Australian Journal of Crop Science AJCS

AJCS 13(01):17-25 (2019) ISSN:1835-2707
doi: 10.21475/ajcs.19.13.01.p1023

Adaptability of a U.S. purple-fleshed sweetpotato breeding population in Uganda

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Abstract

Purple-fleshed sweetpotato varieties are important for their nutraceutical value due primarily to their high anthocyanin content. These varieties also often have high dry matter content preferred by consumers and processors in sub-Saharan Africa. However, improved purple-fleshed sweetpotatoes are not available in Uganda. This study was conducted to evaluate the adaptability of purple-fleshed sweetpotato genotypes for storage root yield, dry matter and anthocyanin content in Uganda. A bi-parental population of 159 clones from the cross NCP06-020 × NC09-188 introduced to Uganda from North Carolina State University was evaluated with three local checks in two sites and two seasons in Uganda. The trials were planted in two locations using alpha lattice design with two replicates and five sweetpotato vine cuttings per genotype. Storage roots and vines were harvested after five months and the agronomic characteristics were recorded. Dry matter and anthocyanin content of storage roots were analysed after harvesting. The mean storage root yield of clones across the two locations was 37.8 t/ha and 24.2 t/ha in the first season (2015A) and second season (2015B); respectively, with an overall mean of 31.0 t/ha. Storage root dry matter content ranged from 21.5 to 33.7% across locations and seasons with an overall mean of 29.1%. Storage root anthocyanin content across the two locations ranged from 0 to 12.6 mg/100g FW with the overall mean of 3.9 mg/100g FW. A total of ten genotypes showed significantly stable performance ($P \leq 0.001$) across two locations and two seasons. Highly significant difference between genotypes for dry matter content, anthocyanin content and total storage root yields revealed significant genetic variability among the tested genotypes, which can be exploited for future crop improvement.

Keywords: Anthocyanin; dry matter; stability; yield.
Abbreviations: ALT_Alternaria blight, DMC_Dry matter content, FW_Fresh weight, GxL_ Genotype by location interaction, GxLxS_Genotype by location by season interaction, GxS_ Genotype by season interaction, LxS_Location by season interaction, PFSP_Purple-fleshed sweetpotato, SPVD_Sweet Potato Virus Disease, TRY_Total root yield.

Introduction

Purple-fleshed sweetpotatoes (PFSPs) have attractive light to intense purple coloration due to varying accumulation of anthocyanin pigments in their storage roots. PFSPs are known to have beneficial health effects and they have been used as a source of natural food colorant due to their high levels of anthocyanins and polyphenols (Steed and Truong, 2008). Natural plant colorants are highly demanded by consumer market and food processing industries as a replacement for synthetic dyes such as the banned FD&C Red 2 dye (Francis, 1989; Fabre et al., 1993). This need has come from legislative action and consumer concern against synthetic food additives that are said to have negative effects on human health (Francis, 1989; Fabre et al., 1993). The safety of products containing artificial colors has been a point of debate for decades, with adversaries claiming that they are potentially toxic, carcinogenic and contribute to the pollution of environment (Ratna and Padhi, 2012).

Anthocyanins have a high potential for use as natural colorants due to their attractive orange, red, purple, and blue colors. PFSP possesses much higher anthocyanin content, dietary fiber, total phenolics content and total antioxidant capacity than other types of sweetpotato. The anthocyanin content in storage roots of PFSP is comparable to that of highest anthocyanin producing crops like blueberries, blackberries, cranberries and grapes (Nicole et al., 2010). Studies conducted in US have found that purple-fleshed sweetpotatoes are different from orange-fleshed varieties not only in higher anthocyanin content, but also in higher dry matter and starch contents (Nicole et al., 2010).

