International Journal of Research Studies in Agricultural Sciences (IJRSAS)
Volume 7, Issue 8, 2021, PP 13-22
ISSN No. (Online) 2454–6224
DOI: http://dx.doi.org/10.20431/2454-6224.0708002
www.arcjournals.org

Genetic Diversity Studies for Tuber Yield and Yield Related Traits in Potato *(Solanum tuberosum* L.*)* Genotypes

Awoke Ali Zeleke*

Ethiopian Institute of Agricultural Research (EIAR), Kulumsa Agricultural Research Centre, Asela, Ethiopia

Corresponding Authors:** ***Awoke Ali Zeleke, *Ethiopian Institute of Agricultural Research (EIAR), Kulumsa Agricultural Research Centre, Asela, Ethiopia*

Abstract: *Genetic diversity is a pre request for successful breeding program. The study was conducted at Adet in 2018/19 under field condition in simple lattice design with three replication. The aim of the study was to identify genetically divergent potato genotypes having desired traits for further potato breeding activity. A total of 36 potato genotypes were evaluated for 18 quantitative traits in simple lattice design. The analysis of variance revealed that highly significant ($p < 0.001$) difference among the tested potato genotypes for all quantitative traits except stem number per hill. The studied 36 potato genotypes were grouped in to five distinct clusters. Cluster V was the largest cluster which consisted of eleven genotypes (30.56%) and cluster III comprise three genotypes (8.33%). Clusters I and IV having divergence distance can be used as a parent for further breeding or crossing. The highest and lowest intra cluster distance was observed in cluster III (4.97) and V (2.37) respectively. A total of six principal component with an Eigen value >1 accounted for 78.22% of the total variation in the studied potato genotypes.*

Keywords: *Cluster, Eigen value, Genetic diversity, Intra, Inter*

1. Introduction

Genetic diversity with respect to variability considered as an important factor as well as essential pre request for successful any crop improvement programs for obtaining high yielding progenies. Estimation of genetic diversity is an important tool that helps to know the source of genes for a particular trait within the available genotypes. Genetic diversity among the segregating population also helps to select suitable types as parents and also for commercial cultivation (Sattar *et al.,* 2011). Mostafa *et al.* (2011) also hypothesized that genetic diversity studies provides the understanding of genetic relationships among populations and hence directs assigning lines to specific heterogeneous groups useable in identification of parents and hence choice selection for hybridization or crop improvement program. The quantification of genetic diversity made it possible to select diverse parents for successful hybridization program.

Objectives

Hence, the present study was undertaken to identify genetically divergent potato genotypes having desired traits for further potato breeding activity

2. Materials and Methods

Description of the Study Area

The experiment was conducted at Adet Agricultural Research Center's experimental station in Northwestern Ethiopia. It is nearly 450 km away from Addis Ababa and 42 km from the Capital City of Amhara Regional State Bahir Dar. Geographically, it is located at $11^0$16'N latitude and $37^0$29'E longitude at an altitude of 2240 meter above sea level. The mean annual rain fall is 869 mm and the mean annual temperature is 18.56^{0}C (Ethiopian National Meteorological Agency Bahir Dar Branch, 2018). The soil type of the study area is Nitosol soil.

Experimental Design, Treatments and procedures

A total of 36 potato genotypes consisting of 33 advanced genotypes were introduced from International Potato Center (CIP) and three recently released potato varieties as standard checks were

used (Table 1). All of the 36 genotypes were planted at Adet Agricultural Research Center on station during the main cropping season in 2018/19. The genotypes arranged in simple lattice design with two replications and each gross plot were 3 m x 3 m = 9 m^2 consisting of four rows, which accommodated 10 plants per row and thus 40 plants per plot. The net plot size is 1.5 m x 2.4 m=3.6 m^2. The spacing between rows and plants were 0.75 m and 0.30 m, respectively. The spacing between plots and adjacent replications were 1 m and 1.5 m, respectively. The experimental field was cultivated to a depth of 25-30 cm by a tractor and ridges were made manually after leveling. The planting depth was maintained at 10-15 cm. Fertilizer application was made as per the specific recommendation for the location, in which NPS as a source of phosphorus was applied at a rate of 180 kg /ha and Urea as a source of nitrogen was applied at rate of 117 kg/ha. NPS was applied once during planting in the rows, while urea was applied in split application half at emergence and half at 50% flowering as a side dress application. All other agronomic practices such as weeding, cultivation and spraying Redomil chemical were kept uniform for all treatments in each plot. The two middle rows were used for data collection.

