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Evaluation of Plant Nutrition Traits Based Genetic Variability to Identify N-P-K Use Efficient Genotypes in Cassava

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Abstract

A total of 132 elite genotypes were evaluated to identify N-P-K use efficient genotypes in cassava. The genetic variation was studied through the principal component, cluster, biplot and dendrogram analysis. Principal component analysis (PCA) extracted seven principal components with a cumulative variability of 73.3% with the highest variability (24.1%) in PC1 and the least in PC7 (4.7%). Hierarchical cluster analysis resulted in eight clusters having 62, 29,13,18, 2,5,2 and 1 genotypes in clusters one to eight respectively with each cluster having genotypes with almost similar characters. Biplot indicated the characters important for each genotype and the dendrogram had eight groups with the same genotypes composition as in cluster analysis. These analyses revealed the distinct variation among these genotypes and the genotypes in clusters 1, 2, 3, and 4 were later screened as nutrient use efficient (NUE) too. These included NPK efficient genotypes *viz.,* Acc. No. 7, 775, 788, 796 (cluster 1), Acc. No. 130, 766 (cluster 2), Acc. No. 696 (cluster 3), NP efficient genotypes *viz.,* Acc. No. 890, 896 (cluster 1), Acc. No. 115 (cluster 4) and PK efficient genotypes *viz.,* Acc. No. 662, 905, 906, 908 (cluster 1), Acc. No. 750 (cluster 3). Biplot analysis revealed the characters linked to the genotypes are significant for genotypes in clusters 1,2,3 and 4 which in turn were later delineated as NUE genotypes. These accessions can form a broad genetic base in breeding programmes to evolve genotypes with better NUE.

Key words: Cassava, nutrient use efficiency, tuber yield, physiological efficiency, cluster analysis, principal component analysis, biplot, dendrogram.

Introduction

Among the tropical tuber crops, cassava (*Manihot esculenta* Crantz) deserves much significance. The reasons being the highest area under cultivation globally, suitability to grow under marginal environments, tolerance to biotic and abiotic stresses (More et al., 2020), higher biological efficiency in the form of dry matter production per unit area and quality starch worthy of making value added food and industrial products (More et al., 2019).The experience on soil fertility and plant nutrition of cassava at ICAR-Central Tuber Crops Research Institute (CTCRI) under the long term fertilizer experiment (LTFE) since 1977 revealed the high positive response of cassava to integrated nutrient management (INM) practices involving organic manures and chemical fertilizers (Susan John et al., 2005, 2019). The storage root (tuber) yield of cassava to the tune of 30-60 t ha^{-1} implies the fact that they require higher levels of nutrients to replenish the removed nutrients from the soil to sustain the yield.Though we are applying sufficient nutrients to the soil to enhance the yield, the nutrient use efficiency (NUE) of the crop to properly assimilate and utilize the nutrients for plant growth and yield is more important. In this regard, the nutrient available in the soil solution plays a significant role in the pattern and magnitude of nutrient uptake and accumulation and incidentally on plant growth rate and dry matter partitioning. Here, both

root and plant architecture plays a vital role which in turn are inherent plant attributes. There exists drastic variation among accessions concerning their genetic ability to acquire and utilize the soil available nutrients. In this regard, adaptations like root system enlargement (Liu et al., 2004; Jemo et al., 2006), development mechanisms in the rhizosphere or at the cellular level or changes in rhizosphere pH (Marschner et al., 2005) are significant. Efficient use of soil nutrients (either present innate in the soil or applied through external source) by plants to produce biological/economic yield otherwise called physiological efficiency (PE) is inherent. If this can be exploited well, the application of nutrients through external source can be reduced (Sattelmacher et al., 1994; Duncan and Carrow, 1999). In this regard, evaluation of the accessions for identifying genotypes that are physiologically efficient in utilizing the soil nutrients deserves importance. Fageria et al. (2008) indicated PE as one of the best indices to find out the high yielding potential genotypes for breeding programmes. NUE is directly and indirectly linked with many of the plant characters like leaf, stem, storage root fresh weight, their dry matter percentage, dry matter production, nutrient contents and nutrient uptake. There are reports (Baligar et al., 2001; Fageria et al., 2006) in many other crops indicating genotypic variation concerning dry matter production, leaf area index and plant canopy/ architecture. This can indirectly or directly affect nutrient absorption/utilization and incidentally NUE. Agong et al. (2001) reported the need of undertaking systematic study and characterization of germplasm for the current and future agronomic and genetic improvement of crops. Selection and breeding of NUE varieties are important from the point of view of rising fertilizer prices, unavailability during its application time and organic cultivation with low input of fertilizers. As per Smith et al. (1994), the major implication being for identifying or breeding NUE genotypes is to reduce the dependence on chemical fertilizers.

An attempt to screen the elite cassava genotypes was initiated at ICAR-CTCRI, Thiruvananthapuram, Kerala, India to identify NPK use efficient genotypes to reduce the use of NPK chemical fertilizers. As a prelude in the screening process, a preliminary evaluation of around 132 elite cassava genotypes was done concerning soil and plant nutrition attributes. As these traits are directly related to the inherent PE of the crop, the genetic variation among genotypes was studied. This, in turn, will help to identify the potential genotypes with high PE which when used as planting materials can reduce the use of external supply of chemical fertilizers.

Materials and Methods

A total of 132 elite cassava accessions received from the Division of Crop Improvement, ICAR-CTCRI were used for the trial. These genotypes included indigenous and exotic collections, top cross hybrids and interspecific hybrids. The selection of these accessions was primarily based on their high yield, good tuber quality parameters including cooking quality, better plant architecture, biotic and abiotic stress tolerance. The stress factors considered were drought, diseases tolerance especially to cassava mosaic disease (CMD), tuber rot and pest tolerance to white fly, mealy bug and scale insects. The tuber quality traits evaluated were high starch, low cyanogenic glucosides and better β carotene contents. They were planted in a row trial at ICAR-CTCRI farm (Ultisol) at the rate of 10 plants per row without adding any fertilizers and manures.The major determinant used to identify the best genotypes from these genotypes was PE for major nutrients *viz.,* N, P, K. Moreover, traits like canopy architecture, storage root yield, tuber quality traits, CMD tolerance were also given priority. The entire plants were harvested at ten months after planting (MAP) and all these characters were assessed.

As regards to the fresh plant (leaf, stem, storage root) yield, at harvest, from the 10 plants of each row representing each accession, two sample plants were uprooted. The weight of the stems was taken, converted for a single plant and then to a per hectare basis. In the case of total leaf yield from sprouting till harvest, standing as well as fallen leaves and the fresh weight of 10 leaves at each sampling taken at tri-monthly intervals was used. The total tuber yield of 10 plants of each row was taken, converted to per plant and then on per hectare basis. Leaf, stem and tuber dry matter percentage was computed by drying 50 g each of the fresh samples in a hot air oven at ± 64°C till constant weight is attained and converted to percentage. The fresh leaf, stem and storage root yield and their corresponding dry matter percentage were used to calculate their dry matter production following the formula as given below.

Plant (leaf, stem, storage root) matter production (t ha^{-1}) = Plant dry matter percentage × plant fresh yield (t ha^{-1}). By adding the dry matter production of leaf, stem and tuber, arrived at the total plant dry matter production.

