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Genetic diversity in drought tolerant Potato (*Solanum tuberosum* L.) genotypes in Simada, North western Ethiopia

Berhan Gashaw[1*], Mohammed Wassu [2] and Abebe Tesfaye[3]

[1] *Amhara Agricultural Research Institute, Sirinka Agricultural Research Center, Woldia, Ethiopia*
[2] *Haramaya University, School of plant science, Dire Dawa, Ethiopia*
[3]*Amhara Agricultural Research Institute, Adet Agricultural Research Center, Bahir Dar, Ethiopia*

**Corresponding author: berhanegashaw@yahoo.com*

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Abstract: Developing drought tolerant potato varieties is one of the research priorities in Ethiopia. To this end, 100 drought tolerant potato genotypes were introduced to the country. Estimation of genetic diversity is a key in the process of variety development. This research was conducted at Simada research site of Adet Agricultural Research Center in 2016 main rain season to determine genetic diversity among 105 potato genotypes towards of which five were checks. The experiment was carried out in Augmented design and data were generated for 20 traits. Mean squares of the analysis of variance showed highly significant ($P \leq 0.01$) differences among genotypes for all traits except for plant height, small and medium size tubers percentage this indicating 17 traits used for further genetic diversity analysis. Genetic distances of genotypes measure by Euclidean distance was ranged from 1.11 to 12.60 and Unweighted Pair-group Method with Arithmetic means (UPGMA) formed dendrogram in which grouped potato genotypes in to 20 distinct clusters. The genotypes grouped in different clusters characterized by one or more desirable traits resulted wide range of intra and inter clusters average genetic distances suggested the higher chance of developing varieties through direct selection or crossing of genotypes to produce heterotic hybrids.

Keywords: Augment design, Drought, Euclidean distance and Genetic diversity

Introduction

Potato (*Solanum tuberosum* L.) is the leading horticultural crops in the mid and high lands of Ethiopia with production of over 3.66 million Mt from an area of over 296,578 hectares of land (CSA, 2016). In this area it provides food, employment, and

income as a cash crop (Scott *et al*., 2000) and helps in food security while contributing to a better land use ratio by raising the aggregate efficiency of agricultural production systems (Gastelo *et al*., 2014). In hectare base potato provide more dry matter and protein than most cereal crops (Harris, 1992). Moreover, it is an excellent source of carbohydrates as compared to cereals. It is good source of phosphorus, potassium, calcium, iron and vitamins, and especially vitamin C (Horton, 1987). Therefore, the crop has high potential to secure food and nutrition in developing countries such as Ethiopia.

The value of germplasm is determined by its genetic diversity, availability, and utility in which, potato stands out among all other crops (Bamberg and Del Rio, 2005). Earliest forms of cultivated potato and their wild relatives provide diverse source of genetic variation, which could be a foundation of various traits for potato improvement. This variation gave broad adaptation of agro ecological regimes. They are equally diverse in morphological traits (Hanneman, 1989).

Potato breeding aims to develop potential varieties that make sure highest and stable production in a diverse environmental condition. As stated by Mondal (2003) genetic divergence analysis estimates the degree of diversity existed among selected genotypes. In addition, genetic diversity is studied to identify specific parents for wider genetic variation and being heterosis when they are crossed. Knowing the nature and degree of genetic diversity of being hybridized helps the breeder in choosing the distant parents for purposeful hybridization (Samsuddin, 1985).

Hybridization provides a chance to combine the desirable traits from two or more lines into a single genotype. The effectiveness, however, depends on the genetic divergence among the lines being hybridized. The more the divergence, the more the chances of developing superior yielding genotypes. However, in Ethiopia such genetic information is lacking, because no attempt has made on genetic diversity of drought tolerant potato genotypes in moisture stress areas of the country. Getachew *et al*. (2016) indicated the absence of creating variability through crossing in the country as a result of this introduction and evaluating variability of genotypes introduced abroad is necessary for wide adaptability across regions in the country. Therefore, the study was conducted to estimate the genetic diversity of potato genotypes developed for moisture stress areas for tuber yield and yield related traits.

Materials and Methods

Description of the Experimental Site

The experiment was carried out at Adet Agricultural Research Center, Simada trial site in 2016/17 main rain season. Simada is located in Amhara National Regional State South Gondar Administrative Zone, 770 km North of Addis Ababa and 105 km

South East of Debrtabor. The study site is located at 110 21' 0" N latitude and 38 0 25' 0" E longitudes and at an altitude of 2407 meter above sea level and has red brown Nitosol soil type. It has annual mean temperature of 16.80C, maximum monthly mean temperature 23.30C and minimum monthly mean temperature 10.30C. The experimental site receives mean annual rainfall of 838.7mm which is abundant enough of but show erratic distribution Table 1.

