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Phenotypic diversity using principal components and cluster analysis in Potato genotypes grown in Mambilla Plateau, Taraba State, Nigeria

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Abstract

Potato due to its early maturity, high yield and excellent food value can improve food security, increase household income and alleviate poverty. This study was conducted at Mambilla Plateau in 2021 and 2022 cropping season to investigate the extent of genetic diversity among twelve potato genotypes using principal component and cluster analysis. It was established according to the randomized complete block design with three replications. Data were collected on growth, yield and internal quality traits. The results revealed that the 1st six principal component (PC_1 - PC_6) with Eigen values greater than 1 accounted for 87.53 % of the total variation. The 1st principal component with variance of 25.14 % was dominated positively by number of branches per plant, weight of tubers per plant, weight of tuber per plot, and total tuber yield per hectare, while the 2nd principal component with 22.10 % of the variance was associated positively with days to first flower, number of leaves per plant, weight of tubers per plant and number of tubers per plot. Whereas the 3rd, 4th, 5th and 6th had proportional variance of 14.40 %, 10.50 %, 8.0 %, and 7.2 % respectively. The genotypes were grouped into two clusters, with four individuals in cluster 1 and eight individuals found in cluster 2. The maximum genetic distance was found between Caruso and Madam (7.87) and showed maximum divergence, while the minimum Euclidean distance was observed between Lady Christly and Green leaf Nicola (2.09). Genotypes belonging to different clusters having maximum genetic divergence can be effectively utilized in crop improvement programme.

Keywords: Potato, genotypes, principal component, cluster analysis, genetic diversity

Introduction

Potato (*Solanum tuberosum* L.) originated in the high plain Andes of Peru and Bolivia, where the crop have been cultivated for over 2400 years (Hawkes, 1994; Acquaah, 2012) [2, 10]. The potential of potato for providing food, preservation and eradication of poverty are the most important cause of potato distribution all over the world (Bradshaw and Bonierbale, 2010) [5]. Today, potatoes are cultivated in more than 161 countries globally, on an area of 25 million hectares (Tessema *et al*., 2022) [26], and has the potentials for improving food security, increasing household income and poverty alleviation due to its early maturity, high yield and excellent food value (Devaux *et al*., 2014) [6]. The tubers can be consumed in various forms like boiled, roasted, baked, fried and or in processed forms like French fry, chips and potato powder (Farzana *et al*., 2021) [8], and also used as livestock feed (Patel *et al*., 2018) [16]. It is an excellent low fat source of carbohydrates, rich in vitamins and minerals such as vitamin B and C, Calcium, and phosphorus (Panigrahi *et al*., 2017; Puttongsiri *et al*., 2012) [15, 18]. Potato tubers are known to combat prostate cancer and breast cancer due their higher antioxidant content (Kumari *et al*., 2018) [11]. The juice and slices of raw potato tubers with their anti-aging property remove dark circles and prevent wrinkles of the face and make the face glow (Sahair *et al*., 2018) [20]. Genetic variation and diversity play significant role in the success of a breeding programme (Md Hossain *et al*., 2023) [13], hence, genetic differences are beneficial tools for effectively selecting parents for hybridization (Salgotra and Chauhan, 2023) [21]. Prabha *et al*. (2018) [17] pointed out that information on the nature and degree of genetic diversity helps the plant breeders while selecting parents for crop improvement. Gebreselassie and Ajema (2022) [9] highlighted that multivariate statistical tools have found extensive use in describing and summarizing the inherent variation in the population of crop genotypes. Some of the tools that have found extensive application in multivariate statistics include principal component analysis (PCA), discriminant canonical analysis (DCA) and cluster analysis (CA) (Afuape *et al*., 2019) [3]. Principal component analysis is useful in grouping varieties of crops based on their similarities and a common techniques in variability studies and numerical classification (Dum, 2007) [7]. Lohani *et al*. (2012) [12], pointed out that grouping of genotypes in cluster reflects the relative divergence of cluster and permits a convenient selection of genotypes with overall phenotypic similarity for hybridization. In spite of the great potentials and long historical production of potato in the Mambilla Plateau, no statistical data is available for the crop and production is constraint by the absence of high stable tuber yield, susceptible to biotic and abiotic stresses. Therefore the study was undertaken to determine the extent of similarity and divergence among the potato varieties used for the research.