The leaf, stem and storage root samples kept for dry matter calculation, after taking their dry weight, ground and used for the chemical analysis of nutrients *viz.,* N, P, K. Triacid (Nitric: Perchloric: Sulfuric acids in the ratio 10:3:1) digest of the sample was used for P and K analysis and single acid digestion using sulfuric acid was done for N as per Piper (1970). P content in the leaf, stem and tuber samples were determined by phospho-molybdous-vanadate yellow colour method using a visible spectrophotometer (Systronics VIS 1203). K in these samples was directly read with the plant acid extract using a flame photometer (Systronics, 128). The Kleldhal system was used in the case of N determination[Kelplus-classic SX (VA)].

Leaf, stem and storage root uptake were determined separately by multiplying their dry matter production with their respective N,P, K contents. Total plant uptake of N, P, K was determined by adding leaf, stem and tuber uptake.

Among the different attributes, PE of N, P, K, which is the basic inherent determinant to understand the nutrient utilization efficiency of a crop (Isfan,1990) was assessed following the formula

PE (N/P/K) kg kg^{-1} = Biological yield (total plant dry matter production) (kg $plant^{-1}$)/Nutrient uptake (N/P/K) (kg $plant^{-1}$).

The genotypic variation among these accessions was understood by arbitrary classification criteria having an upper and lower value concerning each of the studied parameters as well as through different statistical tools.

Statistical tools in the genetic variability analysis

The different statistical methods included principal component (PCA) cluster, biplot and dendrogram analysis.

For performing the PCA and cluster analysis, the missing values on the different characters studied were imputed by the Multiple Imputation by Chained Equations (MICE) algorithm using Fully Conditional Specification (FCS) as described in Van Buuren and Oudshoorn (2011). MICE package in R environment for statistical computing not only allows for performing imputations but includes several functions for identifying the missing data pattern(s) present in a particular dataset. Under MICE, Predictive Mean Matching (PMM), a semi-parametric imputation approach was used which is similar to the regression method except for each missing value. This method fills in a value randomly from the observed donor values whose regression predicted values are closest to the regression predicted value for the missing value from the simulated regression model (Heitjan and Little, 1991; Schenker and Taylor, 1996).

Principal component analysis (PCA)

PCA was done to determine the extent of variability among the accessions by grouping them as principal components (PC) with the percentage of variability in each PC due to the studied characters (Jolliffe and Cadima, 2016).

Cluster analysis

Agglomerative hierarchical cluster analysis (Van Hintum,1995) with a complete linkage method has been carried out for classifying the 132 cassava accessions based on the degree of similarity and dissimilarity.

Biplot analysis

Biplot PCA was also done with percent variability in PC1 and PC2 on the X and Y axes respectively to reveal the characters linked to each accession (Gabriel, 1971).

Dendrogram analysis

A dendrogram was constructed based on Euclidean distance as per the hierarchical cluster analysis.

Results and Discussion

Screening was done for 132 cassava genotypes and was grouped concerning the characters *viz.,* plant (leaf, stem, storage root) fresh yield, plant dry matter percentage, total plant dry matter production, plant nutrient (N, P, K) contents, physiological efficiency of the genotypes concerning nutrients *viz.,* N, P, K and total plant nutrient (N, P, K) uptake.The results based on the arbitrary criteria are as follows.

Plant fresh yield

The plant fresh yield comprised of storage root (tuber), stem and leaf yields. The storage root yield ranged from

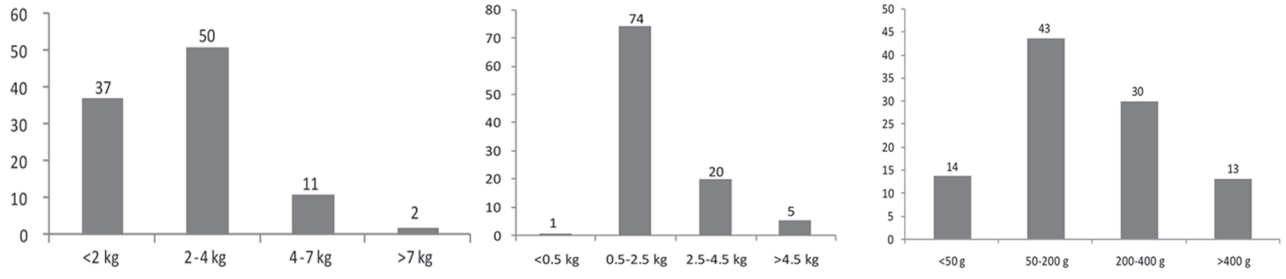
1.5 to 10.9 kg plant^{-1} with a mean value of 2.7 kg plant^{-1}. Out of the total genotypes, 37, 50, 11, 2% possessed storage root yield as <2, 2-4, 4-7 and >7 kg plant^{-1}. The number of genotypes corresponding to their percentages are presented in Fig. 1a. In the case of fresh weight of stem (stem yield), it ranged from 0.1 to 7.4 kg plant^{-1} at harvest with a mean value of 2.1 kg plant^{-1}. There were 1% genotypes with stem yield < 0.5 kg plant^{-1} and 5% with more than 4.5 kg plant^{-1}. Out of the genotypes, 74 and 20 % respectively had stem yield in the range of 0.5-2.5 and 2.5-4.5 kg plant^{-1}. The details on the number of genotypes with different stem yields are given in Figure 1b. Leaf yield ranged from 20-1150 g plant^{-1} with a mean value of 231.1 g plant^{-1}. In 14% genotypes, the leaf yield was <50 g plant^{-1}and 13% had > 400g leaf yield per plant. Out of these genotypes, 43 and 30% respectively had leaf yield ranging from 50-200 g and 200-400 g respectively (Fig.1c). These observations adhere to the reports of Agong et al. (2001) in tomato and Susan John et al. (2020) in cassava that, there is significant variation among genotypes concerning plant fresh and dry weights.

Plant dry matter percentage

The mean leaf dry weight percentage (LDW%) of 132 genotypes was 33.9% with values ranging from 14.8 to 46.3%. About 1 and 2% respectively of the genotypes had LDW%< 15% and >45%. However, 13 and 84% of the genotypes possessed LDW% to the tune of 15-30 and 30-45% respectively (Fig.2a). The stem dry weight percentage (SDW%) ranged between 24.4-48.8% with a mean value of 36.2%. Out of the total accessions, 3,47,44 and 6% had SDW% as <25, 25-35, 35-45 and >45% respectively (Fig. 2b). The storage root (tuber) dry weight percentage (TDW%) of the accessions ranged from 7.0-51.6% with a mean value of 39.1%. About 2 and 1% of the accessions recorded TDW% as <10 and >50% respectively. However, 5 and 92% of the accessions had TDW% in the range of 10-25 and 25-50% respectively (Fig. 2c). These findings confirm the studies of Santos et al. (2019) in the selection of superior lineages of *Ricinus communis* with greater variability in the weight of seeds per plant. Moreover, Susan John et al. (2020) in cassava found drastic variation concerning plant dry matter production in the screening and selection of K use efficient genotypes.

