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Physiological Efficiency of Cassava as Influenced by Genotypes Over Period of Maturity in the Screening of K Use Efficient Genotypes

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Abstract

Plant nutrition of cassava is important on account of its high yield to the tune of 30-50 t ha-1. Among the major nutrients, the key nutrient, K plays a significant role in enhancing tuber yield and improving tuber quality. This relevance of K urged in undertaking research to screen K use efficient cassava genotypes with a view to reduce the external application of K. The initial evaluation of 83 elite cassava genotypes conducted at ICAR-CTCRI to exploit their physiological efficiency (PE) of K grouped the genotypes into five clusters with 9, 48, 17, 5 and 4 genotypes respectively in each cluster. The parameters contributing to PE viz., biological yield and total plant nutrient uptake were influenced by plant dry matter yield, dry matter percentage and K contents of the genotypes. This paper narrates the genetic diversity among clusters, among the intervals of maturity and their interaction as well as the significant effect of the parameters associated with PE under different clusters and stage of maturity in the identification of K efficient genotypes. The study revealed significant effect of number of storage roots and tuber length at 6 MAP under cluster 1, tuber girth at 10 MAP, leaf and stem K at 6 MAP under cluster 2, storage root dry matter percentage at 6 MAP under cluster 3, leaf and stem dry matter percentage at 8 MAP under cluster 4, storage root K at 10 MAP under cluster 5 in affecting the PE. As most of these attributes are significantly high during 6 MAP, it can be established that, screening for NUE should be done at 6 MAP. Since the tuber quality attributes being important in the selection of genotypes, the analysis indicated lowest cyanogen under cluster 2 at 10MAP and highest starch under cluster 4 at 6 MAP. Among the six genotypes identified as K efficient through preliminary evaluation, Aniyoor, 7 Sahya (2) and 7III E3-5 came under cluster 1 and W-19, CR 43-8, 6-6 under cluster 2. This information with respect to each cluster towards their contribution in influencing the inherent PE of the genotypes as well as the variability in growth stages in influencing the associated attributes can form crucial factors in selecting parent materials for breeding purpose in evolving K efficient genotypes.

Key words: Clusters, biological yield, plant nutrient uptake, tuber quality, storage root K, tuber girth

Introduction

Among the torpical tuber crops, cassava is rated as the most important owing to the extent of area under cultivation, high productivity, tolerance to abiotic and biotic stresses, good quality storage root (tuber), starch suitable for preparing many value added industrial products and the acceptability of the cooked tuber as an energy rich tasty food in the cassava growing countries. Globally, cassava is grown in an area of 25.59 million ha producing 277.81 million tonnes with a productivity of 11.30 tha^{-1} (FAO, 2019).

Our experience on the nutrient management of cassava for the last four decades under a long term fertilizer experiment (LTFE) indicated a high positive response of cassava to the application of fertilizers and manures under INM (Susan John et al., 2019). The blanket recommendation of cassava is arrived as N: P_2O_5: K_2O @ 100:50:100 kg ha^{-1}. K is considered as the key nutrient for cassava productivity and tuber quality (Susan John et al., 2010), hence this research work of screening nutrient use efficient (NUE) genotypes for the nutrient K was initiated. The present paper forms a part of the pre evaluation of 83 elite cassava genotypes undertaken for identification of potassium (K) efficient cassava genotypes which can reduce the application of K fertilizers from external sources. Moreover, muriate of potash(MoP), the chemical fertilizer source of K is imported, hence the unit cost of K is too high. In this regard, Fageria et al. (2008) and Gorny and Garczynski (2008) suggested the scope for inclusion of NUE genotypes as planting material in nutrient management programmes to reduce the use of chemical fertilizers.

The NUE is achieved on account of the root system of the K use efficient crop which can extract the unavailable fixed soil K as well as the LAI of the crop in harnessing for higher photosynthetic efficiency. In the process of evaluation of the germplasm for identifying K use efficient genotypes, physiological efficiency (PE) was taken as the basic parameter which in turn is an inherent attribute. Biological yield and total plant K uptake are the parameters to be calculated for determining PE which in turn depends on plant characters like plant (leaf, stem and storage root) dry matter production, plant dry matter percentage and plant K contents. In dry matter production, the tuber dry matter is governed by tuber yield which in turn depends on tuber number, tuber length and tuber girth. These were also recorded along with other criteria for selection of NUE genotypes like tuber quality attributes (cyanogen and starch) and growth characters (plant height, stem girth) at 6,8 and 10 months after planting (MAP) of cassava. This paper describes the variation of these parameters among clusters over time towards the fag end of maturity (at the above intervals) based on the five clusters we have already evolved through cluster, principal component, biplot and dendrogram analysis (Susan John et al., 2020) as well as the contribution of these parameters to physiological efficiency (PE) in the screening and selection of K use efficient genotypes.The ultimate outcome of this research is to utilize the identified NUE genotypes/varieties or to use them as parent materials to breed varieties with better NUE so that the dependence on chemical fertilizers can be reduced (Smith et al. 1994).

Materials and Methods

In the screening trial for the identification of K use efficient cassava genotypes, the 83 elite genotypes were planted in a row trial with 10 plants per genotype in each row. The cut stems (setts) of these genotypes were planted on ridges without giving any manure and fertilizer to exploit the genetic potential of the crop in assimilating the innate fertility of the soil to crop biomass otherwise termed as physiological efficiency. Biometric/growth characters *viz.,* height and girth of the stem, leaf, stem and storage root (tuber) dry matter, leaf, stem and tuber K, starch and cyanogenic glucosides, tuber characters *viz.,* number, length, girth and yield at two months interval as 6, 8, 10 MAP were recorded.

In the case of plant height, the length of the stem from the base of the plant from where the first branch formed to the top most part of the plant was taken using a metre scale. In the case of stem girth, the diameter of the base of the first branch formed was taken using a twine and is measured in a metre scale. As regards to leaf, stem and tuber dry matter, destructive sampling was done at 6, 8 and 10 MAP from two plants of each row. After separation of the leaves along with petioles, their fresh weight was taken in addition to the fresh weight of the stem and that of tuber. From each of these, 100g fresh weight was taken and oven dried at ± 65°C till we get a constant weight and hence determined the leaf, stem and tuber dry weight percentage. In the case of leaf dry weight, the retained and fallen leaves counted at these intervals as well as the per leaf dry weight at the respective intervals was utilized for arriving the same.

The tuber characters *viz*., length of tuber from the sample plants was measured using a metre scale and girth of the same tuber was taken with a twine and measured in a metre scale. Similarly, the number of tubers from each sample plant was recorded. From the dried and ground leaf, stem and tuber samples, the K content at the above intervals was determined following tri acid digestion (Piper, 1970) and K analysis using flame photometer (Systronices, 128). The starch content was determined in the dried tuber flesh at the aforementioned intervals as per Chopra and Kanwar (1976) and converted on fresh weight basis using the tuber dry weight percentage determined during the three intervals. The cyanogenic glucoside content of fresh cassava tubers immediately after harvest at each interval was determined following Indira and Sinha (1969).