Table1. *list of potato genotypes and accession code*

No.	Accession code	No.	Accession code	No.	Accession code	No.	Accession code
1	CIP-308517.501	10	CIP-308530.501	19	CIP-308511.507	28	CIP-308499.501
2	CIP-308527.501	11	CIP-308525.01	20	CIP-308499.001	29	CIP-308530.002
3	CIP-308510.03	12	CIP-308500.01	21	CIP-308482.506	30	CIP-308523.500
4	CIP-308985.01	13	CIP-308522.503	22	CIP-308522.502	31	CIP-308482.504
5	CIP-308526.502	14	CIP-308527.502	23	CIP-308518.001	32	CIP-308516.501
6	CIP-3038522.504	15	CIP-395077.120	24	CIP-308487.500	33	CIP-308482.505
7	CIP-308517.500	16	CIP-308511.508	25	CIP-308516.500	34	Gudanie (CIP-386423.13)
8	CIP-308526.501	17	CIP-308522.501	26	CIP-308532.500	35	Belete (CIP-393371.58)
9	CIP-308499.502	18	CIP-308485.002	27	CIP-308522.500	36	Dagim (CIP-396004.337)

All genotypes was introduced from CIP (International Potato Center) & the released varieties were from Adet Agricultural Research Center

Data Collection

The Data were collected on phenological, growth parameters, tuber yields and yield related traits, tuber quality traits and late blight severity percentage.

Tuber quality attributes was calculated as follows:

Tuber dry matter content (TDMC) (%): Five fresh tubers were randomly taken from each plot, washed, weighed and sliced at harvest, dried for seven days under sun and finally in oven at 75^{o}c for 72 hours until a constant weight attained and dry matter percent calculated according to (William and Woodbury, 1968).

$$\text{Dry matter} = \frac{\text{weight of sample after drying(g)}}{\text{initial fresh weight of sample(g)}} * 100$$

Specific gravity of tubers (SG): was determined by the weight in air and in water method. Five kg tuber of all shapes and sizes were randomly taken from each plot. The tubers were washed with water. Then after the sample were first weighed in air and then re-weighed suspended in water. Specific gravity was calculated according to (Kleinkopf *et al*., 1987) formula.

$$\text{Specific gravity} = \frac{\text{Weight in air}}{\text{Weight in air} - \text{Weight in water}}$$

Starch (%): The percentage of starch was calculated from the specific gravity as follows:

Starch (%) =17.546 + 199.07 × (SG-1.0988) (Talburt and Smith, 1959). Specific gravity (SG) was determined as indicated above by the weight in air and weight in water method.

Total soluble solids (^{0}Brix): The Brix of the raw potato samples was determined using a method as described by Pardo *et al.* (2000) using hand refractometer. The Brix was measured in the juice obtained after washing, crushing and extracting juice of the tuber samples.

Disease data: Assessment of severity of late blight under field conditions in percent was recorded on a plot basis taking into account the number of plants developing disease symptoms in a leaf and/or many leaves and plants free from disease following the procedures of Henfling (1987).

3. Statistical Data Analysis

Analysis of Variance

The collected data were subjected to analysis of variance (ANOVA) for Simple Lattice by SAS computer software (9.0). Duncan Multiple Range Test (DMRT) was used to compare means at 5% and 1% level of significance.

Cluster analysis and genetic divergence

Cluster analysis is one of the most common and efficient methods of multivariate statistical analysis for grouping genotypes. Clustering of genotypes was performed using SAS proc cluster procedure (SAS, 2002). Square statistics (D^2) developed by Mahalanobis, (1936) was used to cluster genotypes into different groups. Genetic divergence was determined using the generalized Mahalanobis's (D^2) statistics as follows:

$D^2ij = (Xi - Xj)\ S^{-1}(Xi-Xj)$

Where: D^2ij = the distance between two groups i and j, Xi and Xj = the two vectors mean i^{th} and j^{th} accessions respectively, S^{-1}= is the inverse of the pooled divergence matrix.