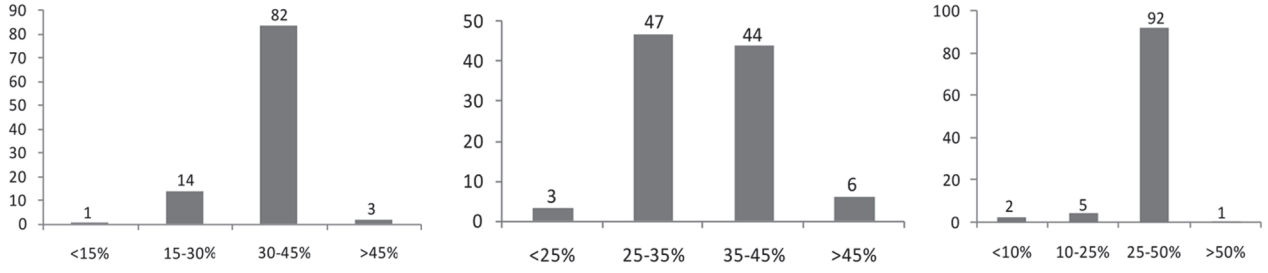
Total plant dry matter production (TPDMP)

The mean total plant dry matter of the evaluated genotypes was 1.82 kg plant^{-1} with values ranging from 0.75-6.38 kg plant^{-1}. Among the 132 genotypes, 9 and 8% respectively had TPDMP as <1 and >3.5 kg



a. Tuber yield b. Stem yield c. Leaf yield

Fig.1. Percentage of genotypes with varying tuber, stem and leaf fresh wieght



a. Leaf dry weight percentage b. Stem dry weight percentage c. Tuber dry weight percentage

Fig.2. Percentage distribution of genotypes with varying plant dry matter percentage

plant^{-1}. However, 64 and 19% indicated TPDMP to the tune of 1-2 and 2-3.5 kg plant^{-1} respectively (Fig. 3). In this regard, Ene et al. (2016) in cucumber found significant variation among genotypes concerning agronomic traits like vine length, number of branches, number of leaves, leaf area, fruit length, fruit girth, fruit weight per plant, number of fruits per plant, mean fruit weight and total fruit yield. Susan John et al. (2020) also established significant variation among genotypes

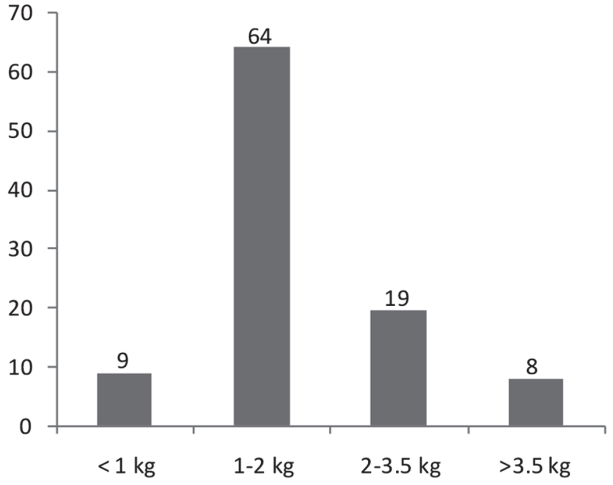


Fig.3. Percentage distribution of genotypes with varying total plant dry matter production

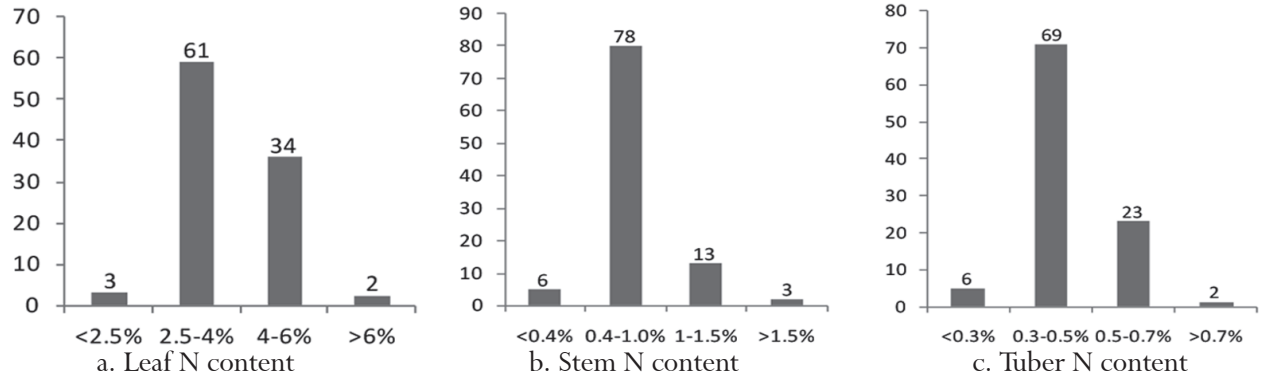
concerning total plant dry matter production in the screening of K use efficient cassava genotypes.

Plant nutrient content (dry weight basis)

The mean N content in the leaf, stem and storage root at harvest was 3.86, 0.76, 0.44% respectively. These values ranged 2.37-6.29% in leaf, 0.33-1.65% in stem and 0.26-0.64% in storage root. Out of the total genotypes, 3, 59,36, 2% of the genotypes had leaf N in the range of <2.5, 2.5-4, 4-6 and > 6% respectively (Fig. 4a). There were 5% genotypes having <0.4% N, 80% with 0.4-1%, 13% with 1-1.5% and 2% with >1.5% stem N (Fig. 4b). In the case of storage root N, 5, 71, 23, 1% of the genotypes gave tuber N to the tune of <0.3, 0.3-0.5, 0.5-0.7 and >0.7% respectively (Fig. 4c).

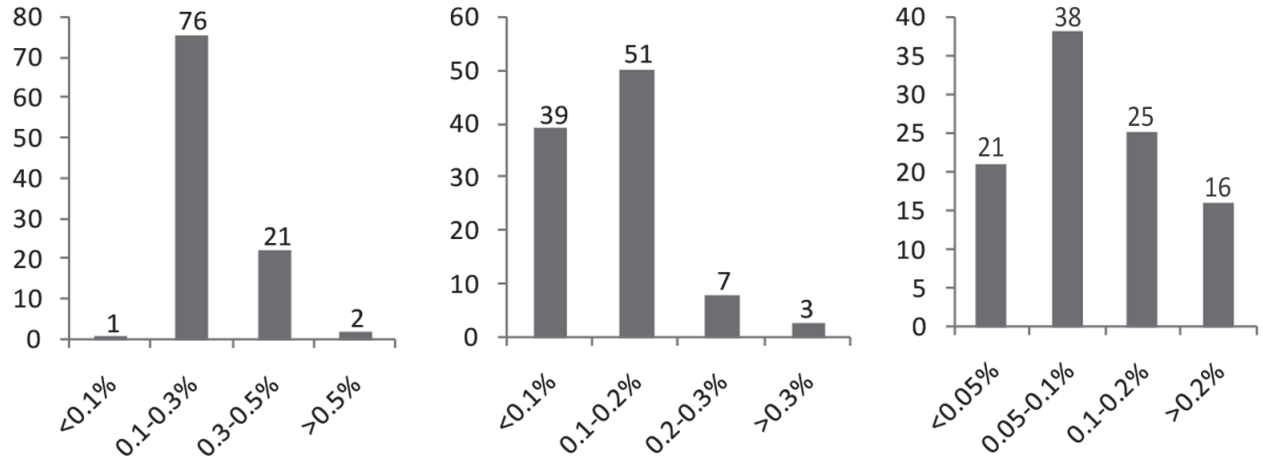
The leaf, stem and tuber P ranged as 0.057-0.621%, 0.036-0.359% and 0.023-0.296% respectively with mean values as 0.231, 0.121 and 0.111% respectively. As regards to leaf P, 1, 75, 22 and 2% of the genotypes had <0.1, 0.1-0.3, 0.3-0.5 and >0.5% leaf P respectively (Fig. 5a). A total of 39, 50, 8 and 3% accessions had <0.1, 0.1-0.2, 0.2-0.3 and >0.3% stem P respectively (Fig. 5b). There were 21, 38, 25 and 16% of the accessions had storage root P as <0.05, 0.05-0.1, 0.1-0.2 and >0.2%, respectively (Fig. 5c).