The objective of the present study was to explore the variation among the clusters over period of time (6, 8 and 10 MAP) and understand this with respect to the different genotypes in the clusters. The variation among the five clusters with respect to genotypes in each cluster was assessed by grouping the data on the aforementioned observations over 6, 8 and 10 MAP in the five clusters and employing completely randomized design (CRD) by taking the independent variables as clusters, while treatments were genotypes in the clusters and intervals. In other words, the variation among genotypes in these five clusters for parameters like leaf, stem and tuber dry weight percentage, tuber attributes like number, length, girth and yield, plant growth characters like plant height and stem girth, plant K and tuber quality parameters like starch and cyanogenic glucosides were done in CRD with five clusters comprising of the number of genotypes as 9, 48, 17, 5 and 4 in clusters one to five respectively at the three intervals as 6, 8 and 10 MAP were studied. This in turn can give the contribution of the evaluated attributes towards PE as well as the best stage of maturity for screening in the selection/breeding of K use efficient genotypes.

Results and Discussion

Cluster analysis was undertaken to group the genotypes into clusters having similar traits with respect to the characters studied. Hierarchical cluster analysis with complete linkage method has been suggested for classifying entries of germplasm collections based on degree of similarity and dissimilarity (Van Hintum, 1995) and was carried out using R environment for statistical computing (R version 3.4.1). Susan John et al., (2020) grouped these 83 genotypes based on cluster, principal component, biplot and dendrogram analysis by following the procedure suggested by Van Hintum (1995) wherein the agglomerative hierarchical cluster analysis of the 83 genotypes resulted in respectively 9, 48, 17, 5 and 4 genotypes in each cluster. The principal component analysis explained more than 77% of the variability for the first five components.

The details of the five clusters comprising of the genotypes in each cluster is presented in Table 1. As indicated in the methodology, based on cluster analysis, there were five clusters (1,2,3,4,5) with the number of genotypes as 9, 48, 17, 5 and 4 respectively in the five clusters. Cluster 1 contained the genotype Aniyoor later released as the first K efficient cassava variety under the name Sree Pavithra and the genotype 7 III E3-5, identified as NPK efficient. Some very promising released varieties with valuable traits like cassava mosaic disease (CMD) tolerance (Sree Rekha), high yielding high starch hybrid varieties (H97, H 165), high starch triploids (Sree Harsha), high starch top cross hybrids (Sree Rekha, Sree Prabha) suitable for industrial purposes, high yielding shade tolerant edible hybrid varieties (Sree Sahya, Kalpaka, Sree Prakash), high yielding short duration varieties (Sree Vijaya, Sree Jaya and Vellayani Hraswa) fell under cluster 2. Cluster 3 comprised of the popular local edible genotype Neelagiri and cluster 4 included

Table 1. Cluster composition of the evaluated genotypes of cassava under the preliminary evaluation trial

Cluster	Number of genotypes	Cluster members
1	9	Aniyoor, C59/8R, ID2(6-7), 7 III E3-5, CR54 A-3, MN7, 7 Sahya (2), 43-7, TEMNI
2	48	IH3/2, Sree Rekha, CR43-11, Sree Sahya, H97, Sree Vijaya, IH5/2, 4/31, 4/21, Kalpaka, 7 IVA-I, CR 43-8, 7III E 1-6, H 226, Sree Jaya, Sree Prabha, H 165, Sree Prakash, II D 79-6, I D 7C 1-3, C-1848, C-21, M4 , H 7 IV E3-5, 7 III C 8-2, 4-2, 5-3, 6-6, 17/5, 16-12, I H5/15, CR 43-2, W-19, 4/3, Sree Harsha, 2-18, CR 9A 125, Kadakkal, Ummanvella, New 1,25/26, Ullichuvala, CR 59 -8, New 2, 99/14 (3), 7 Ulli-2, Vellayani Hraswa, 6-2MN4
3	17	7 IVC 4-4, 35/8, 7 III C2-5, Neelagiri, CR5/8, 7/49/MN3, 7MN2, CR43-2, 4-21, CR43-7, 35/8(2), CR114-0, CR 26-1, 25/2, CR43-5, CR 43-11, 4-31
4	5	MNGA, Ambakkadan, I H5-8, 7-99MNA, T Amba
5	4	7/39, Sree Visakham, 7MN6, CR43-6

the CMD resistant variety MNGA by name Sree Padmanabha and Ambakkadan another high yielding popular genotype known for its stable yield coupled with good cooking quality and cluster 5 contained the most promising culinary hybrid variety rich in β carotene (Sree Visakham).

The statistical analysis revealed the differences among clusters, intervals and the interaction between clusters and intervals on the studied parameters which definitely enable in identifying significant attributes as well as the growth stage of the crop in delineating the genotypes for better K use efficiency.

Plant dry weight percentage

Here the results on variation in leaf, stem and tuber dry weight percentage of the cassava genotypes in five clusters at different intervals as well as the interaction between clusters and intervals is described as follows:

Leaf dry weight percentage

In the case of leaf dry weight percentage (LDW%), there was no significant difference among clusters and the overall mean of the cassava genotypes of five clusters over the three intervals was 27.59%. The mean LDW % of the cassava genotypes of the clusters 1, 2, 3, 4, 5 during the three intervals were 28.51, 27.41, 28.38, 29.01, 26.77% respectively. There was significant difference for cassava genotypes LDW% among the three intervals *viz.,* 6, 8, 10 MAP with mean values as 28.21 (6 MAP), 29.75(8 MAP) and 26.08% (10 MAP) respectively. LDW% of cassava genotypes at 6 and 8 MAP were on par and at 10 MAP, it was significantly lesser to both 6 and 8 MAP. Significant interaction effect of clusters and intervals was noticed and the genotypes in cluster 4 at 8 MAP (31.80%) had the maximum and was on par with genotypes in cluster 1 at 8 MAP (29.77%). This was found on par with the LDW % recorded for all clusters at all the stages except cluster 1 at 6 MAP and clusters 2, 3, 4, 5 at 10 MAP. The cassava genotypes in cluster 5 at 6 MAP (24.22%) indicated the lowest LDW% which was on par with cassava genotypes in clusters 1, 2 and 5 at 6 MAP, cluster 5 at 8 MAP and clusters 2, 3, 4 at 10 MAP (Table 1). The variation observed with respect to clusters and age can be justified as per the reports of Távora and Barbosa (1994) that, leaf yield is a function of the plant age and variation in climatic conditions, especially temperature, which can either accelerate or delay the leaf production (Table 2, Fig.1, 2).