The anthocyanins found in storage roots of purple-fleshed sweetpotato exist in forms of mono- or di-acylates of cyanidin and peonidin, which enables them to be a powerful and stable food colorant (Philpott et al., 2003; Terahara et al., 2004). These forms of anthocyanin provide purple-fleshed sweetpotatoes with higher antioxidant activity compared to white-, yellow- and orange-fleshed sweetpotatoes (Teow et al., 2007). Anthocyanins from purple-fleshed sweetpotato can serve as natural colorants due to their high heat and light stability (Tsukui et al., 2002; Philpott et al., 2003; Terahara et al., 2004 Steed and Truong, 2008). In Japan, a successful industry has arisen based on using purple-fleshed sweetpotatoes as sources of anthocyanins as natural food colorants (Suda et al., 2003).

Natural colorants derived from purple-fleshed sweetpotatoes and carrots are rich in acylated anthocyanins and they exhibit higher stability than purple corn and red grape colorants, which have higher levels of nonacylated anthocyanins (Bolívar and Luis, 2004). Many studies have reported the predominance of acylated anthocyanins in pigmented purple-fleshed sweetpotato clones. Increased hydroxylation decreases stability whereas methylation increases stability (Brouillard, 1982). Additional research has shown that acylated substituents are more stable during processing and storage (Giusti and Wrolstad, 2003) and the stability of anthocyanins can be increased with inter-molecular copigmentation (Francis, 1989).

PFSP's contain a range of phytochemical substances with various pharmacological properties. These phytochemical substances posses anti-oxidant, anti-cancer, anti-diabetic, wound healing, anti-ulcer, anti-bacterial and anti-mutagenic activities (Vandana and Sonkamble, 2012). Anthocyanins are commonly suggested as a natural medicine to reduce coronary heart disease and to improve visual acuity (Mazza and Miniati, 1993) and in industrial field to formulate cosmetic products and food preservation and colorant agents (Mervat and Hanan, 2009).

Many adult consumers in sub-Saharan Africa (SSA) prefer high dry matter content sweetpotato varieties and many PFSPs are reported to have high dry matter content. These same materials may have potentially different starch properties from the orange-fleshed varieties and this presents challenges for the commercial production of purees and other value-added food products from high anthocyanin PFSPs (Steed and Truong, 2008). This study was conducted to evaluate the performance and adaptability of purple-fleshed sweetpotato genotypes for storage root yield, dry matter and anthocyanin content as a prerequisite for the establishment of a PFSP breeding program in Uganda.

Results

Segregation of PFSP for storage root flesh color

Segregation of storage root color was observed in the bi-parental population after harvesting. Among the 191 F1 seeds sown, 159 clones were selected and evaluated. A total of 92 clones segregated for different levels of cream color (light cream, intermediate cream and pale yellow), while the remaining 67 clones exhibited segregation for different purple color types (light purple, intermediate and dark purple).

Agronomic performance of purple-fleshed sweetpotato clones

Effects of three way interaction (Genotype x location x season) were significant for *Alternaria* blight (*Alternaria spp.)* severity ($P \leq 0.001$), SPVD severity and harvest index ($P \leq 0.01$) and significant for dry matter content ($P \leq 0.05$). The analysis of variance for DMC, HI and total storage root yields of evaluated clones were highly significant ($P \leq 0.001$) across location and across seasons. The interaction between location and season was significant for sweetpotato weevil damage ($P \leq 0.001$), total root yield ($P \leq 0.01$), and significant for *Alternaria* severity ($P \leq 0.05$) (Table 1). Multivariate ANOVA indicated that there was no significant difference for interaction of genotypes by location and between genotypes tested (Table 2).

Frequency distribution of genotype performance for TRY, DMC, anthocyanin content, ALT severity, SPVD severity and weevil infestation

Storage root yield exhibited a normal distribution for genotypes, across seasons in two locations with an overall mean of 31.0 t/ha. Many genotypes at the Serere site (117; 96%) ranged from 21.0 to 40.9 t/ha with a grand mean of 31.6 t/ha, while the Bulindi site had 96 genotypes (60%) with above 30.3 t/ha (Fig. 1). The frequency distribution of mean genotype of DMC across seasons in two locations had a normal distribution with an overall mean of 29.1%. Serere had 77% of the genotypes ranging from 21.0 to 30.9% of DMC, while most genotypes in Bulindi had a high range of 31.0-40.9% of DMC, with a mean of 29.5% (Fig. 2).