The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi- square (x^2) and were tested for significance at (1% and 5%) probability levels against the tabulated value of (x^2) for 'P' degree of freedom, where P is the number of parameters considered (Singh and Chaudhary, 1985). Cubic clustering criteria (CCC), Pseudo F statistic and pseudo t^2 statistic generated by SAS were examined to decide the number of optimum clusters. Average intra and inter cluster D^2 values were estimated using the formula given by Singh and Chaudhary (1985), $\sum \frac{D^2 i}{n}$ where, $\sum D_i^2$ is the sum of distance between all possible combinations (n) of the genotypes included in a cluster. Square of intra-cluster distance = $\sum Di^2$ / n and Square of inter-cluster distance = $\sum Di^2$ / ninj Where; $\sum Di^2$ = Sum of distance between all possible combinations, ni = number of genotypes in cluster i and nj = number of genotypes in cluster j.

Principal Component Analysis

Principal component analysis (PCA) was computed to find out the characters, which accounted more to the total variation. The data were standardized to mean zero and variance of one before computing principal component analysis. The principal component based on correlation matrix was calculated using proc princomp procedure in SAS software. According to Gutten's lower bound principle that eigenvalues <1 should be ignored (Kumar *et al*., 2011).

4. Results and Discussions

Analysis of variance

The result of Analysis of variance showed that there is highly significant ($p \leq 0.001$) difference among the tested potato genotypes for all traits except stem number per hill (Table 2). The findings on variance for tuber yield and its components indicates the existence of substantial amount of variability for most of the traits in experimental material studied. This provides an opportunity for a breeder to select best genotypes for their better tuber yield and other yield related traits. Addisu *et al*., 2013; Rahman, 2015; Getachew *et al*., 2016; Ebrahim *et al.*, 2017 so many authors reported the existence of significant variation among potato genotypes for different traits.

Table2. *Analysis of variance for 18 traits at Adet Agricultural Research center in 2018/19 in simple lattice design*

Traits	Mean	Rep **(1)**	Genotype **(35)**	Error **(35)**	CV	R^2	LSD
DE	15.74	0.68	13.56**	0.42	4.12	0.98	1.34
DF	48.13	3.13	11.48**	1.43	2.48	0.93	2.46
DM	93.46	23.4	48.74**	1.89	1.47	0.98	2.83
SN	5.12	3.92	2.3ns	1.66	25.15	0.74	2.67
PH	66.84	83.2	131**	2.24	7.3	0.85	10.32
LAI	3.76	2.68	0.97**	0.14	10.12	0.88	0.82
MTNPH	8.70	11.14	16.98**	2.66	18.84	0.87	3.18
UMTNPH	2.90	0.80	2.2*	1.05	35.78	0.68	2.07
TTNPH	11.6	17.91	13.81**	2.24	13	0.91	3.09
ATW	78.13	926.08	618.4**	179.26	17.14	0.78	27.3
MTY	29.28	0.13	195.1**	13.02	12.32	0.94	6.97
UMTY	3.08	0.36	4.36**	1.63	41.2	0.73	2.66
TTY	32.36	0.05	206.7**	12.30	10.81	0.94	6.95
DMC	23.03	2.12	14.89*	6.98	11.47	0.68	5.78
SG	1.14	0.0058	0.0034*	0.00185	3.77	0.66	0.09
STA	28.88	134.4	130.3**	38.68	21.53	0.78	12.51
TSS	3.91	6.69	0.84**	0.30	13.97	0.77	1.26
LB	59.58	50.0	1191.8**	17.86	7.09	0.98	8.49

Note: DE- Days to 50% emergence, DF- days to 50% flowering, DM- days to maturity, PH –plant height in cm, SN-stem number per hill, LAI- leaf area index, MTNPH- marketable tuber number per hill/ plant, UMTNPH- un marketable tuber number per hill/plant, TTNPH- total tuber number per hill/plant, ATW-average tuber weight (g/tuber), MTY-marketable tuber yield (t/ha), UMTY-un marketable tuber yield (t/ha), TTY total tuber yield (t/ha), DMC- dry matter content (%), SG-specific gravity, STA starch percentage (g/100g), TSS- total soluble solid (^{0} brix), LB-late blight severity percentage (%),CV- coefficient of variation, R^2 - coefficient of determination

