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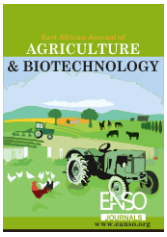

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Original Article

Genetic Diversity in Potato *(Solanum tuberosum L.)* Genotypes for Yield and Processing Attributes at Holetta, Central Highlands of Ethiopia

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Euclidean Distances, Clustering, Principal Component Analysis, Tuber Quality, External Quality, Solanum Tuberosum.

ABSTRACT

Potato (*Solanum tuberosum* L.) is a versatile crop and a source of inexpensive energy in the human diet in many countries. It can be used as fresh products and commercially processed foods such as French fries and chips. Potato varieties development research previously conducted in Ethiopia related to processing quality were limited in their scope of quality parameters. This experiment was conducted at Holetta Agricultural Research Centre, Ethiopia during the main crop season of 2017. Twenty-four potato genotypes were evaluated for 23 quantitative and six qualitative traits in randomized complete block design with three replications to determining the nature and magnitude of common genetic diversity and to screen out genetically diverse parents by using cluster and principal component analysis. The first eight principal components accounted for 90.26% of the observed variations among 24 potato genotypes. The first three PC accounted for 60.43% of the variation. The genetic distances among the 24 potato genotypes ranged from 3.40 to 11.80 and the genotypes were grouped into eight clusters based on quantitative and qualitative traits. Cluster II consisted of 25%, Cluster IV, I, III contained 20.83%, 16.67% and 12.5% of genotypes, respectively, while Cluster VI, VII and VIII each consisted of one genotype. In conclusion, genotypes grouped under Cluster II and VIII worth further evaluation to obtain genotypes with highest total tuber yield, the specific gravity of tuber, dry matter content, total starch content, acceptable tuber physical and frying quality with other desirable traits.

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INTRODUCTION

The potato is a versatile food crop and a cheap source of food in many countries. It is the third most important food crop in terms of consumption in the world after rice and wheat (Birch *et al*., 2012; Hancock *et al*., 2014). The genetic diversity of potatoes *Solanum* Section Petota (*Solanaceae*) may be grouped in wild and cultivated potatoes. The cultivated potatoes *Solanum tuberosum* are tetraploid (2n=4x= 48), while the native are highly diverse, diploids (2n=2x=24), triploids (2n=3x=36), tetraploids (2n=4x=48), pentaploids (2n=5x=60) and hexaploids (2n=6x=72) (Huamán and Spooner, 2002). For a successful breeding program, the presence of genetic diversity and variability is vital in obtaining the desirable traits for developing new varieties. Information on genetic diversity in elite germplasm is essential for identifying promising lines for traits of interest (Ali *et al*., 2008) and estimating genetic distinctiveness among parents. Selection of genetically diverse parents is mandatory for the exploitation of transgressive segregation (Joshi *et al*., 2004).

Large genetic distances among parents is a prerequisite for securing useful heterosis in the progeny. Diversity in plant genetic resources provides the opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (high yield potential, disease resistance, product colour, etc.) and breeder-preferred traits (pest and disease resistance and photosensitivity, etc.). Genetic diversity facilitates breeders to develop varieties for specific traits like quality improvement and tolerance to biotic and abiotic stresses (Bhandari *et al.*, 2017). There are statistical tools that help breeders to identify genetic diversity and to isolate traits that are useful in developing target variety characteristics.

Cluster analysis and principal component analysis (PCA) are frequently used statistical tools for exploring genetic diversity while

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securing relative basic differences among study samples. Cluster analysis is a classification method, which is used to arrange a set of cases into similar groups that share relationships. The of set cases within a cluster is more similar to each other than those in other clusters and helps to generate summary information of data among the study samples. In addition, cluster analysis is used to explore similarities and diversity in a collection of study subjects (Gevrekçi *et al*., 2004).

In Ethiopia, several improved potato varieties have been released by different research centres and institutions since the establishment of the potato research and development program. However, most of the released varieties have not satisfied the farmer and consumer expectations, especially for processing attributes. Therefore, the present study was designed to explore the nature and magnitude of genetic diversity and the characters contributing in potato genotypes for tuber quality, yield and yield-related traits and also to identify genetically diverse parents for developing varieties with superior traits for high yield, user-preferred quality attributes by using cluster and principal component analyses.

MATERIALS AND METHODS

Experimental Site, Design and Materials

A total of 24 potato genotypes were used for the experiment. These included 21 genotypes and three released varieties (*Table 1*). The 24 genotypes were planted at Holleta Agricultural Research Centre experiment station during the main cropping season of 2017. The experiment was laid out in randomized complete block design (RCBD) with three replications and each plot was 3.6 m (length) x 4.5 m (width) (16.2 m^2 gross plot size) consisted six rows each containing 12 plants and thus 72 plants per plot. The spacing between rows and plants was 0.75 m and 0.30 m, respectively. The spacing between plots and adjacent replications was 1 m and 1.5 m, respectively.