The frequency distribution of anthocyanin content across the two locations was skewed to the right with an overall mean of 3.9 mg/100g FW. At Bulindi site, the mean genotypic anthocyanin content ranged from 0.0-14.33mg/100g FW with some clones having higher anthocyanin content than the purple parent mean (12.9mg/100g FW), while at Serere site it ranged from 0-10.0mg/g FW and across sites from 0-12.16mg/100g FW (Fig. 3).

The highest mean *Alternaria* severity was observed at Bulindi and the lowest mean was observed at Serere. The Serere site had many genotypes (132; 82%) with low *Alternaria* severity scores of 1-2, while Bulindi had 103 (64%). In the higher range of mean *Alternaria* severities (4.1-6.0), Bulindi had 15 genotypes while Serere had only one genotype.

Most of the 161 genotypes (72%) had mean SPVD severity scores ranging from 2.1 to 4.0. The highest mean SPVD severity (3.3) was observed at Bulindi and the lowest (2.6) was observed at Serere and the mean score across sites was 2.9. Considering scores of 4.1-6.0, which represent susceptible genotypes, Bulindi site had more genotypes (33; 20%) than Serere site (5; 3%) (Fig. 4).

A total of 155 genotypes had mean sweetpotato weevil damage severity ratings ranging between 2.1 and 4.0 at Bulindi site, while at Serere site 78 (48%) had weevil damage in the same range. Weevil infestation severity of 4.1-6.0 was more in Serere site with 83 genotypes (51%) and Bulindi had 6 (4%) (Fig. 5).

Top ten genotypes selected with high yielding, DMC and anthocyanin content

The top ten genotypes were selected for further breeding using Elston's Weight Free Index (Index used for the purpose of ranking selection with respect several traits at a time): EWFI=(x_1-d_1) (x_2-d_2) (x_3-d_3) (x_i-d_j) (Mark and Todd, 1986) where x_i = the mean of the trait, dj=minimum value of the trait). Dry matter content of selected genotypes ranged from 28.64-32.31% with the mean of 30.24% for clone 31 exhibiting the highest DMC. Total root yield of top ten selected genotypes ranged from 25.97-51.01t/ha with the mean of 42t/ha and genotype 51 having the highest yield. Genotype 97 showed the highest anthocyanin content (9.38mg/100 FW), which ranged from 3.69-9.38mg/100FW.

Discussion

In season 2015A, the mean total yield of storage roots of the purple-fleshed sweetpotato clones across two locations was 47.5 and 28.2 t/ha in Serere and Bulindi, respectively, with an overall mean of 37.8 t/ha. Genotypes showed highly significant differences in yield across locations and seasons. This suggests that there is sufficient genetic variability among the tested genotypes for future exploitation for crop improvement. The effects of interaction between genotype and location were significant for total storage root yield across locations in season 2015B. This is consistent with previous reports of significant G x E interactions in sweetpotato (Manrique and Hermann, 2000; Mehmet et al., 2011; Yada et al., 2011). The large contribution of the environment to the variation observed in total storage root yield implies that sweetpotato exhibits large non-additive genetic effects on the total yield. The observed presence of significant effects of genotype x environment interaction in sweetpotato in both yield and quality traits have been reported previously (Grüneberg et al., 2005).

Total storage root yield across locations and growing seasons exhibited a normal distribution (Fig. 1), with 72% of the genotypes in Serere site performing well across seasons with an overall mean of 31.0 t/ha, while at Bulindi 45% of the genotypes performed well across seasons with an overall mean of 31.0 t/ha. These yield values are within the yield range of sweetpotato genotypes released in Uganda (Mwanga et al., 2009; Mwanga et al., 2011), and they are also within the range reported by various authors (Woolfe, 1992; Barbet et al., 1998); therefore, in terms of yield at least, these materials or progeny derived from them, should be acceptable to farmers. The low total storage root yield in Bulindi in season 2015A could be due to the deficiency of rain during the first days after planting, which led to poor establishment, and rooting. Effective rooting is most essential for successful crop establishment and yield from cuttings (Belehu, 2003).