Genetic Divergence Analysis

Clustering of genotypes

The distribution of 36 potato genotype were grouped into five (5) distinct clusters (Table 3). This indicated the presence of diversity among the tested genotypes. Cluster V was the largest cluster which consisted of 11 genotypes (30.56%), followed by cluster II and IV consisted of 8 genotypes (22.22%), cluster I consisted of 6 genotypes (16.67%), cluster III consisted three genotypes (8.33) (Table 9). Many authors reported the presence of diversity among potato genotypes classifying in different number of distinct clusters. Mondal *et al.* (2007) studied genetic diversity of 31 potato genotypes (parents and their hybrid progenies) the diversity was determined using multivariate analysis and the genotypes grouped into five different clusters. The maximum numbers of genotypes were included in clusters II and V. Cluster V had maximum and cluster I had minimum intra-cluster distance. Nasiruddin (2017) studied 31 potato genotypes and detected in to five clusters according to cluster analysis in which cluster IV had the maximum number of genotypes (each containing 11 genotypes). The lowest number of genotypes (only two) had in cluster I. Rangare (2017) evaluated 44 potato genotypes and grouped in to five distinct clusters in which cluster III consists of maximum number of (16) genotypes and cluster I consist of minimum (2) potato genotypes. Rahman (2015) evaluated 21 potato genotypes and grouped into five highly divergent clusters on the basis of D^2 values. The clusters divergence was proved by the high inter- cluster and low intra clusters D^2 values.

Table3. *Distribution of 36 potato genotypes in to different cluster groups*

Clusters	**No. genotypes**	**Percentage (%)**	**Genotypes & CIP code**
I	6	16.67%	CIP-308517.501, CIP-308527.502, CIP-308526.502, CIP-308517.500, CIP-308500.01, Gudanie (CIP-386423.13)

II	8	22.22%	CIP-308527.501, CIP308530.501, CIP-308525.01, CIP-308522.503, CIP-308487.500, CIP308499.5 01, CIP-308523.500, Dagim (CIP 396004.337)
III	3	8.33%	CIP-308510.03, CIP308526.501, CIP-308522.501
IV	8	22.22%	CIP-308985.01, CIP-308511.507, CIP-308499.001, CIP-308532.500, CIP-308522.500, CIP-308482.504, CIP-308482.505, CIP-308530.002
V	11	30.56%	CIP-308511.508, CIP-395077.120, CIP-308499.502, CIP-308485.002, CIP-308516.501, CIP-308482.506, CIP-308522.502, CIP-308518.001, CIP-308516.500, CIP-3038522.504, Belete (CIP-393371.58)

Cluster mean analysis

The mean values of five clusters across 18 tuber yield and yield related traits of 36 potato genotypes are listed below in Table 4. The cluster mean values revealed considerable differences among the clusters for different characters. Genotypes in cluster I and III require the longest (18.54 and 17.94) days to 50% emergence while genotypes in cluster V took the shortest days (13.73) to 50% emergence respectively. Genotype grouped in cluster III (51.14) and I (50.06) take the highest days to attain 50% flowering while genotypes in cluster II take minimum (46.92) days to 50% flowering. Genotypes in cluster III (99.89) require maximum days to maturity and genotype in cluster II require minimum (88.44) days to maturity.

The highest plant height was recorded from genotypes included in cluster III (72.69) and I (69.28) while the lower plant height was measured from genotypes grouped in cluster II (64.29).The maximum stem number per hill was obtained from genotypes grouped in cluster I (6.13 and V (5.87) and minimum stem number per hill was obtained in cluster III (3.73).The highest leaf area index was measured from genotypes included in cluster IV(4.31) while the lowest leaf area index was measured from genotype grouped in cluster II (3.44) and III (3.48).

The maximum marketable tuber number per hill was obtained from genotype grouped in cluster I (13.02) followed by cluster III (9.265). Genotypes in cluster IV gave (6.34) minimum marketable tuber number per hill. Maximum unmarketable tuber number per hill was obtained from genotypes in cluster V (4.13) and minimum unmarketable tuber number per hill was obtained in genotypes included in cluster I (2.02). Genotypes in cluster I and V gave (15.08 and 13.42) maximum total tuber number per hill, and genotypes in cluster IV gave (8.83) minimum total tuber number per hill respectively.

The highest average tuber weight was measured from genotypes grouped in cluster III (101.92) followed by IV (88.50) and the lowest average tuber weight was measured from genotypes grouped in cluster I (62.53).Genotypes grouped in cluster III and I gave higher marketable tuber yield (41.11 and 39.00 respectively), while genotype grouped in cluster II gave (19.36) lower marketable tuber yield. Unmarketable tuber yield had higher mean value from genotypes grouped in cluster V (4.73) and lower in genotypes grouped in cluster I (2.04).The higher total tuber yield per hectare was obtained from genotype grouped in cluster III (44.83) followed by I (41.04) while the lower total tuber yield per hectare was obtained from genotype included in cluster II (21.18).