The mean K content of leaf, stem and storage root (Fig. 6 a,b,c) of the genotypes tested were 0.79, 0.43, 0.72% respectively, with values ranging as 0.15-1.78, 0.08-1.24, 0.19-2.12% respectively. A total of 10% genotypes had leaf K less than 0.5%. The majority of the genotypes (70%) had leaf K content ranging from 0.5-1% and 19% in the range of 1-2% and 1% with >2% leaf K. About 1% of the genotypes had stem K content <0.1%, whereas 77% had 0.1-0.5%, 18% had 0.5-1% and 5% had > 1% stem K content. In the case of tuber K content, 52, 27, 14 and 7% of the genotypes possessed K content as <0.5, 0.5-1.0, 1-2 and >2% respectively (Fig. 6). This, in turn, corroborates the reports of Chavez et al. (2005) and Susan John et al. (2020) in cassava indicating significant variation in the mineral content of plant tissues



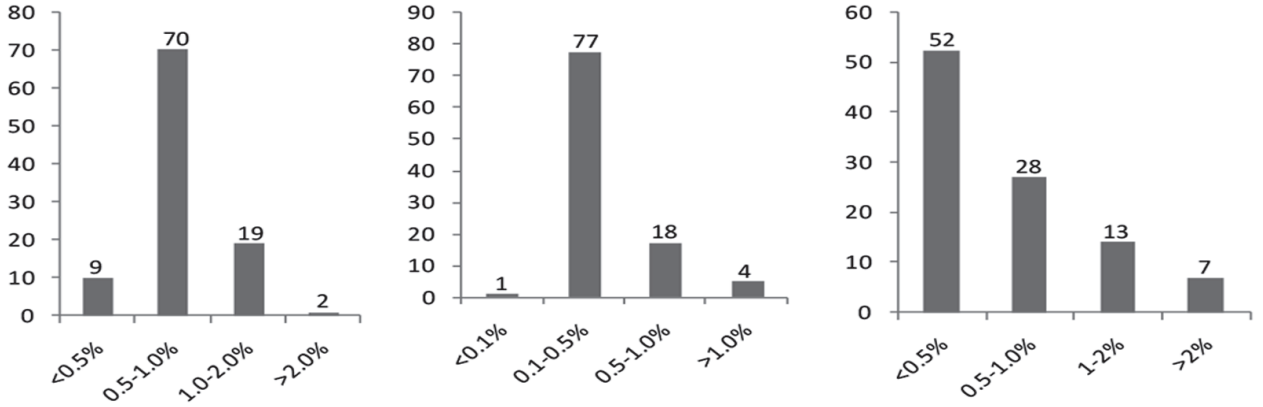
a. Leaf N content b. Stem N content c. Tuber N content

Fig.4. Percentage distribution of genotypes with varying plant N contents



a. Leaf P content b. Stem P content c. Tuber P content

Fig.5. Percentage distribution of genotypes with varying plant P contents



a. Leaf K content b. Stem K content c. Tuber K content

Fig.6. Percentage distribution of genotypes with varying plant K contents

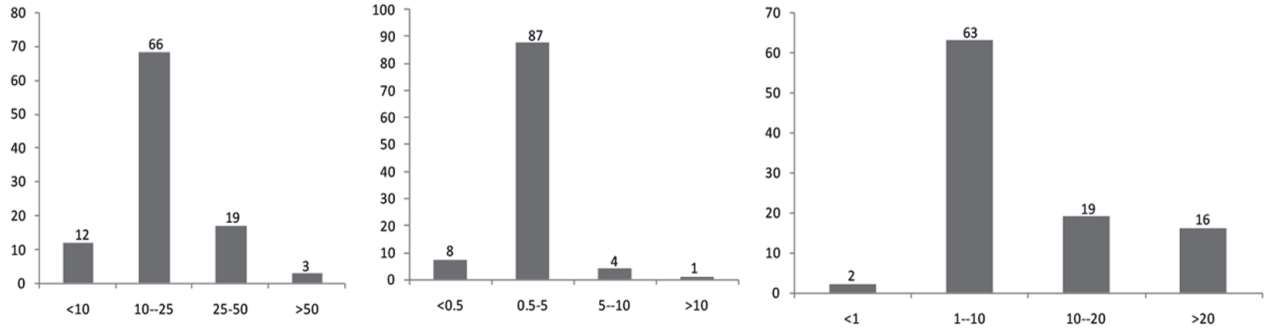
especially K due to significant genetic differences in nutrient uptake and utilization among genotypes.

Nutrient uptake

The mean N, P, K uptake per plant was 20.6, 1.93, 10.05 g plant^{-1} respectively with values ranging as 3.9-75.9, 0.26-13.51, 0.52-44.19 g plant^{-1} respectively. In the case of N uptake, 12% of the genotypes had N uptake $<$10 g plant^{-1} and 3% had N uptake more than 50 g plant^{-1}. There were 68 and 17% genotypes with N uptake as 10-25 and 20-50 g plant^{-1} respectively. As regards to P uptake, 7, 88, 4 and 1% of the genotypes recorded P uptake as $<$0.5, 0.5-5, 5-10 and $>$10 g plant^{-1} respectively. K uptake of these genotypes varied as $<$1.0, 1-10, 10-20 and $>$ 20 g plant^{-1} respectively in 2, 66, 19 and 13% genotypes (Fig. 7 a,b,c). This result corroborates the findings of Rengel and Paul (2008) that, there are genotypic differences in K efficiency, uptake and utilization for all major economically important plants. Susan John et al. (2020) reported genotypic variation in the leaf, stem and tuber K uptake while computing PE for K in the screening K use efficient genotypes.

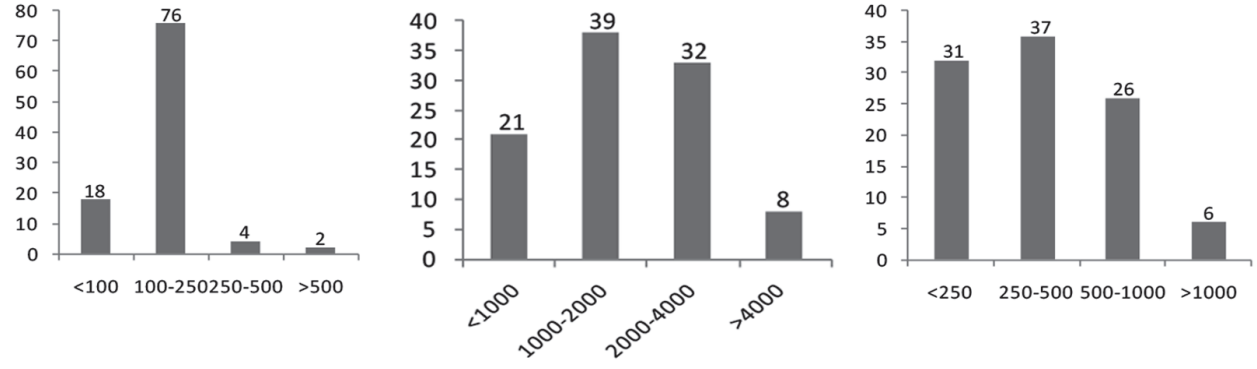
Physiological efficiency (PE)