3.2. Treatments, Experimental Design and Field management

Hundred potato genotypes developed for moisture stress (drought prone) areas of the world by International Potato Center (CIP) from Peru and as standard check four released potato varieties (Belete, Gera, Shenkolla and Guassa) in Ethiopia and one farmer's cultivar (local) were included in the trail. The lists of genotypes and checks are given in Table 2. The field trial was arranged in Augmented Block design with 5 blocks. Each block contained 20 genotypes and 5 checks. The genotypes were appeared once, whereas the checks were planted at each block. First 20 genotypes were assigned for each block randomly and then the genotypes plus checks were randomized to each experimental plot separately in a block.

Medium size (35-45 mm diameter) and vigour sprouted potato tubers were planted first week of July at spacing of 75 and 30 cm between rows and plants, respectively, in a gross plot size of 2.25m2 (0.75 m x 3 m) which accommodate 10 plants. Agronomic practiced were done at the appropriate time to facilitate root, stolon and tuber growth for the crop. Before two weeks of harvesting as the crop attained maturity (yellowing of stems and senescence of leaves) dehullming was done to thicken the tubers.

Table1 - Mean monthly weather condition of the experimental site in 2016.

S, No	Month	Rainfall (mm)	Maximum T (°C)	Minimum T (°C)
1	Jan	0.0	25	NA
2	Feb	0.0	27	NA
3	Mar	17.8	28.2	12
4	Apr	43.7	26.9	11.8
5	May	129.2	24.3	11.8
6	Jun	108.0	24.2	10.7
7	Jul	291.3	20.2	10.5
8	Aug	205.1	20.4	10.4
9	Sep	43.6	13.5	4.9
		Total 838.7		

Source: Ethiopian Meteorological Agency Bahir Dar branch. NA=not available

Table 2 - List of potato genotypes used in the experiment

No.	Accession code	No.	Accession code	No.	Accession code	No.	Accession code
1	16SET5.1	26	11SET3.3	51	24SET5.9	76	F30.4
2	16SET5.2	27	11SET3.4	52	19SET7.1	77	F 16.1
3	16SET5.3	28	11SET3.5	53	19SET7.2	78	F16.2
4	16SET5.4	29	11SET3.6	54	19SET7.3	79	F16.3
5	16SET5.5	30	11SET3.7	55	19SET7.4	80	F26.1
6	16SET5.6	31	11SET3.8	56	5SET6.1	81	F26.2
7	16SET5.7	32	25SET6.1	57	5SET6.2	82	F29.1
8	16SET5.8	33	25SET6.2	58	5SET6.3	83	F29.2
9	16SET5.9	34	25SET6.3	59	5SET6.4	84	F29.3
10	16SET5.10	35	25SET6.4	60	5SET6.5	85	F10.1
11	16SET5.11	36	25SET6.5	61	2SET8.1	86	F10.2
12	16SET5.12	37	25SET6.6	62	2SET8.2	87	F14.1
13	20SET4.1	38	22SET7.1	63	2SET8.3	88	F14.2
14	20SET4.2	39	22SET7.2	64	3SET6.1	89	F14.3
15	20SET4.3	40	22SET7.3	65	3SET6.2	90	F22.1
16	20SET4.4	41	22SET7.4	66	23SET3.1	91	F22.2
17	20SET4.5	42	22SET7.5	67	23SET3.2	92	28SET6.1
18	20SET4.6	43	24SET5.1	68	4SET8.1	93	28SET6.2
19	20SET4.7	44	24SET5.2	69	4SET8.2	94	F18
20	20SET4.8	45	24SET5.3	70	4SET8.3	95	F20
21	20SET4.9	46	24SET5.4	71	27SET7.1	96	F28
22	20SET4.10	47	24SET5.5	72	27SET7.2	97	F23
23	20SET4.11	48	24SET5.6	73	F30.1	98	F24
24	11SET3.1	49	24SET5.7	74	F30.2	99	F15
25	11SET3.2	50	24SET5.8	75	F30.3	100	F21.1

Standard Check: Belete, Shenkolla, Guassa, Gera and Local

Data Collection

Phenology parameters (days to emergence, days to 50% flowering and physiological maturity) were collected from the entire plots. Leaf area, plant height and stem number per plant were collected from five plants randomly taken from the central plants and the average value was considered per plant basis. Tuber size distribution (very small < 20g, small 20 to < 39 g, medium 39-75g, and large >75 g according to Lung'aho *et al*. (2007) and other yield and yield components were measured from the net plot.

Bulking rate (g day-1): Was calculated as total weight of tubers harvested from net plot divided by number of days taken from days to 50% flowering to physiological maturity (CIP, 2014).

Tuber dry matter content (%): Representative clean and unpeeled tubers were chopped into small pieces and about 200g chopped fresh samples were dried by 80OC for about 72 hours to a constant weight at regular intervals. The percent of dry matter was calculated according to CIP (2007) as:

Dry matter (%) = (Weight of sample after drying (g))/(Initial weight of sample (g)) x100%

Specific gravity of tubers: Five kg of all size representative tubers randomly taken from the bulk of total tuber yield. Specific gravity was computed as the proportion of weight in air to weight in air minus weight in water method (Kleinkopf and Wassermann, 1987).

