

# Phenotypic Diversity for Agronomic and Yield Characters among Potato (*Solanum tuberosum* L.) Genotypes in Mambila Plateau, Taraba State, Nigeria

\*Zanzam, M.S and Jandong, A.E

Department of Agronomy, Taraba State University, Jalingo

**Abstract:-** Twelve potato genotypes comprising of improved and local varieties were evaluated for genetic potentials in agronomic, yield and internal qualities in Nguroje area of the Mambila Plateau, Taraba State, during the rainy season of 2022. The experiment was arranged in a Randomized Complete Block Design, which was replicated three times. Results of analysis of variance showed significant difference among the genotypes for all the traits except specific gravity, indicating the existence of significant variation within the genotypes. Phenotypic coefficient of variation was generally higher than their corresponding genotypic coefficient of variation revealing the influence of environment on expression of the characters. Higher phenotypic and genotypic coefficient of variation were recorded for starch content (44.30, 41.55), number of leaves per plant (35.34, 31.09), and leaf length (34.44, 26.44). High broad sense heritability and genetic advance as a percent of mean were observed for Days to first flower (98%, 28.87 %), weight of tuber per plot (88%, 39.60%), yield of tuber per hectare (88%, 39.56%), starch content (83%, 75.76%), and number of leaves per plant (77%, 56.06%). Tuber yield per hectare was significantly and positively correlated to number of branches per plant (0.42\*\*), leaf width (0.36\*), weight of tubers per plant (0.88\*\*), and weight of tubers per plot (0.99\*\*). The first four principal components accounted for 87.64 % of the total variation, of which the 1<sup>st</sup> component explained 43.1 %, the 2<sup>nd</sup>, 3<sup>rd</sup> and the 4<sup>th</sup> component constituted 21.1 %, 15.6 %, and 7.8 % respectively. Result of cluster analysis revealed that the varieties were grouped into 3 main clusters. Genotypes falling in cluster 1 and 3 showed highest mean values for yield and internal quality traits, while genotype in cluster 2 recorded highest for growth characters. The diversity exhibited among the genotypes signifies its potential for effective breeding.

**Keywords:-** Potato, Tuber, Yield, Genotypes, Phenotypic coefficient of variation, genotypic coefficient of variation

## I. INTRODUCTION

Potato (*Solanum tuberosum* L.), originated in the high plains of the Andes Cordillera, Peru, where it is largely cultivated for food (Rolot, 2001). It is the world's fourth most important food crop and among the five crops that feed the world, others being wheat, corn, sorghum and rice (Acquaah, 2012; FAO, 2014; Zaheer and Akhtar, 2016). Haverkort *et al.* (2009), reported that potato is the third most important food security crop, and the leading non-grain food

commodity in the world (FAO, 2013). The crop is grown in cool- temperate regions and at higher altitudes in the tropics (Wagner *et al.*, 2014). Bradshaw *et al.* (2010), reported that providing food, preservation and eradication of poverty are the most important cause of potato distribution in the world. The production of potato in Africa and Asia has rapidly overtaken all other food crops since early 1960s (Haan and Rodriguez, 2016), which account for more than half of global potato production (Devaux *et al.*, 2014). The crop is an excellent low fat source of carbohydrates, rich in vitamin and minerals such as vitamin C and B, Calcium and Phosphorus (Panigrahi *et al.*, 2017; Puttongsiriet *et al.*, 2012). Sahair *et al.* (2018) reported that potato contains large amount of vitamins present in form of beta-carotene, vitamin C, A, B1, B2, B6, and Folic acid. Ahmed *et al.* (2015), observed that tuber of potatoes act as anti- ulcer, anti-gout, anti-arthritis, anti-inflammatory, anti- scurvy, diuretic, and are known to combat prostate and breast cancer in human due to their higher antioxidant content (Kumari *et al.*, 2018).

Variability for a given crop character is a basic prerequisite for its improvement (Engida *et al.*, 2007; Meenakshi *et al.*, 2017; Panigrahi *et al.*, 2017; Patel *et al.*, 2018a). Sestra *et al.* (2007) and Janaki *et al.* (2015), revealed that variability in the available cultivars may be due to differences in genetic constitution of the cultivars or in the environment in which they grow. Singha and Ullah (2020), highlighted that phenotypic and genotypic coefficient of variation are useful tools in identifying the amount of variability present in a population. Hajam *et al.* (2018), reported that genotypic coefficient of variation does not offer full scope to estimate the variation that are heritable and hence, estimation of heritability becomes necessary. Mondal (2003), also asserted that heritability estimates with genetic advance in percent could give more useful picture of expected yield under phenotypic selection than heritability alone. The knowledge of correlations among the traits is important (Bhatia, 2004), and would provide estimates on degree of association between tuber yield and its various components (Patel *et al.*, 2018b). Lohani *et al.* (2012) pointed out that grouping of genotypes in cluster reflects the relative divergence of cluster and permits a convenient selection of genotypes with their overall phenotypic similarity for hybridization programme.

Inadequate information on the genetic potential of potatoes for development of new variety necessitates undertaking the evaluation of phenotypic diversity present among some potato varieties grown in the area.

## II. MATERIALS AND METHODS

### A. Planting material

The planting material used for the study were twelve genotypes of potato, of which five cultivars were sourced from farmers on the Mambilla Plateau, Taraba State, six germplasm were collected from National Root Crop Research Institute (NRCRI) Potato Research Sub-station, Vom, Jos, Plateau State and one variety from a farmer in Bokkos area of Plateau State (Table 1).