It is an inherent physiological attribute of the crop to efficiently utilize the soil available nutrients for total plant biomass production. It is described as the biological yield (kg ha^{-1}) produced for each kg of total crop uptake of nutrients (N,P, K; kg ha^{-1}). The mean value of PE computed in the case of N, P, K of the tested genotypes were 169,2204 and 470 kg kg^{-1} respectively. The distribution of PE of N among these genotypes was $<$100, 100-250, 250-500 and $>$500 kg kg^{-1} for 18, 76, 4 and 2% respectively of the total genotypes. PE for



a. Plant N uptake (g plant^{-1}) b. plant P uptake (g plant^{-1}) c. Plant K Uptake (g plant^{-1})

Fig.7. Percentage distribution of genotypes with varying plant nutrient uptake



a. PE (N) b. PE (P) c. PE (K)

Fig. 8. Percentage distribution of genotypes with varying physiological efficiency

P was in the range of <1000, 1000-2000, 2000-4000 and >4000 kg kg^{-1} with 21, 38, 33 and 8% respectively of the total genotypes. In the case of PE for K, 32, 36, 26 and 6% of the genotypes had values as <250, 250-500, 500-1000 and >1000, kg kg^{-1}respectively (Fig.8 a,b,c). These findings conform to the reports of Fageria and Baligar (2005) that, there is significant variation in physiological efficiency due to drastic genetic differences among genotypes of the same species in nutrient uptake and utilization. Susan John et al. (2020) established significant variation among genotypes in the case of PE (K) through different statistical tools while identifying K use efficient genotypes.

Genetic divergence of cassava genotypes for NPK use efficiency and physiological efficiency

The variability among the accessions concerning the studied characters was done through principal component analysis (PCA), cluster analysis, biplot and dendrogram. The above analyses primarily aim in studying the genetic divergence among groups which in turn could be made by clubbing together those accessions which behave similarly concerning the parameters evaluated.

Principal component analysis (PCA)

Among the different parameters evaluated, those which have significance in imparting the variability was studied through PCA. PCA analysis indicated the extent of variability among the genotypes as well as the characters significantly contributing to the variability. In this case, as per Table 1, PCA analysis extracted seven PCA components with a cumulative variability of 73.3% with highest variability in PC1 (24.1%) followed by PC2 (12%), PC3 (11.8%), PC4 (7.8%), PC5 (6.6%), PC6(6.2%) and PC7(4.7%). Pahadi et al. (2017) for the selection of best genotypes for maize breeding had undertaken PCA of the major agronomic traits and the first two PCA explained 74% of the total variability. In the present study, among the different parameters, the important plant characters that contributed significantly to PC1 included storage root P and K contents and total plant P and K uptake. PC2 was significantly influenced by fresh leaf, stem and storage root yield, leaf dry weight

Table 1. PCA Analysis of the studied traits of cassava genotypes

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value (Root)	2.248	1.586	1.577	1.281	1.182	1.142	0.998
% variation expressed	24.1	12.0	11.8	07.8	6.6	6.2	4.7
Cumulative variation expressed (%)	24.1	36.1	47.9	55.7	62.4	68.6	73.3
Leaf dry weight	-0.045	0.303	-0.222	0.221	-0.273	0.282	-0.161
Stem dry weight	-0.252	-0.052	-0.277	0.047	-0.053	0.003	-0.283
Tuber dry weight	-0.136	-0.097	-0.181	0.207	-0.433	0.120	0.398
Leaf yield	0.138	0.401	0.236	0.124	0.075	-0.043	0.207
Stem yield	-0.267	0.416	0.016	-0.093	-0.048	-0.070	0.093
Tuber yield	-0.258	0.424	0.011	-0.057	0.114	-0.016	-0.052
Leaf N	0.234	0.124	0.367	0.060	-0.451	0.151	0.138
Stem N	-0.138	-0.213	-0.044	0.225	0.541	-0.048	-0.207
Tuber N	0.048	-0.071	-0.213	0.030	0.424	-0.058	0.644
Leaf P	0.035	-0.008	0.340	-0.062	-0.047	0.318	0.242
Stem P	0.102	0.027	-0.127	-0.184	0.262	0.666	-0.051
Tuber P	-0.321	-0.155	-0.005	-0.229	0.070	0.014	0.108
Leaf K	0.045	0.012	0.215	-0.405	-0.047	-0.237	0.018
Stem K	-0.026	-0.104	0.383	-0.328	0.074	0.196	-0.254
Tuber K	-0.285	-0.256	0.054	-0.183	-0.048	-0.125	0.195
PE N	0.107	0.105	-0.351	-0.528	-0.095	0.068	0.085
PE P	0.254	0.208	-0.074	-0.146	-0.008	-0.434	-0.118
PE K	0.215	0.199	-0.349	-0.246	0.192	0.028	0.030
N uptake	-0.291	0.321	0.127	0.155	0.302	-0.053	0.036
P uptake	-0.371	0.131	-0.018	-0.095	0.036	0.136	-0.003
K uptake	-0.374	-0.011	0.092	-0.190	-0.124	-0.031	0.080

percentage and total plant N uptake. In the case of PC3, the plant characters that contributed significantly were leaf N and P contents, stem K content and PE(K). Similarly, leaf K content and PE(N) contributed significantly to PC4. Tuber dry weight percentage and stem N content contributed significantly to PC5. PC6 was influenced significantly by stem P content and PE(P). Stem dry weight percentage and storage root N contributed significantly to PC7 (Table 1). This study corroborates the reports of Susan John et al.(2020) in the screening of K use efficient genotypes where the five principal components extracted explained more than 77% of the variability.

Cluster analysis

In the preliminary evaluation trial on screening for NPK use efficient genotypes, the 132 genotypes evaluated based on the characters described *viz.,* plant fresh yield, plant dry matter percentage, total plant dry matter production, plant nutrient (N,P, K) contents, nutrient (N, P, K) uptake and physiological efficiency (N, P, K) were grouped into 8 clusters following the hierarchical cluster analysis with complete linkage methods and the cluster components are presented in Table 2.

These eight clusters from one to eight respectively had 62, 29, 13, 18, 2, 5, 2 and 1 accessions with almost similar plant characters studied for each cluster. Cluster 1 had the highest and cluster 8 had the least number of accessions. The mean values of the different parameters of the eight clusters with the grant centroid values are presented in Table 3.