Table 1: List of potato genotypes used for evaluation

No.	Accession code	No.	Accession code
1	CIP-396034.268	13	CIP-394611.112
2	CIP-393220.54	14	CIP-392617.54
3	CIP-395017.229	15	CIP-381381.20
4	CIP-392797.27	16	CIP-398180.289
5	CIP-395112.19	17	CIP-.398190.89
6	CIP-399075.7	18	CIP-398190.404
7	CIP-393280.64	19	CIP-391058.175
8	CIP-398098.65	20	CIP-396034.103
9	CIP-393385.39	21	CIP-391046.14
10	CIP-396027.205	22	Belete (CIP-393371.58)
11	CIP-393077.159	23	Gudanie (CIP-386423.13)
12	CIP-399002.52	24	Dagim (CIP-396004.337)

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Data Collection

Phenology and Growth Parameters

Phenology and growth data were recorded as days to 50% flowering, days to physiological maturity, plant height (cm), average stems number and leaf area index (cm^{-3})

Yield and Yield Components

The data collected for yield variables included shoot dry weight (g), tubers dry weight (g), dry total biomass weight (g), number of tubers per hill, average tuber weight (g/tuber), tuber size distribution:- small (< 35 mm), medium (35 to 50 mm), and large (>50 mm) as a percent of total harvested tubers, total tuber yield (t ha^{-1}), marketable tuber yield (t ha^{-1}) and unmarketable tuber yield (t ha^{-1}). The amount of tuber number in different size categories was changed to percentage (Ekin *et al*., 2009).

External and Internal Tuber Quality Traits

Tuber geometric mean diameter (Dg) (mm): The sizes as a geometric mean diameter of ten randomly selected tubers from each plot were determined by measuring the length (L), width (W) and thickness (T) using digital Vernier calliper with an accuracy of 0.01 mm. The geometric mean diameter (D_g) was calculated using the cube root of the product of L, W and T.

$$Dg = (LWT)^{0.33} \quad [1]$$

Where: L is the length, W is the width and T is the thickness of the tuber.

Tuber length (L) to width (W) ratio (L/W = Ɍ): This was computed as the ratio of tuber length (L) to tuber width (W).

$$Ɍ = L/W \quad [2]$$

Tuber sphericity was determined by using the formula as described by Ahmadi *et al.* (2008).

$$\Phi = (Dg/ L) \times 100 \quad [3]$$

Where: Φ is sphericity of the tuber (mm^{-1}), D_g is the geometric mean diameter (mm) and L is tuber length (mm)

Surface area (S) (mm^2): Tubers surface area was determined according to Baryeh (2000)

$$S = \pi Dg^2 \quad [4]$$

Where: S is the surface area (mm^2) and D_g is the geometric mean diameter (mm)

Tuber shape: This was described by eight types of tuber shape, which was transformed into numerical scores from 1 to 8, where 1 = compressed, 2 = round, 3 = ovate, 4 = obovate, 5 = elliptic, 6 = oblong, 7 = long-oblong and 8 = elongate (Huaman *et al*., 1977).

Tuber eye depth: This described by five levels denoted by numerical scores from 1 to 5, where 1= Protruding, 2 = Shallow, 3 = Medium, 4 = Deep, and 5 = Very deep (Huaman *et al*., 1977).

Tuber skin colour: This was assessed visually at harvesting according to a colour card (Huaman *et al*. 1977) on a 1-9 scale, where 1 = white-cream, 2 = yellow, 3 = orange, 4 = brown, 5 = pink, 6 = red, 7 = red-rose, 8 = purple and 9 = blackish.

Tuber flesh colour: This was evaluated visually using the colour card (Huaman *et al*., 1977) on a code of 1-8, where 1 = white, 2 = cream, 3 = yellow (bright), 4 = yellow, 5 = intense yellow, 6 = red, 7 = purple, 8 = violet.

Chips and French Fries Colour: Potato chips and French fry colour is important in processed and fried potato products. Uniformly-sized

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(100–150 g) tubers were peeled and collected in cool tap water and sliced using potato slice cutter and collected in tap water. The slices were blot-dried on paper towels to remove the free water. Before frying the potato slices, sunflower cooking oil was heated for 10 to 15 minutes until it reached 176 °C and ascertained with a thermometer. For each potato variety, 700 g of slices were fried 3 to 4 minutes at 176-180 °C using an electronic deep fat fryer until bubbling ceased (Amoros *et al*., 2000). The chips and French fry colour was determined using a standard colour chart with a scale of 1 to 5 (1 = the lightest colour-white to cream), 2 = light tan, 3 = dark tan, 4 = brown and 5 = dark brown. Chips and French fries colour between grade 1 and 2 is commercially acceptable (Amoros *et al*., 2000; CIP, 2007).