### B. Study site

The study was conducted on the Mambilla Plateau (Nguroje) during the 2022 cropping season at the farmers' field. The Mambilla Plateau is located in the South Eastern part of Taraba state, Nigeria. It has an average elevation of 1,524 m (5,000 ft.) above sea level and is in the northern fringes of the Bamenda Highlands of Southern Cameroon. It is located at latitude 7°20'N and longitude 11°43'E. It harbors the Chappal Waddi Mountains, which is considered the highest point in Nigeria, with an average height of about 2,419 m (7,936 ft.) 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 (Ardo and Abubakar, 2016).

### C. Experimental design and Field management

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications on a gross plot size of 12m<sup>2</sup> (3m x 4m). Distance of 1 m between replicates and 0.5m between plots was maintained, each replicate consisted of twelve plots and the experimental block consists of thirty six plots. The seed tubers were planted at the spacing of 70 cm between rows and 30 cm within rows, and at the depths of 5 cm. The plants were earthed up and weed control was done manually when necessary.

### D. Data Collection

Data were collected on both agronomic and yield parameters: percentage emergence, days to first flower, plant height, number of branches per plant, leaf length, leaf width, number of leaves per plant, number of tubers per plant, marketable tuber size, weight of tubers per plant, number of tubers per plot, weight of tubers per plot, yield of tubers per hectare, tuber dry matter content, specific gravity and the starch content. Ten plants were selected from each plots, tagged and used for data collection.

Table 1: Genotypes used and area of collection

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

### E. Statistical Analysis

Data collected were subjected to the analysis of variance (ANOVA) using the SAS statistical analysis package (SAS Institute Inc. 2009, USA). Means were separated using Duncan's multiple range test (DMRT) at 5% level of probability (Duncan, 1955). Components of variance were estimated from the expected mean squares and broad sense heritability were computed using the method described by Singh and Chaudhary (1985).

$$\delta^2_g = \frac{M_g - M_e}{r}$$

$$\delta^2_e = M_e$$

$$\delta^2_p = \delta^2_g + \delta^2_e$$

$$\delta^2_g = \text{genotypic variance, } \delta^2_p = \text{phenotypic variance,}$$

$$\delta^2_e = \text{error variance, } M_e = \text{mean square error, } M_g =$$

mean square genotype,

r = replication.

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\delta^2_p}}{\bar{X}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\delta^2_g}}{\bar{X}} \times 100$$

$\delta^2_g$  = genotypic variance,  $\delta^2_p$  = phenotypic variance,  $\bar{X}$  = grand mean

$$H = \frac{\delta^2_g}{\delta^2_p}$$

$\delta^2_g$  = genotypic variance,  $\delta^2_p$  = phenotypic variance

Genetic advance and Genetic Advance as percent mean were calculated using the method of Johnson *et al.*, (1955)

$$\text{Genetic Advance (GA)} = H \times K \times \delta^2_p$$

$$\text{Genetic Advance as percent of mean (GAM)} = \frac{\text{GA}}{\bar{X}} \times 100$$

H = Broad sense Heritability, K = Selection differential at 5%,  $\delta^2_p$  = Phenotypic standard deviation, GA = Genetic advance,  $\bar{X}$  = grand mean. Multivariate analysis comprising of Principal component analysis (PCA) and cluster analysis were performed to classify the level of closeness and similarity among the genotypes using R software version 4.1.3.

### III. RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variation in almost all the characters studied, indicating the existence of variability among the potato genotypes. The genotypes differed significantly ( $p \leq 0.05$ ) for percentage emergence, leaf length and highly significant ( $p \leq 0.01$ ) for days to first flower, plant height, number of branches, leaf width, number of leaves per plant, number of tubers per plant, number of tubers per plot, weight of tubers per plant, weight of tubers per plot, tuber yield and starch content, while non-significant was obtained for specific gravity (Table 2). This observations were similar to those of Bekele and Haile (2019), who also reported highly significant difference ( $p \leq 0.01$ ) among all the genotypes of potato tested except plant height which recorded non-significant. Mananno *et al.* (2021), also observed highly significant difference ( $p \leq 0.01$ ) for all traits of potato computed except proportion of medium tuber size and specific gravity. Replication effects were non-significant for all the characters except for weight of tubers per plot ( $p \leq 0.05$ ), implying less influence of replication on the expression of the characters. However, Nasiruddin *et al.* (2017), reported non-significant effects for all replication items, when working on potato.

In this study, wide ranges were obtained for all the characters tested (Table 3), suggesting the presence of variability among the genotypes. Moderate coefficient of variability (CV) (Table 3) values were observed for most of the characters, where, leaf length recorded the highest CV of 22.03%, while the lowest CV was obtained for days to first flower with 1.48%. The low to moderate CV exhibited by most of the characters signifies high precision for the experiment.

Phenotypic variance ( $\delta^2_g$ ) and genotypic variances ( $\delta^2_p$ ) were generally higher than their corresponding environmental variance for all characters except for percentage emergence where the environmental variance recorded a little higher value (30.75) than the genotypic variance (29.95), indicating influence of the environmental factors on the expression of this character. This observation is in line with the work of Asefa *et al.* (2016) and Tessema *et al.* (2022), where they observed higher phenotypic variance compared to their genotypic and environmental variance in potato. Similarly, the estimates of phenotypic coefficient of variation (PCV) were higher in magnitude than the genotypic coefficient of variation (GCV) in all the characters. The differences between the two are relatively low for most of the characters, suggesting less influence of the environment on the expression of those characters. Rangare and Rangare, (2013), Asefa *et al.* (2016), Nasiruddin *et al.* (2017), Hajamet *et al.* (2018) and Anoumaa *et al.* (2023) previously reported similar results on potato.

