Cassava Breeding Annual Report, 2019/2020

Multilocation Evaluation Trials In Uganda and Tanzania

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EXECUTIVE SUMMARY

Cassava is the second most important staple crop after banana and maize in Uganda and Tanzania respectively. The major two economic important diseases that threaten its production are Cassava mosaic disease (CMD and Cassava brown streak disease (CBSD). Breeding for resistance is the most effective and efficient method of their control. The IITA's regional breeding program based in Uganda has initiated breeding trials aimed at developing new varieties that combine dual resistance to the two diseases along with other farmer/end-user preferred characteristics like high fresh root yield, high dry matter content, mealiness and low cyanogenic potential. The trials were established at Sendusu and Serere, Uganda and at Bunda, Chato, Chambezi, Ukerewe and Ukiriguru in Tanzania.

Fifteen promising genotypes were evaluated across the two contrasting sites in Uganda whereas twelve were evaluated in Tanzania across the five sites. Five genotypes were identified in Uganda (MM16/0642, MM16/0801, MM16/0814, MM16/1016 and MM16/1487) and four in Tanzania (KBH16B/087, KBH16B/316, KBH16B/504 and KBH16B/521). These genotypes showed high resistance to cassava mosaic disease (CMD) and had lower cassava brown streak disease (CBSD) root incidence than the improved checks. Furthermore, the identified genotypes had high marketable dry root yield that were comparable to the commercial checks. We recommend that these genotypes should be passed on to NARO (Uganda) and TARI (Tanzania) for on-farm evaluation to get farmers' opinion about their performance and end-use characteristics. This information will be needed by the National Variety Release Committees in both countries if these genotypes will be tabled for official release.

These results show that our breeding program is making very good progress in developing new varieties that are better than the currently grown popular officially released varieties. This will ensure that new varieties will be higher yielding, more pest and disease resistant and more climate resilient along with meeting both farmers'/end-user preferences.

Introduction

Cassava is the second most important staple for Tanzania and Uganda after maize and bananas respectively. In Kenya it is only important in the coastal and western regions. Tanzania produces about 4.2 million tons from about 800,000 hectares whereas Uganda produces 2.8 million tons from 852,000 hectares of land. Although Kenya produces only about 0.86 million tons from 63,725 hectares, it ranks top in yield among the east African countries (FAO, 2015). However, this production is threatened by the two devastating viral diseases; Cassava Mosaic Disease (CMD) and Cassava Brown Streak Disease (CBSD). The two diseases are the greatest threat to cassava production in the whole sub-Saharan Africa where cassava is important. The most cost effective, efficient and sustainable means of increasing cassava productivity is to deploy high-yielding and disease-resistant varieties. Therefore, the IITA's regional breeding program (in Uganda and Tanzania) has continued screening cassava germplasm to identify dual resistant genotypes that also combine high dry matter root yield with other end-user preferred characteristics like mealiness.

Materials and Methods

The trials in Uganda were planted at Sendusu and Serere during the long rain season in April 2019. Fifteen promising genotypes that were in advanced stages of evaluation were used namely: MM06/0123, MM16/0025, MM16/0229, MM16/0521, MM16/0577, MM16/0642, MM16/0728, MM16/0770, MM16/0801, MM16/0814, MM16/0978, MM16/1016, MM16/1487, MM16/1583, and MM16/1612. Two checks were used: NARO-CASS 1 (commercial variety) and TME 14 (CBSD susceptible check. In Tanzania the trials were planted in January 2019 for the four sites in the Lake Zone (mid-altitude agroecology) namely; Bunda (Mara region), Chato (Geita region), Ukerewe (Mwanza region) and Ukiriguru (Mwanza region) and in April 2019 for the site in the coastal lowlands at Chambezi (Coast region). Twelve genotypes that were in advanced stages of evaluation were used, namely; KBH2014B/017, KBH2015B/036, KBH2015B/065, KBH2015B/071, KBH2015B/129, KBH2015B/157, KBH2016B/020, KBH2016B/087, KBH2016B/185, KBH2016B/316, KBH2016B/504 and KBH2016B/521. One improved and one local check was used at each site. The improved check for the Lake Zone sites was Mkombozi, whereas for Chambezi it was Mkuranga 1. The local checks for the Lake zone sites were Kalingisi or Lwakitangaza whereas, for Chambezi the local check was Albert. Cuttings for planting were taken from the previous season's crop to establish the new trials. The trials were arranged in a RCBD design with two and three replications in Uganda and Tanzania respectively. The plot sizes were 7m x 6 m for the trials in Uganda and 5m x 5m for the trials in Tanzania. The spacing of 1m x m was used for placing the cuttings. The plots were kept weed free and no fertilizers or chemical pesticides were applied during the crop growth cycle.

Plants were assessed for virus disease symptoms at 3 and 6 months after planting (MAP). CBSD leaf severity assessment was conducted using a scoring scale of 1 to 5 where, 1 = asymptomatic; 2 = slight feathery leaf chlorosis without stem symptoms; 3 = pronounced leaf feathery chlorosis, mild stem lesions and no stem dieback; 4 = severe leaf feathery chlorosis, severe stem lesions and no dieback; and 5 = defoliation, severe stem lesions and dieback (Gondwe et al. 2003). Simultaneously, CMD severity was scored on a scale of 1-5, where: 1 = no symptoms; 2 = up to 25% leaf area chlorotic, mild leaf distortion,

and no stunting; 3 = 25% - 50% leaf area chlorotic, moderate leaf distortion, no stunting; 4 = 50% - 75% leaf area chlorotic, severe leaf distortion, and moderate stunting; and 5 = 75% - 100% leaf area distortion, small leaflets, almost no lamina, and severe stunting. Incidences of CBSD and CMD were calculated as the percentage of CBSD or CMD symptomatic plants in each treatment plot (Fodong et al., 2002). Mean CMD and CBSD severity scores were calculated as the averages of scores value.

Harvesting was done at 12 months after planting (MAP) by uprooting all plants in the net plot area. The roots were detached from the plants, . and cut transversally about 5 cm from both ends to separate them into marketable (CBSD root necrosis severity score of class ≤ 2) and unmarketable (CBSD root necrosis severity score of class ≥ 3), counted and weighed to estimate marketable (MFRY), non-marketable and total fresh root yield (TFRY) components. The percentage marketable fresh root yield (PMFRY) was calculated as the ratio of MFRY (t/ha) to the total fresh root yield (TFRY) (t/ha) expressed as a percentage. To confirm the status of the roots in both the marketable and unmarketable categories, all the roots were cut transversally by making five cross-sectional cuts in each of the roots. CBSD symptoms were then scored from each cut using a scale of 1-5 where 1 = no root necrosis; 2 = mild root necrotic lesions (1–10% of the root surface area necrotic); 3 = pronounced root necrotic lesions (11–25%); 4 = severe root necrotic lesions (26–50%) combined with mild root constriction; and 5 = very severe root necrotic lesion (>50%) coupled with severe constriction (Kawuki et al., 2016). The most frequent severity score among the cuts was recorded to represent that plot. Root samples were taken from the marketable roots on a sub-plot basis to determine root dry matter content using the specific gravity (SG) method as described by Kawano et al. (1987). In brief, SG was determined by weighing approximately 3 kg of fresh roots in air and re-weighing the same roots when completely submerged in water. SG was then calculated using the following formula:

SG = Weight in air/ (Weight in air – Weight in water)   (1)

The SG was then used to calculate dry matter content (DMC) using the following formula described in Kawano et al. (1987).