Materials and methods

The study was conducted at the Mambilla Plateau (Nguroje) during the 2021 and 2022 cropping season at the farmers' field. The Mambila Plateau is located at latitude 7°20'N and longitude 11°43'E. The area has an average elevation of 1,524 m above sea level and is in the Northern fringes of the Bamenda Highlands of Southern Cameroon. It harbors the Chappal Waddi Mountains, which is considered the highest point in Nigeria, with an average height of about 2,419 m above sea level. The area enjoys low temperatures ranging between 12 to 25°C in most parts of the year, and it receives over 1,850 mm of rainfall annually, endowed with a semi temperate climate that is favourable for agricultural crop production and livestock rearing.

The genotypes comprised of twelve potato varieties, six of the potato varieties were sourced from the National Root Crop Research Institute (NRCRI), substation Vom, Plateau State, five of the varieties were obtained from the Mambilla Plateau, and one of the variety was collected from farmer in the potato producing area in Bokkos Local Government Area of Plateau State, as showed in Table 1. The experiment was laid out in a Randomized Complete Block Design with three replications. The genotypes were sown at the spacing of 70 x 30 cm at the depth of 5-10 cm. All other management practice was carried out as recommended.

Data collection

Ten plants were selected from each plots, tagged and used for data collection, data were collected on percentage emergence (%), days to first flower, plant height (cm), number of branches per plant, leaf length (cm), leaf width (cm), number of leaves per plant, number of tubers per plant, marketable tuber size, weight of tubers per plant (g), number of tubers per plot, weight of tubers per plot (kg), yield of tubers per hectare (ton/ha), tuber dry matter content (%), specific gravity (g), and the starch content (%). Data collected were subjected statistical tool using Statistics for Agricultural Research (STAR), vision 2.0.1 (2014) [25] utilized for principal component and cluster analysis.

Table 1: Genotypes used and area of collection

S/N	Genotypes	Areas of collection
1	Superior	Nguroje, Mambilla, Taraba State
2	Bawon doya	Bokkos, Jos, Plateau State
3	Red Irish	Nguroje, Mambilla, Taraba State
4	Yellow Cece	Nguroje, Mambilla, Taraba State
5	Yellow leaf Nicola	NRCRI, Vom, Plateau State
6	Cameroun variety	Nguroje, Mambilla, Taraba State
7	Green leaf Nicola	NRCRI, Vom, Plateau State
8	Marabel	NRCRI, Vom, Plateau State
9	Bertita	NRCRI, Vom, Plateau State
10	Madam	Nguroje, Mambilla, Taraba State
11	Caruso	NRCRI, Vom, Plateau, State
12	Lady Christly	NRCRI, Vom, Plateau, State

Results and discussion

Principal component analysis

The total variation for the principal components analysis was divided in 16 principal components. The first six principal components with Eigen values > 1 accounted for 87.53 % of the total variation among the genotypes tested. The first principal component (Table 2) accounted for 25.14 % of the total variation, while the 2nd, 3rd, 4th, 5th and 6th components accounted for 47.29 %, 61.69 %, 72.25 %, 80.25 % and 87.53 % of the total variation respectively. Similar results were reported by Rymuza (2015) [19], Seid *et al*. (2021b) [23] and Md Hossain et *al*. (2023) [13]. The eigen values and proportion of the variance (Table 2) associated with each principal component decreased gradually with principal component 1 having the highest stand of 4.02 and 25.10, and stop at principal component 6 having 1.16 and 7.20 respectively.

In this study, the contribution of the characters tested to each principal component was present in Table 3, the first principal component (PC_1) accounted for 25.14 % of the proportional variance and was dominated positively by traits such as number of branches per plant (0.401), leaf width (0.384), weight of tubers per plant (0.383), weight of tubers per plot (0.335), and tuber yield per hectare (0.322). The first principal component was predominantly related to yield and yield contributing characters and reported maximum variation than other principal components. This indicates that this component proven more important towards the genetic diversity among the genotypes, hence individuals selected from this component (PC_1) will be desirable in breeding program for improving the traits contributing to high variability. The second principal component (PC_2) with 22.10 % of the proportional variance contribution was highly associated positively with days to first flower (0.333), number of leaves per plant (0.330), weight of tubers per plant (0.436), and number of tubers per plot (0.465), but negatively determined by plant height (-0.350), and number of leaves per plant (-0.330). These negative contributions, if selected should be viewed as a measured of decreasing potato tuber yield per hectare. The positive loadings in the third principal component (PC_3) with proportion variance of 14.41 % was obtained by tuber yield per hectare (0.345), whereas negative loadings were exerted by percentage emergence (-0.342), number of leaves per plant (-0.324), weight of tubers per plant (-0.330), and starch content (-0.360). This signifies that these characters affected total tuber yield per hectare of potato differently.