Higher PCV and GCV values (Table 3) were observed for starch content (44.30, 41.55), number of leaves per plant (35.34, 31.09), leaf length (34.44, 26.44), leaf width (25.35, 22.46), number of branch per plant (22.71, 20.71), weight of tubers per plot (21.85, 20.53), tuber yield per hectare (21.83, 20.50), and weight of tubers per plant (21.37, 20.38). Conversely, moderate to low PCV and GCV were noted for plant height (19.72, 17.21), number of tubers per plant (16.32, 13.49), tuber dry matter (15.29, 12.69), days to first flower (14.30, 14.22), specific gravity (13.47, 7.38), marketable tubers (9.84, 2.15), percentage emergence (8.30, 5.83), and number of tubers per plot (7.63, 5.55). The findings in this study on PCV and GCV was consistent with the results of Mishra *et al.* (2017) and Tessema *et al.* (2022) on potato. In addition, Anoumaa *et al.* (2023) reported low PCV and GCV for dry matter content and percentage marketable tubers and further suggested that low coefficient of variation obtained indicated pronounced effect of environment on the expression of these characters.

Days to first flower (98%), weight of tubers per plant (90%), weight of tubers per plot (88%), yield of tuber (88%), starch content (83%), number of branches (83%), leaf width (78%), number of leaves (77%), and plant height (76%) recorded higher broad sense heritability, while lower heritability was recorded for percentage emergence (49%), specific gravity (30%), and percentage marketable tubers (3%) respectively (Table 3). High broad sense heritability values observed indicated that these characters are more genetically influenced, therefore, selection of these traits will be effective for potato improvement. This is in agreement with previous reports of Ozturk and Yildirim (2014), Maharana *et al.* (2017), Mishra *et al.* (2017), Hajamet *et al.* (2018), and Mananno *et al.* (2021).

High genetic advance as percent of mean (Table 3) were obtained for days to first flower (28.87%), plant height (30.87%), number of branches (38.89%), leaf length (40.99%), leaf width (40.57%), number of leaves per plant (56.06%), number of tuber per plant (44.84%), weight of tubers per plant (37.65%), weight of tubers per plot (39.60%), tuber yield per hectare (39.56%), tuber dry matter (21.44%) and starch content (75.76%). Higher genetic advance as a percent of mean in majority of traits tested have been previously reported by Nasiruddin *et al.* (2017), Patel *et al.* (2018a), Singha and Ullah (2020), and Anoumaa *et al.* (2023). Consequently, Days to first flower (98%, 28.87%), weight of tuber per plot (88%, 39.60%), yield of tuber per hectare (88%, 39.56%), starch content (83%, 75.76%), and number of leaves per plant (77%, 56.06%)

recorded high heritability and high genetic advance as percent of mean, hence, this indicates greater influence of genetic factors than the environmental factors on the phenotypic appearance of the characters.

Number of branches per plant, leaf width, number of leaves per plant, weight of tubers per plant, weight of tuber per plot, tuber yield, and starch content exhibited higher phenotypic and genotypic coefficient of variation, with high broad sense heritability coupled with high genetic advance as percent of mean indicating that these characters are most likely governed by additive gene effects and selection for improved may be highly rewarding.

Correlations (Table 4) among the traits showed the present of significant and positive correlation for some of the characters. Tuber yield per hectare was significantly and positively correlated to number of branches per plant (0.42\*\*), leaf width (0.36\*), weight of tubers per plant (0.88\*\*), and weight of tubers per plot (0.99\*\*). Number of branches per plant was significantly and positive correlated with leaf width (0.75\*\*), number of tubers per plant (0.34\*), weight of tuber per plant (0.44\*\*), weight of tuber per plot (0.43\*\*). Similarly, leaf length was significantly and

positively correlated to number of leaves per plant (0.61\*\*). Highly significant and positive interrelationship existed between weight of tubers per plant with weight of tubers per plot (0.88\*\*). Nevertheless, significant and negative correlations were observed between plant height (-0.43\*\*), number of branches (-0.35\*), leaf length (-0.34\*), leaf width (-0.47\*\*), number of leaves (-0.56\*\*), weight of tuber per plant (-0.58\*\*), weight of tuber per plot (-0.37\*), and yield per hectare (-0.38\*) with days to first flower were obtained. Significant and positive correlations of some of the traits with tuber yield indicates those traits are governed under additive gene and selection of these characters for tuber yield improvement will be effective. Patel *et al.* (2018b) reported significant and positive association between total tuber yield with number of stems per plant and average weight of tubers per plant. However, the current results on correlations were contrary to those of Tripura *et al.* (2016), who observed significant and positive relationship between total yield and number of tubers per plant. Panigrahi *et al.* (2017), also reported significant and positive correlation between total yield per hectare and marketable tuber yield at both early and late harvest.

Table 2: Mean squares measured for sixteen characters studied

Source of variation	DF	PE	DFD	PH	NB	LL	LW	NL	NTP	TS	WTP	NTPL	WTPP	TY	TDM	SG	SC
Replication	2	22.4	2.23	1.74	0.07	0.15	0.08	1707.0	1.45	12.69	0.003	822.86	79.24*	52.56	1.44	0.01	6.56
Genotypes	11	120.6*	224.8**	106.78**	3.009**	2.06*	1.622**	23757.9**	9.12**	54.20**	0.090**	3020.08**	168.51**	116.12**	21.021**	0.026 <sup>NS</sup>	185.77**
Error	22	30.75	0.811	10.03	0.193	0.39	0.144	2106.1	1.22	47.10	0.003	691.21	7.144	4.96	2.757	0.0087	8.101

\* = Significant, \*\* = Highly significant at 0.05 and 0.01 level of probability, PE = Plant emergence, DFD = Days to 1<sup>st</sup> flower, PH = Plant height, NB = Number of branches per plant, LL = Leaf length, LW = Leaf width, NL = Number of leaves per plant, NTP = Number of tubers per plant, TS = Marketable tuber size, WTP = Weight of the tubers per plant, NTPL = Number of tubers per plot, WTPP = Weight of tubers per plot, TY = Tuber yield per hectare, TDM = Tuber dry matter content, SP = Specific gravity, SC = Starch content.

