems), which performed peak detection and fragment size matching from the reference data. Allele calls were automatically made when a peak from a data sample matched the location of a bin. Completed results were run in AlleloBin software (Prasanth et al., 1997) to correct any errors in the scored alleles resulting from slippage of DNA polymerase during PCR resulting into stutter peaks (Schlotterer and Tautz, 1992). The allele calls were then converted to binary data using ALS-Binary software (Prasanth and Chandra, 1997) for the subsequent analyses.

Statistical data analysis. The polymorphic information content (PIC), the measure of the usefulness of each marker in distinguishing one individual from another, was determined (Weir, 1996) as:

$$PIC = 1 - \sum P_i^2$$

where P_i is the frequency of the i^{th} allele.

To investigate the diversity among the accessions, the number of alleles per locus was computed, and genetic distances among all pairs of individuals were calculated using the Nei and Li coefficient (Nei and Li, 1979). The distance matrix was then subjected to cluster analysis using the unweighted pair group method using arithmetic averages (UPGMA) algorithm of NTSYS-pc software version 2.2 (Rohlf, 1993) to generate a dendrogram (Sneath and Sokal, 1973). Principal component analysis (PCA) was used to graphically display genetic relationships (Gower, 1966).

Results and Discussion

Polymorphic information content. The PIC value reflecting genetic diversity of the 10 microsatellite loci ranged from 0.23 for locus IB-S07 to 0.76 for locus IB-R12 with an average of 0.62 (Table 3). Except for primers IB-S07 and IB-R08, the other primers were highly polymorphic with PIC values higher than 0.50. IB-R12 was the most polymorphic primer. The high average PIC value observed in this study is an indication of the use of more informative sweetpotato SSR markers.

Polymerase chain reaction amplifications and number of alleles detected. Initial analysis by gel electrophoresis revealed high yield for most of the PCR reactions. The number of alleles detected per locus ranged from two for locus IB-R08 to six for IBCIP-

13 with an average of four and the allele sizes ranged from 39 to 373 bp (Table 3). Because sweetpotato might be an autohexaploid crop with a large genome (Cervantes-Flores et al., 2008), the number of alleles per locus is expected to range from one to six, although no single genotype showed up to six alleles at a particular locus. However, as a result of the polyploid and highly outcrossing nature of sweetpotato, allele dose effects such as simplex, duplex, and triplex could not be differentiated in this study. There was no relationship between the number of repeats and polymorphism. The 192 genotypes were clearly distinguished by the 10 SSR primers suggesting that SSR markers have good discriminatory power for genotyping sweetpotato germplasm. For example, only six SSR primer pairs generated scorable allelic information for typing 113 Latin American sweetpotato cultivars (Zhang et al., 2000a). Four SSR primer pairs also discriminated among 57 East African sweetpotato genotypes (Gichuru et al., 2006). The level of polymorphism detected by SSRs in this study was higher than that detected by other SSR techniques used by Gichuru et al. (2006) and Zhang et al. (2000a). This could be because of a good choice of highly polymorphic SSR markers used in the study. Tseng et al. (2002), however, obtained greater polymorphism in sweetpotato using SAMPL as a remedy to the limitation of dosage effect detection in SSRs as previously proposed by Buteler et al. (1999).

Genetic distances among sweetpotato genotypes. The frequency of pairwise genetic distance coefficients for the SSR analysis is shown in Figure 1. The SSR-based genetic distance coefficients ranged from 0.0 to 1.0 with a mean of 0.57. The relatively high mean genetic distance and wide range of genetic

Table 2. Simple sequence repeat primer sequences, dyes, coload sets, and polymerase chain reaction product dilutions.