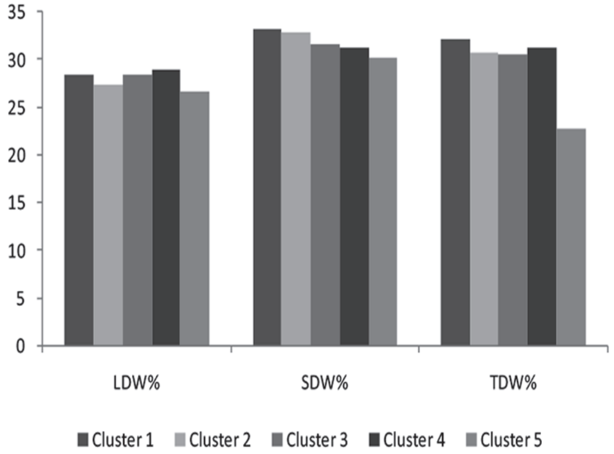

Fig.1. Variation among clusters on PDW%

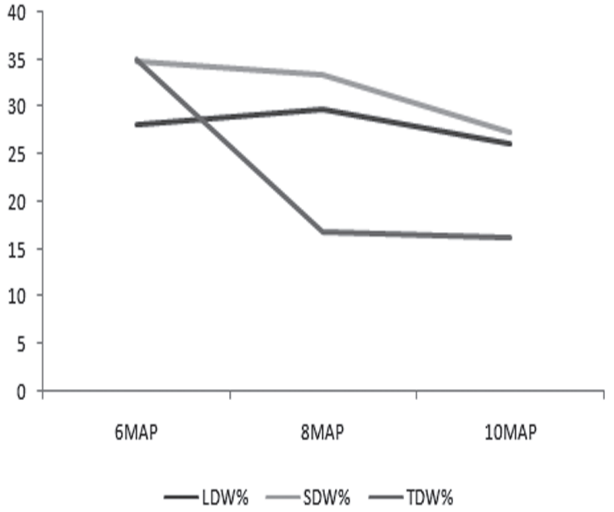

Fig.2. Variation on PDW% at three intervals

There was no significant difference among clusters for stem dry weight percentage (SDW %). SDW % computed at 10 MAP showed a significant reduction over the SDW % at 6 and 8 MAP which in turn were on par. The overall mean of the SDW % of cassava genotypes was 32.30% and the mean of cassava genotypes in five clusters over the three intervals respectively were 33.15, 32.81, 31.56, 31.36, 30.22%. The mean of SDW% of cassava genotypes over 6, 8 and 10 MAP were 34.81, 33.31 and 27.35% respectively. As regards to the interaction effect of clusters and intervals, cassava genotypes of cluster 2 at 8 MAP had the maximum SDW % (38.19%) which was on par with the SDW % of cassava genotypes in clusters 1,2, 3, 5 at 8 MAP, and cassava genotypes in clusters 3, 4, 5 at 6 MAP. Cassava genotypes

Table 2. Variation among clusters on plant dry weight percentage over three intervals

Clusters	Intervals			
	Leaf dry weight percentage			
	1	2	3	Mean(C)
1	27.36^{abcde}	29.77^{a}	28.40^{abcf}	28.51^{a}
2	26.99^{bcde}	28.98^{a}	26.25^{de}	27.41^{a}
3	28.91^{abcd}	29.67^{abc}	26.58^{cde}	28.38^{a}
4	30.25^{ab}	31.80^{a}	24.97^{def}	29.01^{a}
5	27.55^{abcde}	28.54^{abcde}	24.22^{e}	26.77^{a}
Mean (I)	28.22^{a}	29.75^{a}	26.08^{b}	27.59
	Stem dry weight percentage			
	1	2	3	Mean(C)
1	33.71^{bcdf}	37.52^{ab}	28.21^{eg}	33.15^{a}
2	32.26^{cdf}	38.19^{a}	27.98^{e}	32.81^{a}
3	37.45^{abc}	32.82^{abcde}	24.42^{g}	31.56^{a}
4	36.81^{abcd}	30.00^{bcdeg}	27.27^{efg}	31.36^{a}
5	33.81^{abcde}	28.00^{abcdeg}	28.85^{deg}	30.22^{a}
Mean (I)	34.81^{a}	33.31^{a}	27.35^{b}	32.30
	Tuber dry weight percentage			
	1	2	3	Mean(C)
1	37.48^{ab}	31.85^{cde}	27.22^{egh}	32.18^{a}
2	35.76^{abc}	31.44^{df}	24.95^{ghi}	30.72^{a}
3	39.17^{a}	31.01^{bcde}	21.77^{ij}	30.65^{a}
4	36.51^{abcd}	30.85^{abcdeg}	26.23^{efghi}	31.20^{a}
5	35.01^{abcde}	16.96^{hij}	16.28^{j}	22.75^{b}
Mean (I)	36.79^{a}	24.42^{b}	23.29^{c}	30.06

of cluster 3 at 10 MAP had the least SDW % (24.42%) which was on par with those in clusters 1, 4, 5 at 10 MAP, clusters 4 and 5 at 8 MAP (Table 2, Fig.1, 2).

Tuber dry weight percentage

With regard to tuber dry weight percentage (TDW %), there was no significant difference among the genotypes in different clusters as in the case of LDW and SDW %. However, the stages of the crop showed significant difference with 6 MAP showing the highest TDW % (36.79%) followed by TDW % at 8 MAP (24.42%) and at 10 MAP (23.29%). Ebah-Djedji et al., (2012) could not find any significant statistical difference among improved cassava genotypes in tuber dry matter, may be due to the fact that, root development varies with stages of plant growth and development (Fageria et al., 2006).The overall mean of the cassava genotypes in five clusters was 30.02% and the cluster means were 32.18, 30.72, 30.65, 31.20 and 22.75% respectively. As regards to the interaction between clusters and intervals, it was found that, cluster 3 at 6 MAP had the highest TDW% (39.17%) which was on par with the average for the genotypes in clusters 1, 4 and 5 at 6 MAP and clusters 2 and 4 at 8 MAP. Cluster 5 at 10 MAP had the lowest TDW% which was on par with cluster 5 at 8 MAP and clusters 3, 4 and 5 at 10 MAP (Table 1, Fig.1, 2). In this regard, Akparobi et al. (1999) reported a positive relation of high leaf dry matter production to high root yield in cassava and Kamara et al.(2003) viewed that, the total plant dry matter production is a good estimator of the degree of adaptation of a genotype to the environment in which it is grown.