Table 3: Means and their standard error, range, coefficient of variability, heritability and genetic advance as a percent of mean

Characters	Mean ± SE	Range Min - max	CV %	Environmental variance	Genotypic variance	Phenotypic variance	Genotypic Coefficient variation	Phenotypic Coefficient variation	Heritability (%)	Genetic Advance	Genetic advance as % mean
PE	93.86±5.55	65.00 - 100.00	5.91	30.75	29.95	60.70	5.83	8.30	49	7.86	8.37
DFD	60.75±0.90	50.00 - 77.00	1.48	0.81	74.66	75.47	14.22	14.30	98	17.54	28.87
PH	32.98±3.17	17.60 - 46.20	9.72	10.03	32.25	42.28	17.21	19.72	76	10.18	30.87
NB	4.68±0.44	2.70 - 6.90	9.35	0.19	0.94	1.13	20.71	22.71	83	1.82	38.89
LL	2.83±0.62	1.40 - 6.40	22.03	0.39	0.56	0.95	26.44	34.44	58	1.16	40.99
LW	3.18±0.38	1.70 - 4.60	11.94	0.14	0.51	0.65	22.46	25.35	78	1.29	40.57
NL	273.22±45.89	120.00 - 580.00	16.87	2106.10	7217.26	9323.36	31.09	35.34	77	153.16	56.06
NTP	12.02±1.11	8.20 - 16.90	9.12	1.22	2.63	3.85	13.49	16.32	68	5.39	44.84
TS	71.50±6.86	60.00 - 82.00	9.60	47.10	2.36	49.46	2.15	9.84	5	0.72	1.01
WTP	0.85±0.06	0.55 - 1.28	7.09	0.003	0.03	0.033	20.38	21.37	90	0.32	37.65
NTPL	501.79±26.29	401.60 - 573.40	5.21	691.21	776.29	1467.50	5.55	7.63	52	41.03	8.18
WTPP	35.73±2.67	20.10 - 49.70	7.55	7.14	53.79	60.93	20.53	21.85	88	14.15	39.60
TY	29.69±2.22	16.80 - 41.40	7.58	4.96	37.05	42.01	20.50	21.83	88	11.75	39.58
TDM	19.45±1.66	14.02 - 26.10	8.54	2.76	6.09	8.85	12.69	15.29	68	4.17	21.44
SG	1.05±0.09	0.70 - 1.27	8.85	0.009	0.006	0.02	7.38	13.47	30	0.08	7.62
SC	18.52±2.85	6.60 - 47.10	15.35	8.10	59.22	67.32	41.55	44.30	83	14.03	75.76

PE = Plant emergence, DFD = Days to 1<sup>st</sup> flower, PH = Plant height, NB = Number of branches per plant, LL = Leaf length, LW = Leaf width, NL = Number of leaves per plant, NTP = Number of tubers per plant, TS = Marketable tuber size, WTP = Weight of the tubers per plant, NTPL = Number of tubers per plot, WTPP = Weight of tubers per plot, TY = Tuber yield per hectare, TDM = Tuber dry matter content, SP = Specific gravity, SC = Starch content.



Table 4: Simple Correlation Coefficients for growth, yield and quality traits in potato genotypes

	PE	DFF	PH	NB	LL	LW	NL	NTP	TS	WTP	NTPL	WTPPL	TY	TDM	SG	SC
PE	1															
DFF	-0.09	1														
PH	0.23	-0.43**	1													
NB	-0.17	-0.35*	-0.34*	1												
LL	0.03	-0.34*	0.06	0.27	1											
LW	-0.01	-0.47**	-0.19	0.75**	0.24	1										
NL	0.02	-0.56**	0.15	0.23	0.61**	0.21	1									
NTP	0.21	0.24	-0.39	0.34*	0.15	0.14	-0.09	1								
PMT	0.17	-0.25	0.14	0.24	0.13	0.18	0.26	0.19	1							
WTP	0.12	-0.58**	0.18	0.44**	0.003	0.37*	0.11	-0.26	0.31	1						
NTPL	0.37*	0.30	-0.30	0.16	-0.17	0.17	-0.004**	0.58**	0.01	-0.15	1					
WTPPL	0.08	-0.37*	0.09	0.43**	-0.18	0.35*	-0.03	-0.26	0.28	0.88**	-0.003	1				
TY	0.07	-0.38*	0.09	0.42**	-0.17	0.36*	-0.03	-0.23	0.29	0.88**	-0.007	0.99**	1			
TDM	0.02	0.26	-0.19	0.08	-0.08	-0.08	-0.05	0.16	0.08	0.09	0.09	0.13	-0.12	1		
SG	-0.12	-0.19	0.03	0.11	0.09	0.02	0.23	-0.08	-0.12	-0.08	-0.06	-0.13	-0.13	-0.14	1	
SC	0.21	-0.12	-0.05	0.27	0.0002	0.09	0.08	0.49**	0.23	0.25	0.29	0.12	0.13	-0.09	0.01	1

\*= Significant at 0.05, \*\* = highly significant at 0.01 level of probability, PE=Plant emergence, DFF = Days to 1<sup>st</sup> flower, PH = Plant height, NB = Number of branches per plant, LL = Leaf length, LW= Leaf width, NL = Number of leaves per plant, NTP = Number of tubers per plant, TS= Marketable tuber size, WTP = Weight of the tubers per plant, NTPL =Number of tubers per plot, WTPPL= Weight of tubers per plot, TY = Tuber yield per hectare, TDM = Tuber dry matter content, SP= Specific gravity, SC = Starch content.