Primer	Forward	Reverse	Dye	Coload set	Product dilution
IB-R16	GACTTCCTTGGTGTAGTTGC	AGGGTTAAGCGGGAGACT	VIC	1	1:100
IB-R19	GGCTAGTGGAGAAGGTCAA	AGAAGTAGAACTCCGTCACC	PET	1	1:60
IBCIP-13	CGTGCTTGAGGTCTGAGTAGAA	TTCCCTAGAAGCTGCGTGAT	NED	1	1:60
IB-R03	GTAGAGTTGAAGAGCGAGCA	CCATAGACCCATTGATGAAG	PET	2	1:75
IBCIP-9	AGACTGCTAGGGTTATCTCTCCA	GACATTGCCAAGGACACTGA	6-FAM	2	1:50
IB-S09	GCTGCTCAATCCCTCTCCTT	GGAATCTGATACAGCGTGGT	NED	2	1:50
IB-R08	GGCGACACCTTAGAGTAT	CACCCCTATTACAA	PET	2	1:50
IB-R12	GATCGAGGAGAAGCTCCACA	GCCGGCAAATTAAGTCCATC	NED	3	1:100
IB-S07	GCTTGCTGTGGTTTCGAT	CAAGTGAAGTGATGGCGTTT	6-FAM	3	1:100
IBCIP-7	GGTTTGACCGTGGAGTTGTT	GGACGAACCTTCCCAAATCA	PET	3	1:50

Table 3. Primer, repeat motifs, annealing temperature (T_m), size range, alleles per locus, total number of alleles, and polymorphic information content (PIC) of 10 primers.

Primer	Repeat motif	T _m (°C)	Size range	Alleles per locus	Total alleles	PIC
IB-R16	(GATA) ₄	60	201–213	3	428	0.65
IB-R19	(CAG) _{5b}	60	190–208	4	392	0.68
IBCIP-13	(ACC) ₃ +(CGG) ₂ +(TGC) ₃ +(GTC) ₂	60	196–373	6	477	0.68
IB-R03	(GCG) ₅	60	243–258	4	463	0.71
IBCIP-9	(CCA) ₂ AC(ACC) ₆	50	42–63	4	461	0.68
IB-S09	(AT) ₁₁	50	193–203	4	318	0.72
IB-R08	(T3A) ₄	50	204–216	2	230	0.36
IB-R12	(CAG) _{5A}	60	303–342	5	496	0.76
IB-S07	(TGTC) ₇	60	162–178	4	193	0.23
IBCIP-7	(CCA) ₂ +3+(CCG) ₂ +1+3(CCA) ₃ +(CG) ₄	50	39–99	6	492	0.74
Mean				4	395	0.62

Fig. 1. Frequency distribution of pairwise genetic distance estimates among 192 sweetpotato genotypes.

distances among landraces indicates moderately high genetic diversity. Most distance coefficients were in the range of 0.5 to 0.6, accounting for 60.7% of the pairwise distance coefficients in this study. Genotypes MLE191 and KML942 collected from the neighboring districts of Mbale and Kamuli, respectively, were identified as duplicates, although they differed significantly in their vine and leaf coloration but had similar storage skin and flesh color. MLE191, a popular accession from Mbale, could have been brought to Kamuli for cultivation by a farmer who could not name it or vice versa (McGregor et al., 2001). Likewise, genotypes ARA237 from the Arua district and KSR663 from the Kisoro

Fig. 2. Dendrogram showing genetic relationships among 192 Ugandan sweetpotato genotypes.

district also had a distance coefficient of 0.0 (duplicates). These districts are both bordered by the Democratic Republic of Congo from where the farmers could have brought this accession. This environment could have affected the pigmentation traits leading to differential scoring of these traits on the accessions. The highest pairwise genetic distance was observed between genotypes BSH748 and MLE163 from Bushenyi and Mbale districts, respectively. A high mean genetic distance of 0.58 was also found among sweetpotato genotypes from China, the world's leading producer (He et al., 2006). In contrast, Gichuru et al. (2006) observed low diversity among some East African sweetpotato genotypes probably because of the small number of accessions collected from few districts and also fewer number of SSR primers (four primer pairs) used in the study. Similar low diversities have been observed among the sweetpotato genotypes from Tanzania (Elameen et al., 2008), Papua New Guinea (Zhang et al., 1998), and the United States (He et al., 1995). The relatively high genetic diversity of sweetpotato in Uganda can be attributed to the self-incompatibility leading to chance seedlings in farmers' fields and vegetative propagation of the crop and directed selection in the crop for various uses such as human food, livestock feed, and poultry feed coupled with new introductions and mutations. High levels of polymorphism among sweetpotato plants are maintained through vegetative propagation and self-incompatibility in the crop (He et al., 1995).