It is understood from Table 3 that, the highest values of the studied parameters are distributed in clusters 5,6, 7 and 8. A comparison of the studied characters concerning the grand centroid revealed the superiority of the different clusters and is explained below:

Genotypes under cluster 4 had the maximum tuber dry weight percentage (44.68%). Genotypes under cluster

Table 2. Cluster composition of the evaluated genotypes of cassava

Cluster	Number of genotypes	Cluster members
1	62	Accession numbers 7, 7-2, 62(5), 63, 64, 87, 121, 602, 632, 635, 646, 662, 665, 696(1), 704, 725, 735, 775, 779 (5), 788, 789, 790, 796, 800, 810, 825, 830, 833, 850, 854, 855, 856, 859,862, 864, 865, 865, 870, 871, 874, 876, 881, 882, 883, 884, 886, 887, 888, 889, 890, 892, 896, 899, 900, 902, 905, 906, 907, 908, M4, H 1687 (Sree Visakham)
2	29	Accession numbers 11, 21, 26, 28, 35, 37, 49, 53, 56, 58, 67, 73, 74, 75, 80, 89, 104, 109, 143, 163, 565, 568, 569, 572, 576, 585, 599, 866, 879
3	13	Accession numbers 209, 660, 666, 696, 727, 750, 755, 776, 802, 873, 897, 901, 904
4	18	Accession numbers 4, 16, 24, 39, 65, 69, 71, 82, 103, 107, 115, 120, 124, 126, 133, 142, 581, 878
5	2	Accession numbers 60, 102
6	5	Accession numbers 84, 119, 125, 695, 698
7	2	Accession numbers 130, 766
8	1	Accession numbers147

Table 3. Mean values of the different parameters of the eight clusters

Variables	Cl1	Cl2	Cl3	Cl4	Cl5	Cl6	Cl7	Cl8	Grand Centroid
Leaf dry weight (%)	34.81	28.41	34.91	37.84	42.79	26.59	34.72	20.46	32.57
Stem dry weight(%)	34.68	37.95	32.70	41.57	43.22	30.78	37.86	34.97	36.72
Tuber dry weight (%)	39.90	38.99	33.20	44.68	36.16	26.87	38.12	38.79	37.09
Fresh Leaf yield ($g\ plant^{-1}$)	287.47	78.62	375.38	127.78	200.00	420.00	220.00	40.00	218.66
Fresh stem yield ($g\ plant^{-1}$)	1.83	1.67	1.38	3.51	6.10	1.93	2.45	1.80	2.58
Fresh tuber yield ($kg\ plant^{-1}$)	2.54	2.15	2.12	4.06	9.70	2.36	1.95	5.10	3.75
Leaf N (%)	4.02	3.29	4.95	3.16	2.62	5.50	3.01	2.92	3.68
Stem N(%)	0.70	0.90	0.66	0.737	0.77	0.83	0.46	0.77	0.73
Tuber N (%)	0.44	0.46	0.49	0.402	0.42	0.35	0.59	0.48	0.45
Leaf P (%)	0.22	0.24	0.32	0.187	0.25	0.33	0.15	0.32	0.25
Stem P (%)	0.11	0.11	0.21	0.114	0.09	0.13	0.30	0.08	0.14
Tuber P (%)	0.06	0.18	0.07	0.169	0.25	0.08	0.10	0.21	0.14
Leaf K (%)	0.76	0.72	0.90	0.729	0.95	0.97	0.92	2.27	1.03
Stem K (%)	0.35	0.46	0.44	0.420	0.32	1.08	0.27	1.24	0.57
Tuber K (%)	0.40	1.30	0.37	1.12	0.62	0.59	0.36	2.05	0.85
Physiological Efficiency (N) ($kg\ kg^{-1}$)	154.94	121.28	142.29	204.96	151.13	116.55	1248.20	217.56	294.61
Physiological efficiency (P) ($kg\ kg^{-1}$)	2936.7	1306.7	1744.9	1176.9	942.49	2292.10	6492.70	1231.50	2265.50
Physiological Efficiency (K) ($kg\ kg^{-1}$)	592.13	252.83	537.34	194.93	355.65	221.86	3286.80	125.43	695.87
N uptake($g\ plant^{-1}$)	18.34	18.86	17.86	29.28	64.74	20.69	6.00	23.44	24.90
P uptake ($g\ plant^{-1}$)	1.10	2.13	1.16	4.06	11.09	1.17	0.54	4.14	3.17
K uptake($g\ plant^{-1}$)	5.13	12.88	4.67	21.92	31.17	10.61	1.35	40.66	32.57

5 had the maximum leaf (42.79%) and stem (43.22%) dry weight percentage, fresh stem (6.1 kg plant^{-1}) and tuber (9.7 kg plant^{-1}) yield, tuber P% (0.252%), total plant N (64.74 g plant^{-1}) and P uptake (11.09 g plant^{-1}). Genotypes under cluster 6 had the highest fresh leaf yield (420 g plant^{-1}), leaf N (5.50%) and leaf P (0.33%). Tuber N (0.59%), stem P (0.30%), PE (N) (1248.2), PE (P) (6492.7), PE(K) (3286.8) were highest for genotypes under cluster 7. Leaf K (2.27%), stem K (1.24%), tuber K (2.05%) and total plant K uptake (40.66 g plant^{-1}) was maximum for genotypes under cluster 8. Susan John et al. (2020) could find five clusters while screening 83 elite genotypes for screening K use efficient genotypes in cassava.

The inference from PCA and cluster analysis helped in delineating the significant parameters relevant to nutrient use efficiency of the crop as tuber dry weight, fresh tuber yield, tuber K, physiological efficiency of N, P, K and total N, P, K uptake in this study. Taking into account these characters as important for the clusters formed in influencing the NUE parameters for identifying NUE genotypes, it is seen that, clusters 4, 8, 5 and 1 possess the highest values of the above characters. The identified NPK efficient genotypes *viz.,* Acc. No. 7, 775, 788, 796 fell under cluster 1and Acc. No. 130, 766 under cluster 2 and Acc. No. 696 under cluster 3. The identified NP efficient accessions *viz.,* Acc. No. 890, 896 came under cluster 1 and Acc. No. 115 under cluster 4. The PK efficient genotypes *viz.,* Acc. No. 662, 905, 906, 908 came under cluster 1 and Acc. No. 750 came under cluster 3. In addition, the popular cultivar M4 and the widely accepted and cultivated hybrid H-1687 (Sree Visakham) also came under cluster 1. According to Singh and Dwivedi (2005), Ali et al. (2008) and Suryanarayana et al. (2017), cluster analysis can help to findout the high yielding genotypes as well as the genetic divergence among genotypes which can lead to the distinction of better performing genotypes.

Biplot analysis

The biplot shows the characters important for each genotype and the characters which are closer and behave similarly to enhance nutrient use efficiency. The biplot of the studied characters and the associated genotypes is presented in Fig. 9.