Table 5: Eigen values and the cumulative variability of the principal components

Characters	PC1	PC2	PC3	PC4
Eigen value	7.82	3.83	2.84	1.42
Prop. Var.	0.43	0.21	0.16	0.08
Com. Var. (%)	43.09	64.21	79.84	87.64

Table 6: Eigen vectors of the first four principal components

Characters	PC1	PC2	PC3	PC4
Plant emergence	0.002	-0.300	-0.626	<b>0.245</b>
Days to 1 <sup>st</sup> flower	-0.012	0.197	-0.087	-0.016
Plant height	-0.044	0.169	<b>0.216</b>	0.171
Number of branches per plant	0.006	<b>0.367</b>	<b>0.286</b>	-0.248
Leaf length	0.013	0.134	-0.074	-0.319
Leaf width	0.007	0.163	-0.222	-0.297
Number of leaves per plant	<b>0.967</b>	-0.067	0.028	-0.048
Number of tubers per plant	0.016	<b>0.469</b>	0.001	<b>0.246</b>
Marketable tuber size	0.003	<b>0.321</b>	0.092	<b>0.304</b>
Weight of the tubers per plant	-0.002	-0.316	-0.401	<b>0.422</b>
Number of tubers per plot	<b>0.207</b>	0.104	0.039	0.177
Weight of tubers per plot	-0.102	-0.285	0.208	-0.294
Tuber yield per hectare	-0.085	-0.077	-0.134	-0.019
Tuber dry matter content	-0.017	-0.308	<b>0.504</b>	-0.056
Specific gravity	0.000	0.181	-0.463	-0.086
Starch content	-0.026	0.096	<b>0.319</b>	<b>0.440</b>

The total variation was divided in 16 principal components, and the first four principal components with Eigen values > 1 accounted for 87.64 % of the total variability among the 12 potato genotypes. The 1<sup>st</sup> principal component (PC<sub>1</sub>) accounted for 43.1 % of the total variation. The 2<sup>nd</sup> (PC<sub>2</sub>), 3<sup>rd</sup> (PC<sub>3</sub>) and the 4<sup>th</sup> (PC<sub>4</sub>) explained 21.1%, 15.6 % and 7.8 % of individual variation (Table 5) (fig. 1). The Eigen value and proportion of variance associated with each principal component decreased gradually with PC<sub>1</sub> having the largest and stopped at 1.42 and 0.08 respectively. Similar results were presented by Tessema *et al.* (2022), who identified four principal components with eigen value >1 and contributed 87.53 % of the total variability on 21 potato genotypes. Seidet *al.* (2021), who observed that the

first five principal components account for 88.20 % of the variance on 24 genotypes of potato.

The contribution of the characters studied to each principal component was presented in Table 6.

PC<sub>1</sub> was highly associated with number of leaves per plant and number of tubers per plot. The

PC<sub>2</sub> was determined by number of branches per plant, number of tubers per plant, marketable tuber size. Plant height, number of branches per plant, weight of tubers per plot, tuber dry matter and starch content contributed to PC<sub>3</sub>. The PC<sub>4</sub> was dominated by characters such as percentage emergence, number of tubers per plant, marketable tuber size, weight of tubers per plant and starch content. The

projection of component characters on PC<sub>1</sub> and PC<sub>2</sub> showed that weight of tubers per plot, weight of tubers per plant, number of branches, leaf width and marketable tuber size

are positively associated with yield of tubers per hectare (tons).