Cluster analysis. The standard distance matrix-generated dendrogram grouped the

genotypes into four major clusters (Fig. 2). Within each cluster, the genotypes mainly did not group according to geographic origin. For instance, Cluster 1 has 16 genotypes collected from the districts of Mbale, Kamuli, Kumi, Rakai, Mpigi, Pallisa, Lira, and Kisoro. Similarly, Cluster 2 consisted of genotypes from Kumi, Rakai, and Luweero districts. Cluster 3 had the largest number of genotypes and many subclusters, and Cluster 4, likewise, did not show a geographic pattern. Clustering among some East African cultivars indicated a lack of geographic association as well (Gichuru et al., 2006). However, clear regional patterns of clustering were observed among the sweetpotato genotypes from Latin America (Zhang et al., 2000a, 2004). The lack of geographic associations among the Ugandan genotypes may be a result of gene flow because farmers have routinely shared planting material over the years of sweetpotato cultivation in Uganda. Self-incompatibility and high outcrossing favors gene flow in sweetpotato (He et al., 1995).

Principal component analysis. Principal component analysis was also conducted to analyze the genetic relationships among the individual accessions. The first two principal components accounted for 23.1% and 17.6% of the variance in the PCA plot of the genotypes, respectively. Similar to the cluster analysis results, PCA did not result in a discernible grouping of genotypes by the regions of collection (Fig. 3). Tseng et al. (2002) observed similar results between UPGMA clustering and PCA in the genotyping and assessment of genetic relationships

among elite polycross breeding cultivars of sweetpotato in Taiwan using SAMPL polymorphisms.

Conclusion

The 10 fluorescent-labeled microsatellites detected on ABI 3730 have distinguished the 192 Ugandan sweetpotato genotypes. The relatively high level of genetic diversity is an indication of the broad genetic base for sweetpotato in Uganda. The identification of 190 diverse genotypes of varying characteristics for use in hybridization schemes in the region will enhance accession development and contribute to sweetpotato productivity in SSA. These East African sweetpotato genotypes have several unique important characteristics like high dry matter content, high resistance to virus diseases, and vigorous foliage cover, although they have low root beta-carotene content (Gichuki et al., 2003). The genotypes are ready for cleaning and in vitro conservation at NaCRRI and CIP, Lima, Peru. Sources of genes for these characteristics have been identified in the distinct genotypes of the Ugandan sweetpotato collection. Two duplicates identified from this morphologically distinct collection confirm the advantage of molecular characterization over morphological characterization. This efficient genotyping will enhance low-cost conservation and use of these superior genotypes. To enhance breeding for orange-fleshed cultivars, genotypes MLE172 from Mbale and KMI83, both having high dry matter, are recommended as parental genotypes. Meanwhile, KBL616, KBL648, KSR659, KSR676, and

Fig. 3. Two-dimension principle component analysis plot of 192 Ugandan sweetpotato genotypes.

KRE693 are highly recommended as parental genotypes for breeding *Alternaria* blight resistance in the region. The genotypes SRT27, SRT47, MBL191, MSD382, HMA496, RAK808, RAK835, KML875, and MPG1122 are high-yielding and moderately resistant to both SPVD and *Alternaria* blight. These are recommended for breeding high-yielding cultivars of sweetpotato. Finally, to improve SPVD resistance, SRT37, KMI83, MSK1026, MPG1103, MPG1117, and LUW1290 are the recommended parental genotypes to be used in breeding. Passport data and complete description of the germplasm are available at: http://www.viaxivitamu.org/ugasp_db/index.php.

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