Total starch content (g/100g): Starch content in percent was computed from specific gravity as established by Talburt and Smith (1959) as cited by Yildrim and Tokuşoğlu, (2005) as: Starch content (%) = 17.546 + 199.07 × (specific gravity-1.0988), where specific gravity was comes from weight in air and weight in water method.

Data Analysis

Analysis of Variance

The analysis of variance was computed by using the Statistical package for augmented design (SPAD) software (Abhishek *et al*., 2010). Means that differ significantly were separated using critical difference and genetic distance was analysed using STATISTICA-7 basic statistical analysis software (StatSoft Revision, 2002.). All traits were considered for further genetic diversity analysis for which mean squares of accessions are significant.

Genetic divergence and clustering

Genetic distance of 105 potato genotypes was estimated using Euclidean distance (ED). Euclidean distance (ED) was calculated from the collected quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Sneath and Sokal (1973) as follows:

$$EDjk = \sqrt{\sum_{i=1}^{n} (Xij - Xik)^2}$$

EDjk = distance between genotypes *j* and *k*; *xij* and *xik* = quantitative traits mean values of the ith trait for genotypes *j* and *k*, respectively; and n= number of traits. Euclidean distance was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic means (UPGMA). Dendrogram helps clustering of genotypes based on genetic distance matrix. In addition, mean average distance (ED) was calculated for each genotype by averaging the distance of a particular potato genotype over the other 104 genotypes. The calculated average distance was used to estimate which potato genotype is closest or distant to the others.

Results

Analysis of Variance

Analysis of variance (ANOVA) of 17 quantitative traits for the 105 potato genotypes is presented in Table 3. The analysis of variance revealed the presence of highly significant ($P<0.01$) differences among genotypes for all traits except plant height, small and medium size tubers. In separate comparison of tests vs controls the analysis of variance showed significant ($P<0.05$) differences for all the traits except for unmarketable tuber yield and very small size tuber in percent. It was also revealed significant ($P<0.05$) differences among controls (check varieties) for all traits except for plant height, average tuber weight, small and large size tubers proportion in percent. It was also observed significant differences among tests (new entries) for all traits except for plant height, small and medium size tubers.

Genetic Divergence and Clustering

Estimation of Euclidean distance and Clustering of Genotypes

Genetic distances of 105 potato genotypes were estimated by using Euclidean distance (ED). The ED of 5460 pair of genotypes is difficult to show in table. The ED of 5460 pair of genotypes ranged from 1.11 between Belete and Shenkolla and

12.59 between 19SET7.1 and 3SET6.1. The overall mean ED was 6.106 with 1.565 and 25.6% standard deviation (SD) and coefficient of variation, respectively. Among pairs of genotypes, 1 and 9 pairs had ED of <1.106 and >11.449, respectively. Other 5, 122 and 720 pair of genotypes had ED that ranged from 1.106 to 2.255, 2.256 to 3.404 and 3.405 to 4.553, respectively, while 1511, 1521 and 903 pairs had ED that ranged from 4.554 to 5.702, 5.703 to 6.851 and 6.852 to 8.000, correspondingly. The remaining 453 pairs had 8.0001 to 9.150 ED, 164 pairs had ED ranged from 9.151 to 10.299 and 51 pairs of genotypes had ED of 10.300 to 11.448 (Figure 1).

The highest average Euclidean distance was calculated for 19SET7.1 (9.11) and other 13 genotypes had mean ED that ranged from 7.09 to 8.60 to others. This indicated that these genotypes were most distant from others. On the other hand, the local check cultivar (4.86) followed by 20SET4.7 (4.89) were the most closest to other genotypes with low mean ED. Other two genotypes 16SET5.4 and 1SET3.3 also had mean ED of 4.94 and 4.98, respectively. The remaining 87 genotypes had mean ED 5 to 7 (near to mean ED of genotypes) Table 3.

Clustering of genotypes was conducted using Unweighted Pair-Group Method with Arithmetic means (UPGMA) method based on Euclidean distance (ED) matrices. The dendrograms from cluster analysis at cut point of 5 (means ED of genotypes minus standard deviation) resulted in grouping 105 potato genotypes into 20 different clusters (Figure 2). The number of genotypes with their list in each cluster is given in Table 4. Distribution of the genotypes revealed that the maximum genotypes grouped in Cluster XIV (14) shared 13.33% followed by Cluster X and XII each comprised 12 genotypes and sharing 11.43% of the total number of genotypes. On the other hand, Cluster III, XVII, XVIII and XX each contained single genotype in which they share 3.8% of the total distribution. Other four Clusters viz Cluster IV, IX, XIII, and XIX each comprised 2 genotypes constitute of 7.62% of the total distribution. Cluster VI, VIII and Cluster VII and XI contained 7(6.67%) and 8 (7.62%) genotypes respectively while Custer II and I had 11(10.46) and 5 (4.76%) genotypes respectively.