Plant dry weight percentage

From the aforementioned interpretation, it was understood that, there is drastic variation among clusters which in turn is comprised of many genotypes. Similarly, there is drastic difference with respect to total plant dry weight percentage (PDW%) at different period of maturity. In the present study, among the clusters, there was no significant difference on leaf, stem and tuber dry matter percentage. However, there was a significant reduction in these parameters towards harvest (10 MAP). Among the clusters, cassava genotypes of clusters 4, 2, 3 had the highest leaf, stem and tuber DW% and 5, 3, 5 had the least of these values. Among the three intervals of sampling, 8MAP recorded the highest LDW and SDW% and 10MAP for TDW%. The least PDW% was recorded at 10 MAP for all the three plant parts (Table 1). These type of variation observed particularly over a period of maturity is in conformity with the reports of Augustin et al., (1977) and White et al., (1974) that, plant growth rates and soil nutrient availability can influence the pattern and magnitude of nutrient uptake, accumulation and partitioning of dry matter into different parts of the plant. Moreover, as per the findings of Sagrilo et al. (2002), high leaf dry matter yield can result in initial reduction in storage root yield due to coinciding exactly with the restructuring period of the plant photosynthetic apparatus and the later increase and stabilization possible may be related to the intensification of assimilate production by the photosynthetic apparatus.

Adjei-Nsiah (2010) reported similar findings in total dry matter production of five different cassava varieties. Fageria et al., (2006) revealed that, P and N deficient plants usually have more drymatter partitioned to roots than shoots, presumably due to higher export of photosynthates to roots.

Tuber characters

Tuber characters included tuber attributes like length, girth, number and yield. As in the case of PDW%, variation among clusters, intervals and interaction between clusters and intervals is presented for the above tuber traits as follows:

Tuber number

There was significant difference among clusters on tuber number. The mean tuber number of cassava genotypes in the five clusters was 9.075 with mean values as 11.46, 8.82, 8.61, 4.67 and 8.92 for the clusters 1, 2, 3, 4 and 5 respectively. Cassava genotypes in cluster 1 had significantly the highest tuber number on par with cluster 5 followed by clusters 2 and 3 on par with 5. Cassava genotypes in cluster 4 had significantly the lowest tuber number. There was no significant variation among 6, 8 and 10 MAP on tuber number as the number of tubers recorded were 8.25, 8.31 and 8.92 respectively. The interaction effect of clusters and intervals were significant with cassava genotypes of cluster 1 at 6 MAP having the maximum number of tubers on par with the same cluster at 8 and 10 MAP and cassava genotypes in cluster 5 at the three intervals. Cassava genotypes of cluster 4 at 6 MAP had the least number of tubers on par with cassava genotypes in clusters 3 at 6 MAP, clusters 4 at 8 and 10 MAP and in cluster 5 at all the three intervals (Table 3, Fig.3,4). These findings corroborates to the reports of Peterson et al., (1984) in winter wheat and Hobman et al. (1987) that, less plant growth occurs at comparatively unfavorable conditions compared to favorable field experimental situations where there will be better distribution of assimilates to the storage roots in proportion to the canopy growth.

Tuber length

In the case of tuber length, though no significant effect was seen at 6, 8 and 10 MAP, the genotypes in different clusters showed significant variation with cluster 1 cassava genotypes having lengthy tubers and cluster 4 having short tubers. The mean of tuber length of the different genotypes was 32 cm and the mean values for cassava genotypes in each of the five clusters were 37.96, 31.45, 32.34, 17.31 and 32.97cm respectively. In this regard, clusters 1 and 5 were on par and clusters 2, 3 and 5 were also on par. The mean tuber length at 6, 8 and 10 MAP were 33.38, 27.62 and 30.21cm respectively. The interaction effect of clusters and intervals were also significant with cluster 1 at 6 MAP giving the most lengthy tubers (44.57cm) on par with cassava genotypes in cluster 3 at 6 MAP and cluster 5 at 6 and 10 MAP. The shortest tuber was seen in cassava genotypes of cluster 4 at 10 MAP (14.50 cm) which was on par with cassava genotypes of clusters 4 and 5 at 8 MAP and cluster 4 at 6 MAP (Table 3, Fig. 3, 4).

Tuber girth

Tuber girth showed significant variation among clusters and also at different intervals. The overall mean of the tuber girth of the cassava genotypes in five clusters were 18.93 cm. Among the five clusters, cassava genotypes in cluster 1 had tubers with maximum girth (21.15 cm) on par with cassava genotypes in cluster 5 (18.75 cm). However, clusters 1, 2, 3 were on par to cluster 5 and tubers of cluster 4 were significantly the thinnest with a tuber girth of 11.19 cm. As regards to the tuber girth at the three intervals, cassava tubers of genotypes at 6 MAP had significantly the least girth (15.30 cm) and the tuber girth at 8 (18.18 cm) and 10 MAP (18.28 cm) were on par. Cassava genotypes in cluster 2 at 10 MAP had the maximum tuber girth on par with those in cluster 1 at 8 and 10 MAP and those in cluster 5 at all the three intervals. The thinnest tuber was seen in cassava genotypes in cluster 4 at 6 MAP which was on par with those in cluster 3 at 6 MAP, cluster 4 at 8 and 10 MAP and cluster 5 at 6 and 8 MAP (Table 3, Fig. 3, 4).

Tuber yield

The overall mean tuber yield of the cassava genotypes in five clusters was 3.45 kg plant^{-1} and there was significant difference among clusters with cassava genotypes in cluster 1 having significantly the highest tuber yield (6.45 kg plant^{-1}) followed by cassava genotypes in cluster 2 (3.17 kg plant^{-1}), cluster 3(2.88 kg plant^{-1}) and cluster 5 (2.60 kg plant^{-1}) which in turn were on par (Table 3, Fig. 3, 4). However, cassava genotypes in cluster 4 had significantly the lowest yield to the tune of 0.42 kg plant^{-}

^{1} on par with cassava genotypes in cluster 5. As regards to the tuber yield of cassava genotypes at 6, 8, 10 MAP, no significant variation was noted with average yield as 3.22, 3.15, 2.95 kg plant^{-1} at 6, 8 and 10 MAP respectively. As regards to the interaction effect of clusters and intervals, cassava genotypes in cluster 1 at 6 MAP (5.98 kg plant^{-1}), 8 MAP (6.44 kg plant^{-1}) and 10 MAP (6.93 kg plant^{-1}) had significantly the maximum tuber yield which in turn were on par and also on par with cluster 5 at 6 MAP (4.55 kg plant^{-1}). Cassava genotypes in cluster 4 at 6 MAP had the lowest tuber yield (0.075 kg plant^{-1}) on par with those in clusters 3 and 4 at all intervals and cluster 5 at 8 and 10 MAP. This can be explained on the basis of the fact that, dry matter partitioning and leaf area development are critical factors in terms of crop productivity which determines light interception and hence crop yield (Milthorpe and Moorby, 1974). This can again be justified with the findings of Howeler (2002) that, the amount of nutrients removed in the root harvest,is highly dependent on crop growth rate and yield, which in turn depends on climate, soil fertility and genotypic character.

Plant growth characters

The plant growth characters studied included plant height and stem girth at three intervals *viz.,* 6, 8 and 10 MAP. As in the case of earlier characters, these characters were also studied for their variation among clusters, among intervals and also for the interaction between clusters and intervals.