Higher tuber dry matter percentage was measured from genotypes grouped in cluster III (26.54) and lower tuber dry matter percentage was measured from genotypes grouped in cluster V and IV (22.04 and 22.25 respectively).Maximum specific gravity was recorded from genotypes grouped in cluster III (1.20) and minimum specific gravity was recorded from genotypes group in cluster IV (1.10).

Genotypes grouped in cluster III measure higher tuber starch percentage (38.83) followed by cluster II (34.22) while genotypes grouped in cluster IV (18.73) gave lower tuber starch percentage. Total soluble solid had higher mean value from genotypes grouped in cluster III (4.60) and lower mean value from genotypes grouped in cluster IV (3.67).Late blight severity percentage was higher on genotypes grouped in cluster II (84.69) followed by IV (70) and lower on genotypes in cluster III (30).

According to the cluster mean analysis of characters, developing varieties for tuber yield through selection and further evaluation of genotypes from Cluster I and III is possible to obtain genotypes with highest total tuber yield, specific gravity of tuber, dry mater content and total starch content with other desirable traits. Ebrahim *et al.* (2017) reported the grouping of 24 potato genotypes in to eight cluster that had highest total tuber yield, specific gravity of tuber, dry mater content, total starch content, acceptable tuber physical and frying quality and other desirable traits. 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.

Table4. *Mean values of five clusters for 18 characters in 36 potato genotypes*

Clusters					
Traits	**I**	**II**	**III**	**IV**	**V**
DE	18.54	15.47	17.94	15.82	13.73
DF	50.06	46.92	51.14	47.99	47.23
DM	96.67	88.44	99.89	94.34	92.96
PH	69.28	64.29	72.69	65.66	66.62
SN	6.13	4.56	3.73	4.43	5.87
LAI	3.83	3.44	3.48	4.31	3.62
MTNPH	13.02	7.08	9.26	6.34	8.96
UMTNPH	2.02	2.10	2.50	2.65	4.13
TTNPH	15.08	9.17	10.85	8.83	13.42
ATW	65.98	62.53	101.92	88.50	82.08
MTY	39.00	19.36	41.11	24.01	31.80
UMTY	2.04	2.08	2.40	2.94	4.73
TTY	41.04	21.18	44.83	26.95	36.52
DMC	23.87	23.22	26.54	22.25	22.04
SG	1.15	1.15	1.20	1.10	1.15
STA	28.90	34.22	38.83	18.73	29.68
TSS	4.25	3.85	4.60	3.67	3.78
LB	45.42	84.69	30.00	70.00	49.55

Note: DF- Days to 50% emergence, DF- days to 50% flowering, DM- days to maturity, PH –plant height in cm, LAI- leaf area index, MTNPH- marketable tuber number per hill/ plant, UTNPH- unmarketable tuber number per hill/plant, TTNPH- total tuber number per hill/plant, ATW-average tuber weight (g/tuber), MTY-marketable tuber yield (t/ha), UMTY-un marketable tuber yield (t/ha), TTY- total tuber yield (t/ha),DMC-dry matter content (%), SG-specific gravity, STA-starch content percentage TSS-total soluble solid, LB-late blight severity percentage (%)

Estimation of inter and intra cluster distance

The results of both inter and intra cluster of 36 potato genotypes for their 18 characters are listed in Table 5 below. The maximum inter cluster distance was obtained between cluster I and IV (69.72) followed by II and V (67.33), I and II (61.98) while minimum inter cluster distance was found between cluster II and III (32.40) followed by II and IV (38.41).Genotypes belongs to cluster I and IV were genetically diversified and it can be used for crossing purpose. The highest intra cluster distance was observed in cluster III (4.97) followed by cluster I (3.58) indicated that genotypes grouped in this clusters are most diverse than other genotypes while the lowest intra cluster value was observed in cluster V (2.37).

Rahman (2015) reported the intra and inter clusters D^2 values among 21 genotypes revealed that cluster II and V showed minimum intra cluster D^2 value (0.00) distance followed by cluster III (14.03), whereas, maximum intra cluster D^2 value (19.04) was shown by cluster IV followed by cluster I (18.70) indicated that genotypes included in this cluster are very diverse and was due to both

natural and artificial selection forces among the genotypes. Minimum inter cluster D^2 value was observed between the clusters IV and V (21.44) indicated close relationship among the genotypes included in these clusters. Maximum inter clusters D^2 value was observed between the clusters I and V (57.13) indicated that the genotypes belongings to these groups were genetically most divergent.