Cluster Mean Analysis

The mean values of 17 quantitative traits in each cluster are given in Table 5. Cluster XIX took 75 days to mature which was consider as early mature followed by cluster IV (81.5) and XI (83.72), whereas late maturing groups were cluster V, IX and XV with 103.6, 101.8 and 97 days, respectively.

Among clusters, Cluster XII, XVIII and XX revealed maximum mean values for most quantitative traits. Maximum cluster mean value for tuber yield per plant (0.92 kg), marketable tuber yield (32.5 ton ha^{-1}), total tuber yield (35.05 ton ha^{-1}) and tuber bulking rate (169.37 g/day) found in Cluster XII. In addition Cluster XII was

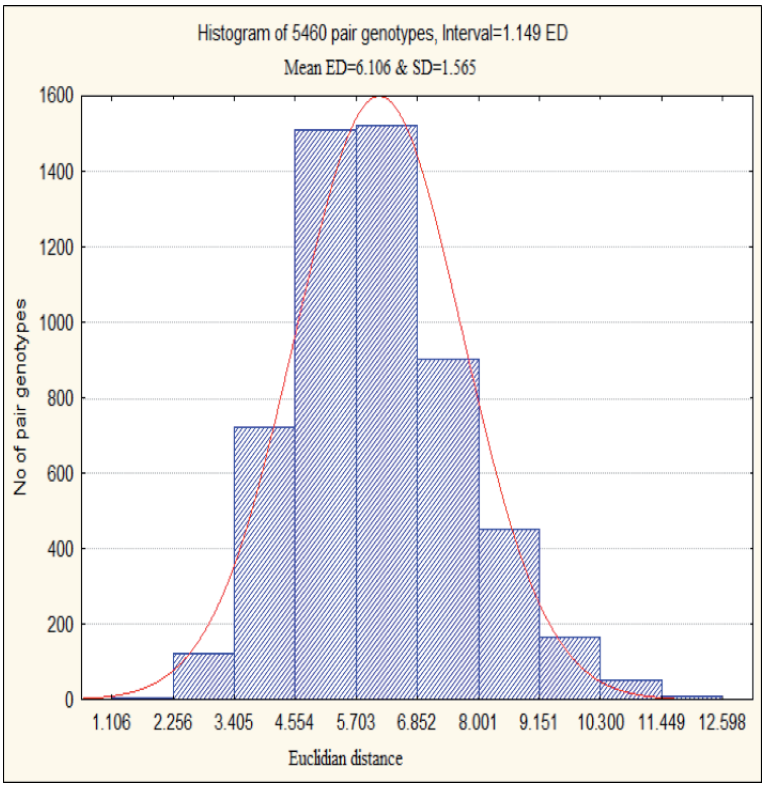

Figure 1 - 5460 pair of genotypes distribution with interval of 1.149 ED (Euclidean distance), 6.106 mean Euclidean distances, and SD (standard deviation) of 1.565.

among the highest for mean value of average tuber weight (0.52 gm), and large tuber size percent (22.78). Cluster XVIII recorded the highest for leaf area (15 cm^2), and it was also among the highest clusters for marketable tuber yield (28.6 ton ha^{-1}), total tuber yield (32.5. ton ha^{-1}) and bulking rate (154.46 g/day). For tuber number per plant (39) and very small size tuber percept (59) the highest mean value was obtained in Cluster XX. Cluster XX also had high mean value for tuber yield per plant (0.86kg) and total tuber yield (32.3. ton ha^{-1}).

Cluster XVI had the lowest mean value for tuber yield per plant (0.3 kg), average tuber weight (19.14 g), and large tuber size percent (1.32). The lowest mean value for marketable yield (14.3 ton ha^{-1}) and total tuber yield (16 ton ha^{-1}) were found in Cluster XV. Cluster XV was also low in bulking rate (85.67g/day).

Table 3 - Mean squares and their significance for 17 traits of 105 potato genotypes evaluated at Simada during 2016.