DMC = (158.3 x SG) – 142.0   (2)

Data were subjected to analyses of variance (ANOVA) using the GenStat Discovery software (VSN International, http://www.vsni.co.uk). The least significant difference (LSD) was used to separate the means.

Results

Uniform Yield Trial, Sendusu and Serere, Uganda

The analysis of variance (ANOVA) table for the 11 traits evaluated among the 15 promising genotypes is given under Table 1. Highly significant (p<0.001) differences were detected among the genotypes for all the traits except for root necrosis severity (RNS) which was significant at p<0.05. Highly significant (p<0.001) differences were detected between the sites for cassava brown streak disease incidence (CBSDI), cassava brown streak disease severity (CBSD), total fresh root yield (TFRY), dry matter content

(DMC), marketable dry root yield (MDRY), and total dry root yield (TDRY). Furthermore, highly significant (p<0.001) genotype x site (GxS) interaction effects were detected for only TFRY, MDRY, and TDRY. However, the GxS interaction effects were significant (p<0.05) for CBSDI and CBSDS (Table 1).

The performance of the 15 genotypes for the various traits are given in Table 2. High (p<0.01) to highly significant (p<0.001) differences among the genotypes were detected for both CBSD and CMD incidences and severities at both sites. One genotype only (MM16/1487) did not show any CBSD leaf symptoms at both sites. Five genotypes (MM16/0521, MM16/0577, MM16/0814, MM16/1583 and TME 14) had all plants showing CBSD leaf symptoms (100.0% incidence) at Sendusu. Sendusu had a higher mean CBSDI (75.6%) than Serere (35.1%) and had a higher CBSDS (2.5) than Serere (1.9).

Nine of the genotypes (MM06/0123, MM16/0521, MM16/0642, MM16/0801, MM161016, MM16/1484, MM16/1583 and TME 14) had no CMD symptoms at Sendusu. Five of them (MM16/0642, MM16/0801, MM16/0814, MM16/1016 and MM16/1487) had no CMD symptoms at both sites. Serere had a higher CMD incidence (24.3%) than Sendusu (18.1%).

High (p<0.01) to highly significant (p<0.001) differences were detected among the genotypes for TFRY and TDRY, MFRY and MDRY at both sites. TFRY at Sendusu ranged from 11.6 t/ha (MM16/0521) to 109.9 t/ha (MM16/1487) with a mean of 38.3 t/ha, whereas, at Serere it ranged from 4.9 t/ha (MM16/1016) to 30.9 t/ha (MM16/0025) with a mean of 16.1 t/ha (Table 2). MFRY at Sendusu ranged from 11.5 t/ha (MM16/0521) to 109.9 t/ha (MM16/1487) with a mean of 35.4 t/ha whereas, at Serere MFRY ranged from 4.2 t/ha (MM16/0521) to 30.9 t/ha (MM16/0025) with a mean of 14.2 t/ha (Table 12).

TDRY at Sendusu ranged from 4.5 t/ha (MM16/0521) to 42.3 t/ha (MM16/1487) with a mean of 14.8 t/ha. At Serere TDRY ranged from 1.6 t/ha (MM16/1016) to 11.5 t/ha (MM16/0025) with a mean of 5.7 t/ha. At Sendusu, MDRY ranged from 3.3 t/ha (TME 14) to 42.3 t/ha (MM16/1487) with a mean of 13.7 t/ha. At Serere, MDRY ranged from 1,5 t/ha (MM16/1583) to 11.5 t/ha (MM16/0025) with a mean of 5.0 t/ha (Table 2).

Differences among genotypes for dry matter content (DMC)were only significant (p<0.050 at Sendusu, where it ranged from 35.3% (MM16/0978) to 42.0% (NARO-CASS 1) with a mean of 38.3% (Table 2). At Serere, DMC ranged from 30.2% (TME 14) to 34.2% (MM16/0801) with a mean of 30.2%.

Genotypic differences for percentage marketable fresh root yield (PMFRY) were highly significant (p<0.001) at Sendusu and significant (p<0.05) at Serere. At Sendusu, PMFRY ranged from 38.1% (TME 14) to 100.0% (MM16/0801, MM16/1016, MM16/1487 and MM16/1612) with a mean of 89.6%. At Serere, PMFRY ranged from 12.6% (TME 14) to 100.0% (MM16/0025, MM16/0229, MM16/0642, MM16/0814 and MM16/1016) with a mean of 85.5% (Table 2).

Highly significant (p<0.001) genotypic effects were detected for root necrosis incidence (RNI) at Sendusu, whereas, at Serere only significant differences (p<0.05) were detected. At Sendusu, four genotypes (MM16/0801, MM16/1016, MM16/1487 and MM16/1612) did not have root necrosis (0.0% RNI). Only one genotype (MM16/1016) showed no root necrosis at both sites. The highest root necrosis incidence at

both Sendusu and Serere was recorded from TME 14 (63.7% and 87.1% respectively). TME 14 is the susceptible check for CBSD (Table 2).

Advanced Yield Trial, Tanzania

The ANOVA Table for the 11 traits evaluated across five sites in Tanzania is presented in Table 3. Highly significant (p<0.001) genotypic differences were detected for all the traits. Highly significant site differences (p<0.001) were detected for all the traits except for CMD severity (CMDS) and root necrosis severity RNS). High significant (p<0.01) to highly significant (p<0.001) GxS interaction effects were detected for all the traits except for CBSDI, CMDS and DMC. Furthermore, significant (p<0.05) GxS interaction effects were detected for CBSDI and CMDS (Table 3.

Highly significant genotypic effects (p<0.001) were detected for CBSDI across all the sites except at Chambezi (Table 4). Two genotypes (KBH2016B/087 and KBH2016B/316) did not show CBSD leaf symptoms across all the sites. The local checks had the highest CBSDI across all the sites. Chambezi was the site with the highest CBSD leaf symptom incidence (35.9%) as well as the highest CBSD leaf symptom severity (2.3). The lowest CBSD leaf symptom severity (1.4) was recorded at Ukiriguru (Table 5).

Significant differences (p<0.05) to highly significant genotypic effects (p<0.001), were detected for CMD incidence (CMDI) across all the sites (Table 6). Five genotypes (Improved check, KBH2015B/157, KBH2016B/504, and KBH2016B/521) did not show CMD symptoms across all the sites. The highest CMD incidence was recorded at Chato (15.3%), whereas, the lowest CMD incidence (3.5%) was recorded at Ukerewe (Table 6). The highest CMD severity (CMDS) was recorded at Ukiriguru (1.5) across the sites, whereas, the lowest (1.3) was recorded at Ukerewe (Table 7).