Plant height

In the case of plant height, though there was no significant difference among the three intervals on plant height, there observed significant difference among cassava genotypes of clusters with cassava genotypes in clusters 1 and 2 having significantly the tallest plants with height to the tune of 2.60 and 2.57 m respectively which in turn was on par with cluster 5 (2.73 m). The mean plant height at 6, 8 and 10 MAP respectively were 2.45, 2.36 and 2.31 m. As regards to the interaction between clusters and intervals, it is found that, cassava genotypes in cluster 2 at 8 MAP had the maximum plant height (2.69 m) on par with those in cluster 1 at three intervals, cluster 2 at 8 and 10 MAP, cluster 3 at 6 MAP and cluster 5 at all the three intervals. The mean plant height over the five clusters was 2.49 m (Table 4, Fig. 5,6).

Table 3. Variation among clusters on tuber characters

Clusters	Intervals			
	Tuber Number			
	1	2	3	Mean(C)
1	13.00^{a}	11.17^{ab}	10.22^{abc}	11.46^{a}
2	8.73^{c}	8.38^{c}	9.35^{bc}	8.82^{b}
3	7.50^{bcd}	8.50^{bc}	9.82^{bc}	8.61^{b}
4	2.50^{d}	6.00^{cd}	5.50^{cd}	4.67^{c}
5	9.50^{abcd}	7.50^{abcd}	9.75^{abc}	8.92^{ab}
Mean (I)	8.25^{a}	8.31^{a}	8.93^{a}	9.075
	Tuber Length (cm)			
	1	2	3	Mean(C)
1	44.57a	35.32^{b}	34.00^{b}	37.96^{a}
2	31.16^{b}	30.25^{bc}	32.94^{b}	31.45^{b}
3	35.62^{ab}	29.28^{bcd}	32.13^{b}	32.34^{b}
4	19.17^{cde}	18.25^{de}	14.50^{e}	17.31^{c}
5	36.40^{abcd}	25.00^{bcde}	37.50^{ab}	32.97^{ab}
Mean (I)	33.38^{a}	27.62^{a}	30.21^{a}	32.00
	Tuber girth (cm)			
	1	2	3	Mean(C)
1	18.36^{cde}	22.53^{ab}	22.56^{ab}	21.15^{a}
2	15.87^{ef}	19.95^{bc}	21.61^{a}	19.14^{b}
3	14.55^{defg}	17.31^{cde}	16.25^{def}	16.04^{c}
4	9.70^{g}	12.63^{efg}	11.25^{fg}	11.19^{d}
5	$18.00^{abcdefg}$	$18.50^{abcdefg}$	19.75^{abcd}	18.75^{abc}
Mean (I)	15.30^{b}	18.18^{a}	18.28^{a}	18.93
	Tuber yield (kg/plant)			
	1	2	3	Mean(C)
1	5.98^{a}	6.44^{a}	6.93^{a}	6.45^{a}
2	2.48^{cd}	3.54^{b}	3.49^{b}	3.17^{b}
3	3.00^{bcd}	3.00^{bcd}	2.64^{bcd}	2.88^{b}
4	0.075^{d}	0.88^{cd}	0.31^{cd}	0.421^{c}
5	4.55^{abc}	1.88^{bcd}	1.39^{cd}	2.60^{bc}
Mean (I)	3.22^{a}	3.15^{a}	2.95^{a}	3.452

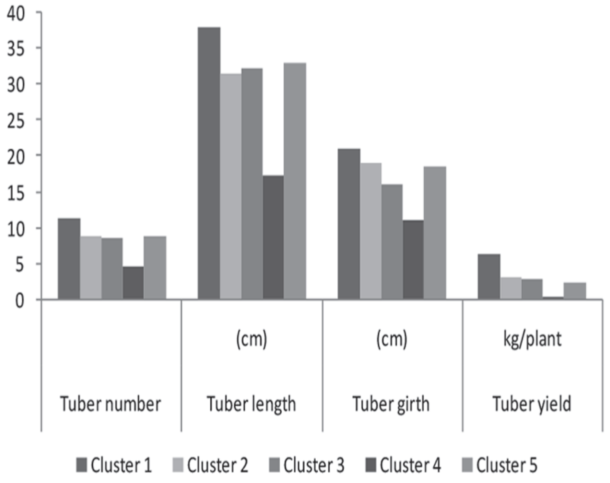

Fig.3. Variation among clusters on tuber characters

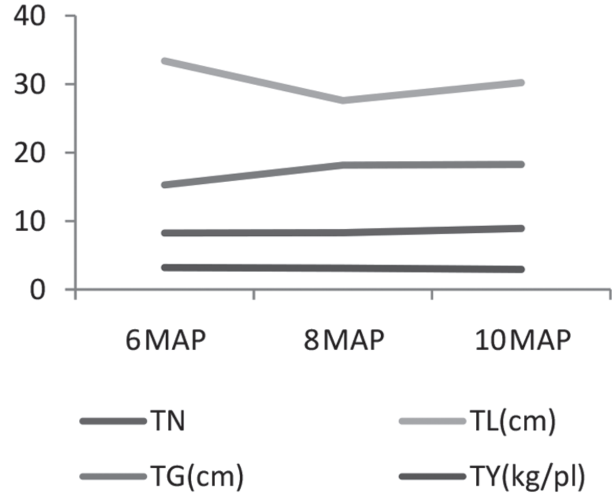

Fig.4. Variation of tuber characters at different intervals

Stem girth

The mean stem girth of cassava genotypes over the five clusters was 7.52 cm. There was significant difference among clusters with cassava genotypes of cluster 1 having the thickest stem (9.67 cm) which was on par with those in cluster 2 (9.21cm) and cluster 3 (9.39 cm). The stem was thinnest in cassava genotypes of cluster 5 (2.73cm). The intervals also showed significant variation with the significantly thickest stems at 10 MAP (7.99 cm) and the stems were having girth as 7.37 and 7.21 cm respectively at 6 and 8 MAP which in turn were on par. The interaction effect of clusters and intervals was significant with the thickest stems in cluster 3 at 10 MAP (10.17cm). The stems of cassava genotypes were thinnest in cluster 5 at 6 MAP (2.64 cm), 8 MAP (2.79 cm) and 10 MAP (2.75 cm) which in turn was on par (Table 4, Fig.5,6). The variation observed among clusters can be justified with respect to nutrient absorption and utilization by different cultivars as per the reports of Baligar et al., (2001) that, plant species and cultivars within species differ in absorption and utilization of nutrients, mainly due to their morphological, physiological and biochemical processes and their interaction with climatic, soil, fertilizer, biological and management practices.