	Mean squares						
	Block (4)	Treatment (104)	Among control (4)	Among tests (99)	Tests vs control (1)	Error	CV (%)
DE	1.36	6.67**	17.96**	5.29**	98.57**	0.76	5.64
DF	1.76	21.2**	33.56**	19.99**	90.74**	1.51	2.19
DM	51.24	44.62**	15.94*	41.25**	492.03**	3.49	2.02
LA	0.5	2.21**	2.69**	2.01*	19.11**	0.37	4.48
SNP	0.16	2.21**	1.86**	2.15**	9.21**	0.25	12.11
TNP	1.28	24.86**	10.05**	42.57**	61.99**	0.59	4.92
TYP	0.002	0.04**	0.015**	0.037**	0.04*	0.003	9.02
AVT	19.1	149.54**	24.53NS	152.46**	360.15**	12.75	9.18
MKY	6.97	27.94**	11.47*	28.72**	16.83*	2.57	6.76
UMY	0.04	1.9**	2.87**	1.86**	0.19NS	0.16	16.63
TY	6.66	27.08**	17.07**	27.55**	20.66**	2.12	5.56
BRP	1234.61	1264.29**	879.84**	1238.92**	5313.81**	107.91	7.79
VSP	74.51	137.5**	299.77**	132.06**	26.19NS	37.02	18.59
LTP	5.65	77.47**	11.71NS	80.87**	3.23NS	8.95	20.6
DMC	0.41	8.68**	2.72*	7.96**	103.73**	0.81	3.47
SG	0.00007	0.00081**	0.0004*	0.00074**	0.01**	0.00008	0.83
TSC	2.77	32.21**	14.04*	29.26**	396.61**	3.17	13.61

*and**=significant at P<0.05 and P<0.01, respectively. NS=Non-significant, DE= days to emergence, DF=days to 50% of plants flowering, DM=days to 90% maturity, LA=leaf area (cm^2), STN=stem number per plant, TNP=tuber number per plant, TYP=tuber yield per plant(kg), AVT=average tuber weight(gm), MKY=marketable tuber yield (ton ha^{-1}), UMK=unmarketable tuber yield (ton ha^{-1}), TY=Total tuber yield (ton ha^{-1}), BRP=bulking rate per plot(g/day),VSP=very small size tubers percentage, LTP=large size tubers percentage, DMC=tuber dry matter content (%), SG=specific gravity of tuber, TSC= total starch content (gm/100gm), CV (%) = coefficient of variation in percent.

Cluster XVII showed the highest value for all tuber quality parameters, dry matter (31.28%), and specific gravity (1.114) and among the highest for total starch content (20.55%). In addition, Cluster III had high tuber dry matter (30.78%), specific gravity (1.114) and the highest for total starch content (20.66%). In contrary, cluster XIX revealed the lowest in dry matter (19.8), specific gravity (1.04) and total starch content (5.38). Specific gravity was also low in cluster XIV and XVIII 1.04 for each.

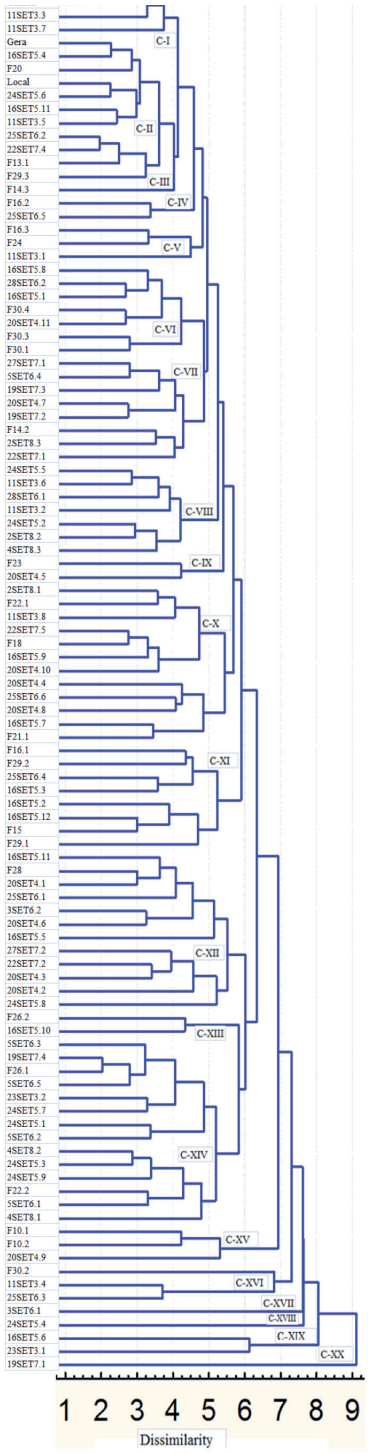

Figure 2. Dendrograms from UPGMA Clustering of 105 potato genotypes from 17 agromorphology traits at cut point 5 Euclidean distances

Table 4 - Distribution of genotypes in to 20 clusters based on Euclidean distance of 105 potato genotypes tested at Simada 2016.