Weight of tubers per plot (0.392), tuber yield per hectare (0.303), and starch content (0.350) contributed positively to the forth principal component (PC_4) with proportion variance of 10.50 %, while, negative contributions were observed for leaf length (-0.386), leaf width (-0.347), and percentage marketable tuber size (-0.320). The fifth principal component (PC_5) with proportional variance of 8.0 % was highly influenced positively by percentage emergence (0.561), plant height (0.345), percentage marketable size (0.338), and tuber dry matter content (0.470), but with weak negative loading from some characters. In the sixth principal component (PC_6), percentage marketable tuber size (0.302), and starch content (0.650) contributed positively to PC_6 cumulatively. Tuber dry matter content (-0.380) explained the negatively associated with the PC_6. This highlighted the richness of those characters with positive loadings when selecting traits for improvement. These findings are consistent with previous studies of Seid *et al*. (2021a) [22] and Tessema *et al*. (2022) [26].

The first two principal components PC_1 and PC_2 plot (fig.1) that had eigen values greater than three and contributing 47.29 % of the variation were plotted to observe the relationship between twelve potato genotypes. The genotypes are grouped into four groups, the group consists of genotypes appearing on the top right axis (PC_1 score), this group include Madam, Caruso and Lady Christly and are associated with yield characters, the second top left has genotypes like Bawon doya, Yellow Cece, Cameroun variety and Marabel which are associated with both growth and yield parameters, while, the third group bottom right comprises of Superior, Red Irish and Yellow leaf Nicola, and are associated with yield and internal quality, similarly, the fourth group which is the bottom left, this group is dominated by Green leaf Nicola and Bertita, they are also associated with yield traits. The PCA plot grouped the genotypes into four principal axes according to the relationship among the genotypes and selection for hybridization are best achieved between genotypes that are diverge.

Table 2: Eigen values and the cumulative variability of the principal components

	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Eigen value	4.02	3.54	2.30	1.69	1.28	1.16
Prop. Var.	25.14	22.10	14.41	10.50	8.00	7.20
Com. Var. (%)	25.14	47.29	61.69	72.25	80.25	87.53

Table 3: Eigen vectors of the first six principal components

Characters	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Plant emergence	0.175	0.044	-0.342	0.028	0.561	0.231
Days to 1st flower	-0.294	0.333	0.146	0.007	0.137	0.036
Plant height	0.009	-0.350	0.193	0.241	0.345	0.059
Number of branches per plant	0.401	0.175	0.142	0.200	0.199	0.055
Leaf length	0.204	-0.214	0.266	-0.386	0.155	-0.261
Leaf width	0.384	0.100	0.148	-0.347	0.177	-0.115
Number of leaves per plant	0.144	0.330	-0.324	0.222	-0.128	-0.238
Number of tubers per plant	0.079	0.436	-0.330	0.062	0.088	0.131
Marketable tuber size	0.280	0.051	0.227	0.320	0.338	0.302
Weight of the tubers per plant	0.383	0.209	0.203	0.261	0.073	0.088
Number of tubers per plot	0.106	0.465	-0.062	0.004	0.042	0.128
Weight of tubers per plot	0.335	0.153	-0.193	0.392	0.145	-0.245
Tuber yield per hectare	0.322	-0.121	0.345	0.303	0.045	0.176
Tuber dry matter content	0.012	0.197	0.160	0.001	0.470	0.380
Specific gravity	0.047	-0.025	-0.293	-0.191	0.163	0.650
Starch content	0.219	0.190	-0.360	0.350	-0.184	0.085