Highly significant (p<0.001) genotypic effects for total fresh root yield (TFRY) were detected across all the sites except at Ukerewe. The effects at Ukerewe were significant at p<0.05 (Table 8). At Bunda TFRY ranged from 4.4 t/ha (KBH2015B/157) to 31.7 t/ha (KBH2016B/087) with a mean of 15.9 t/ha. At Chambezi, TFRY ranged from 0.16 t/ha (KBH2015B/065) to 26.8 t/ha (KBH2016B/521) with a mean of 9.66 t/ha. At Chato, TFRY ranged from 2.7 t/ha (KBH2015B/071) to 15.8 t/ha (KBH2016B/316 with a mean of 8.2 t/ha. At Ukerewe, TFRY ranged from 4.2 t/ha (KBH2016B/504) to 25.2 t/ha (KBH2016B/087) with a mean of 12.2 t/ha. Furthermore, at Ukiriguru, TFRY ranged from 3.1 t/ha (KBH2015B/036) to 24.3 t/ha (Local Check) with a mean of 10.7 t/ha (Table 8).

Genotypic effects for dry matter content (DMC) were significant (p<0.01) to highly significant (p<0.001) only at Chato and Ukerewe (Table 9). At Chato, DMC ranged from 27.3% (KBH2016B/316) to 36.1% (KBH2016B/020) with a mean of 31.9%. At Ukerewe, DMC ranged from 27.2% (KBH2016B/521) to 35.8% (KBH2016B/020) with a mean 31.2% (Table 9).

Genotypic effects were highly significant (p<0.001) for marketable dry root yield (MDRY) across all the sites except at Ukerewe (Table 10).At Bunda, MDRY ranged from 0.3 t/ha (KBH2014B/017) to 9.1 t/ha (KBH2016B/087) with a mean of 3.7 t/ha, which was the highest among the sites. At Chambezi MDRY ranged from 0.0 t/ha (KBH2015B/065 and KBH2015B/129) to 8.7 t/ha (KBH2016B/521) with a mean of 2.7 t/ha. At Chato, MDRY ranged from 0.7 t/ha (KBH2015B/071) to 4.7 t/ha (KBH2016B/020) with a mean of

2.2 t/ha. At Ukerewe, MDRY ranged from 1.1 t/ha (KBH2016B/504) to 7.5 t/ha (KBH2016B/087) with a mean of 3.3 t/ha. Lastly, at Ukiriguru, MDRY ranged from 0.4 t/ha (KBH2015B/036) to 5.8 t/ha (KBH2016B/316) with a mean of 2.9 t/ha (Table 10).

Highly significant (p<0.001) genotypic effects were detected for total dry root yield (TDRY)across all the sites except at Ukerewe (Table 11).At Bunda, TDRY ranged from 1.2 t/ha (KBH2014B/017) to 9.1 t/ha (KBH2016B/087) with a mean of 4.4 t/ha, which was the highest among the sites. At Chambezi, TDRY ranged from 0.1 t/ha (KBH2015B/065) to 8.7 t/ha (KBH2016B/521) with a mean of 3.0 t/ha. At Chato, TDRY ranged from 0.9 t/ha (KBH2015B/071) to 5.5 t/ha t/ha (KBH2016B/020) with a mean of 2.1 t/ha. At Ukerewe, TDRY ranged from 1.0 t/ha (KBH2015B/036) to 5.6 t/ha (KBH2016B/521) with a mean of 3.8 t/ha. Furthermore, at Ukiriguru, TDRY ranged from 1.0 t/ha (KBH2015B/036) to 8.3 t/ha (Local Check) with a mean of 3.1 t/ha (Table 11).

Genotypic effects were significant (p<0.05) to highly significant (p<0.001) for percentage marketable fresh root yield (PMFRY) across all the sites except at Ukerewe where they were non-significant (Table 12). AT Bunda, PMFRY ranged from 17.5% (KBH2014B/017) to 100.0% (KBH2016B/185, KBH2016B/316 and KBH2016B/504) with a mean of 78.8%. At Chambezi, PMFRY ranged from 0.0% (Local Check) to 100.0% (KBH2016B/316, KBH2016B/504 and KBH2016B/521) with a mean of 63.0%. At Chato, PMFRY ranged from 71.1% (Local Check) to 100.0% (KBH2015B/129, KBH2016B/316 and KBH2016B/504) with a mean 85.8%. AT Ukerewe, PMFRY ranged from 57.3% (Improved Check) to 100.0% (KBH2015B/065, KBH2015B/157, KBH2016B/087, KBH2016B/316, KBH2016B/504 and KBH2016B/521) with a mean of 87.7%, which was the highest across the sites. Finally, at Ukiriguru, PMFRY ranged from 35.5% (KBH2015B/071) to 100.0% (KBH2015B/157, KBH2016B/087, and KBH2016B/504) with a mean of 78.8%. Only one genotype (KBH2016B504) recorded 100.0% PMFRY (no root necrosis) across all the five sites (Table 12).

High significant (p<0.01) to highly significant (p<0.001) genotypic effects were detected for root necrosis incidence (RNI)across all the sites except at Ukerewe where the effects were significant at p<0.05 (Table 13). At Bunda, RNI ranged from 0.0% (KBH2016B/185, KBH2016B/316, and KBH2016B/504) to 36.3% (KBH2014B/017) with a mean of 22.0%. At Chambezi, RNI ranged from 0.0% (KBH2016B/316, KBH2016B/504 and KBH2016/521) with a mean of 37.4%, which was the highest among the sites.AT Chato, RNI ranged from 0.0% (KBH2015B/129, KBH2016B/316 and KBH2016B/504) to 66.2% (KBH2014B/017) with a mean of 15.8%. At Ukerewe, RNI ranged from 0.0% (KBH2016B/087, KBH2016B/316, KBH2016B/504 and KBH2016B/521) to 44.8% (KBH2014B/017 with a mean of 13.9% which was the lowest among the sites. Finally, at Ukiriguru, RNI ranged from 0.0% (KBH2016B/087 and KBH2016B/504) to 68.6% (KBH2015B/036) with a mean of 25.2%. Only one genotype (KBH2016B/504) had no root necrosis (0.0% RNI) across all the sites (Table 13).

High significant (p<0.01) to highly significant (p<0.001) genotypic effects were detected for root necrosis severity (RNS)across all the sites except at Chato where they were non-significant (Table 14). At Bunda, RNS ranged from 1.0 (KBH2016B185, KBH2016B/316and KBH2016B/504) to 4.6 (KBH2015B/036) with a mean of 2.5. At Chambezi, RNS ranged from 1.0 (KBH2016B/316, KBH2016B/504 and KBH2016B/521) to 4.7 (Local Check) with a mean of 2.7. At Chato, RNS ranged from 1.0 (KBH2015B/129, KBH2016B/316 and KBH2016B504) to 4.0 (KBH2014B/017) with a mean of 2.5. At Ukerewe, RNS ranged from 1.0

(KBH2016B/087, KBH2016B316, KBH2016B/504 and KBH2016B/521) with a mean of 2.5. Finally, at Ukiriguru, RNS ranged from 1.0 (KBH2015B157, KBH2016B/087 and KBH2016B/504) to 4.5 (KBH2015B/036) with a mean of 2.6. Only one genotype (KBH2016B/504) had RNS of class 1.0 (no root necrosis) across all the sites (Table 14).