Verma and Singh (2016) studied 44 potato genotypes and grouped them into 11 distinct clusters and reported that the maximum intra and inter cluster distance was noticed in cluster IX (1.931) and between cluster IV and IX (6.514), respectively. Mishara (2016) evaluated 25 potato genotypes and grouped in to four clusters then he reported the highest intra cluster distance was observed in cluster IV (2.610) and lowest in cluster II (2.226). However, the maximum inter-cluster divergence was observed between the clusters I and II (5.243) and the minimum inter-cluster distance was observed in between cluster I and IV (3.000).

Table5. *Intra (bold diagonal) and Inter cluster distance (off bold)*

Cluster	I	II	III	IV	V
I	**3.58**	61.98	48.29	69.72	39.11
II		**3.01**	32.40	38.41	67.33
III			**4.97**	57.39	58.35
IV				**3.01**	57.26
V					**2.37**

Principal Component Analysis for Quantitative Traits

The principal component analysis of 18 traits among 36 potato genotypes is described in Table 6 below. From the total of 18 principal components extracted, the first six PC's with an Eigen value >1 accounted for 78.22% of the total variation and the first, second and third PC's with an eigenvalue (5.4, 2.8 and 2.2) accounted (30.06%, 45.58% and 57.88%) of the total variability among the studied 36 potato genotypes respectively. The first six components were retained in analysis because eigen values are >1. The others factors having eigenvalue < 1 were ignored. These were ignored due to Gutten's lower bound principle that eigenvalues <1 should be ignored (Kumar *et al*., 2011). 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 57.88%.

The PC- 1 showed positive factor loading for most traits except leaf area index, unmarketable tuber number and yield (t/ha), and late blight severity percentage and The cumulative contribution of PC1 was due to the contribution (>0.25) of days to maturity , marketable and total tuber number per hill, marketable and total tuber yield per hectare. 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 dry matter content percentage, specific gravity and starch content percentage may be more effective.

PC- 2 indicated positive loading factor for plant height, stem number per hill, unmarketable and total tuber number per hill, average tuber weight, marketable tuber yield, un marketable tuber yield and total tuber yield. Stem number per hill, unmarketable tuber number per hill and un marketable tuber yield per hectare contributed (>0.25) to PC 2 more than other traits.

Traits contributed positive factor loading to PC-3 are days to maturity, plant height, un marketable tuber number per hill, un marketable and total tuber yield, average tuber weight, dry matter content percentage specific gravity, starch content percentage and total soluble solid. Average tuber weight, dry matter content percentage, specific gravity and starch content percentage was greatly contributed (>0.25) to PC 3 than other traits.

PC-4 showed positive factor loading for stem number per hill, marketable and total tuber number per hill, specific gravity, starch content percentage, total soluble solid, and late blight severity percentage. Traits such as stem number per hill specific gravity and starch content percentage was accounted positive (>0.25) to PC 4 than other traits.

PC-5 showed a positive factor loading for Days to 50 % emergence, days to 50% flowering, unmarketable and total tuber number per hill, un marketable tuber yield, starch content percentage, total soluble solid and late blight severity percentage. Days to 50 % emergence and flowering, un marketable tuber number per hill and un marketable tuber yield per hectare was accounted positive (>0.25) to PC 5 than other traits.

Mostafa *et al.* (2011) reported that the PCA analysis had Eigen values up to 1.0 presenting cumulative variance of 80.1%. Principal component one (PC1) with eigenvalue of 3.82 contributing 38.3% of the total variability, PC2 eigenvalue of 2.79 accounted for 28 % of the total variability and PC 3 had eigenvalue of 1.38 contributed to 13.8% of the total variability observed among the 22 potato cultivars. Ghebreslassie *et al.* (2017) studied 21 potato genotypes and reported that based on the initial Eigen value ≥ 1 scored the PCA analysis indicated that the first four components explained about 85% of the total variability among the studied materials.PCA1 with eigenvalue of 6.0 contributed 37.50% of variation, PCA 2 had eigenvalue of 3.85 accounted 24.08% of variation,PCA3 with eigenvalue of 2.37 contributed to 14.08% of variation and PCA4 with an eigenvalue of 1.32 accounted 8.25% of the total variation among the observed 21 potato genotypes. Ebrahim et al. (2017) also reported 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. Of these, the first, the second and the third principal components constituted 28.69%, 18.74% and 13.00% of the variation respectively.