As per the biplot diagram, germplasm accessions *viz.,* Acc. Nos.4, 115, 697 were associated with better fresh

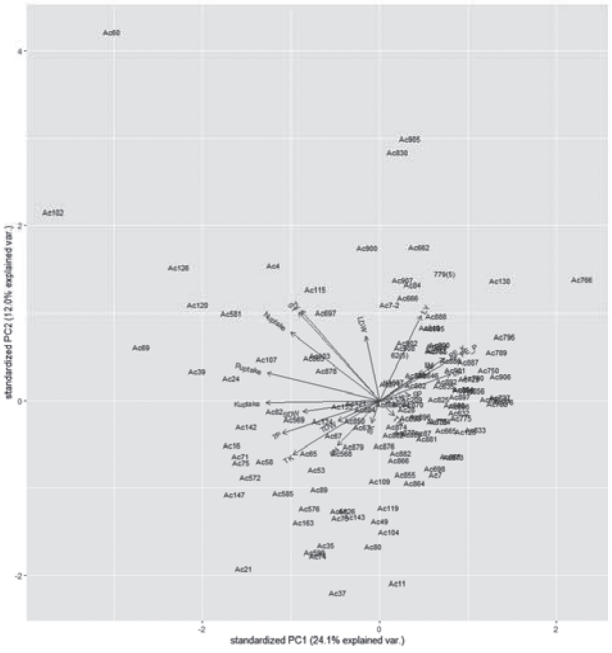


Fig. 9. Biplot analysis for nutritional and morphological traits of 132 genotypes evaluated for nutrient use efficiency

tuber and stem yield. Acc. Nos. 103, 883, 878 were associated with high N uptake. Acc. No. 107 had high P uptake. Acc. Nos.121 and 82 had high K uptake. Tuber N is higher with Acc. Nos. 565 and 874, Tuber P with Acc. No. 124 and tuber K with Acc. Nos. 884, 850, 67 and 65. PE (N, P, K) is linked with Acc. Nos. 646, 802, 901, 880 and M4. On correlating the inferences from cluster analysis with biplot result, it can be seen that, the genotypes delineated through biplot with characters as linked above which are employed in the ultimate selection of NUE genotypes fall under the following clusters. Cluster 4 is significant for characters *viz.,* fresh tuber yield, stem yield, total plant N, P, K uptake, tuber P and PE (N, P, K). Cluster 1 is significant for characters as tuber yield, plant N and K, tuber N and K and PE (N, P, K). Cluster 2 with tuber N and K and cluster 3 with PE (N, P, K) as per cluster analysis. Ultimately it can be seen that, the genotypes linked to the respective traits afore mentioned above are falling in the clusters linked to that particular trait. Thus, the inferences from cluster and biplot can be linked for the selection of K use efficient genotypes (Susan John et al., 2020).

Dendrogram analysis

The cluster dendrogram (Fig.10) divides the genotypes into eight groups which were found adhering to the

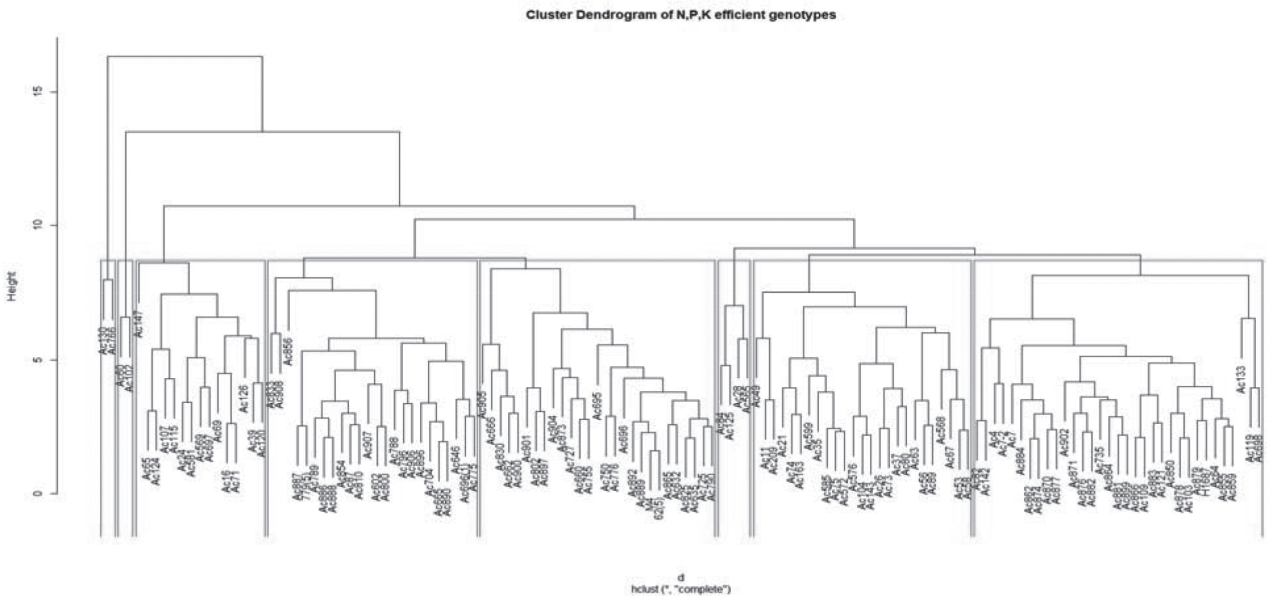


Fig.10. Cluster dendrogram of 132 accessions evaluated for nutrient use efficiency.

results from the cluster and principal component analysis. It is seen from the dendrogram that, the eight groups as per the dendrogram analysis had the same number and component genotypes as evolved from cluster and PCA. Thus, dendrogram analysis can be used in the selection of K use efficient genotypes in cassava (Susan John et al., 2020).

Hence, cluster, biplot and dendrogram revealed the drastic genetic divergence among the groups. PCA evaluated the variability among the different PC's concerning the characters studied as well as the characters significant for each PC. This in turn helped in arriving at a valid conclusion on the plant characters significant in making groups as per cluster, biplot and dendrogram. However, genotypes under cluster 4 and 1 are important concerning identifying NUE genotypes. The 15 genotypes selected from this study as NUE were distributed in the same groups as delineated by the three different statistical tools. Hence, the wide genetic diversity established in cassava for the soil-plant nutrition traits can very well be used in further crop improvement programmes especially in breeding for NUE genotypes. In this regard, the reports of Cavicchi and Silvetti (1976) and Broschat (1979) to include more morphological, agronomic and biochemical traits in multi-trait selection programme for the improvement of horticultural characteristics needs thorough research and attention.

Conclusion

The present study was undertaken as a preliminary evaluation trial for identifying NPK use efficient genotypes from the most elite accessions of cassava germplasm. The study revealed the wide variation among the accessions concerning plant characters associated with soil and plant nutrition. The evaluated traits were dry matter percentage, plant dry matter production, plant nutrient contents, physiological efficiency, fresh leaf, stem, storage root yield and total plant uptake of nutrients. In this regard, 132 elite cassava genotypes available in the cassava germplasm of ICAR-CTCRI were evaluated for genetic of the characters through an arbitrary method (fixing some criteria with an upper and lower value). This was further confirmed through PCA, cluster, biplot and dendrogram analysis. The arbitrary method established the drastic variation among genotypes concerning the characters studied. Grouping of these genotypes through PCA with almost similar traits resulted in evolving seven principal components with a cumulative variation of 73.3%. Cluster analysis as well as dendrogram grouped the genotypes into eight distinct clusters, each cluster with genotypes of almost similar characters. The biplot analysis made by linking the accessions with the evaluated plant characters also revealed the same trend as that of cluster and dendrogram. Though the cluster analysis indicated clusters 2,4,5,6,7,8 as having the

maximum values of the characters studied, the 15 genotypes later screened from this trial as NUE fall under the clusters 1, 2, 3 and 4 (widely varying clusters) as per the three analysis. These NUE genotypes can help in evolving improved cultivars or hybrids with high nutrient use efficiency so that the dependence on chemical fertilizers can be overlooked.

References

Agong, S.G., Schittenhelm, S. and Friedt, W. 2001. Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* L.) germplasm. *J. Food Tech. Africa,* **6**(1): 13-17.

Ali, Y., Atta, B.M, Akhter, J., Monneveux, P. and Lateef, Z. 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pakistan J. Bot*., **40**: 2087-2097.