Discussion

Fifteen promising genotypes were evaluated across two contrasting sites (Sendusu and Serere) in Uganda. Both sites are now hot spots for both CMD and CBSD enabling the selection of disease resistant genotypes. Planting materials of these clones (MM16 series) have now been recycled for three seasons. This is enough recycling frequency to be confident that genotypes that do not show disease symptoms are resistant/tolerant (Kawuki et al. 2016). The highly significant differences observed among the genotypes for almost all the traits indicate that there is high genetic variability among them to enable identification and selection of elite performing ones. The only sustainable and cost-effective means of control of the two economically important viral diseases (CMD and CBSD) is to develop and deploy cassava varieties with dual resistance to both CBSD and CMD. Currently, all the officially released varieties in all the CBSD endemic countries, are tolerant to CBSD and they, therefore, serve as sources of inoculum for the spread of CBSD to new areas. Contrary to tolerant varieties, truly resistant cultivars are not readily infected, even when exposed to large amounts of vector borne inoculum; when infected develop inconspicuous symptoms and not associated with obvious deleterious effects on growth and yield and support low virus content and thus to be poor source of inoculum (Thresh et al., 1998). Two genotypes (MM16/1016 and MM16/1487) were observed to show resistance to both CMD and CBSD. MM16/1487 also had the highest marketable dry root yield at Sendusu which was comparable to that of the commercial check (NARO-CASS 1). Three other genotypes (MM16/0642, MM16/0801 and MM16/0814) showed high resistance to CMD and had root necrosis incidences less than 5.0% which was much better than that of the commercial check (NARO-CASS 1). These five genotypes are the best candidates for further evaluation under on-farm conditions to get farmers' opinion about their agronomic and end-user characteristics.

Twelve promising genotypes were evaluated in Tanzania across five sites. Four of the sites (Bunda, Chato, Chambezi and Ukerewe) are disease hot-spots and therefore very ideal for screening cassava germplasm for resistance to diseases. The high significant (p<0.01) to highly significant (p<0.001) Genotype x Site interaction effects detected for all the traits except for CBSDI, CMDS and DMC imply that selection for good performing genotypes should be site specific. Four promising genotypes (KBH2015B/157, KBH2016B/504, and KBH2016B/521) did not show CMD symptoms across all the sites. Significant genotypic effects detected for root necrosis incidence (RNI) across all the sites imply that selection for resistant genotypes would be effective. Only one genotype (KBH2016B/504) had no root necrosis (0.0% RNI) across all the sites. However, three other genotypes (KBH16B/316, KBH16B/316, and KBH16/521 had very low root necrosis incidences (ranging from 2.0% to 6.0%) that was much lower than that of the commercial checks. These four genotypes are the best candidates for further evaluation under on-farm conditions to get farmers' opinion on its merits.

Conclusion and recommendations

The results from these trials in Uganda and Tanzania showed that there was high disease pressure across all the sites to justify the selection of promising genotypes for further on-farm evaluation. Five genotypes were identified in Uganda (MM16/0642, MM16/0801, MM16/0814, MM16/1016 and MM16/1487)and four in Tanzania (KBH16B/087, KBH16B/316, KBH16B/504 and KBH16B/521). We recommend that these should be passed on to NARO (Uganda) and TARI (Tanzania) for on-farm evaluation to get farmers' opinion about their performance and end-use characteristics. This information will be needed by the National Variety Release Committees in both countries if these genotypes will be tabled for official release.

Acknowledgements

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Table 1: Analysis of Variance (ANOVA) for 15 promising genotypes evaluated under UYT at Sendusu and Serere, Uganda, 2019/2020 season.

SOV	DF	Mean Squares					
		6CBSDI+	6CBSDS	6CMDI	6CMDS	TFRY	DMC
Rep	1	22.5	0.2353	12.04	0.2353	2.5	23.398
Genotype (G)	19	3528.8***	1.7036***	3820.75***	2.6246***	1038.87***	12.283*
Site (S)	1	29228.1***	5.1607***	108.66	0.1607	6003.5***	114.512***
G x S	13	1007*	0.5069*	44.27	0.1607	518.74***	9.659
Residual	33	370.6	0.205	50.71	0.205	43.43	6.143

Table 1 cont'd: Analysis of Variance (ANOVA) for 18 promising genotypes evaluated under AYT1 at Sendusu and Serere, Uganda, 2018/2019 season.

SOV	DF	Mean Squares					
		MDRY	TDRY	PMFRY	RNI	RNS	
Rep	1	0.982	1.262	25.2	116.7	0.0588	
Genotype (G)	19	179.891***	166.315***	1201.3***	1154.8***	1.5124*	
Site (S)	1	885.083***	981.303***	67.6	38.4	0.0714	
G x S	13	81.054***	83.726***	123.6	112.5	0.4945	
Residual	33	7.084	5.855	236.7	190.7	0.6952	

+ 6CBSDI = CBSD incidence (%) at 6 MAP, 6CBSDS = CBSD severity score at 6 MAP, 6CMDS = CMD severity score at 6 MAP, 6CMDI = CMD incidence (%) at 6 MAP, RNI = CBSD root necrosis incidence (%), KKFRY = Marketable fresh root yield (t/ha), TFRY = Total fresh root yield (t/ha), DMC = Dry matter content (%), MDRY = Marketable dry root yield (t/ha), TDRY = Total Dry root yield (t/ha), PMFRY = Percentage Marketable root weight, RNI = Root necrosis incidence (%), RNS = CBSD root necrosis severity score, CV = Coefficient of variation (%), LSD = Least significant difference, *** Statistically Significant at p = 0.001, ** significant at p = 0.01 *significant at p =0.05

Table 2: Performance of 15 promising genotypes evaluated under UYT at Sendusu and Serere, Uganda, 2019/2020 season.

S/N	Clone	Pedigree	6CBSDI+		6CBSDS		6CMDI		6CMDS	
			Sendusu	Serere	Sendusu	Serere	Sendusu	Serere	Sendusu	Serere
1.	MM06/0123	Kibaha HS	100.00	66.70	3.00	3.00	0.00	5.26	1.00	2.00
2.	MM16/0025	MM06/0130 X MM06/0130	7.50	0.00	1.50	1.00	28.03	74.79	3.00	3.00
3.	MM16/0229	MM06/0130 X MM06/0130	97.50	11.10	2.50	1.50	2.50	0.00	1.50	1.00
4.	MM16/0521	MM06/0128 x MM06/0128	100.00	32.50	3.00	2.00	0.00	5.00	1.00	1.50
5.	MM16/0577	MM06/0128 X MM06/0128	100.00	79.20	3.00	2.50	2.63	5.26	1.50	1.50
6.	MM16/0642	MM06/0128 X MM06/0128	60.00	0.00	3.00	1.00	0.00	0.00	1.00	1.00
7.	MM16/0728	MM06/0128 X MM06/0128	97.50	32.00	2.00	2.00	78.89	80.45	3.00	3.00
8.	MM16/0770	MM06/0123 x MM06/0128	0.00	0.00	1.00	1.00	72.50	78.89	3.00	2.50
9.	MM16/0801	MM06/0123 x MM06/0128	97.50	75.40	3.00	3.00	0.00	0.00	1.00	1.00
10.	MM16/0814	MM06/0123 x MM06/0128	100.00	46.50	3.00	2.50	0.00	0.00	1.00	1.00
11.	MM16/0978	MM06/0123 x MM06/0128	90.00	33.20	2.50	2.00	20.00	43.29	3.00	3.00
12.	MM16/1016	MM06/0123 x MM06/0128	97.40	0.00	3.00	1.00	0.00	0.00	1.00	1.00
13.	MM16/1487	MM06/0123 x MM06/0123	0.00	0.00	1.00	1.00	0.00	0.00	1.00	1.00
14.	MM16/1583	MM06/0123 x TME 14	100.00	92.50	3.00	3.00	0.00	2.50	1.00	1.50
15.	MM16/1612	TME 14 HS	68.90	0.00	2.00	1.00	100.00	94.87	3.00	3.50
	NARO-CASS 1	Kibaha HS	30.00	46.40	3.00	2.00	20.00	6.25	2.50	1.50
	TME-14		100.00	81.10	3.00	3.00	0.00	16.37	1.00	2.50
	Mean		75.66	35.10	2.50	1.91	19.09	24.29	1.74	1.85
	LSD_G		12.07***	44.93***	0.64***	1.157**	8.16***		0.64***	1.21**
	CV		7.50	60	12.10	28.5	20.20		17.50	30.9