Table6. *Eigenvectors, Eigenvalues, proportion and cumulative percentage of variation explained by five principal components (PCs) for morphological and tuber yield characters of 36 potato genotypes tested at Adet Agricultural Research Center in 2018/2019 cropping season*

Eigen vector					
Traits	**PC 1**	**PC 2**	**PC 3**	**PC 4**	**PC 5**
DE	0.087	-0.351	-0.045	-0.106	0.544
DF	0.173	-0.237	-0.017	-0.143	0.548
DM	0.328	-0.047	0.081	-0.235	-0.116
PH	0.211	0.073	0.095	-0.074	-0.033
SN	0.121	0.253	-0.294	0.324	-0.138
LAI	-0.004	-0.039	-0.163	-0.348	-0.322
MTNPH	0.343	-0.061	-0.354	0.110	-0.028
UMTNPH	-0.004	0.515	0.125	-0.002	0.302
TTNPH	0.317	0.159	-0.342	0.166	0.092
ATW	0.107	0.163	0.498	-0.311	-0.092
MTY	0.417	0.033	-0.011	-0.042	-0.076
UMTY	-0.028	0.492	0.152	-0.061	0.324
TTY	0.413	0.106	0.024	-0.056	-0.014
DMC	0.143	-0.237	0.316	-0.044	-0.203
SG	0.130	-0.067	0.323	0.502	-0.025
STA	0.072	-0.102	0.337	0.521	0.021
TSS	0.175	-0.288	0.100	0.048	0.043
LB	-0.383	-0.136	-0.110	0.097	0.054
Eigen value	5.412	2.793	2.214	2.110	1.550
Proportion	30.06	15.52	12.30	11.72	8.61
Comulative	**30.06**	**45.58**	**57.88**	**69.60**	**78.22**

5. Conclusions And Recommendations

Conclusions

The research results indicated the presence of wide variations among potato genotypes for tuber yield and yield related traits. The D^2 value both inter and intra cluster distance also an indicator of wide genetic diversity among genotypes. The maximum inter cluster distance was obtained between cluster I and IV (69.72) while minimum inter cluster distance was found between cluster II and III (32.40). The highest intra cluster distance was observed in cluster III (4.97) while the lowest intra cluster value was observed in cluster V (2.37). Genotypes grouped in cluster I and III gave maximum marketable and total tuber yield t ha^{-1}. Genotype CIP-308522.501, CIP-308526.502, CIP-308517.500, CIP-308500.01 and CIP-308626.501 gave higher total tuber yield t ha^{-1} and less late blight severity percentage than the released potato varieties. The studied 36 potato genotypes were grouped into five

(5) distinct clusters. Cluster V was the largest cluster which consisted of eleven genotypes (30.56%) while cluster III was the lowest consisted of three genotypes (8.33%). A total of six Principal component with an Eigen value ≥1 accounted for 78.22% of the total variation among the studied 36 potato genotypes.

Recommendations

It can be recommended that intercrossing among the genotype belonging to genetically diverse clusters (I and IV) and showing superior mean performance might prove beneficial for obtaining desirable sergeants in the coming generation. Most of the advance potato genotypes gave higher total tuber yield t ha^{-1} and less late blight severity percentage than the released varieties.

ACKNOWLEDGMENT

The first author acknowledges Adet Agricultural Research Center for giving the tested potato genotypes and supported in the field from planting to harvesting period. The authors also would like to express their special gratitude and warm appreciation to Ethiopian Institute of Agricultural Research (EIAR) for fully financing the study.

REFERENCES

[1] Addisu Fekadu, Yohannes Petros and Habtamu Zelleke. 2013. Genetic variability and association between agronomic characters in some potato *(Solanum tuberosum L.)* genotypes in SNNPRS, Ethiopia. International Journal of Biodiversity and Conservation 5(8): 523-528.

[2] Anamika Verma and Dhirendra Singh.2016 Assessment of genetic diversity and association among agro-morphological characters in potato *(Solanum tuberosum L.).* Department of Vegetable Science, College of Agriculture, G. B. Pant University of Agriculture and Technology, Pantnagar -263145, India,50 (4) : 345-349.

[3] Ebrahim S., Wasu, M. and Tesfaye, A. 2018. *Genetic Variability in Potato (Solanum tuberosum L. Genotypes for Tuber Quality, Yield and Yield Related Traits at Holetta, Central Highlands of Ethiopia*. (MSc.Thesis, Haramaya University).