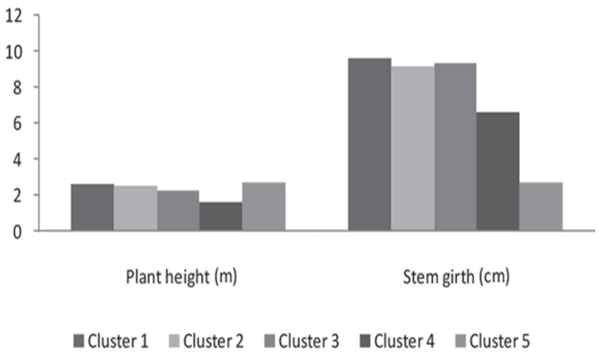

Fig.5. Variation among clusters on plant growth characters

Plant K content

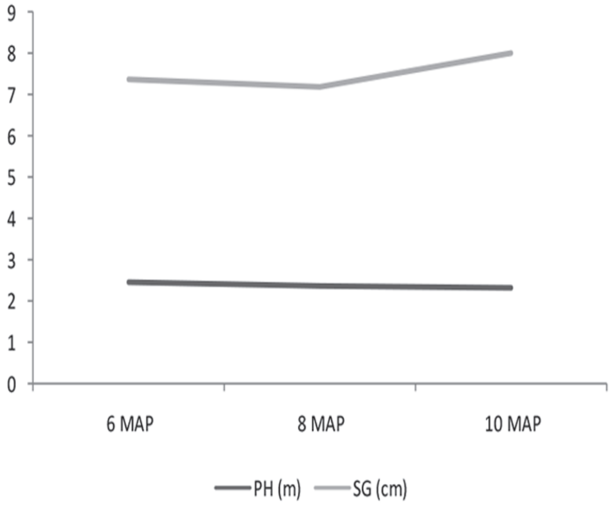

Fig.6. Variation of plant growth characters at different intervals

Table 4. Variation among clusters on plant growth characters

	Plant height (m)			
Clusters	Intervals			
	1	2	3	Mean(C)
1	2.54^{ab}	2.57^{ab}	2.68^{ab}	2.60^{a}
2	2.43^{b}	2.69^{a}	2.60^{ab}	2.57a
3	2.87^{ab}	2.02^{cde}	1.95^{de}	2.28^{b}
4	1.67^{e}	1.71^{de}	1.66^{e}	1.68^{c}
5	2.73^{abc}	2.79^{abcd}	2.68^{ab}	2.73^{ab}
Mean (I)	2.45^{a}	2.36^{a}	2.31^{a}	2.493
	Stem girth (cm)			
	1	2	3	Mean(C)
1	9.97^{bcd}	8.99^{bcde}	10.06^{a}	9.67^{a}
2	8.72^{de}	8.94^{cde}	9.99^{a}	9.21^{a}
3	9.92^{bcde}	8.08^{ef}	10.17^{a}	9.39^{a}
4	5.63^{fg}	7.25^{def}	6.96^{b}	6.61^{b}
5	2.64^{g}	2.79^{g}	2.75^{c}	2.73^{c}
Mean (I)	7.37^{b}	7.21^{b}	7.99^{a}	7.52^{b}

The plant K content studied included leaf, stem and tuber K. The statistical analysis performed indicated variation among clusters, among intervals as well as the interaction between clusters and intervals.

Leaf K

In the case of leaf K, no significant difference was seen among clusters and also among the three intervals. The mean leaf K content over the three intervals of the cassava genotypes in five clusters was 1.34% and the mean of cassava genotypes in clusters 1, 2, 3, 4 and 5 were 1.23, 1.38,1.35,1.19 and 1.27% respectively. The mean of the three intervals were 1.37, 1.27 and 1.21% respectively at 6, 8 and 10 MAP. Cassava genotypes in cluster 2 at 6 MAP had the highest leaf K (1.65%) on par with those in all clusters at 6 MAP, in clusters 3,4,5 at 8MAP and in cluster 5 at 10 MAP. Cassava genotypes in cluster 1 at 10 MAP had the least leaf K (1.00%) on par with those in cluster 1 at 8 MAP, in cluster 2 at 10 MAP, and in clusters 3, 4, 5 at all intervals (Table 5, Fig. 7,8).

Stem K

There was significant difference among clusters on stem K with an overall mean K content of 0.927% with cluster mean of 0.663, 0.959, 1.094, 0.906 and 1.027% respectively for cassava genotypes in clusters 1, 2, 3, 4 and 5. Cassava genotypes of cluster 3 had the highest stem K (1.09%) and was on par with clusters 2, 4 and 5. Cassava genotypes of cluster 1 had significantly lower stem K content to the tune of 0.66% and was on par with those in clusters 4 and 5. The mean stem K content at 6, 8 and 10 MAP were 1.01, 0.95 and 0.84% respectively. Cassava genotypes of cluster 2 at 6MAP had the highest stem K (1.14%) on par with those in clusters 3, 4, 5 at all intervals. Cassava genotypes in cluster 1 at 10 MAP had significantly the least stem K content (0.58%) on par with those in clusters 1 at all intervals, cluster 2 at 8 MAP, cluster 3 at 8 MAP, clusters 4 and 5 at all intervals.

Tuber K

Though there was no significant difference among the three intervals on tuber K, the clusters differed significantly with cluster 5 having significantly the highest tuber K content (1.59%) on par with those in cluster 2 (1.22%). Cassava genotypes in cluster 4 had the least tuber K content (0.85%) on par with those in clusters 1 (0.95%) and cluster 3 (1.13%). The mean tuber K content at 6, 8, 10 MAP were 1.08, 1.28 and 1.10% respectively where the overall mean of the cassava genotypes of five clusters was 1.17%.Cassava genotypes in cluster 5 at 8 MAP had the maximum tuber K content (1.76%) on par with those in cluster 2 at 8, 10 MAP, in

Table 5. Variation among clusters on plant K attributes

	Leaf K (%)			
Clusters	Intervals			
	1	2	3	Mean(C)
1	1.40^{abc}	1.29^{bcd}	1.00^{d}	1.23a
2	1.65^{a}	1.34^{b}	1.15^{cd}	1.38a
3	1.42^{abcd}	1.33^{abcd}	1.29^{bcd}	1.35a
4	1.24^{abcd}	1.15^{abcd}	1.18^{bcd}	1.19a
5	1.13^{abcd}	1.25^{abcd}	1.44^{abcd}	1.27a
Mean (I)	1.37^{a}	1.27a	1.21a	1.34
	Stem K(%)			
	1	2	3	Mean(C)
1	0.758^{bcd}	0.651^{cd}	0.580^{d}	0.663^{b}
2	1.138^{a}	0.828^{bcd}	0.912^{bc}	0.59^{a}
3	1.19^{ab}	1.045^{abcd}	1.044^{ab}	1.094^{a}
4	0.900^{abcd}	1.059^{abcd}	0.758^{abcd}	0.906^{ab}
5	1.042^{abcd}	1.142^{abcd}	0.898^{abcd}	1.027^{ab}
Mean (I)	1.006^{a}	0.945^{a}	0.838^{a}	
	Tuber K(%)			
	1	2	3	Mean(C)
1	0.77^{e}	1.12^{abce}	0.97^{bef}	0.95^{c}
2	1.02^{bef}	1.39^{a}	1.26^{acd}	1.22^{ab}
3	1.02^{abce}	1.38^{abc}	0.99^{bef}	1.13^{bc}
4	0.95^{abce}	0.74^{cef}	0.87^{bcde}	0.85^{c}
5	1.62^{abc}	1.76^{ab}	1.39^{abc}	1.59^{a}
Mean (I)	1.08a	1.28^{a}	1.10^{a}	