Cluster	Accession	No	Cluster	Accession	No	Cluster	Accession	No	Cluster	Accession	No
C-I (5)	BELETE	1	C-VII (8)	27SET7.1	1	C-XI (8)	F16.1	1	C-XIV	5SET6.2	8
	GUASSA	2		5SET6.4	2		F29.2	2	Continued	4SET8.2	9
	SHENKOLLA	3		19SET7.3	3		25SET6.4	3		24SET5.3	10
	11SET3.3	4		20SET4.7	4		16SET5.3	4		24SET5.9	11
	11SET3.7	5		19SET7.2	5		16SET5.2	5		F22.2	12
C-II (11)	Gera	1		F14.2	6		16SET5.12	6		5SET6.1	13
	16SET5.4	2		2SET8.3	7		F15	7		4SET8.1	14
	F20	3		22SET7.1	8		F29.1	8	C-XV (3)	F10.1	1
	LOCAL	4	C-VIII (7)	24SET5.5	1	C-XII (12)	16SET5.11	1		F10.2	2
	24SET5.6	5		11SET3.6	2		F28	2		20SET4.9	3
	16SET5.11	6		28SET6.1	3		20SET4.1	3	C-XVI (3)	F30.2	1
	11SET3.5	7		11SET3.2	4		25SET6.1	4		11SET3.4	2
	25SET6.2	8		24SET5.2	5		3SET6.2	5		25SET6.3	3
	22SET7.4	9		2SET8.2	6		20SET4.6	6	C-XVII (1)	3SET6.1	1
	F13.1	10		4SET8.3	7		16SET5.5	7	C-XVIII (1)	24SET5.4	1
	F29.3	11	C-IX (2)	F23	1		27SET7.2	8	C-XIX (2)	16SET5.6	1
C-III (1)	F14.3	1		20SET4.5	2		22SET7.2	9		23SET3.1	2
C-IV (2)	F16.2	1	C-X (12)	2SET8.1	1		20SET4.3	10	C-XX (1)	19SET7.1	1
	25SET6.5	2		F22.1	2		20SET4.2	11			
C-V (3)	F16.3	1		11SET3.8	3		24SET5.8	12			
	F24	2		22SET7.5	4	C-XIII (2)	F26.2	1			
	11SET3.1	3		F18	5		16SET5.10	2			
C-VI (7)	16SET5.8	1		16SET5.9	6	C-XIV (14)	5SET6.3	1			
	28SET6.2	2		20SET4.10	7		19SET7.4	2			
	16SET5.1	3		20SET4.4	8		F26.1	3			
	F30.4	4		25SET6.6	9		5SET6.5	4			
	20SET4.11	5		20SET4.8	10		23SET3.2	5			
	F30.3	6		16SET5.7	11		24SET5.7	6			
	F30.1	7		F21.1	12		24SET5.1	7			

Table 5. Mean value of 17 quantitative traits of the 20 clusters for 105 potato genotypes tested at Simada 2016.

	Clusters																			
Traits	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
DE	13.59	14.96	14.48	13.9	14.95	16.5	18.41	17.65	17.98	14.15	13.83	15.33	13.4	16.9	16.9	18.21	21.48	19.5	14.1	14.70
DF	56.79	55.94	53.08	52.3	54.41	57	57.98	53.91	63.98	54.55	54.03	53.6	56.8	56.9	61.6	59.15	64.08	55.1	39.7	53.90
DM	95.42	93.31	90.24	81.5	103.6	86.7	94.07	94.41	101.8	93.34	83.72	90.62	89.5	90.2	97	95.04	92.24	92.2	75.00	88.00
LA	14.31	12.65	13.96	13.2	13.44	12.6	14.02	14.21	13.73	13.13	11.6	14.02	11.5	14.9	10.8	12.1	13.37	15.7	13.7	13.50
SNP	3.31	4.776	5.58	3.99	5.503	4.55	3.068	3.136	3.2	4.993	6.964	4.522	4.09	3.47	2.7	3.627	2.45	2.45	4.65	5.43
TNP	15.75	14.43	12.22	11.1	19.2	15.3	15.62	11.72	12.5	21.4	19.34	16.1	9.71	13.9	8.2	19.64	9.12	14.8	17.0	39.00
TYP	0.576	0.561	0.44	0.49	0.567	0.39	0.456	0.601	0.59	0.645	0.669	0.92	0.69	0.68	0.36	0.3	0.5	0.82	0.44	0.86
AVT	35.86	38.52	37.76	44.7	30.67	28.6	31.92	52.78	43.01	28.18	33.38	52.44	63.1	47.7	48.6	19.14	67.77	50.7	24.7	20.00
MY	22.94	23.06	18.35	21.3	21.27	19.9	19.00	25.53	26.87	23.44	23.99	32.57	25.6	26.1	14.3	17.75	24.69	28.6	17.2	22.90
UMY	3.178	1.554	1.68	0.91	2.703	2.61	2.79	1.12	1.675	3.814	2.423	2.486	0.92	2.08	1.73	3.84	1.08	3.86	2.84	9.42
TY	26.12	24.62	20.03	22.2	23.98	22.5	21.79	26.65	28.55	27.25	26.41	35.05	26.5	28.1	16	21.59	25.78	32.5	20.00	32.30
BRP	135.9	144.3	134.9	133	159.3	116	158.1	179.2	116.9	182	157.5	176.9	140	163	104	100.3	170	355	177.0	151.0
VSP	38.56	25.85	16.03	15.4	34.72	44.4	40.95	23.17	24.52	46.38	30.03	20.28	24	30.2	34	49.75	20.26	38.2	48.70	59.00
LTP	14.18	12.04	13.28	18.6	17.96	8.57	7.857	24.45	16.03	7.028	6.682	22.78	37.5	19.6	22.2	1.322	17.55	20.2	6.26	2.57
DM	27.48	27.02	30.78	23.6	24.14	24.8	28.38	27.82	24.22	26.62	25.69	25.81	24.1	22.1	24.6	28.56	31.28	22.2	19.80	24.80
SG	1.094	1.082	1.114	1.07	1.072	1.06	1.096	1.093	1.067	1.078	1.075	1.079	1.07	1.04	1.06	1.086	1.114	1.04	1.04	1.05
TSC	16.58	14.22	20.66	11	12.18	9.48	17.06	16.46	11.21	13.35	12.9	13.59	11	5.52	9.3	14.93	20.55	6.47	5.38	8.23