Specific gravity of tubers (Sg) (gcm^{-3}): The specific gravity of tubers was determined using the air, underwater weight method. Five kilograms of fresh tubers of different shapes and sizes were randomly selected from each plot per genotype in a net bag. The tubers were washed with tap water and allowed to dry. The tubers were first weighed in air and then re-weighed suspended in water. The specific gravity of each sample was determined according to the formula (Gould, 1995).

$$\text{Specific gravity} = \frac{\text{Weight in air}}{\text{Weight in air–Weight in water}} \ldots\ldots [5]$$

Dry matter content (%): The total dry matter content (DMC) was calculated according to Porras *et al.* (2014). Five tubers of each variety were chopped (about 500 g total) into small 1-2 cm cubes. The cubes were mixed thoroughly and two sub-samples of 200 g each taken. The exact weight of each sub-sample was recorded as fresh weight. Subsequently, each sub-sample was placed in an oven set at 80 °C and dried for 48 hours until constant weight. Each sub-sample were weighed immediately and recorded as dry weight. The dry matter content for each sub-sample was then computed.

$$\text{Dry matter content (\%)} = \frac{\text{dry weight}}{\text{fresh weight}} * 100 \ldots [6]$$

Total starch content (g/100g): The total starch content was estimated from dry matter percent. Starch content (%) = 17.55 + 0.891 * (tuber dry weight% – 24.182) (AOAC, 1980).

Data Analysis

Determination of Genetic (Euclidean) Distance and Genotype Clustering

The genetic distances of 24 potato genotypes were estimated using Euclidean distance (ED) calculated from quantitative and qualitative traits after standardization Sneath and Sokal (1973) as;

$$ED_{jk} = \sqrt{\sum_{i=1}^{n} \left(Xij - Xik\right)^{2}}^{\frac{2}{2}} \ldots\ldots\ldots\ldots [7]$$

ED_{jk} is Euclidean distance between genotypes *j* and *k*; X_{ij},; X_{ik} is phenotype traits values of the i^{th} character for genotypes *j* and *k*, respectively and *n* is the number of phenotype traits used to calculate the distance.

The distance matrix from phenotype traits was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrogram for the test genotypes. In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other 23 genotypes. The calculated average distances (ED) were used to estimate the closeness of the genotypes.

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Principal Component Analysis

Principal component analysis (PCA) was computed to explore characters, which accounted most to the total observed variation. The data were standardized to zero mean and variance of one before computing principal component analysis. The principal component analysis was based on correlation matrix was calculated using SAS software where according to Gutten's lower bound principle, eigenvalues <1 should be ignored (Kumar *et al*., 2011).

RESULTS AND DISCUSSION

Clustering Among Evaluated Potato Genotypes

Assessment of genetic distances measured by Euclidean distances using cluster analysis resulted in 276 pairs of potato genotypes (*Table 2*). The four highest Euclidean distance among genotype pairs were between CIP396027.205 with CIP392617.54, CIP-396027.205 with CIP394611.112, CIP398098.65 and CIP396027.205 and CIP-396027.205 with Belete, in descending order (*Table 2*). The four lowest Euclidean distances among genotype pairs were between CIP-395017.229 with CIP392797.27, CIP391058.175 with CIP-391046.14, CIP-393220.54 with CIP-391058.175 and CIP398098.65 with CIP-394611.112 in ascending order (*Table 2*). Further, Euclidean distances were higher among introduced genotypes than among the released varieties. This indicated that there is a higher chance of improving tuber yield, physical and internal tuber quality traits through selection and hybridization of potato genotypes for yield and processing quality.

Generally, 36 genotype pairs (13.0%) of had genetic distances between 3.38 and 5.48, 124 genotype pairs (44.9%) had genetic distances between 5.49 and 7.58, 86 genotype pairs (31.2%) had genetic distance between 7.59 to 9.67 while 30 genotype pair (10.9%) had genetic distances between 9.68 and 11.78 (*Figure 1*)

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Table 2: Euclidean distances based on 23 quantitative and 6 qualitative traits of 24 potato genotypes evaluated at Holetta, in 2017

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1	6.28	5.81	5.02	4.59	8.26	4.79	6.12	8.03	8.35	5.10	8.53	6.47	5.82	4.89	5.50	5.55	4.79	5.33	6.50	7.18	6.10	7.03	7.80
2		6.78	6.21	6.99	8.01	7.54	8.78	6.19	6.4	4.40	9.38	9.02	8.57	6.32	6.34	7.28	6.69	3.62	6.50	3.99	8.59	5.21	5.91
3			3.39	5.41	7.73	7.33	9.14	8.91	8.25	6.60	11.02	9.35	6.57	6.65	6.99	5.74	6.39	6.23	8.70	6.83	8.14	7.03	6.56
4				5.55	7.18	6.55	7.70	8.57	8.66	6.60	10.68	7.84	5.41	5.38	5.64	4.77	5.85	4.99	8.00	6.01	6.90	5.93	6.52
5					9.70	6.61	7.53	8.62	9.06	6.20	10.68	8.46	6.43	6.82	7.08	6.26	5.54	7.23	6.90	8.80	8.33	7.30	7.68
6						8.53	9.29	10.26	10.3	8.30	9.26	9.42	10.1	8.45	9.31	8.13	9.85	7.11	10.00	7.33	10.04	6.67	7.90
7							6.04	8.02	9.32	6.40	7.16	5.31	6.71	4.73	6.21	7.20	6.15	6.21	5.90	8.31	6.14	6.26	8.22
8								8.79	11.6	8.20	8.99	3.70	6.74	6.08	6.82	6.28	6.88	7.42	7.70	9.63	6.20	7.43	10.34
9									5.56	4.70	9.38	9.48	10.4	7.29	8.42	9.79	9.17	6.94	7.40	8.43	9.36	7.58	9.07
10										4.90	10.36	11.72	11.8	8.57	9.10	10.6	10.65	7.80	9.10	8.01	11.60	9.14	8.07
11											7.59	8.89	8.68	6.51	7.04	8.03	7.27	5.40	5.90	6.38	8.64	6.88	6.73
12												9.11	10.90	8.87	9.52	10.7	10.24	8.57	9.80	10.10	9.90	8.98	10.86
13													7.35	5.52	6.47	7.05	7.36	7.28	8.00	9.54	5.51	7.34	10.58
14														5.55	6.06	4.75	4.71	6.87	9.10	8.99	4.88	7.67	9.85
15															4.62	5.90	6.05	4.46	7.40	7.18	4.67	5.42	8.32
16																4.55	6.43	4.96	8.00	6.74	6.57	6.49	7.40
17																	5.48	5.75	9.20	7.24	6.58	6.40	8.04
18																		5.57	7.00	7.44	5.24	6.60	8.80
19																			7.20	3.45	6.08	4.09	6.23
20																				8.14	8.96	7.32	7.55
21																					8.81	6.06	5.25
22																						7.35	10.96
23																							6.74