+6CBSDI = CBSD incidence (%) at 6 MAP, 6CBSDS = CBSD severity score at 6 MAP, 6CMDI = CMD incidence (%) at 6 MAP 6CMDS = CMD severity score at 6 MAP,   CV = Coefficient of variation (%), LSD = Least significant difference,

*** Statistically Significant at p = 0.001, ** significant at p = 0.01 *significant at p =0.05, , CV = Coefficient of variation (%), LSD = Least significant difference, *** Statistically Significant at p = 0.001, ** significant at p = 0.01

*significant at p =0.05

Table 2 Cont'd: Performance of 15 promising genotypes evaluated under UYT at Sendusu and Serere, Uganda, 2019/2020 season

	Clone	Pedigree	TFRY+_t/ha		MFRY_t/ha		TDRY_t/ha		MDRY_t/ha	
			Sendusu	Serere	Sendusu	Serere	Sendusu	Serere	Sendusu	Serere
1.	MM06/0123	Kibaha HS	42.42	15.95	27.72	10.52	15.54	5.30	10.16	3.52
2.	MM16/0025	MM06/0130 X MM06/0130	42.67	30.90	39.58	30.90	16.22	11.53	15.05	11.53
3.	MM16/0229	MM06/0130 X MM06/0130	55.28	8.35	53.44	8.35	21.65	3.26	20.92	3.26
4.	MM16/0521	MM06/0128 x MM06/0128	11.61	8.18	11.52	4.18	4.52	2.81	4.49	1.62
5.	MM16/0577	MM06/0128 X MM06/0128	21.88	13.69	19.87	12.61	8.38	4.63	7.60	4.28
6.	MM16/0642	MM06/0128 X MM06/0128	52.44	19.37	50.43	19.37	19.19	6.53	18.46	6.53
7.	MM16/0728	MM06/0128 X MM06/0128	31.73	13.03	26.89	12.44	11.67	4.80	9.88	4.60
8.	MM16/0770	MM06/0123 x MM06/0128	19.62	21.71	19.21	19.87	7.99	7.56	7.83	6.92
9.	MM16/0801	MM06/0123 x MM06/0128	28.89	22.38	28.89	21.71	10.94	8.77	10.94	8.51
10.	MM16/0814	MM06/0123 x MM06/0128	45.59	16.37	43.92	16.37	18.09	5.51	17.44	5.51
11.	MM16/0978	MM06/0123 x MM06/0128	18.79	12.69	16.53	11.44	6.40	4.78	5.61	4.32
12.	MM16/1016	MM06/0123 x MM06/0128	20.54	4.93	20.54	4.93	8.06	1.61	8.06	1.61
13.	MM16/1487	MM06/0123 x MM06/0123	109.89	25.97	109.89	25.72	42.31	8.01	42.31	7.94
14.	MM16/1583	MM06/0123 x TME 14	14.28	6.26	11.86	4.01	5.40	2.29	4.48	1.47
15.	MM16/1612	TME 14 HS	26.89	21.04	26.89	20.21	9.97	7.04	9.97	6.77
16.	NARO-CASS 1	Kibaha HS	86.92	21.63	85.67	16.95	36.54	8.38	36.01	6.58
17.	TME-14		21.88	11.27	8.52	1.25	8.47	3.44	3.30	0.37
	Mean		38.31	16.10	35.37	14.17	14.79	5.66	13.68	5.02
	LSD_G		15.96***	10.96**	17.86***	10.84***	6.07***	3.51**	6.74***	3.61***
	CV		19.7	32.1	23.2	36.1	19.4	29.2	22.7	33.9

+TFRY = Total fresh root yield (t/ha), MFRY = Marketable fresh root yield (t/ha, TDRY = Total Dry root yield (t/ha), MKDRY = Marketable dry root yield (t/ha), , CV = Coefficient of variation (%), LSD = Least significant difference, *** Statistically Significant at p = 0.001, ** significant at p = 0.01 *significant at p =0.05

Table 2 Cont'd : Performance of 15 promising genotypes evaluated under UYT at Sendusu and Serere, Uganda, 2019/2020 season

	Clone	Pedigree	DMC_%		PMFRY_%		RNI		RNS	
			Sendusu	Serere	Sendusu	Serere	Sendusu	Serere	Sendusu	Serere
1.	MM06/0123	Kibaha HS	36.64	33.28	64.60	69.60	33.00	21.40	2.50	1.50
2.	MM16/0025	MM06/0130 X MM06/0130	38.14	37.19	92.60	100.00	8.20	0.00	2.00	1.00
3.	MM16/0229	MM06/0130 X MM06/0130	39.16	37.23	96.70	100.00	5.90	0.00	1.50	1.00
4.	MM16/0521	MM06/0128 x MM06/0128	38.91	36.57	99.50	63.10	4.20	37.50	1.50	2.00
5.	MM16/0577	MM06/0128 X MM06/0128	38.22	33.66	92.20	89.70	6.80	9.50	1.00	2.00
6.	MM16/0642	MM06/0128 X MM06/0128	36.59	34.94	95.70	100.00	4.50	0.00	2.00	1.00
7.	MM16/0728	MM06/0128 X MM06/0128	36.85	36.56	83.20	93.00	16.10	8.80	3.00	2.00
8.	MM16/0770	MM06/0123 x MM06/0128	40.60	34.81	97.30	92.50	3.80	8.90	1.50	2.00
9.	MM16/0801	MM06/0123 x MM06/0128	37.95	39.16	100.00	96.90	0.00	3.60	1.00	1.50
10.	MM16/0814	MM06/0123 x MM06/0128	39.62	33.56	95.70	100.00	1.90	0.00	1.00	1.00
11..	MM16/0978	MM06/0123 x MM06/0128	35.29	38.77	86.40	90.70	13.90	9.60	2.50	3.00
12.	MM16/1016	MM06/0123 x MM06/0128	39.24	32.52	100.00	100.00	0.00	0.00	1.00	1.00
13.	MM16/1487	MM06/0123 x MM06/0123	38.48	31.26	100.00	99.20	0.00	2.20	1.00	1.50
14.	MM16/1583	MM06/0123 x TME 14	37.83	36.72	83.00	72.40	13.90	21.40	2.00	2.00
15.	MM16/1612	TME 14 HS	37.23	33.53	100.00	96.40	0.00	4.30	1.00	2.00
16.	NARO-CASS 1	Kibaha HS	42.04	38.47	98.40	78.20	1.10	20.50	1.50	3.00
17.	TME-14		38.68	30.22	38.10	12.60	63.70	87.10	3.00	3.50
	Mean		38.32	35.2	89.60	85.50	10.40	13.80	1.71	1.82
	LSD_G		2.85*	NS	18.00***	43.24*	17.61***	38.18*	NS	NS
	CV		3.50	8.2	9.50	23.8	79.70	130.3	42.8	49.3