The low total storage root yield in Bulindi could also be attributed to a high *Alternaria* blight disease pressure. The mean severity scores were very high in Bulindi with a mean severity score of 3.2 while in Serere was 1.3. Similarly, genotype by environment by season interactions (Table 1) mean square values was highly significant for *Alternaria* blight. Bulindi is a hot spot of *Alternaria* blight diseases compared to Serere site. Many authors have reported the damage due to *Alternaria* blight in many sweetpotato farmers' fields in Uganda especially in central and south western Uganda but its severity differs from one district to another (Mwanga et al., 2003; Osiru, 2008).

In season 2015B, the total root yield in Serere and Bulindi were 15.8 t/ha and 32.8 t/ha, respectively. The lowest total storage root yield in Serere was probably caused by excessive drought, which affected the total yield. In season 2015B, the two-way interaction between genotype and location was significantly different for all the traits studied because of severe drought. Drought stress is a major constraint to sweetpotato production in many parts of Sub-Saharan Africa (Mwije et al., 2014). In Uganda drought stress effects have also restricted sweetpotato farmers to local landraces (Yanggen and Nagujja, 2006). Mudiope et al. (2000) reported that NaSARRI is a region where drought is a major constraint to sweetpotato production.

Sweetpotato weevils are also a significant sweetpotato production constraint in SSA. In season 2015A, the mean of weevil damage severity was 1.32, which is relatively low, while the mean weevil damage in season 2015B was 6.7. The distribution of weevil infestations across sites between the two seasons showed severity scores ranging from 4.1-6.0. Serere had many susceptible genotypes 83 (51%) falling within the range of 4.1-6.0 while Bulindi had 6 (3%) (Figure 5). The results of this study showed that Serere had severe weevil pressure. This damage was too much during the period of severe drought. These findings confirm what other authors have reported that sweetpotato weevil infestations are one of the major constraints to sweetpotato production in Uganda (Nicole, 1997; Ebregt et al., 2004; Muyinza et al., 2007). Likewise, different authors have reported that sweetpotato weevil damage was more abundant during the hot and dry part of the growing season than the cool and wet growing one (Talekar, 1983). The three-way interaction (genotype by location by season) was highly significant for sweet potato virus disease. The distribution of mean genotype sweet potato virus disease severity across locations in two seasons (Figure 5) showed that in Bulindi most genotypes 149 (92%) had mean severity scores ranging from 2.1 to 6, while Serere site had 115 (71%). This implies that Bulindi was more favorable to sweet potato virus disease infection than Serere in this study. These results confirm what Aritua et al. (2000) reported that in some regions of southern and western Uganda especially around Lake Victoria shores where SPVD is common, rainfall is more regularly spread throughout the year; this appears to have an overall beneficial effect on vectors by ensuring a constant supply of food.The frequency distribution genotype means of anthocyanin content across locations (Figure 3) was skewed to the right and anthocyanin content ranged from 0 to 12.6 mg/100 FW with an overall mean of 3.9 mg/100g FW. These results are within the range of several purple-fleshed sweetpotato varieties reported in Japan and USA with ranges from 2 to 40 mg/100g FW (Suda et al., 2008; Truong et al., 2010; Truong et al., 2012). However, the anthocyanin content of the purple-fleshed sweetpotato populations in this study was lower than anthocyanin content of red potato and red radish that ranges from 15-45 mg/100g FW for each commodity (Rodriguez-Soana et al., 1998). In comparison with commercial purple-fleshed sweetpotato cultivars in United States (<100mg/100g FW), the anthocyanin values in this study were very low. These

Table 1. ANOVA to test disease score severity and yield related traits across seasons in two sites.