Where, 1= CIP-396034.268, 2= CIP-393220.54, 3 = CIP-395017.229, 4 = CIP-392797.27, 5 = CIP-395112.19, 6 = CIP-399075.7, 7 = CIP-393280.64, 8 = CIP-398098.65, 9 = CIP-393385.39, 10 = CIP-396027.205, 11 = CIP-393077.159, 12 = CIP-399002.52, 13 = CIP-394611.112, 14 = CIP-392617.54, 15 = CIP-381381.20, 16 = CIP-398180.289, 17 = CIP-398190.89, 18 = CIP-398190.404, 19 = CIP-391058.175, 20 = CIP-396034.103, 21 = CIP-391046.14, 22 = Belete, 23= Gudaine, 24 = Dagim

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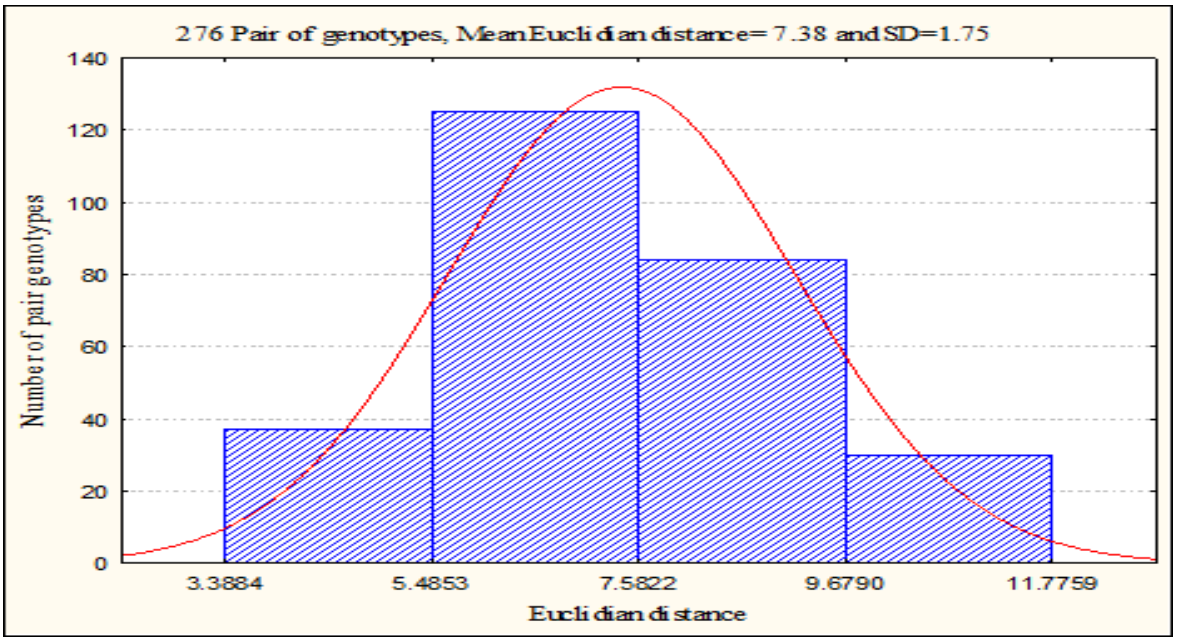
Figure 1: Distribution of 276 pairs of 24 potato genotypes evaluated into different categories of Euclidean distances (Mean Euclidean distance is 7.38 and standard deviation is 1.75) at Holetta in 2017



In this study, the mean genetic distance of each potato genotype to the other 23 genotypes was calculated to generate information about the most distant and closest genotypes (*Table 3*). Genotypes CIP 399002.52 (9.59), CIP396027.205 and CIP399075.7 in descending order had the highest Euclidean distances; while CIP391058.175, CIP396034.268 and CIP381381.20 had the lowest Euclidean distance in ascending order (*Table 3*). Including the two standard checks, Belete and Dagim, 11 potato genotypes (45.8%) had mean genetic distance greater than the mean while 13 potato genotypes (54.2%) including Gudene had mean genetic distance below 7.38. This result indicated the presence of considerable dissimilarities among the genotypes that could be used as parents in the potato breeding program in Ethiopia. Similar findings were also reported among potato genotypes Tesfaye *et al*. (2013); Wassu (2014); Luthra (2009); Panigrahi *et al*. (2014); Haydar *et al*. (2007); Mondal *et al*. (2007); Datta *et al*. (2015); Rangare and Rangare (2017).