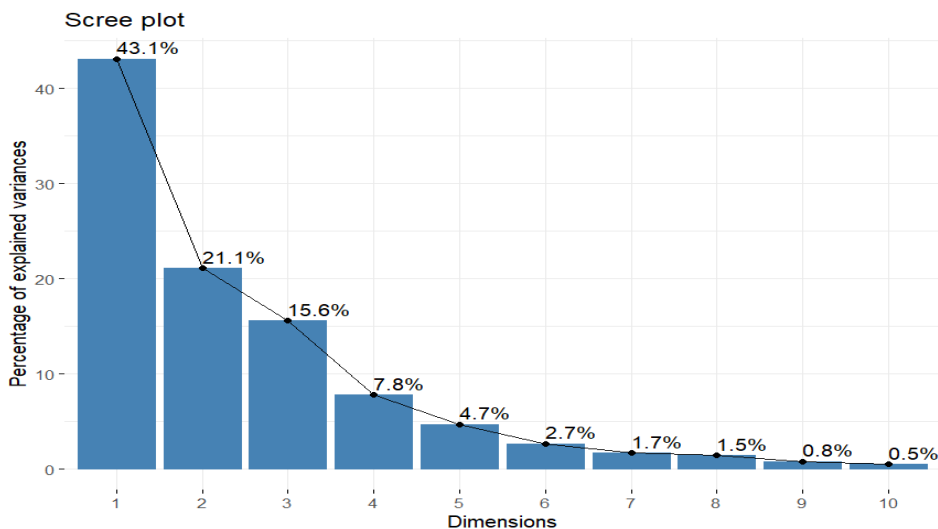


Fig. 1: Scree plot exhibiting PC<sub>s</sub> with their cumulative variability

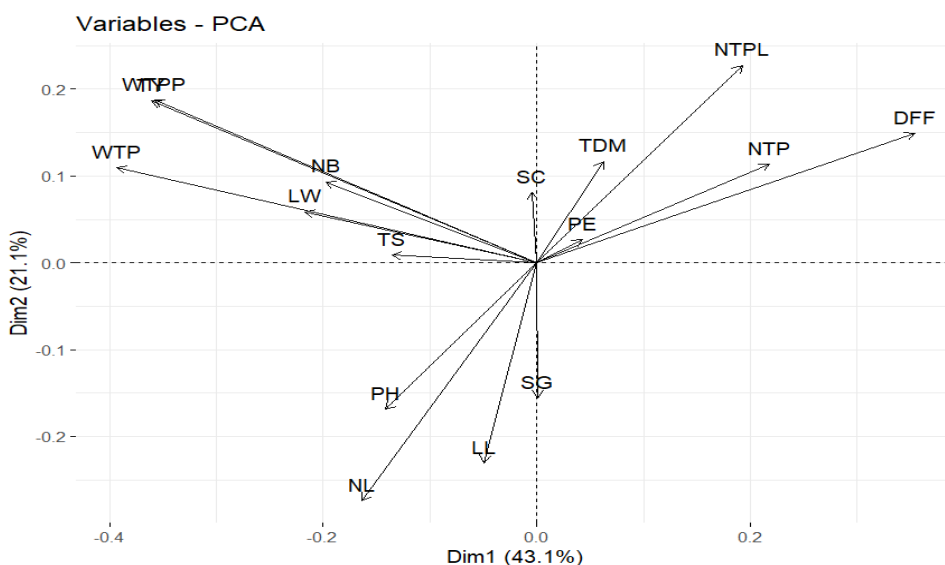


Fig. 2: Principal component biplot for characters tested in potato

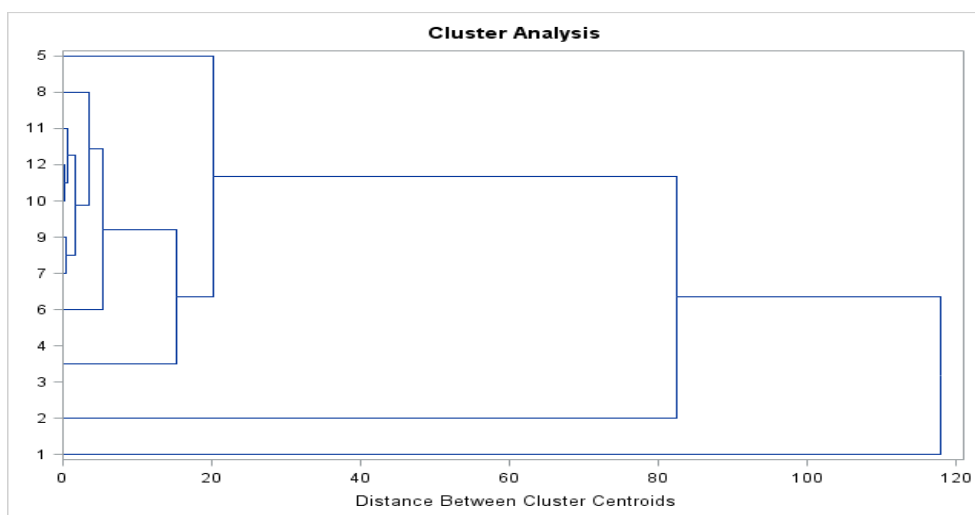


Fig. 3: Cluster dendrogram based on the genotypes used

Cluster analysis grouped the 12 genotypes into 3 distinct clusters and the distance between the clusters as showed in dendrogram (figure 3). Cluster 1 contained ten genotypes and it is the largest with genotypes such as Yellow leaf Nicola, Marabel, Caruso, Lady Christly, Madam, Bertita, Green leaf Nicola, Cameroun variety, Yellow Cece and Red Irish. Cluster 2 had only genotype, Bawon doya, while cluster 3 also contained one genotypes Superior. Abebe *et al.* (2013) reported that 25 varieties of potato used for the study were clustered into 3 clusters. Anoumaa *et al.* (2023), also reported 2 clusters groups on 138 potato accessions. In the present study, the cluster mean revealed that genotypes in cluster 1 recorded high values for number of tubers per plant (11.77), marketable tuber size (74.33), and number of tubers per plot (460.27). The genotypes in cluster 2 are characterized by high mean for

number of branches (5.13), leaf length (5.03cm), leaf width (3.37cm), number of leaves per plant (524.00), and specific gravity (1.11g/cm). Days to first flower (52.67), plant height (42.07cm), weight of tubers per plant (1.18 kg), weight of tubers per plot (47.17 kg), tuber yield per hectare (39.33 tons), tuber dry matter (21.36), and starch content (19.30) showed high mean values in the 3 clusters that contributed to divergence among the genotypes. Genotypes falling in cluster 1 and 3 showed highest mean values for yield and internal quality traits, while genotype in cluster 2 recorded highest for growth characters. Anoumaa *et al.* (2023) reported that cluster 1 recorded the highest dry matter and total tuber yield, while, percentage marketable tuber and plant height had the highest mean values in cluster 2 in potato.

Table 6: Mean values of the three clusters for 16 traits of potato genotypes

Characters	Cluster 1	Cluster 2	Cluster 3
Plant emergence	96.48	96.67	96.25
Days to 1 <sup>st</sup> flower	51.33	50.33	52.67
Plant height (cm)	37.18	33.53	42.07
Number of branches per plant	4.58	5.13	3.83
Leaf length (cm)	3.99	5.03	2.47
Leaf width (cm)	3.10	3.73	2.27
Number of leaves per plant	444.14	524.00	337.33
Number of tubers per plant	11.77	10.41	8.6
Marketable tuber size (%)	74.33	74.05	73.67
Weight of the tubers per plant (kg)	0.95	0.78	1.18
Number of tubers per plot	460.27	443.21	420.40
Weight of tubers per plot (kg)	35.95	27.53	47.17
Tuber yield per hectare (tons)	29.97	22.97	39.33
Tuber dry matter content	19.45	18.02	21.36
Specific gravity	1.08	1.11	1.03
Starch content	16.36	14.17	19.30

#### IV. CONCLUSION

From the above, considerable variation exists among the potato genotypes for most of the characters tested, genetic factors more influenced the characters of the 12 genotypes observed in this study as compared to environmental factors. The most striking differences are the number of branches per plant, leaf width, number of leaves per plant, weight of tubers per plant, weight of tubers per plot, tuber yield per hectare and starch content. The diversity exhibited among the genotypes signifies its potentials for effective breeding.