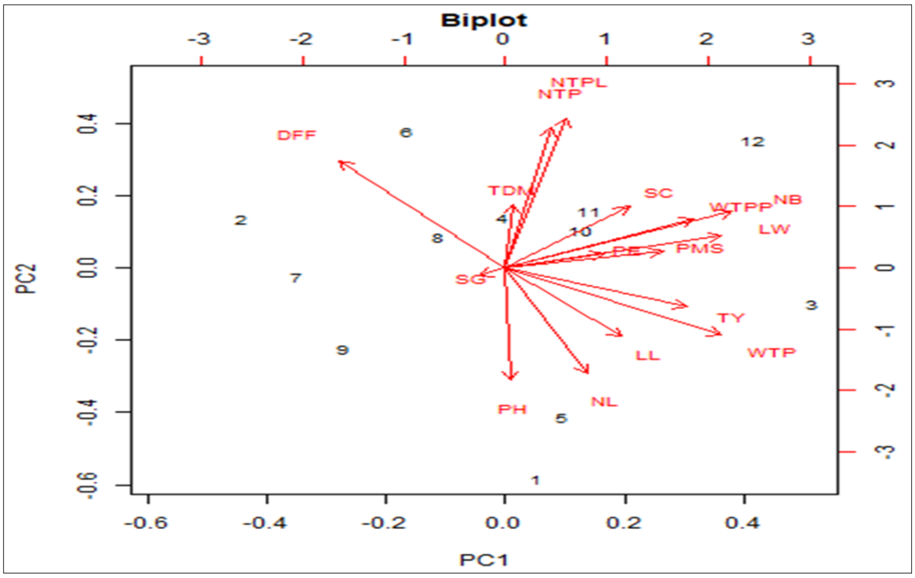

Fig 1: Biplot for principal component analysis for combined data

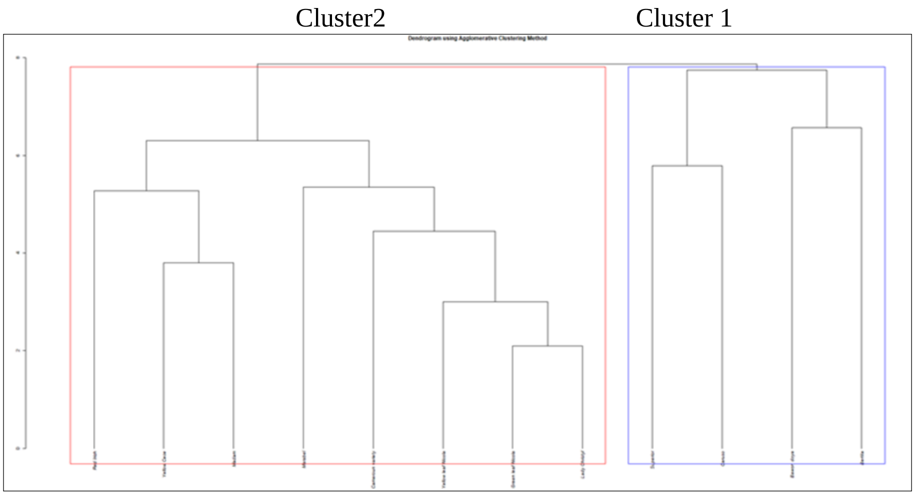

Fig 2: Dendrogram using agglomerative clustering method for combined data

Table 4: Cluster means values for sixteen characters in Potato

Characters	Cluster 1	Cluster II
Plant emergence	97.25	92.62
Days to 1st flower	48.25	59.38
Plant height	39.75	34.50
Number of branches per plant	5.00	4.38
Leaf length	3.50	2.62
Leaf width	3.50	3.25
Number of leaves per plant	350.25	247.38
Number of tubers per plant	11.75	12.00
Marketable tuber size	73.00	69.25
Weight of the tubers per plant	1.00	1.00
Number of tubers per plot	491.25	509.50
Weight of tubers per plot	41.00	34.75
Tuber yield per hectare	33.50	28.50
Tuber dry matter content	18.25	19.88
Specific gravity	1.00	1.00
Starch content	22.75	16.38

Table 5: Euclidean or Genetic distances for combined analysis 2021/2022

	Superior	**Bawon doya**	**Red Irish**	**Yellow Cece**	**Yellow leaf Nicola**	**Cameroun variety**	**Green leaf Nicola**	**Marabel**	**Bertita**	**Madam**	**Caruso**	**Lady Christly**
Bawon doya	6.59											
Red Irish	7.61	7.10										
Yellow Cece	6.78	6.01	5.27									
Yellow leaf Nicola	5.66	5.60	3.93	3.58								
Cameroun variety	5.62	5.84	5.61	4.08	3.90							
Green leaf Nicola	5.73	5.65	4.51	4.89	2.56	4.36						
Marabel	7.16	7.17	5.93	6.30	5.17	5.35	4.52					
Bertita	7.74	6.56	5.42	5.25	4.43	6.95	4.78	5.87				
Madam	7.49	7.85	4.96	3.80	4.07	4.50	5.72	6.03	6.67			
Caruso	5.78	6.87	7.37	7.13	5.32	6.67	3.88	5.69	5.84	7.87		
Lady Christyl	6.59	5.71	3.92	4.84	2.99	4.44	2.09	3.84	5.04	5.27	5.46	