SOV	d.f.	SPVD	ALT	WEEVIL	TRY	HI	DMC
Location	1	147.48 ns	44.47 ns	2541.16 ns	475.4 ns	2.08 ns	173.99 ns
Season	1	23.38 ns	130.37 ns	2082.08 ns	61238.6ns	2.74 ns	5966.43ns
LxS	1	2.84 ns	713.41 *	2550.73 ***	104842 **	1.56 ns	436.11 ns
Rep (LxS)	4	110.12 ***	42.57 ***	24.01 ***	2403.4 ***	1.24 ***	983.37***
Genotype	161	3.67 ns	2.88 ns	1.16 ns	512.2 ***	0.06 ***	38.88 ***
GxL	161	3.09 ns	3.07 ns	1.08 ns	243 ns	0.03 ns	20.34 ns
GxS	161	2.56 ns	2.54 ns	1.29 ns	275 ns	0.03 ns	16.19 ns
GxLxS	161	2.93 **	2.8 ***	1.03 ns	241.6 ns	0.03 **	17.73 *
Error	465-560	2.08	1.23	0.86	211.64	0.02	13.58

*, **, *** significant at P ≤ 0.05, P ≤ 0.01, P ≤ 0.001 respectively; ns not significant at 0.05 probability; SOV: Source of variation; d.f: degree of freedom; SPVD: Sweet Potato Virus Disease; Alt: *Alternaria* blight; TRY: Total Root Yield; HI: Harvest Index; DMC: Dry matter content, LXS: Interaction of Location by Season; Rep (LxS): Replication by location by Season; GXL: Interaction of genotype by Location; GXS: Interaction of genotypes by season; GXLXS: Interaction of genotypes by Location by season.

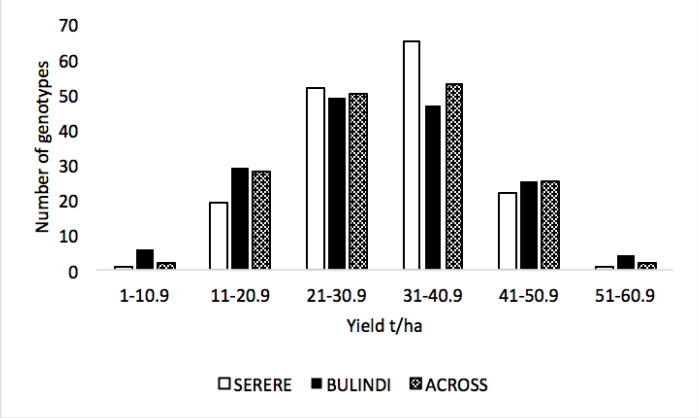

Fig 1. Distribution frequency of total root yield across seasons in two locations; Serere and Bulindi.

Table 2. Multivariate ANOVA testing stability of genotypes.

SOV	d.f.	MS	F-Test	F-Prob
Location	1	21195.3	152.924	2.22E-23
Genotype	66	243.3	1.355	0.110084
Genotype x Location	66	179.6	1.296	0.108288
Error	124	138.6		

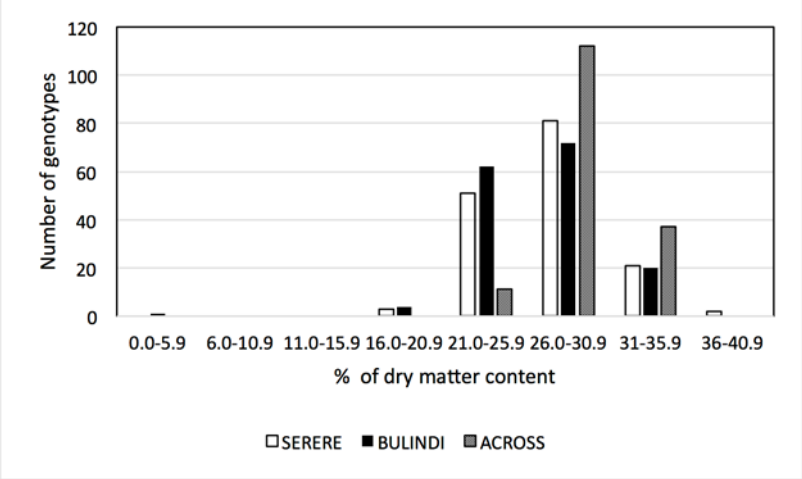

Fig 2. Distribution frequency of DMC across seasons in two locations; Serere and Bulindi.

Table 3. Mean of yield performance for purple population.