Baligar, V.C., Fageria, N.K. and He, Z.L. 2001. Nutrient use efficiency in plants. *Commun. Soil Sci.Plant Anal*., **32**: 921-950.

Broschat, T.K. 1979. Principal component analysis in horticultural research. *Hort. Sci.,* **14**: 114-117.

Cavicchi, S. and Silvetti, E. 1976. Yield in tomato. I. Multiple regression between yield and yield components. *Genetica Agraria*, **30**: 293-313.

Chávez, A.L., Sánchez, T., Jaramillo, G., Bedoya, J.M., Echeverry, J., Bolaños, E.A., Ceballos, H. and Iglesias, C.A. 2005. Variation in quality traits in cassava roots evaluated in landraces and improved clones. *Euphytica*, **143**: 125-133.

Duncan, R. R. and Carrow, R. N. 1999. Turf grass molecular genetic improvement for abiotic/edaphic stress environment. *Adv. Agron.,* **67:** 233-306.

Ene, C.O., Ogbonna, P.E., Agbo, C.U., and Chukwudi, U.P. 2016. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean J. Agric. Res*., **76**(3): 307-313.

Fageria, N.K. and Baligar, V.C. 2005. Nutrient availability. In: D. Hillel (Ed.) *Encyclopedia of Soils and Environment*. Elsevier, San Diego, California. pp. 63-71.

Fageria, N.K., Baligar, V.C. and Clark, R. 2006. *Physiology of Crop Production*. CRC Press, Boca Raton. pp.356. https://doi.org/10.1201/9781482277807.

Fageria, N. K, Baligar, V.C. and Li, Y.C. 2008. The role of nutrient efficient plants in improving crop yields in the twenty first century. *J. Plant Nutrition,* **31:** 1121-1157.

Gabriel, K.R. 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrica*, **58**(3): 453-467.

Heitjan, D.F. and Little, R.J.A. 1991. Multiple computation for the fatal accident reporting system. *Applied Statistics,* **40**(1): 13-29. https://doi.org/10.2307/2347902.

Isfan, D.1990. Nitrogen physiological efficiency index in some selected spring barley cultivars. *J. Plant Nutrition,* **13**(8): 907-914.

Jemo, M., Abaidoo, R.C., Nolte, C. and Horst, W.J. 2006. Genotypic variation for phosphorus uptake and di nitrogen fixation in cowpea on low phosphorus soils of Southern Cameroon. *J. Soil Sci. Plant Nutrition*, **169**: 816-825.

Jolliffe, I.T. and Cadima, J. 2016. Principal component analysis: a review and recent development. *Philosophical Transactions of the Royal Society, a Mathematical, Physical and Engineering Sciences,* **374**(2065): 20150202. http://dx.doi.org/10.1098/rsta.2015.0202

Liu., Y., Mi, G., Chen, F., Zhang, J. and Zhang, F. 2004. Rhizosphere effect and root growth of two maize (*Zea mays* L.) genotypes with contrasting P efficiency at low P availability. *Plant Sci*., **167**(2): 217-223

Marschner, P.Z., Soloiman and Rengel, Z. 2005. Growth, phosphorus uptake and rhizosphere microbial community composition of a phosphorus efficient wheat cultivar in soil differing in pH. *J. Soil Sci. Plant Nutrition*, **168**: 343-351.

More, S.J., Ravi,V., Saravanan, R. and Suresh Kumar, J. 2020. The quest for high yielding drought-tolerant cassava variety. *J. Pharmacognosy and Phytochemistry*, **9**(6S): 433-439. https://www.phytojournal.com/archives/2020/vol9issue6S/PartJ/S-9-6-60-756.pdf

More, S.J., Ravi, V. and Saravanan, R. 2019. Tropical tuber crops. In: de Freitas ST, Pareek S (eds.) *Post harvest physiological disorders in fruits and vegetables.* CRC Press, Boca Raton, pp 719–757. https://doi.org/10.1201/b22001

Piper, C.S. 1970. *Plant and Soil Analysis*. Hans Publications, Bombay, India.

Rengel, Z., Paul, M.D. 2008. Crops and genotypes differ in efficiency of potassium uptake and use. *Physiol. Plant*, **133**(4): 624-636. http://doi.org/10.1111/j.1399-3054.2008.01079.X.

Santos, L. A., Silva, S. A., Souza, D.R., Araujo, G.D., Almeida, V.D. and Neves, C.G. 2019. Genetic parameters in agronomic characters for selection of superior lineages of *Ricinus communis* L. *Ciencia Rural,* **49**(1): e20180547. https://doi.org/10.1590/0103-8478cr20180547.

Sattlemacher, B., Horst, W.J. and Becker, H. C. 1994. Factors that contribute to genetic variation for nutrient efficiency of crop plants. *Zeitschrift fur Pflanzenernahrung und odenkunde,* **157**: 215-224.

Schenker, N. and Taylor, J.M.G. 1996. Partially parametric technologies for multiple imputation. *Computational Statistics and Data Anal.* **22**(4): 425-446.

Singh, S.P. and Dwivedi, V. K.2005. Genetic divergence in wheat (*Triticum aestivum* L.). *Agric. Sci. Digest*, **25**(3): 201-203.

Smith, M. E, Miles, C. A and Van, B. J. 1994. Genetic improvement of maize for nitrogen use efficiency. *Fourth Eastern and Southern Africa Region Maize Conference,* 28 March -1 April, 1994, Harare, Zimbanwe. pp.39-43.

Suryanarayana, L., Reddi Sekhar, D., Ratna Babu, D., Ramana, A.V. and Srinivasa Rao, V. 2017. Cluster and principal component

analysis in maize. *International J.Current Microbiol. Applied Sci*., **6**(7): 354-359.

Susan John, K., Ravindran, C.S. and James George, 2005. Long term fertilizer experiments-Three decades experience in cassava.*Technical bulletin Series No. 45*, ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala. 89 p.

Susan John, K., Anju, P. S., Chithra, S., Shanida Beegum, S.U., Suja,G., Anjana Devi, I.P., Ravindran, C.S., James George, Sheela, M.N., Ravi, V., Manikantan Nair, M., Pallavi Nair and Remya, D.2019. Recent Advances in the Integrated Nutrient Management (INM) Practices of Tropical Tuber Crops. *Technical Bulletin Series No. 75*, ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala, India, 68 p.

Susan John, K., Sreekumar, J., Sheela, M.N., Shanida Beegum, S.U., More, S.J. and Suja, G. 2020. Pre evaluation of cassava (*Manihot esculenta* Crantz) germplasm for genotypic variation in the identification of K efficient genotypes through different statistical tools. *Physiol. Molecular Biol. Plants*, **26**(9): 1911–1923. https://doi.org/10.1007/s12298-020-00867-2

Van Buuren, V. S. and Oudshoorn, C.G. 2011. MICE: Multivariate Imputation by Chained Equations in R. *J. Statistical Software*, **45**(3): DOI: 10.18637/jss.v045.i03

Van Hintum T.J.L. 1995. Hierarchical approaches to the analysis of genetic diversity in crop plants. In: Hodgkin T, Brown A.H.D., Van HintumT.J.L., Morales EAV (Eds.) Core *Collection of Plant Genetic Resources*. John Wiley & Sons, Chichester, UK, pp: 23-34.