DF=days to 50% of plants flower, DM=days to 90%maturity, LA=leaf area (cm^2), SNP=stem number per plant, TNP=tuber number per plant, TYP=tuber yield per plant(kg), AVT=average tuber weight (gm), MKY=marketable tuber yield (ton ha^{-1}) UMK=unmarketable tuber yield (ton ha^{-1}), TY=Total tuber yield (ton ha^{-1}), BRP=bulking rate per plot(g/day),VSP=very small tuber percentage, LTP=large tuber percentage, DM=tuber dry matter content(%), SG=specific gravity of tuber, TSC= total starch content (gm/100 gm).

Table 6 - Minimum, maximum and mean genetic distance of within and with other clusters.

	Within clusters					With other clusters				
Cluster	Mean	SD	CV (%)	Min	Max	Mean	SD	CV (%)	Min	Max
I(5)	5.27	0.19	3.75	4.98	5.52	5.91	0.71	12.01	5.22	7.19
II(11)	5.18	0.26	4.98	4.89	5.81	5.87	0.98	16.69	5.22	7.14
III(1)						6.32	0.56	8.86	5.65	7.61
IV(2)	5.76	0.07	1.34	5.7	5.81	6.15	0.64	10.41	5.47	7.43
V(3)	5.67	0.21	3.78	5.47	5.9	6.1	0.68	11.15	5.43	7.38
VI(7)	5.69	0.37	6.49	5.22	6.3	6.11	0.67	10.96	5.44	7.39
VII(8)	5.8	0.6	10.42	4.89	6.74	6.16	0.63	10.23	5.49	7.45
VIII(7)	5.79	0.43	7.47	5.13	6.26	6.16	0.63	10.23	5.48	7.45
IX(2)	6.05	0.06	0.97	6	6.09	6.28	0.57	9.07	5.62	7.57
X(12)	6.08	0.33	5.46	5.61	6.81	6.29	0.56	8.90	5.63	7.59
XI(8)	6.32	0.52	8.3	5.4	6.96	6.41	0.57	8.89	5.75	7.71
XII(12)	6.51	0.67	10.33	5.68	7.68	6.5	0.6	9.23	5.85	7.81
XIII(2)	6.58	0.96	14.57	5.9	7.25	6.54	0.62	9.48	5.88	7.84
XIV(14)	6.12	0.66	10.8	5.04	7.18	6.32	0.56	8.86	5.65	7.61
XV(3)	7.02	0.55	7.8	6.4	7.42	6.74	0.75	11.12	6.1	8.06
XVI(3)	7.38	0.63	8.51	6.74	7.99	6.91	0.88	12.74	6.28	8.24
XVII(1)						7.09	1.06	14.95	6.47	8.43
XVIII(1)						7.06	1.02	14.45	6.44	8.39
XIX(2)	8.04	0.8	9.97	7.47	8.6	7.23	1.23	17.01	6.61	8.57
XX(1)						7.73	1.94	25.09	7.14	8.57

Min, Max=minimum and maximum Euclidean distance, SD= standard deviation, CV= coefficient of variation.

Intra and Inter Clusters Genetic Distance

The average intra and inter cluster distances was presented in Table 6. The five clusters viz. XIX, XVI, XV, XIII and XII contained genotypes that had higher mean genetic distance than the overall mean Euclidean distance of genotypes ranged from 6.51 to 8.04. The members of these clusters and the three genotypes constructed solitary Cluster XVII, XVIII and XX had >6.49 mean inter cluster genetic distance

with other clusters members which was greater than the overall mean Euclidean distance of genotypes.

Cluster II which contained 11 genotypes had lowest mean genetic distances of 5.18 and 5.87 intra and inter clusters, respectively, followed by Cluster I consisted of five genotypes with 5.27 and 5.91 genetic distances of intra and inter clusters, respectively. In Cluster I, 3 out of 5 genotypes were standard check and in Cluster II, 2 out of 11 genotypes were checks including local variety in which their cluster mean genetic distances were lowest.