Locations/Seasons	2015A	2015B	Across locations
Serere	47.5	15.8	31.6
Bulindi	28.2	32.5	30.3
Across seasons	37.8	24.2	30.9

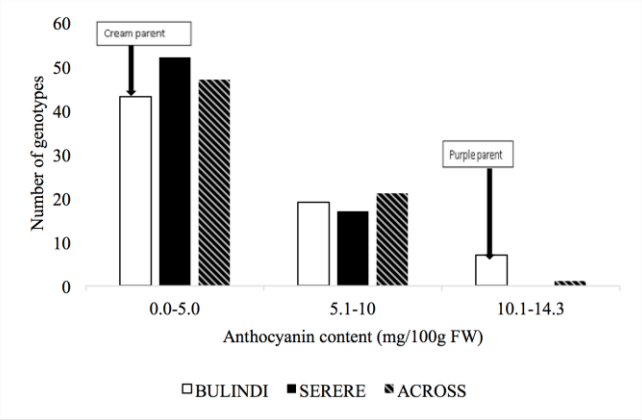

Fig 3. Anthocyanin content (mg/100g FW) across locations; Serere and Bulindi.

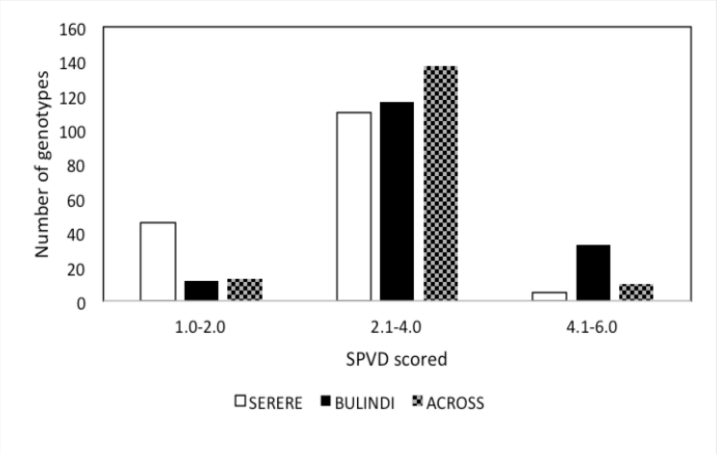

Fig 4. SPVD severity across two locations; Serere and Bulindi (1.0-2.0: resistance; 2.1-4.0: medium; 4.1-6.0: susceptible).

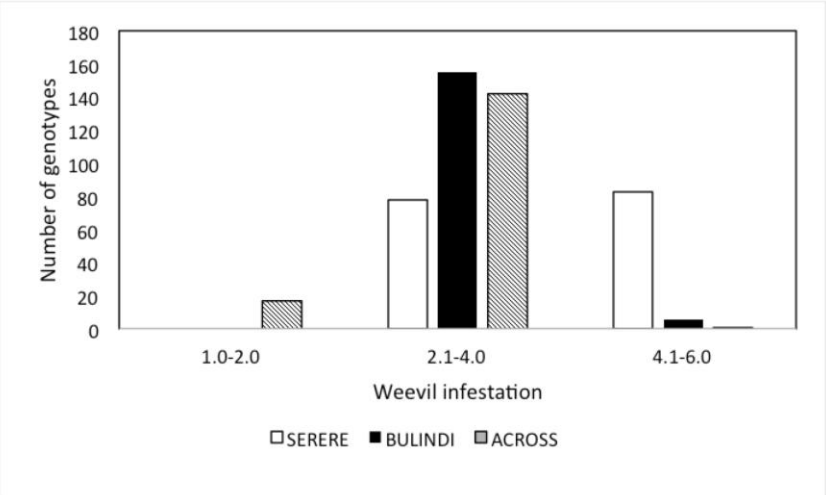

Fig 5. Weevil infestation across locations; Serere and Bulindi (1.0-2.0: resistance; 2.1-4.0: medium; 4.1-6.0: susceptible).