DMC = Dry matter content (%), PMFRY = Percentage Marketable root weight, RNI = CBSD root necrosis incidence (%), RNS = CBSD root necrosis severity score, CV = Coefficient of variation (%), LSD = Least significant difference, *** Statistically Significant at p = 0.001, ** significant at p = 0.01 *significant at p =0.05

Table 3: Analysis of Variance (ANOVA) for 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

SOV	DF	Mean Squares					
		6CBSDI	6CBSDS	6CMDI	6CMDS	TFRY	DMC
Rep	2	901.6	0.3979	218.6	0.0296	57.84	9.19
Genotype (G)	13	12621.4***	7.504***	2159.9***	4.2299***	470.16***	24.39*
Site (S)	4	3170.3***	5.8635***	1037.8***	0.3622	397.14***	215.14***
G x S	52	780.5*	1.0422**	460.3***	0.4956*	84.18***	12.25
Residual	117	521.1	0.5483	112.8	0.3067	33.88	12.89

Table 3 cont'd: Analysis of Variance (ANOVA) for 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season

SOV	DF	Mean Squares					
		MDRY	TDRY	PMFRY	RNI	RNS	
Rep	2	3.118	4.719	291.3	631.6	3.521	
Genoptype (G)	13	41.21***	42.076***	3646.8***	5093.7***	12.7189***	
Site (S)	4	16.276***	22.339***	3241.2***	3524.7***	0.7901	
G x S	52	7.217***	8.521***	1351.8***	1241.6***	2.2579***	
Residual	117	2.867	3.091	461.4	358.8	0.9232	

+6CBSDI = CBSD incidence (%) at 6 MAP, 6C BSDS = CBSD severity score at 6 MAP, 6CMDS = CMD severity score at 6 MAP, 6CMDI = CMD incidence (%) at 6 MAP, , RNI = CBSD root necrosis incidence (%), TFRY = Total fresh root yield (t/ha), DMC = Dry matter content (%), MDRY = Marketable dry root yield (t/ha), TDRY = Total Dry root yield (t/ha), PMKRY = Percentage marketable root weight, RNI = Root necrosis incidence (%), RNS = CBSD root necrosis severity score, CV = Coefficient of variation (%), LSD = Least significant difference, *** Statistically Significant at p = 0.001, ** significant at p = 0.01 *significant at p =0.05

Table 4: Cassava brown streak disease incidence (CBSDI) (%) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		93.1	47.50	97.8	86.80	58.60	76.00
2.	KBH2014B/017		33.30	77.80	12.50	11.10	0.00	27.20
3.	KBH2015B/036		13.70	33.30	5.00	17.50	10.20	16.20
4.	KBH2015B/065		0.00	58.30	0.00	0.00	0.00	11.50
5.	KBH2015B/071		27.80	41.70	25.00	51.70	0.00	29.30
6.	KBH2015B/129		7.40	50.00	18.80	4.10	0.00	16.40
7.	KBH2015B/157		33.60	49.80	0.00	0.00	0.40	17.10
8.	KBH2016B/020		4.30	6.10	0.00	0.00	4.10	3.20
9.	KBH2016B/087		0.00	0.00	0.00	0.00	0.00	0.00
10.	KBH2016B/185		0.00	37.80	0.00	0.00	0.00	7.80
11.	KBH2016B/316		0.00	0.00	0.00	0.00	0.00	0.00
12.	KBH2016B/504		0.00	0.00	0.00	50.30	0.00	10.06
13.	KBH2016B/521		0.00	0.00	0.00	0.30	0.00	0.06
14.	Local Check		93.00	100.00	100.00	95.6	95.8	97.10
	Mean		21.90	35.90	18.50	22.50	11.70	22.40
	LSD_Genotype (G)		22.21***	NS	12.44***	40.69***	23.33***	16.51***
	LSD_Sites (S)		-	-	-	-	-	9.87***
	LSD_GxS		-	-	-	-	-	36.91*
	CV (%)		60.50	107.80	31.10	106.10	118.30	102

Table 5: Cassava brown streak disease severity (CBSD) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		3.5	3.93	2.75	2.73	2.08	3.00
2.	KBH2014B/017		2.07	3.33	2.00	1.33	1.00	1.95
3.	KBH2015B/036		2.67	1.67	1.50	2.17	2.67	2.14
4.	KBH2015B/065		1.00	2.50	1.00	0.99	1.00	1.30
5.	KBH2015B/071		2.77	2.33	3.25	2.01	1.00	2.28
6.	KBH2015B/129		1.67	2.33	2.00	1.02	1.00	1.62
7.	KBH2015B/157		2.67	3.80	1.00	1.00	1.03	1.90
8.	KBH2016B/020		2.50	2.00	1.00	1.00	2.50	1.81
9.	KBH2016B/087		1.00	1.00	1.00	1.00	1.00	1.01
10.	KBH2016B/185		1.00	3.00	1.00	1.00	1.00	1.41
11.	KBH2016B/316		1.00	1.00	1.00	1.00	1.00	1.01
12.	KBH2016B/504		1.00	1.00	1.00	1.75	1.00	1.17
13.	KBH2016B/521		1.00	1.00	1.00	1.00	1.00	1.02
14.	Local Check		3.3	3.93	2.95	2.87	2.967	3.21
	Mean		**1.94**	**2.35**	**1.60**	**1.49**	**1.44**	**1.77**
	LSD_Genotype (G)		1.44**	1.65**	0.97***	0.77***	0.99***	0.53***
	LSD_Sites (S)		-	-	-	-	-	0.32***
	LSD_GxS		-	-	-	-	-	1.20**
	CV (%)		44.40	41.80	28.00	30.40	40.90	41.8