Discussion

Variation was observed among the tested 105 drought tolerant potato genotypes. The ANOVA revealed significant differences for 17 out of 20 tested traits. The considerable differences among genotypes tells the presence of adequate variations that allow applying selection breeding to obtain high yielding variety which combine other desirable traits to improve the yield of potato in the study area. Inline to these results, Khayatnezhad *et al.* (2011) reported significant differences among 10 potato genotypes for main stem per plant, tuber number per plant, average tuber weight, tuber yield per plant, tuber yield, dry matter content, starch content, and big tubers proportion as percentage. Addisu; *et al.* (2013) reported the presence of significant differences among nine regional and national released varieties for phenological traits, number of stem per plant, tuber number per plant, tuber yield and big tubers proportion as percentage. Abraham *et al.* (2014) also found highly significant difference for all phenological traits, stem per plant, tuber yield, tuber per plant, and big tubers proportion as percentage. Wassu and Simret (2015) evaluated 26 potato genotypes at Dire Dawa tolerant to heat stress and reported significant differences among genotypes for tuber yield, yield related traits and tuber dry matter content. Schafleitner *et al.* (2007) study revealed that drought tolerance variation in S. tuberosum and S. tuberosum hybrids. In yield and yield attributes potato genotypes showed significant difference and some genotypes exhibit relatively lower yield loss and less drought susceptibility index under drought condition which implies their tolerance to drought (Luitel *et al.*, 2015).

Significant differences among genotypes for all traits except plant height, small and medium size tubers as present (Table 3) justify using 17 traits for further genetic distance analysis. Estimation of Euclidean distance resulted 5460 pairs of genotypes ranged from 1.11 – 12.59 ED. The distribution of pairs of genotypes resulted normally distributed graph which was resulted by plus or minus standard deviation from over all mean to the left and right, respectively. The result indicated that potato genotypes had wide range of genetic distances though all were developed as tolerant to drought stress. This will allow breeders to select genotypes for character (s) of interest in

addition to tolerant to drought.

Unweighted Pair-Group Method with Arithmetic means (UPGMA) grouped 20 distinct clusters. Among the cluster analysis methods UPGMA provide more accurate grouping information on breeding materials than the other clusters (Aremu et al., 2007). The high number of clusters indicated that the presence of wide genetic diversity among the tested genotypes. The clusters and genotypes in each cluster had diverse traits that can be used for improvement. Among clusters, Cluster XII, XVIII and XX revealed maximum mean values for most quantitative traits. For instance, for tuber yield per plant, marketable tuber yield, total tuber yield, tuber bulking rate, average tuber weight, large tuber size percent, leaf area, tuber number per plant and tuber yield per plant. Hence, those clusters showing superior mean performance could be used for hybridization in order to obtain desirable segregants in the coming generation.

The mean genetic distances of genotypes within each cluster and each cluster members with other 19 clusters were calculated to understand which cluster was containing diverse genotypes and which cluster members were distant from other genotypes in other clusters. The result showed that the members of the five clusters (XIX, XVI, XV, XIII and XII) were more diverse among them and more distant to other genotypes in other clusters while the genotypes that constructed the three solitary clusters (XVII, XVIII and XX) were distant from other genotypes. This suggested the crossing of the members of these cluster among them and with other genotypes in other clusters might produce heterotic progenies. Crosses involving parents belonging to the most divergent clusters would be expected to noticeable maximum heterosis and wide variability in genetic architecture (Singh *et al*., 1987).

Cluster I and II which contained most of the checks including local variety had the lowest genetic distance. This indicating that the checks and the genotypes grouped in these clusters was less divergent. As a result of this, crossing of genotypes among these clusters members may not rewarding in obtaining heterotic hybrids.

In general the mean inter cluster genetic distance was greater than the intra cluster genetic distance for all clusters indicating that considerable amount of genetic diversity existed between genotypes of different groups. This result is in accordance with results of Haydar *et al*. (2009) who studied on 30 potato genotypes and grouped into five clusters and he stated inter-cluster distance exceed intra-cluster distances. Panigrahi *et al*. (2014) set 19 genotypes into seven clusters and reported inter cluster distance were greater than the intra cluster distance. In the composition of clusters higher inter-cluster distances were the main cause of heterogeneity (Datta *et al*., 2015). Mondal *et al*. (2007) studied genetic diversity on 31 potato genotypes and stated intra cluster distance was being much lower than the inter cluster one, suggested, heterogeneous and homogeneous nature between and within groups, respectively.

Conclusion

Genetic diversity is the base for the improvement of crops in which the availability of more diverse materials indicates the chance of getting desirable genes to improve the crops. Hence, creating variability or studying the magnitude of genetic diversity of the germplasm or population is a base for improvement. The study results showed that the genotypes were diverse with significant variations among them for agromorphology traits. The current study results showed that the presence of exploitable genetic diversity among the introduced drought tolerant genotypes in which crossing of distant genotypes with desirable traits to develop varieties for the study area and similar agro-ecology with similar potato production constraints of the country.

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