#### ACKNOWLEDGEMENTS

The authors acknowledged the management of Taraba State University, Jalingo and the TETFund for providing financial support for the execution of the research.

#### REFERENCES

- [1.] Acquah, G. (2012). Principles of Plant Genetics and Breeding. 2<sup>nd</sup> Edition Wiley-Blackwell Publishing. Pp. 647-656.
- [2.] Ahmad, M.F.1., Ahmad, S.M., Raj, K., Keservani, R.K. and Pradhan, A. (2015). Anti-Ulcer Activity of Tuber Extracts of *Solanum tuberosum* (*Solanaceae*) in Rats. *Acta Facultatis Pharmaceuticae. Universitatis Comenianae* : (2): 32-37.
- [3.] Anoumaa M., Kouam E.B., Kanmegne, G., Kamga, Y.B., Djomo Sime, H., and Chimi Nkombo L.L. (2023). Phenotypic variation and genetic divergence studies in Cameroonian potato (*Solanum tuberosum* L.) genotypes. *J Appl Biol Biotech.*, 11(01):210–221.
- [4.] Ardo, M.B and Abubakar, D.M. (2016). Seroprevalence of Horse (*Equus caballus*) Brucellosis on the Mambila Plateau of Taraba State, Nigeria. *Journal of Equine Science.*; 27(1):1-6
- [5.] Asefa G., Wassu, M. and Abebe, T. (2016). Genetic Variability Studies in Potato (*Solanum tuberosum* L.) Genotypes in Bale Highlands, South Eastern Ethiopia. *J. Bio. Agri. and Healthcare.* 6(3):117-119.