Cluster analysis

The genotypes used for the study were grouped into two clusters (Fig. 2). Out of the twelve genotypes tested, cluster one contained four varieties, namely, Superior, Bawon doya, Bertita and Caruso, while cluster two is made up of eight varieties such as Red Irish, Yellow Cece, Yellow leaf Nicola, Cameroun variety, Green leaf Nicola, Marabel, Madam and Lady Christly. The presence of two distinct clusters signifies existence of genetic divergence among the genotypes. Genotypes that are grouped together in a particular cluster are closely related with each other, genetically less diverge, but highly differed from genotypes grouped from other cluster, hence breeding for improvement should target those genotypes that diverge from each other. Anoumaa *et al*. (2023) [44] reported two main clusters on a study conducted with 138 potato genotypes. Gebreselassie and Ajema (2022) [9] in a research with 18 potato genotypes reported that genotypes tested were grouped into two main clusters. However, Md Hossain *et al*. (2023) [13] identified five clusters using 25 potato genotypes, Seid *et al*. (2021a) [22] and Seid *et al*. (2021b) [23] observed six clusters on 24 potato genotypes used, Prabha *et al*. (2018) [18] obtained five clusters in a study conducted with 39 potato genotypes. Abebe *et al*. (2013) [1] also recorded three clusters among 24 varieties of potato studied. Gebreselassie and Ajema (2022) [9] highlighted that genetic diversity among potato genotypes tested might contribute to the occurrence of different clusters. The genotypes in cluster one (Table 4) are characterized by individuals with high mean values for percentage emergence (97.25 %), tall plants (39.75cm), high number of branches per plant (5.00), long leaf (3.50 cm), wide leaf (3.50 cm), high number of leaves per plant (350.25), high percentage marketable tuber size (73 %), heaviest tuber weight per plot (41.01 kg), high total tuber yield per hectare (33.50 tons) and high starch content (22.75 %). In the same vein, cluster two genotypes were characterized by individuals with high mean values for days to first flower (59.38), number of tubers per plant (12.00), number of tubers per plot (509.50), and tuber dry matter content (19.88 %). On another hand, weight of tubers per plant and specific gravity exhibited the same mean values of (1.0 kg) and (1.0 %) respectively. This indicated the presence of genetic variation among the genotypes studied. Similar results can be seen in Seid *et al*. (2021a) [22].

Genetic distances (Euclidean distances) among the genotypes was estimated, the distance ranged from 2.09 to 7.87 (Table 5). The highest genetic distance was observed between Caruso and Madam (7.87), closely followed by the distance between Madam and Bawon doya (7.85), Bertita and Superior (7.85), distance between Madam and Superior (7.49), distance between Caruso and Red Irish (7.37), Marabel and Bawon doya (7.17), Marabel and Superior (7.16), the distance between Caruso and Yellow Cece was (7.13), and the distance between Red Irish and Bawon doya (7.10).While, the lowest Euclidean distance was showed between Lady Christly with Green leaf Nicola (2.09), followed by genetic distance between Green leaf Nicola and Yellow leaf Nicola (2.56), followed by genetic distance between Lady Christly and Yellow (2.99), followed by distance between Yellow leaf Nicola and Yellow Cece (3.58), distance between Madam and Yellow Cece (3.80), distance between Lady Christly and Marabel (3.84), Caruso and Green leaf Nicola (3.88), Cameroun variety and Yellow leaf Nicola (3.90), Lady Christly and Red Irish (3.92), and lastly, Yellow leaf Nicola and Red Irish (3.93). Highest genetic distance observed between Caruso and Madam (7.87) suggested the possibility of genetic diversity among these genotypes and hybridization among these varieties may lead to production of individuals with novel characteristics. Seid *et al*. (2021a) [22] reported Euclidean distance ranged from 2.73 to 10.94 in study on 24 potato genotypes. Panigrahi *et al*. (2014) [14] conducted a research on 17 potato genotypes observed that genetic distance ranged from 3.45 to 13.54. Similarly, Abebe *et al*. (2013) [1], also recorded Euclidean distance ranged of 0.24 to 0.72 on 12 potato genotypes used for the study. Singh *et al*. (2022) [24] reported that higher the distance between clusters greater the diversity between them.

Conclusion

In this study, the 1st six principal components accounted for 87.53 % of the total variation, these six characters contributed more to the total divergence and having significant effect on the phenotype of the population. For the cluster analysis, the genotypes were grouped into two clusters with cluster 1 having four genotypes, while cluster 2 having eight genotypes. The maximum genetics distances between genotypes were observed between Caruso and Madam, hence selecting genetically diverge parents for hybridization breeding programme to produce noble clone will be rewarding.

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