results suggest that the expression of pigments in purple-fleshed sweetpotato were due to genotypic effects and environmental factors as found by Mervat and Hanan (2009). Cultivar 101 with dark purple color had a prominent level of anthocyanin content (14.3 mg/100g FW) in both locations, while cultivar 124 with light cream color produced a small amount at 0.01mg/100 FW. Similar results have been found by many authors who reported that the level of anthocyanin varied from one cultivar to another and the more intense the purple color, the higher the levels of anthocyanin (Montilla et al., 2011; Hua et al., 2015). It was found also that most of the genotypes (90%) in this study were above the cream parent (0mg content) while 7% of the genotypes exhibited transgressive segregation with anthocyanin levels above the purple parent (12.9 mg/100g FW) in the Bulindi site. The results of this study revealed that there is a high potential for further improvement of the anthocyanin content in this purple-fleshed sweetpotato population through breeding in Uganda.

The three-way interaction (genotype by location by season) varied significantly for dry matter content (Table 1). Grüneberg et al. (2005) similarly reported significant effects of genotype by locations interaction on sweetpotato dry matter content. The tested genotypes were also significantly different in dry matter content. These results showed that there is genetic variability among the tested genotypes, which can be exploited for crop improvement. Results also indicated that genotypes expressed the trait differently in different environments. Earlier research reported that dry matter content varied widely with the genotype and locations (Manrique and Hermann, 2000; Mwanga et al., 2007; Rukundo et al., 2013; Shumbusha et al., 2014; Yada et al., 2017). In this study, dry matter content ranged from 21.5 to 33.7% across locations and seasons. These results of dry matter content are within the range found by Brabet et al. (1998) and Shumbusha et al. (2014) who reported that sweetpotato dry matter content >25% is an important component for acceptability of a new sweetpotato variety by sweetpotato growers. Therefore, the moderate to high dry matter content found in this study is within the range for farmers' acceptability.

Materials and methods

Plant material

The breeding population consisted of 191 true seed developed by the Sweetpotato Breeding and Genetics Program of North Carolina State University from a bi-parental cross of NCP06-020 x NC09-188. NCP06-020 is a high yielding purple-fleshed sweetpotato genotype with 4mg/1g dry weight anthocyanin content and high dry matter content (31%), while NC09-188 is a cream-fleshed genotype with high storage root yield, good horticultural traits and disease resistance. The seed was sent to Uganda and sown in sterilized soil in a screen house at National Agricultural Resources Research Institute –Namulonge (NaCRRI). Forty-five days after sowing, seedlings were transplanted into buckets (10L) to stimulate rapid growth in order to get enough planting materials for two sites. After four months, 159 clones were selected based on plant vigor and apparent disease free status of vines. In addition to the selected clones, three landraces were also selected from Sweetpotato Breeding Program at NaCRRI and a total of 162 clones were evaluated.

Description of study sites

Trials were conducted in two cropping seasons (season A: May-October/2015 and season B: October-March 2015/2016) at two locations in Uganda. These locations were the National Semi-Arid Resources Research Institute (NaSARRI), Serere and Bulindi Zonal Agricultural Research and Development Institute (BuZARDI). Serere is located in northeastern Uganda (33^{o} 27' E, 1^{o} 32'N) at an elevation of 1,140 m.a.s.l. This site is characterized by sandy soils with low organic matter content. It is among the low potential dry areas of Uganda due to great variability in its annual rainfall between years (1427mm). The rainfall is bimodal with peaks in April/May and August/September. Mean minimum and maximum temperatures at Serere are 17^{o}C and 33^{o}C, respectively (Kabi et al., 2001). Bulindi is located in Hoima District in Western Uganda. It is situated at 31^{o} 45'E, 1^{o} 45'N, and 1036 m.a.s.l. Annual mean of rainfall distributed in bimodal pattern of March-June season and August-November season is 1309 mm. The minimum and maximum temperatures are 16.8^{o}C and 27.7^{o}C, respectively. The Bulindi soil is mostly black red/clay loams.

Experimental design

Trials were established using a 9x18 Alpha Lattice design with two replications. Five cuttings from each genotype were planted on ridges in each replication. The spacing was 100 cm and 30 cm between rows and plants, respectively. Planting and management practices were similar in both sites, and weeding was carried out whenever it was necessary.