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Table 3: Minimum, maximum and mean Euclidean distances of 24 potato genotypes estimated from 23 quantitative and six qualitative traits evaluated at Holetta in 2017

Genotypes	Minimum	Maximum	Mean	SD	CV (%)
CIP-396034.268	4.59	8.53	6.25	1.26	20.15
CIP-393220.54	3.62	9.38	6.74	1.55	23.01
CIP-395017.229	3.40	11.0	7.20	1.59	22.10
CIP-392797.27	3.40	10.7	6.49	1.58	24.31
CIP-395112.19	4.60	10.7	7.29	1.48	20.26
CIP-399075.7	6.70	10.5	8.77	1.15	13.17
CIP-393280.64	4.73	9.32	6.77	1.17	17.36
CIP-398098.65	3.70	11.6	7.71	1.72	22.36
CIP-393385.39	4.70	10.4	8.28	1.44	17.40
CIP-396027.205	4.80	11.8	9.08	1.88	20.71
CIP-393077.159	4.39	8.89	6.74	1.32	19.63
CIP-399002.52	7.20	11.0	9.59	1.05	10.92
CIP-394611.112	3.70	11.7	7.86	1.87	23.85
CIP-392617.54	4.70	11.8	7.56	2.09	27.69
CIP-381381.20	4.46	8.87	6.33	1.35	21.35
CIP-398180.289	4.55	9.52	6.80	1.37	20.20
CIP-398190.89	4.50	10.7	7.01	1.78	25.36
CIP-398190.404	4.70	10.6	6.96	1.70	24.47
CIP-391058.175	3.45	8.57	6.03	1.36	22.55
CIP-396034.103	5.90	10.5	7.86	1.20	15.27
CIP-391046.14	3.50	10.1	7.39	1.70	23.04
Belete	4.70	11.6	7.63	1.96	25.74
Gudaine	4.09	9.14	6.82	1.11	16.21
Dagim	5.30	11.0	8.06	1.62	20.07
Overall	**3.40**	**11.80**	**7.38**	**1.75**	**23.69**

The descriptive numeric data on qualitative traits of the study genotypes were converted into a binary matrix using a Euclidian distance analysis procedure. The Euclidean distance matrix of the 276-genotype pairs estimated for tuber quality, yield and yield-related traits were used to construct dendrograms based on the Unweighted paired group method with arithmetic means (UPGMA). The 24 potato genotypes grouped in eight clusters. Cluster I consisted of four genotypes (16.7%), cluster II had six (25%) potato genotypes, clusters III and V each contained three genotypes (12.5%), cluster IV had five genotypes (20.8%) while, clusters VI, VII and VIII each had one genotype (*Figure 2*). The three standard checks were in cluster II and IV. The many cluster groups in a small sample of genotypes used in this study reveal as in previous studies that potato has a wide genetic diversity and low

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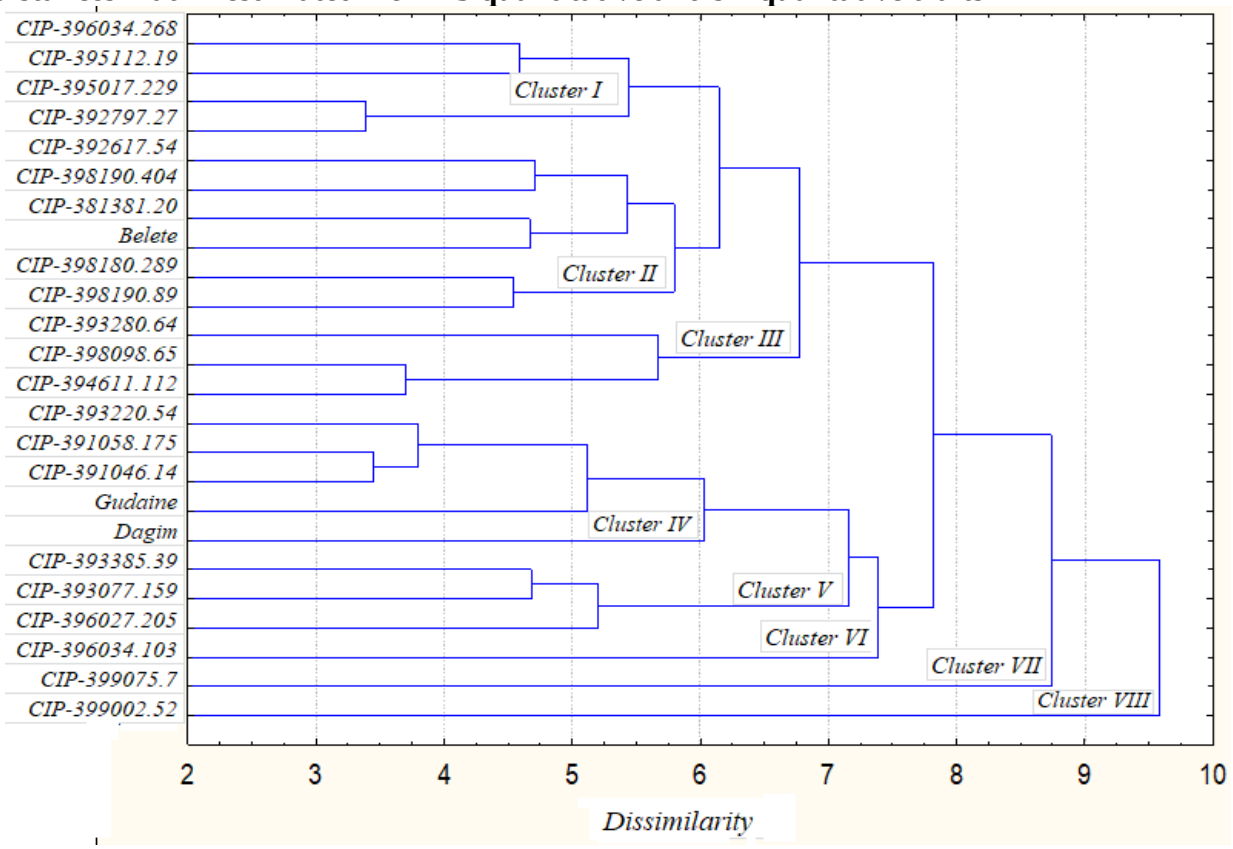
phylogenetic association (Arslanoglu et al., 2011; Rangare and Rangare, 2017; Datta et al., 2015; Joseph et *al.*, 2005; Haydar *et al.*, 2007; Mondal *et al.*, 2007; Tesfaye *et al.*, 2013)