Table 6: Cassava mosaic disease incidence (CMDI) (%) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		0.0	0.00	0.00	0.00	0.00	0.00
2.	KBH2014B/017		3.70	42.20	0.00	6.10	9.26	12.04
3.	KBH2015B/036		3.30	71.70	36.60	0.00	31.38	28.40
4.	KBH2015B/065		18.50	0.00	26.60	0.00	0.00	8.95
5.	KBH2015B/071		0.00	8.30	0.00	0.00	0.00	1.55
6.	KBH2015B/129		0.00	0.00	0.00	0.70	0.00	0.14
7.	KBH2015B/157		0.00	0.00	0.00	0.00	0.38	0.00
8.	KBH2016B/020		20.40	65.40	34.50	27.20	36.46	36.59
9.	KBH2016B/087		0.00	22.20	6.70	6.20	8.75	8.57
10.	KBH2016B/185		1.80	0.00	0.00	0.00	0.00	0.15
11.	KBH2016B/316		0.00	4.20	0.00	0.00	0.00	0.63
12.	KBH2016B/504		0.00	0.00	0.00	0.00	0.00	0.00
13.	KBH2016B/521		0.00	0.00	0.00	0.00	0.00	0.00
14.	Local Check		15.2	0.00	64.9	8.50	6.78	18.88
	Mean		**4.50**	**15.30**	**12.10**	**3.50**	**6.64**	**8.15**
	LSD_Genotype (G)		12.21**	29.37***	19.62***	13.49*	10.71***	7.68***
	LSD_Sites (S)		-	-	-	-	-	4.59***
	LSD_GxS		-	-	-	-	-	17.17***
	CV (%)		162.00	114.50	75.10	225.40	95.90	130.2

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Table 7: Cassava mosaic disease severity (CMDS) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		1.0	1.00	1.00	1.00	1.00	1.00
2.	KBH2014B/017		1.67	1.83	1.00	1.50	2.33	1.67
3.	KBH2015B/036		1.67	2.53	2.40	1.00	3.33	2.19
4.	KBH2015B/065		1.83	1.00	2.00	1.00	1.00	1.37
5.	KBH2015B/071		1.00	1.67	1.00	1.02	1.00	1.13
6.	KBH2015B/129		1.00	1.00	1.00	1.20	1.00	1.00
7.	KBH2015B/157		1.00	1.00	1.00	1.00	1.01	1.00
8.	KBH2016B/020		2.73	2.65	2.25	2.70	2.37	2.54
9.	KBH2016B/087		1.00	1.92	2.00	1.67	2.33	1.79
10.	KBH2016B/185		1.33	1.00	1.00	1.00	1.00	1.07
11.	KBH2016B/316		1.00	1.67	1.00	1.00	1.00	1.14
12.	KBH2016B/504		1.00	1.00	1.00	1.00	1.00	1.00
13.	KBH2016B/521		1.00	1.00	1.00	1.00	1.00	1.00
14.	Local Check		2.8	1.00	2.60	2.00	2.067	2.10
	Mean		**1.43**	**1.45**	**1.45**	**1.30**	**1.53**	**1.42**
	LSD_Genotype (G)		0.88***	0.88**	0.86**	0.90*	1.00***	0.40***
	LSD_Sites (S)		-	-	-	-	-	NS
	LSD_GxS		-	-	-	-	-	0.89*
	CV (%)		36.50	36.20	27.60	40.70	38.80	38.8

Table 8: Total fresh root yield (TFRY) (t/ha) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		12.4	7.23	11.47	9.40	22.12	12.44
2.	KBH2014B/017		4.50	3.64	4.93	13.80	6.7	6.47
3.	KBH2015B/036		6.80	7.10	6.81	14.20	3.13	7.57
4.	KBH2015B/065		21.80	0.16	7.33	5.00	3.27	7.76
5.	KBH2015B/071		14.70	6.03	2.69	10.50	3.66	7.11
6.	KBH2015B/129		12.90	0.64	4.62	12.20	4.81	5.88
7.	KBH2015B/157		4.40	6.77	3.30	4.80	-	4.19
8.	KBH2016B/020		11.20	8.72	15.14	10.20	8.63	10.69
9.	KBH2016B/087		31.70	22.07	10.60	25.20	16.87	21.19
10.	KBH2016B/185		11.30	8.72	8.16	13.80	13.15	10.93
11.	KBH2016B/316		28.70	18.37	15.82	12.90	19.34	18.91
12.	KBH2016B/504		12.70	15.61	6.23	4.20	4.61	8.59
13.	KBH2016B/521		29.40	26.76	6.01	20.90	19.64	20.54
14.	Local Check		20.6	3.12	11.58	13.8	24.33	14.46
	Mean		15.90	9.64	8.19	12.20	10.68	11.20
	LSD_Genotype (G)		11.62***	10.42***	4.91***	11.66*	6.62***	4.21***
	LSD_Sites (S)		-	-	-	-	-	2.52***
	LSD_GxS		-	-	-	-	-	9.42***
	CV (%)		43.50	63.50	27.70	55.90	36.80	52

Table 9: Dry matter content (DMC) (%) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		30.60	30.90	33.06	29.59	33.05	31.48
2.	KBH2014B/017		26.03	30.47	33.60	32.73	31.12	30.96
3.	KBH2015B/036		31.12	30.91	30.95	34.55	32.69	31.96
4.	KBH2015B/065		26.07	27.79	32.40	31.77	37.07	30.86
5.	KBH2015B/071		24.62	28.13	33.70	27.79	30.39	29.01
6.	KBH2015B/129		27.87	26.05	32.55	31.25	33.65	29.98
7.	KBH2015B/157		26.44	30.48	30.02	32.61	32.62	30.42
8.	KBH2016B/020		29.98	32.75	36.14	34.67	37.54	34.26
9.	KBH2016B/087		28.87	30.08	30.41	29.45	33.58	30.52
10.	KBH2016B/185		26.73	30.45	32.00	35.76	34.30	31.89
11.	KBH2016B/316		28.02	30.27	27.27	28.53	33.73	29.60
12.	KBH2016B/504		27.66	31.88	31.97	27.89	33.97	30.75
13.	KBH2016B/521		25.43	32.66	30.99	27.16	33.80	29.96
14.	Local Check		28.46	26.29	32.01	33.72	34.21	31.11
	Mean		**27.71**	**29.94**	**31.93**	**31.25**	**33.69**	**30.91**
	LSD_Genotype (G)		NS	NS	1.47***	4.51**	NS	2.60*
	LSD_Sites (S)		-	-	-	-	-	1.55***
	LSD_GxS		-	-	-	-	-	NS
	CV (%)		19.00	10.30	2.10	8.40	10.50	11.6

Table 10: Marketable dry root yield (MDRY) (t/ha) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		3.16	1.85	3.44	1.57	4.56	2.90
2.	KBH2014B/017		0.32	0.96	1.21	3.17	1.66	1.43
3.	KBH2015B/036		0.86	1.57	1.7	4.05	0.41	1.70
4.	KBH2015B/065		4.61	0.00	1.94	1.70	1.01	1.88
5.	KBH2015B/071		1.48	1.70	0.73	2.79	0.54	1.36
6.	KBH2015B/129		3.31	0.00	1.48	3.35	1.47	1.62
7.	KBH2015B/157		1.87	1.83	0.81	1.64	-	1.29
8.	KBH2016B/020		3.15	2.48	4.73	3.30	3.07	3.33
9.	KBH2016B/087		9.09	6.10	2.91	7.46	5.66	6.23
10.	KBH2016B/185		2.87	2.63	2.15	4.73	4.43	3.34
11.	KBH2016B/316		8.14	5.55	4.3	3.60	5.84	5.46
12.	KBH2016B/504		3.17	4.99	1.99	1.14	1.56	2.56
13.	KBH2016B/521		7.38	8.72	1.54	5.65	4.50	5.55
14.	Local Check		3.11	0.00	2.62	2.72	5.78	2.80
	Mean		3.75	2.74	2.25	3.35	2.88	2.96
	LSD_Genotype (G)		2.70***	3.48***	1.32***	NS	2.09***	1.22***
	LSD_Sites (S)		-	-	-	-	-	0.73***
	LSD_GxS		-	-	-	-	-	2.74***
	CV (%)		42.80	74.60	27.10	69.40	43.00	57.1