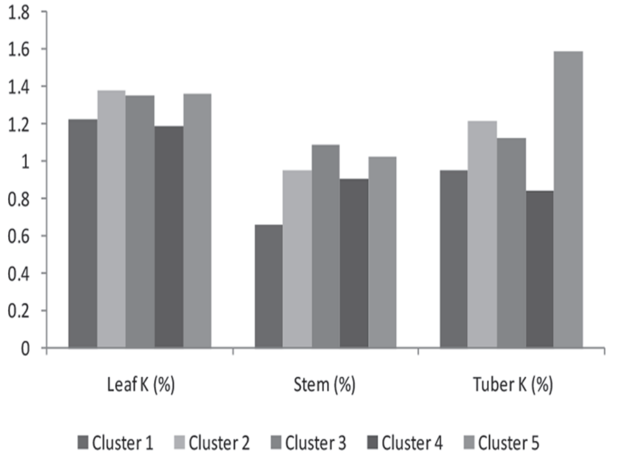

Fig. 7. Variation among clusters on plant K content

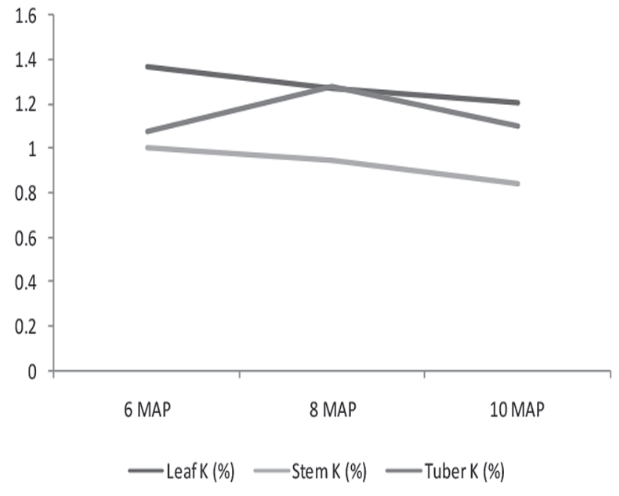

Fig.8. Variation of plant K content at different intervals

cluster 3 at 6, 8 MAP, in cluster 4 at 6 MAP and in cluster 5 at all intervals. Cassava genotypes in cluster 1 during 6 MAP had the least tuber K content (0.77%) which was on par with those in cluster 1 at 8, 10 MAP, in cluster 2 at 6 MAP, in cluster 3 at 6 and 10 MAP and in cluster 4 at all intervals.

The variation in K content of the leaf, stem and tuber noticed among clusters in the present study is in agreement with the reports of Chavez et al. (2000) that, genotype and soil type can influence the mineral content of plant tissues. Moreover, there are reports indicating that, genotypes and management practices can cause variation in the nutrient content of plant tissues (Costa et al., 2002) and Rengel and Paul, (2008) confirmed genotypic differences in the efficiency for uptake and utilization of K in the case of all major economically important plants.

Tuber quality attributes

The tuber quality attributes studied included cyanogenic glucosides (HCN) responsible for bitterness in cassava tubers and starch. Here also, the variation among clusters, among intervals and the interaction between clusters and intervals was studied. Both the attributes were expressed on fresh weight basis.

Cyanogenic glucosides

There was no significant difference among clusters as well as among the three stages of maturity in the case of HCN. Hence, the interaction also was non significant. Sruthi et al., (2019) found no significant effect of stage of growth on HCN content of cassava tubers. Among the clusters, cassava genotypes in cluster 5 had the lowest HCN content (55.02 ppm) and those in cluster 1 had the highest (107.23 ppm). Though there was no significant difference among 6, 8 and 10 MAP with respect to HCN content of tubers, HCN content gradually declined from 6 to 10 MAP. This in turn corroborates to the reports of Sruthi et al., (2019) who found a decreasing trend in HCN from 7-9th month. Cassava genotypes in cluster 2 at 6 MAP (124.72 ppm) had the maximum and 10 MAP (73.81 ppm) had the lowest HCN content in the tubers (Table 6, Fig. 9,10). The HCN content recorded with different genotypes in the present study confirm the reports of Cardoso et al. (2005) that, HCN content of cassava roots ranges from 1 to 1550 ppm. Based on the HCN content and as per the report of Wilson and Dufour,(2002) regarding the categorization of tubers based on HCN as bitter or sweet, 50-75% of the genotypes had sweet tubers with HCN content in the range of 30-75 ppm.

Starch content

In the case of tuber starch content, significant difference was seen among clusters as well as among the three stages of plant growth, *viz.,* 6, 8, 10 MAP. The mean starch content of cassava genotypes over the five clusters was 16.95% and the mean starch content in the tubers of cassava genotypes of clusters 1, 2, 3, 4 and 5 were 16.84, 17.69, 15.11, 17.86 and 11.98% respectively. Cassava genotypes under cluster 2 had the highest starch content (17.69%) and was on par with cassava genotypes in clusters 1 and 4. Cluster 5 had the least starch content to the tune of 11.98% and was on par with those in cluster 3. As regards to the three intervals, highest starch content was recorded at 6 MAP (18.42%) and was on par with 8 MAP (15.72%). At 10 MAP, the starch content was the lowest (13.55%) on par with that of 8 MAP (15.72%). These results are in conformity with the reports of Sruthi et al., (2019) revealing variation among cassava genotypes in starch content and decrease in starch over period of time.

Cassava genotypes under cluster 4 at 6 MAP had the highest starch content in the tuber (21.54%) and was on par with those under cluster 1 at 8 MAP, in cluster 2 at 6, 8 MAP, in cluster 3 at 6, 8 MAP, in cluster 4 at 8 MAP and in cluster 5 at 6 MAP (Table 6, Fig. 9,10). Ebah-Djedji et al. (2012), could not find any significant difference in starch yields from storage roots of improved cassava varieties during harvest and justified it as due to the similarity of the physiological characteristics of improved varieties (Segnou, 2002). According to Cock (1976) and Veltkamp(1985), the difference in starch yields is because of the difference in volume of leaf canopy(number of leaves, leaf area), their interception of solar radiation, thereby the photosynthetic activity and the speed of translocation.