Data collection

During the trial, data were collected on apparent sweet potato virus disease infection and *Alternaria* blight scored using a scale of 1 to 9 according to CIP designations (CIP, 2008). The trials were harvested five months after planting and total marketable and non-marketable storage root weights were recorded for calculating total root yield. Roots classified as marketable roots had over 3 cm diameter with no cracks, insect damage or rotten part (Ekanayake et al., 1990). At harvest storage root weevil damage severity was assessed using the 1-9 scale above. The dry matter content of sweetpotato storage roots was determined using a method of Benesi et al. (2004), later modified by CIP (2008) and Yildirim et al. (2011). Two representative samples were collected from each plot after harvesting. These samples were washed, sliced and mixed to make a composite sample of each clone. Approximately 100 g of the composite sample put in paper bags and weighed prior to drying in oven at 65^{o}C. The weight of each sample was regularly determined after 24 h of drying until a constant weight. Total dry matter content (%) = (Dry weight of sample / Fresh weight of sample) x 100.

The anthocyanin content of sweetpotato storage roots was analyzed using combined approaches of pH differential and absorbance reading with a spectrophotometer (Giusti and Wrolstad, 2001) at NaCRRI Biosciences. Two dilutions of the

same sample were prepared, one with potassium chloride buffer, pH 1.0, and the other with sodium acetate buffer, pH 4.5, using the previously determined dilution factor. The samples were left in the dark to equilibrate for 15 min. Absorbance reads of each sample were determined at 530 nm and at 700 nm (to correct for haze), against a blank cell filled with distilled water. All readings were taken between 15 min and 1 hour after sample preparation. The absorbance (A) of each sample was calculated as follows: A = (A530 – A700) pH 1.0 – (A530 – A700) pH 4.5. The calculation of total monomeric anthocyanin content was done according to the formula:

Monomeric anthocyanin content (mg/liter) = (A × MW × DF × 1000)/ (ε × 1),

where, MW is the molecular weight for sweetpotato anthocyanin = 449.2, DF is the dilution factor, ε is the molar absorptivity = 26900 and 1 is for a standard 1-cm path length for light in a spectrophotometer.

Data analysis

The collected data were analyzed using Genstat (14th Edition) software. This analysis consisted of ANOVA performed on an individual plot basis. The linear model for alpha lattice design for a single location analysis was:

$Y_{ijk} = \mu + R_i + B_i/R_{ij} + G_k + E_{ijk,}$

where Y_{ijk} is the observation effects, μ is the grand mean of the experiment, R_i is replications, B_i/R_{ij} is block per replications, G_k is Genotypes and E_{ijk} is total error of experiment. The linear model for multiple location was: $Y_{ijkL} = \mu + Loc_{L+} Rep/Loc_{ij} + Bloc/Rep/Loc_{Lij} + Gen_k + Gen \times Loc_{LK} + E_{ijk.}$ Where μ is the grand mean of the experiment, Loc_L is locations, Rep/Loc_{ij} is Replications per location, $Bloc/Rep/Loc_{Lij}$ is Blocs per Replications per Location, Gen_k is Genotypes, Gen x Loc_{LK} is interaction of genotypes by location, $E_{ijk.}$ is total error of experiment.

Conclusion

The high yields and yield stability of the purple-fleshed sweetpotato genotypes in this population is an important characteristic for sweetpotato growers. More so, moderate to high dry matter content found is a promising factor for farmers to adopt these genotypes. Anthocyanin results showed the transgressive segregation of low content (for the cream-fleshed sweetpotato genotypes) to high content (for the purple-fleshed genotypes). Additionally, the study revealed that there is a high potential for further use of these purple-fleshed sweetpotato genotypes for use in population improvement and development of purple-fleshed varieties in Uganda.

Acknowledgments

We are greatly indebted to the Alliance for a Green Revolution in Africa (AGRA) for providing financial support for this study. Our acknowledgement also goes to the Rwanda Agriculture Board (RAB), for the study leave to the senior author for conducting the study.

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