Figure 2: Dendrogram depicting dissimilarity of 24 potato genotypes by unweighted Pair group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 23 quantitative and six qualitative traits



Cluster II had shown days to 50% flowering, leaf area index, tubers dry mass weight, total biomass weight, average tuber weight, total tuber yield, marketable tuber yield, oblong tuber shape, shallow and medium eye depth, white- cream tuber skin colour, cream tuber flesh colour, brown chips colour and light tan French fries colour *Table 4*. Cluster III had early maturity, obovate tuber shape, deep eye depth, pink, red and red-purple tuber skin colour, white, cream and yellow (bright) tuber flesh colour, light tan chips colour and white to cream French fries colour. Cluster IV showed early maturity, elliptic tuber shape, shallow eye depth, yellow tuber skin colour, cream and yellow tuber flesh colour, dark tan chips and French fries colour. In cluster V genotypes showed sphericity of the tuber, equally of round tuber shape, very deep eye depth, red tuber skin colour, white tuber flesh colour, dark tan chips and French fries colour. Cluster VI, VII and VIII had contained each one genotype. Cluster VI showed Average stems number, medium-size tubers, the specific gravity of tubers, round tuber shape, very deep eye depth, red tuber skin colour, cream tuber flesh colour, white to cream chips and French fries colour. Cluster VII showed medium maturity, length-width ratio, elliptic tuber shape, shallow eye depth, pink tuber skin colour, Yellow tuber

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flesh colour, white to cream chips and French fries colour. Cluster VIII showed medium maturity, plant height, shoot dry mass weight, average tuber number per hill, unmarketable tuber yield, small size tubers, the specific gravity of tubers, dry matter content, total starch content, ovate tuber shape, shallow eye depth, pink tuber skin, white flesh colour, light tan chips and French fries colour.

According to the cluster mean analysis Table 4 for characters, developing varieties for processing purpose and tuber yield through selection further evaluation of genotypes from Cluster II and VIII is possible to obtain genotypes with highest total tuber yield, specific gravity of tuber, dry matter content, total starch content, acceptable tuber physical and frying quality with other desirable traits. Arslanoglu *et al*. (2011) reported the grouping of 146 local potato genotypes collected from the Eastern Black Sea region of Turkey and into 27 clusters that had higher mean values for desirable morphological traits including tuber shape, skin colour, eye colour, flesh colour, eye depth, skin texture, light sprout colour, growth habit, flower colour. Haydar *et al*. (2007); Mondal *et al*. (2007); Datta *et al*. (2015); Rangare and Rangare (2017) also reported that potato genotypes clusters constructed and that had higher mean values for desirable traits including tuber yield and quality traits.

Table 4. Mean values of eight clusters for 23 quantitative traits and six qualitative traits of 24 potato genotypes evaluated at Holetta in 2017