A critical analysis of the data showed the genotypes in cluster 4 had the highest leaf and stem dry matter percentage at 8 MAP to the tune of 31.8 and 38.2% respectively. Storage root dry weight percentage was maximum for the cassava genotypes in cluster 3 at 6MAP (39.2%). Cassava genotypes in cluster 1 at 6 MAP had the highest average number of storage roots (13) with longest tubers (44.6 cm). Biggest tubers with maximum storage root girth was seen in genotypes in cluster 2 at 10 MAP (21.6 cm). Highest average plant height was found in cassava genotypes in cluster 2 at 8MAP (2.7m) and stem girth in cassava genotypes of cluster 5 at 10 MAP (12.8 cm). Cassava genotypes in cluster 2 at 6MAP had the highest average leaf and stem K to the tune of 1.65 and 1.14 % respectively. In the case of storage root K content, genotypes in cluster 5 at 8MAP had the maximum (1.76%). Cassava genotypes in cluster 2 at 10 MAP possessed the lowest HCN (73.81 ppm) and cassava genotypes in cluster 4 at 6 MAP had the highest starch (21.54%). The significant attributes especially tuber number, tuber length, tuber girth, tuber yield, plant K,

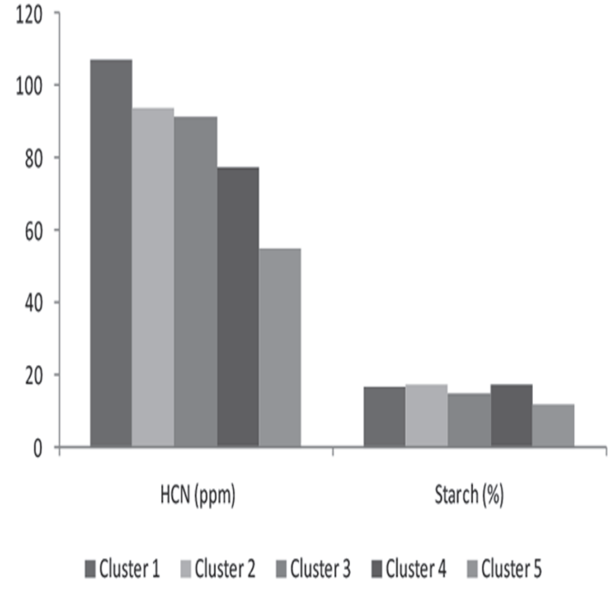

Fig.9. Variation among clusters on tuber quality attributes

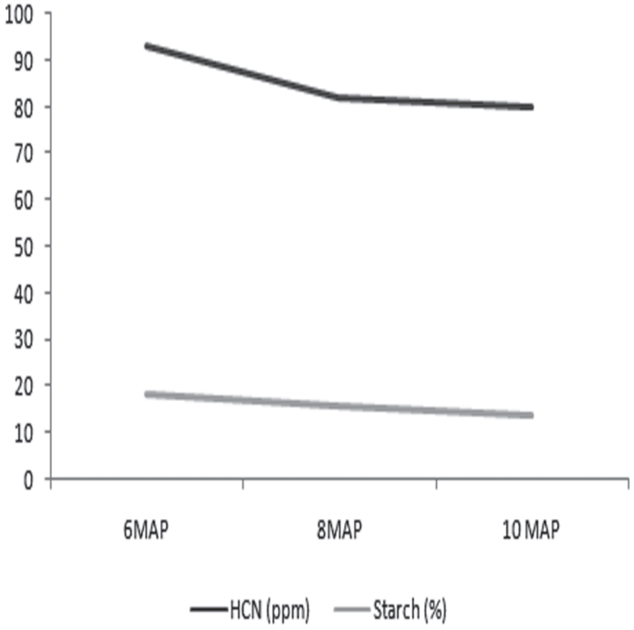

Fig. 10. Variation of tuber quality at different intervals

Table 6. Variation among clusters on tuber quality attributes

	Cyanogenic glucosides (ppm)			
Clusters	Intervals			
	1	2	3	Mean(C)
1	104.76^{ab}	115.38^{ab}	101.54^{ab}	107.23^{a}
2	124.72^{a}	82.45^{b}	73.81^{b}	93.66^{a}
3	70.43^{ab}	93.76^{ab}	110.57^{ab}	91.58^{a}
4	86.38^{ab}	27.94^{b}	50.74^{ab}	77.87^{a}
5	80.28^{ab}	80.28^{ab}	73.05^{ab}	55.02^{a}
Mean (I)	93.31^{a}	81.94^{a}	79.96^{a}	
	Starch (%)			
	1	2	3	Mean(C)
1	16.51^{bc}	17.86^{abc}	16.15^{bc}	16.84^{ab}
2	19.82^{a}	18.16^{ab}	15.08^{c}	17.69^{a}
3	16.70^{abcd}	16.47^{abcd}	12.16^{de}	15.11^{bc}
4	21.54^{ab}	16.66^{abcd}	15.38^{abcde}	17.86^{ab}
5	17.53^{abcde}	9.45^{cde}	8.95^{e}	11.98^{c}
Mean (I)	18.42^{a}	15.72^{ab}	13.55^{b}	

leaf, stem, tuber dry matter production associated to PE are found in genotypes under clusters 1 and 2. Similarly the other quality traits like starch and HCN and growth characters especially stem girth are found significantly high with genotypes under clusters 1 and 2. The six K use efficient genotypes also fell under these clusters too.

Conclusion

The preliminary study in screening K use efficient cassava genotypes was started with pre evaluation of some elite cassava genotypes for different plant attributes. The clustering of genotypes with similar traits at their fag end of maturity from six to ten months at bimonthly intervals threw light on the vast differences that existed among the clusters, among periods of maturity and their interaction. The basic parameter used in the selection of K efficient genotypes was physiological efficiency. The factors directly contributing to it are plant dry matter production, plant dry matter percentage and plant K content. Among the different components of plant dry matter, tuber dry matter is most important which in turn is dependent on tuber yield, tuber number, tuber length and tuber girth. A critical analysis of the data reveals, these parameters are highest for genotypes under cluster 1 and 2. It is interesting to note that, the physiologically efficient genotypes that were selected based on PE such as Aniyoor, 7 III E5-5, 7 Sahya (2), W-19, CR 43-8, 6-6 were belonged to these two clusters. Moreover, other attributes like tuber quality *viz.,* HCN, starch also were seen highest for cassava genotypes under clusters 1 and 2 which contained the K efficient genotypes. Stem girth is noted as one of the best growth characters highly correlated with tuber yield and is seen from the results that, genotypes under clusters 1 and 2 had thickest stems. In addition, other parameters like leaf, stem dry matter percentage, leaf, stem, tuber K content,were not highest for cassava genotypes under clusters 1 and 2, but these parameters were found on par with the highest values under other clusters. As regards to the stage of maturity in affecting these parameters, 6MAP was found better. The information generated for identifying the NUE genotypes will be quite useful in selecting the core NUE genotypes which can later be released as NUE varieties or they can better be used as elite breeding materials in evolving NUE genotypes.

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