- [6.] Bekele, T. And Haile, B. (2019). Evaluation of improved potato (*Solanum tuberosum* L.) varieties for some quality attributes at Shebench Woreda of Bench – Maji Zone, Southwestern, Ethiopia, 14(7):389-394
- [7.] Bhatia, R. (2004). Genetic Variability and Correlation Studies in Gladiolus. M.Sc. Thesis, Punjab Agricultural University Ludhiana.
- [8.] Bradshaw, J.E. and Bonierbale, M. (2010). Potatoes In: Bradshaw, J.E. (ed.). Root and Tuber Crops, Handbook of Plant Breeding, vol. 7, Springer, New York.
- [9.] Devaux, A., Kromann, P. and Ortiz, O. (2014). Potatoes for Sustainable Global Food Security, *Potato Res.*, 57(3):185-199
- [10.] Duncan, D. (1955). Multiple range and Multiple F – tests. *Biometrics*. Pp.11-42.
- [11.] Engida, T., Nigusie, D. and DevakaraSastry, E.V. (2007). Genetic Variability for Yield and Other Agronomic Traits in Sweet Potato. *J. Agron.* 6(1):94-99
- [12.] FAOSTAT (2013). Food and Agricultural Organization (online). *Statistical database. UN, Rome, Italy* Available: <http://www.fao.org/faostat/en/#data>
- [13.] FAOSTAT (2014). Food and Agricultural organization. *Statistical database. UN, Rome, Italy*
- [14.] Haan, S.De and Rodriguez, F. (2016). Potato origin and production. In J.Singh and L. Kaur (eds), *Advances in Potato Chemistry and Technology*. London, UK; Academic Press, Elsevier. Pp. 1-32
- [15.] Hajam, M.A., Bhat, T.A., Rather, A.M., Khan, S.H., Shah, L.R., Hajam, M.A and Paul, S. (2018). Genetic Variability, Heritability and Genetic Advance for Various Qualitative Characters of Potato. *Int. J. Chem. Studies*. 6(6):518-522
- [16.] Haverkort, A.J., Struik, P.C., Visser, R.G.F. and Jacobsen, E. (2009). Applied Biotechnology to combat late blight in Potato caused by *Phytophthora infestans*. *Potato Res* 52:249–264.
- [17.] Janaki, M., Naram L. N., Venkata, C. R and Paratpara, M.R. (2015). Assessment of Genetic Variability, Heritability and Genetic Advance for Quantitative Traits in Chilli (*Capsicum annum* L.) *The Bioscan* (Supplement on Genetics and Plant Breeding) 10(2): 729-733.
- [18.] Johnson, H. W; Robinson, H. F and Comstock, R.E. (1955). Estimation of genetic and Environmental Variability in Soybean. *Agron. J.*, 47: 314-318.
- [19.] Kumari, M., Kumar, M. and Solankey, S.S. (2018). Breeding potato for quality improvement. Potato from Inces to all over the world. Intech open. Pp. 37-59.
- [20.] Lohani, M., Singh, D. and Singh, J.P. (2012). Genetic Diversity Assessment through Principal Component Analysis in Potato (*Solanum tuberosum* L.), *Vegetable Science*, 39(2):207- 209
- [21.] Maharana, J., Panda, C.M. and Jakhar, P. (2017). Genetic Variability among Genotypes and Character Association in Kharif Potato (*Solanum tuberosum* L.) for different Traits. *The Bioscan* 12 (2):1195-1202
- [22.] Meenakshi Badu1, P. Ashok1, T.S.K.K. Kiran Patro1 and Sasikala, K. (2017). Studies on Genetic Variability, Heritability and Genetic Advance for Growth, Yield and Quality Parameters among Orange Flesh Sweet Potato [*Ipomoea batatas*(L.) Lam.] Genotypes. *Int.J. Curr. Microbiol. App.Sci.*, 6(9): 1894-1903
- [23.] Manamno, W., Wassu, M. and Tesfaye A. (2021). Genetic Variability and Correlation of Traits among Progenies of Potato Crosses in Ethiopia, *East African J. Sci.*, 15 (1): 1-16
- [24.] Mishra, S., Singh, J., Sharma, P.K. (2017). Studies on parameters of genetic variability for yield and its attributing traits in potato (*Solanum tuberosum* L.). *Biosci. Biotechnol. Res.*, 14, 489 - 495.
- [25.] Mondal, M.A.A. (2003). Improvement of Potato (*Solanum tuberosum* L.) through hybridization and in vitro culture technique. Ph. D. Thesis, Rajshahi University, Rajshahi, Bangladesh.
- [26.] Nasiruddin, M., Ali Haydar, F.M. and Rafiul Islam, A.K.M. (2017). Genetic diversity in potato (*Solanum tuberosum* L.) genotypes grown in Bangladesh. *International Research Journal of Biological Sciences*, 6 (11):1-8.
- [27.] Ozturk, G. and Yildirim, Z. (2014). Heritability estimates on some Quantitative Traits in Potatoes. *Turkish Journal of Field Crops*. 19(2):262-267.
- [28.] Panigrahi, K.K., Pradhan, J., Panigrahi, P. and Sarkar, K.K. (2017). Genetic Variability, Character Association and Path Coefficient Analysis of Yield Attributes for medium and late Maturing Potato Cultivars. *Int. J. Curr. Microbiol. App. Sci.* 6 (7):2558-2566
- [29.] Patel, A.B., Patel, R.N., Gami, R.A., Patel, J.A. and P.C. Patel (2018a). Genetic Variability among the Potato (*Solanum tuberosum* L.) Genotypes as Affected by Harvesting Period for Processing Purpose and Tuber Yield. *Curr. Agric. Res.* 6(3):372-377
- [30.] Patel, R. A., Bhavani, R.T., Patel, D.K. and Patel, R.J. (2018b). Character Association and Path Coefficient Studies for Yield and its Components in Potato (*Solanum tuberosum* L.). *Int. J. Curr. Microbiol. App. Sci.* 7 (8):1942-1950.
- [31.] Puttongsiri, T., Choosakul, N. and Sakulwilaingam, D. (2012). Moisture Content and Physical Properties of Instant Mashed Potato. International Conference on Nutrition and Food Sciences. IPCBEE VOL.39, IACSIT Press, Singapore
- [32.] Rangare, S.B. and Rangare, N.R. (2013). Genetic variability and character association in potato (*Solanum tuberosum* L.). *Trends in Biosciences*, 6(5):603-607
- [33.] Rolot, J. L. (2001). Potato. In: Romain H. R. (ed). *Crop Production in Tropical Africa*. DGIC Belgium Pp. 188 – 204 .
- [34.] Sahair, R.A., Sneha S., Raghu, N., Gopenath T.S., Karthikeyan, M., Gnanasekaran, A., Chandrashekrappa, G.K. and Basalingappa, K.M. (2018). *Solanum*



- tuberosum* L: Botanical, Phytochemical, Pharmacological and Nutritional Significance. *International Journal of Phytomedicine*, 10(3): 115-124
- [35.] SAS Institute Inc. (2009). SAS System. Cary, NC, USA
- [36.] Seid, E., Wassu, M. and Tesfaye, A. (2021). Genetic Diversity Assessment through Cluster and Principal Component Analysis in Potato (*Solanum tuberosum* L.) Genotypes for Processing Traits. *International Journal of Food Science and Agriculture*, 5(3):440-447
- [37.] Sestra, R., Mihalte, L., Sestra, A., Bondrea, I. and Baciu, A. (2007). The Variability and Heritability of Several Traits at Different Cultivars of Tulips. *Buletinul Usamv-CN*. 64: 1-2.
- [38.] Singh, R. K. and Chaudhary, B.D. (1985). *Biometrical Methods in Quantitative Genetic analysis*. Kalyani Publishers, New Delhi India. Pp.1-349.
- [39.] Singha, L. and Ullah, Z. (2020). Genetic Variability for Yield and its Attributing Traits in Potato (*Solanum tuberosum* L.). *International Journal of Current Microbiology and Applied Science* 9 (2): 1974-1983
- [40.] Tessema, G.L., Mohammad, A.W., Abebe, D.T. (2022). Genetic Variability Studies for Tuber yield and yield attributes in Ethiopian released Potato (*Solanum tuberosum* L.) varieties. *Peer J*, 12860
- [41.] Tripura, A., Das, A., Das, B., Priya, B. and Sharkar, K. (2016). Genetic studies of variability, character association and path analysis of yield and its component traits in potato (*Solanum tuberosum* L.). *Journal of Crop and Weed*, 12(1): 56–63.
- [42.] Wagner, W.L., Herbst, D.R. and Lorence, D.H. (2014). Flora of the Hawaiian Islands. Smithsonian Institution., Washington D.C. USA. <http://botany.si.edu/pacificislandbiodiversity/-hawaiian-flora/index.htm>.
- [43.] Zaheer, K., and Akhtar, M.H. (2016). Potato Production, Usage, and Nutrition—A Review. *Crit. Res. Food Sci. Nutr.* 56, 711–721.