Quantitative and qualitative traits	Cluster I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	51.33	55.5	54.66	54.66	54.44	48	55.33	49
Days to maturity	96.59	96.95	89.47	89.47	90.56	92.67	106	106
Plant height (cm)	78.52	74.55	73.07	73.07	83.59	81.8	104.13	122.7
Average stems number	4.17	3.27	4.31	4.31	5.29	5.53	3.13	3.37
Leaf area index (cm-3)	2.55	2.94	2.22	2.22	2.17	2.45	2.39	2.33
Shoot dry mass weight (g/plant)	192	246.89	180.07	180.07	211.22	168.67	234.67	439
Tubers dry mass weight (g/plant)	771.34	922.28	832.73	832.73	742.78	917	595.67	715
Total biomass weight (g/plant)	963.33	1169.15	1012.8	1012.8	954	1085.7	830.3	1154
Average tuber number per hill	9.17	10.32	10.24	10.24	14.35	9.86	12.27	15.06
Average tuber weight (g/tuber)	77.12	79.14	60.59	60.59	44.38	71.49	47.71	40.75
Total tuber yield (t ha-1)	31.35	36.04	27.33	27.33	27.79	31.4	25.69	27.27
Marketable tuber yield (t ha-1)	28.93	32.5	24.97	24.97	25.16	30.03	23.54	23.58
Unmarketable tuber yield (t ha-1)	2.42	3.54	2.36	2.36	2.64	1.36	2.16	3.69
Small size tubers (%)	29.01	28.1	35.38	35.38	43.15	22.04	46.89	56.67
Medium size tubers (%)	34.37	37.19	46.77	46.77	41.61	51.59	42.13	34.38
Large size tubers (%)	36.62	34.71	17.86	17.86	15.24	26.38	10.98	8.95
Geometric mean diameter (mm3)	59.05	58.03	52.24	52.24	52.01	52.91	57.21	50.24
Sphericity of the tuber (%)	82.55	78.13	74.47	74.47	92.17	89.11	61.98	83.33
Surface area (mm2)	10971.75	10629.33	8630.6	8630.6	8502.67	8794	10287	7933
Length to width ratio	1.2	1.29	1.43	1.43	1.03	1.02	1.87	1.2

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Quantitative and qualitative traits		Cluster I	II	III	IV	V	VI	VII	VIII
Specific gravity of tubers (gcm-3)		1.08	1.09	1.08	1.08	1.08	1.1	1.08	1.1
Dry matter content (%)		20.36	22.32	21.25	21.25	20.28	24.33	20.25	25.75
Total starch content (g/100g)		14.14	15.89	14.94	14.94	14.07	17.68	14.05	18.95
Tuber shape	Compressed (%)	25	-	-	-	33.3	-	-	-
	Round (%)	-		-	-	66.7	100	-	-
	Ovate (%)	25	16.7	33.3	40	-	-	-	100
	Obovate (%)	25	16.7	66.7	-	-	-	-	-
	Elliptic (%)	25	16.7	-	60	-	-	100	-
	Oblong (%)	-	50	-	-	-	-	-	-
Eye depth	Shallow (%)	75	50	-	80	-	-	100	100
	Medium (%)	25	50	33.3	20	-	-	-	-
	Deep (%)	-	-	66.7	-	33.3	-	-	-
	Very deep (%)	-	-	-	-	66.7	100	-	-
Tuber skin colour	White-cream (%)	-	66.7	-	20	-	-	-	-
	Yellow (%)	25	16.7	-	80	-	-	-	--
	Brown (%)	50	16.7	-	-	-	-	-	-
	Pink (%)	25	-	33.3	-	33.3	-	100	100
	Red (%)	-	-	33.3	-	66.7	100	-	-
	Red-purple (%)	--	-	33.3	-	-	-	-	-
Tuber flesh colour	White (%)	25	66.7	33.3	20	66.7	-	-	100
	Cream (%)	75	16.7	33.3	40	33.3	100	-	-
	Bright yellow (%)	-	16.7	33.3	-	-	-	-	-
	Yellow (%)	-	-	-	40	-	-	100	-
Chips colour	White-cream (%)	25	-	33.3	40	-	100	100	-
	Light tan (%)	25	16.7	66.7	-	-	-	-	100
	Dark tan (%)	50	33.3	-	60	66.7	-	-	-
	Brown (%)	-	50	-	-	33.3	-	-	-
French fries' colour	White-cream (%)	25	16.7	100	40	-	100	100	-
	Light tan (%)	50	50	-	-	-	-	-	100
	Dark tan (%)	25	33.3	-	60	66.7	-	-	-
	Brown (%)	-	-	-	-	33.3	-	-	-

Principal Component Analysis of Exploration potato genotype Traits

In this study, principal component analysis (PCA) showed that the first eight principal components accounted for 90.26% of the total variation among 24 potato genotypes for the 23 quantitative and six qualitative traits (*Table 5*). This is because their eigenvalues were greater than 1 while factors having eigenvalue less than one were ignored following Gutten's lower bound principle (Kumar *et al*., 2011). Among principal components, the first, second

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and third accounted for 28.69%, 18.74% and 13.00% of the observed variation, respectively (*Table 5*).

The results of the principal component analysis showed that more than two traits with small contribution accounted for each principal component load and the total contribution of the PC to the variation observed among genotypes. The total contribution of the first three principal component axes was 60.43%. The cumulative contribution of PC1 was due to the individual contribution of leaf area index, average tuber weight, total tuber yield, marketable tuber yield, geometric mean diameter and surface area of tubers that was each greater than 0.25. Shoot dry mass weight, average tuber number per hill, tuber specific gravity, dry matter content, total starch content, plant height and tuber skin colour contributed more to PC2, while average stems number, large size tubers, sphericity of the tuber and tubers eye depth contributed most to PC3. This indicated that these traits had higher contributions to the total differentiation of the genotypes into clusters. Thus, selection efforts based on these traits including physical and frying quality may be more effective.