[4] Ethiopian National Metrological Agency of Bahir Dar Branch.2018.

[5] Getachew Asefa, Wassu Mohammed and Tesfaye Abebe. 2016. *Genetic variability studies in potato (Solanum tuberosum L.) genotypes in Bale highlands, South Eastern Ethiopia*. Journal of Biology, Agriculture and Healthcare, 6(3): 117- 119.

[6] Ghebreslassie, B.M., Tadesse, M., Kasili, R.W. and Githiri, S.M. 2017. Morphological diversity of farmers' and improved potato *(Solanum tuberosum)* cultivars growing in Eritrea.

[7] Heinfnings, J.W.1987. Late blight of potato *(Phytophthora infestans)* Technical information. Lima,Peru, Bulletin 4,22 pp.

[8] Kleinkopf, G.E., Westermann, D.T., Wille, M.J. and Kleinschmidt, G.D.1987.Specific gravity of Russet Burbank potatoes. American potato journal, 64(11), pp.579-587.

[9] Kumar, V., Kato, N., Urabe, Y., Takahashi, A., Muroyama, R., Hosono, N., Otsuka M., Tateishi, R., Omata, M., Nakagawa, H., and Koike, K. 2011. Genome-wide association study identifies a susceptibility locus for HCV- induced hepatocellulare carcinoma. *Natural genetics*, 43(5), p.455.

[10] Mahalanobis, P.C.1936. On the generalized distance in statistics. Proc. Natl. Sci. India B., 2: 49-55.

[11] Mishra, S., 2016. *Genetic variability and character association for yield and its attributing traits in potato (Solanum tuberosum L.).* (Doctoral dissertation, Indira Gandhi Krishi Vishwavidyalya, Raipur).

[12] Mondal, M.A.A., Hossain, M.M., Rasul, M.G. and Uddin, M.S. 2007. Genetic diversity in potato *(Solanum tuberosum L.).* Bangladesh Journal of Botany, 36(2): 121-125.

[13] Mostafa K., Mohammad, H. and Mohammad, M. 2011. Genetic diversity of wheat genotype based on cluster and principal component analyses for breeding strategies. Australian Jour. of Crop Sc. 5 (1): 17-24.

[14] Nasiruddin.M, FM Ali Haydar and AKM Rafiul Islam.201**7.** Genetic diversity in potato *(Solanum tuberosum L.)* genotypes grown in Bangladesh. International Research Journal of Biological Science, Department of botany, University of Rajshahi, Bagladish.Vol.6 (11) 1-8.

[15] Pardo, J.E., Alvarruiz, A., Perez, J.I., Gomez, R. and Varon, R. 2000. Physical-chemical and sensory quality evaluation of potato varieties (*Solanum tuberosum L.).* Journal of Food Quality, 23 (2), pp.149-160.

[16] Rahman, M.H., 2015. *Character association and genetic diversity of potato (Solanum tuberosum L.).*Department of genetics and plant breeding Sher-E-Bangla Agricultural University Dhaka -1207, (MSc. Thesis),Bangladesh.

[17] Rangare, S.B. and Rangare, N.R. 2017. Classificatory analysis of potato *(Solanum tuberosum L.)* Genotypes for yield and yield attributing traits. The Pharma Innovation, 6 (9, Part B), p.94.

[18] SAS Institute Inc. 2002. *Statistical analysis Software version* 9.0. Cary, NC: SAS Institute Inc., USA.

[19] Sattar, M.A., Uddin, M.Z., Islam, M.R., Bhuiyan, M.K.R. and Rahman, M.S., 2011. Genetic divergence in potato (Solanum tuberosum L.). *Bangladesh Journal of Agricultural Research*, *36*(1), pp.165-172.

[20] Talburt, W.F., Smith, O. 1959. Potato Processing; Ed. Westport C. T. The Avi Publishing

[21] William, M.A. and G.W. Woodbury.1968. Specific gravity dry matter relationship and reducing sugar changes affected by potato variety, production area and storage. American Journal of Potato Research, 45 (4): 119-131.

Citation: *Awoke Ali Zeleke, (2021). "Genetic Diversity Studies for Tuber Yield and Yield Related Traits in Potato (Solanum tuberosum L.) Genotypes", International Journal of Research Studies in Agricultural Sciences (IJRSAS), 7(8), pp. 13-22 DOI: http://dx.doi.org/10.20431/2454-6224.0708002*