Table 11: Total dry root yield (TDRY) (t/ha) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		3.89	2.25	3.71	2.78	7.29	3.97
2.	KBH2014B/017		1.20	1.14	1.65	4.65	2.22	2.11
3.	KBH2015B/036		2.07	2.22	2.11	4.86	1.00	2.44
4.	KBH2015B/065		5.82	0.07	2.37	1.59	1.22	2.28
5.	KBH2015B/071		3.16	1.73	0.91	2.96	1.11	1.86
6.	KBH2015B/129		3.39	0.19	1.48	3.79	1.64	1.72
7.	KBH2015B/157		2.15	2.12	0.99	1.59	-	1.41
8.	KBH2016B/020		3.42	2.90	5.47	3.48	3.27	3.68
9.	KBH2016B/087		9.14	6.64	3.22	7.46	5.66	6.40
10.	KBH2016B/185		2.87	2.87	2.61	4.94	4.45	3.52
11.	KBH2016B/316		8.14	5.55	4.30	3.60	6.52	5.59
12.	KBH2016B/504		3.17	4.99	1.99	1.10	1.56	2.55
13.	KBH2016B/521		7.56	8.70	1.84	5.61	6.65	6.07
14.	Local Check		5.65	0.94	3.79	4.61	8.32	4.58
	Mean		4.40	3.02	2.60	3.79	3.62	3.44
	LSD_Genotype (G)		3.04***	3.41***	1.43***	NS	2.26***	1.27***
	LSD_Sites (S)		-	-	-	-	-	0.76***
	LSD_GxS		-	-	-	-	-	2.85***
	CV (%)		41.10	66.40	25.50	57.20	37.00	51.1

Table 12: Percentage marketable fresh root yield (PMFRY) (%) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		78.50	55.30	91.00	57.30	62.4	68.80
2.	KBH2014B/017		17.50	82.10	73.80	59.40	81.40	63.90
3.	KBH2015B/036		41.60	56.30	80.90	70.90	44.10	58.20
4.	KBH2015B/065		83.70	1.60	82.90	100.00	87.30	70.80
5.	KBH2015B/071		44.00	66.70	80.30	95.30	35.50	64.60
6.	KBH2015B/129		96.80	1.60	100.00	87.70	75.00	69.70
7.	KBH2015B/157		96.20	61.30	81.60	100.00	100.00	86.90
8.	KBH2016B/020		92.30	79.60	86.30	94.20	93.50	89.10
9.	KBH2016B/087		99.50	90.90	90.10	100.00	100.00	96.00
10.	KBH2016B/185		100.00	94.00	82.20	95.40	99.60	94.10
11.	KBH2016B/316		100.00	100.00	100.00	100.00	89.20	97.70
12.	KBH2016B/504		100.00	100.00	100.00	100.00	100.00	100.00
13.	KBH2016B/521		98.10	100.00	80.30	100.00	65.40	88.40
14.	Local Check		54.9	0.00	71.10	65.2	70.3	52.00
	Mean		**78.80**	**63.10**	**85.80**	**87.70**	**78.80**	**78.60**
	LSD_Genotype (G)		28.28***	51.83***	15.65*	NS	33.32**	15.49***
	LSD_Sites (S)		-	-	-	-	-	9.26***
	LSD_GxS		-	-	-	-	-	34.64***
	CV (%)		21.40	48.20	8.40	25.10	25.10	27.2

Table 13: Root necrosis incidence (RN) (%) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		20.20	51.00	10.4	39.10	45.50	33.20
2.	KBH2014B/017		86.30	17.70	65.20	44.80	24.80	46.20
3.	KBH2015B/036		66.40	41.20	26.70	24.40	68.60	46.10
4.	KBH2015B/065		20.30	86.80	20.80	0.10	22.20	30.40
5.	KBH2015B/071		38.00	33.30	45.80	27.10	51.30	39.00
6.	KBH2015B/129		0.40	98.40	0.00	13.90	39.60	33.30
7.	KBH2015B/157		6.30	42.00	25.00	6.00	0.00	16.10
8.	KBH2016B/020		10.60	31.20	4.90	2.70	10.80	12.00
9.	KBH2016B/087		1.00	10.20	3.30	0.00	0.00	2.80
10.	KBH2016B/185		0.00	6.20	1.60	5.00	2.60	3.00
11.	KBH2016B/316		0.00	0.00	0.00	0.00	11.00	2.10
12.	KBH2016B/504		0.00	0.00	0.00	0.00	0.00	0.00
13.	KBH2016B/521		2.50	0.00	3.70	0.00	34.80	8.40
14.	Local Check		56.3	100.00	13.30	35.5	39.8	48.90
	Mean		22.00	37.40	15.80	13.90	25.20	23.00
	LSD_Genotype (G)		21.85***	49.16***	24.89**	28.54*	26.17***	13.71***
	LSD_Sites (S)		-	-	-	-	-	8.19***
	LSD_GxS		-	-	-	-	-	30.66***
	CV (%)		59.10	77.20	73.10	120.40	61.60	82.5

Table 14: Root necrosis severity (RNS) among 12 promising genotypes evaluated under AYT across five sites in Tanzania, 2019/2020 season.

S/N	Genotype	Pedigree	Sites					Mean
			Bunda	Chambezi	Chato	Ukerewe	Ukiriguru	
1.	Improved Check		3.47	4.00	2.88	4.35	3.06	3.53
2.	KBH2014B/017		3.17	2.22	4.00	4.15	3.20	3.26
3.	KBH2015B/036		4.61	1.77	3.40	2.67	4.55	3.42
4.	KBH2015B/065		2.64	3.77	2.90	1.42	2.07	2.52
5.	KBH2015B/071		3.10	2.00	3.50	3.01	3.52	3.00
6.	KBH2015B/129		1.33	3.77	1.00	2.49	2.48	2.16
7.	KBH2015B/157		1.58	3.33	3.00	2.42	1.00	2.14
8.	KBH2016B/020		3.90	4.00	2.38	4.33	3.36	3.57
9.	KBH2016B/087		1.67	2.67	2.25	1.00	1.00	1.69
10.	KBH2016B/185		1.00	2.67	2.00	2.67	2.33	2.11
11.	KBH2016B/316		1.00	1.00	1.00	1.00	2.70	1.32
12.	KBH2016B/504		1.00	1.00	1.00	1.00	1.00	1.00
13.	KBH2016B/521		1.92	1.00	2.00	1.00	2.90	1.72
14.	Local Check		4.25	4.72	3.16	4.21	3.13	3.80
	Mean		**2.47**	**2.69**	**2.46**	**2.49**	**2.59**	**2.51**
	LSD_Genotype (G)		1.45***	1.73***	NS	1.97**	0.89***	0.69***
	LSD_Sites (S)		-	-		-	-	NS
	LSD_GxS		-	-	-	-	-	1.55***
	CV (%)		35.00	37.80	38.80	46.40	20.50	38.2