A similar trend in principal component analysis among potato genotypes has also been suggested by Mondal *et al*. (2007); Taheri *et al.* (2007) in potato genotypes. Nickmanesh and Davoud (2014) reported greater eigenvector values for tuber yield and tuber uniformity traits in the first and/or second principal components. Rabeai *et al*. (2008) also identified seven traits with three first major components in normal and drought stress condition.

Table 4: Eigenvalue, percentage, and cumulative variances of the first eight principal components for 23 quantitative and six qualitative traits in 24 potato genotypes evaluate at Holetta, in 2017

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to 50% flowering	0.074	0.073	-0.106	0.345	0.05	0.474	-0.177	-0.163
Days to 50% maturity	0.211	0.185	-0.16	-0.207	0.206	0.054	0.04	-0.15
Plant height (cm)	-0.002	0.286	-0.187	-0.261	0.173	-0.154	0.195	0.051
Average stems number	-0.231	0.116	0.258	0.025	-0.149	0.229	0.082	0.016
Leaf area index (cm^{-3})	0.282	-0.029	-0.011	0.048	0.081	0.131	0.006	-0.211
Shoot dry mass weight (g/plant)	0.157	0.27	-0.147	-0.053	0.232	-0.188	0.084	-0.174
Tubers dry weight (g/plant)	0.211	0.033	0.123	0.369	-0.178	-0.132	0.127	-0.036
Total biomass weight (g/plant)	0.248	0.155	0.032	0.281	-0.039	-0.198	0.144	-0.111
Average tuber number per hill	-0.046	0.309	-0.027	0.146	0.19	0.147	0.293	0.313
Average tuber weight (g/tuber)	0.252	-0.207	0.154	-0.081	-0.133	-0.035	-0.172	-0.05
Total tuber yield (t ha^{-1})	0.302	0.052	0.142	0.064	-0.023	0.115	0.121	0.253

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Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Marketable tuber yield (t ha^{-1})	0.295	0.042	0.169	0.042	-0.055	0.062	0.223	0.164
Unmarketable tuber yield (t ha^{-1})	0.161	0.063	-0.05	0.119	0.121	0.275	-0.37	0.478
Small size tubers (%)	-0.168	0.209	-0.275	0.086	0.222	-0.015	-0.151	-0.026
Medium size tubers (%)	-0.154	0.035	-0.029	0.233	-0.399	0.085	0.4	-0.062
Large size tubers (%)	0.225	-0.195	0.247	-0.2	0.032	-0.034	-0.093	0.056
Geometric mean diameter (mm^3)	0.258	-0.172	0.037	-0.097	0.198	0.16	0.209	0.001
Sphericity of the tuber (%)	-0.101	0.172	0.401	-0.1	0.106	0.017	-0.152	-0.169
Surface area (mm^2)	0.258	-0.177	0.038	-0.093	0.197	0.152	0.204	0.008
Length to width ratio	0.05	-0.149	-0.426	0.099	-0.066	0.063	0.207	0.191
Specific gravity of tubers (gcm^{-3})	0.191	0.284	-0.039	-0.046	-0.266	-0.132	-0.174	0.082
Dry matter content (%)	0.189	0.287	-0.039	-0.042	-0.257	-0.128	-0.187	0.075
Total starch content (g/100g)	0.189	0.288	-0.039	-0.042	-0.256	-0.127	-0.187	0.074
Tuber shape	0.166	-0.076	-0.269	0.268	0.012	0.045	-0.136	-0.443
Eye depth	-0.083	0.25	0.263	0.097	-0.024	0.265	-0.027	-0.209
Tuber skin colour	-0.027	0.289	0.061	-0.196	0.047	0.384	0.039	-0.043
Tuber flesh colour	-0.074	-0.15	-0.271	-0.074	-0.228	0.183	-0.187	0.211
Chips colour	-0.017	-0.06	0.123	0.387	0.346	-0.162	-0.245	0.095
French fries colour	-0.139	0.022	0.168	0.285	0.239	-0.284	0.05	0.234
Eigenvalue	8.32	5.43	3.77	2.37	2.22	1.64	1.35	1.08
Variances (%)	28.69	18.74	13	8.16	7.64	5.65	4.67	3.71
Cumulative variances (%)	28.69	47.43	60.43	68.59	76.23	81.88	86.54	90.26

CONCLUSION

The principal component analysis showed that the first eight principal components accounted for 90.26% of the observed variation among 24 potato genotypes for the twenty-nine qualitative and quantitative traits. The genetic distances of the 24 potato genotypes ranged from 3.40 to 11.80 with the mean, standard deviation and coefficient of variation having the values of 7.38, 1.75 and 23.69%, respectively. Analysis of the cluster mean for characters revealed the possibility of obtaining or developing varieties with highest total tuber yield, the specific gravity of tuber, high dry matter content, high total starch content, acceptable tuber physical and frying quality with other desirable traits for processing purpose and tuber yield through the selection of genotypes in Cluster II and VIII. Finally, the genetic diversity analysis could be helpful to select diverse parents and strengthen for future breeding programs of Ethiopia.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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