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Estimation of Genetic Distance among Potato (*Solanum tuberosum* L.) Crosses in Ethiopia

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ABSTRACT

In Ethiopia, there is very little effort has been carried in determining on genetic information of potato crosses. This study was conducted to determine the genetic distance among 81 potato clones. Parents with their hybrid offspring were evaluated for 18 traits in a 9 x 9 simple lattice design and their genetic diversity was determined using multivariate analysis. The Euclidean distances estimates showed that the genetic distances ranged from 1.57 to 14.35 cM with a mean of 5.77. Cluster analysis revealed that the parents and offspring were grouped into sixteen clusters. The maximum number of clones were grouped in cluster V followed by cluster I with 15 clones and cluster VI with 13 clones. Cluster mean analysis showed a wide range of variation for several characters among single as well as multi-genotypic clusters. Clones produced from biparental crosses of *Jalene* with *Aterababa* and *Belete* with *Aterababa* showed high inter and intra cluster distance than *Shenkola* with *Gera* crosses. The first four principal components accounted for 72.7% of the total variations; where principal component analysis 1and 2 with values of 33.8% and 16.6%, respectively, which contributed to 50% of total variations. Total yield per hectare, tuber yield per plant, marketable tuber yield and stem height had much contribution to the principal component analysis. The current study suggests the higher chance of developing genetically distant clones through local crossing to produce heterotic hybrids. Considering diversity pattern, parents should be selected from I, II, X, XI and XII clusters to improve potato crop.

Keywords: Attitudes; Biparental crosses, Clustering, Euclidean distance, Principal Component Analysis

INTRODUCTION

Potato (*Solanum tuberosum L.*) is the fourth most economically important food crop after wheat, rice, and maize in the world. It is highly heterozygous and has complex tetrasomic inheritance that results in increased number of progeny classes (Muthoni et al., 2015) and makes it difficult to understand the inheritance of traits and implement in a hybridization program.

Potato hybridization is a highly effective means of increasing productivity in a sustainable and environmentally safe way. Hybridization provides a chance to combine the desirable traits from two or more lines into a single clone. Potato population improvement through local crossing not only capture essential genetic resources and move desired traits along variety development pipelines but also help to assure the creation of broad genetic base or distance and dynamic gene pool (Bonierbale et al., 2020).

Genetic distance measures based on morphological traits are one of the main multi-variate techniques that are used to provide criteria for choosing parents. The genetic distance found between clones could be increased by heterosis in the crossing program (Humphreys, 1991). The existence of genetic distance in a particular trait between crosses is also an important prerequisite for its heritable improvement. Genetic distance analysis can estimate the degree of diversity found in clones that generated from crossing (Reddy et al., 2018).

The divergent parents can give more chances to maximize heterozygosity, broaden the genetic base and produce heterotic progenies (Sun et al., 2003). A narrow genetic base would result in inbreeding depression as result of accumulation of deleterious alleles in a population (Gopal, 2014). High level of genetic diversity among potato genotypes possessing different desirable traits is also important for its improvement. However, in Ethiopia, generating potato clones through crossing and investigating genetic diversity on these crosses

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is very limited due to much dependence on introduced materials especially through international potato center (Getachew et al., 2016). Hence, knowing the nature and degree of genetic diversity of hybridized clones helps the breeder in choosing the distant parents for purposeful hybridization and variety development (Shamsuddin, 1985). Therefore, this study was conducted to determine genetic distance or diversity among potato progenies obtained from local crossing and their parental varieties for different agro-morphological traits.

MATERIALS AND METHODS

Description of the Study Site:

The experiment was conducted at Adet Agricultural Research Station during the main growing season in 2018. Adet Agricultural Research Center is located at longitudes ranging from 37° 28’ 38’’ to 37° 29’ 50’’ E and latitudes ranging from 11° 16’ 19’’ to 11° 17’ 28’’ N in the northern highlands of Ethiopia with an average altitude of 2240 meters above sea level (Andualem et al., 2013). The mean annual rainfall during the growing season was 1432 mm with the average minimum and maximum temperatures of 10.81 to 25.55℃.

Experimental Material and Design:

A total of 81 genetic materials which consisted of 75 clones that were generated from crossing of Ethiopian potato varieties by Adet Agricultural Research Center, five parental varieties’ and one latest improved *Dagim* variety were included in this experiment (Table 1). The experiment was laid out in a 9 x 9 simple lattice design. The well-sprouted potato tubers were planted at the spacing of 75 cm between rows and 30 cm between plants. Each clone was planted in a plot size of 1.5 m x 3m having two rows and twenty plants per plot. Fertilizer was applied following the standard recommendation of Adet Agricultural Research Center. All other required agronomic practices were applied as per the recommendation for the crop at the appropriate time.

Data Collection:

Observations were recorded and calculated on sixteen plants from each plot for 18 quantitative traits such as: days to emergency, days to flowering, days to maturity, main stem number, plant height, tuber number per plant, tuber yield per plant, very small tuber numbers, medium sized tubers, large sized tubers, tuber dry matter content, tuber starch content, tuber specific gravity, average tuber weight, marketable tuber number, marketable tuber yield, unmarketable yield, and total tuber yield.

Table 1: List of 75 clones and 5 parents with one standard check variety used in the experiment

Trt	Clones	Trt	Clones
1	J x A.277	42	J x A.23
2	B x A.153	43	J x A.27
3	J xA.296	44	Ge xSh.186
4	B x A.174	45	J x A.130
5	J x A.94	46	B x A.163
6	B x A.225	47	J x A.67
7	Ge x Sh.65	48	*Shenkola*
8	*Belete*	49	Ge x Sh.206
9	J x A.140	50	J x A.146
10	B x A.74	51	B x A.8
11	J x A.170	52	J x A.102
12	B x A.112	53	B x A.213
13	J x A.21	54	J x A.245
14	B x A.184	55	J x A.345
15	B x A.164	56	B x A.201
16	J x A.120	57	*AterAbaba*
17	J x A.187	58	J x A.135
18	B x A.44	59	B x A.603
19	J x A.39	60	J x A.201
20	B x A.198	61	B x A.55
21	Ge x Sh.29	62	J x A.9
22	J x A.42	63	Ge x Sh.100
23	B x A.15	64	B x A.248
24	J x A.49	65	J x A.18
25	B x A.60	66	J x A.123
26	J x A.77	67	B x A.207
27	Gera	68	J x A.186
28	J x A.31	69	B x A.129
29	Ge x Sh.101	70	J x A.122
30	J x A.333	71	J x A.243
31	B x A.228	72	Ge x Sh.90
32	J xA.266	73	Ge x Sh.317
33	J x A.143	74	J x A.196
34	J x A.326	75	J x A.250
35	*Dagim*	76	J x A.119
36	J x A.188	77	J x A.246
37	J xA.60	78	J x A.165
38	B x J.16	79	*Jalene*
39	J x A.34	80	B x A.97
40	Ge x Sh.319	81	Ge x Sh.96
41	B x A.140		

Note: Trt=treatment number, J x A=*Jalen*e x *Aterabab*, B x A = *Belete* x *Aterababa*, Ge x Sh = *Gera* x *Shenkola*, *Dagim* = standard check variety and numbers followed crosses indicated the code of clone experimental materials**.**

Statistical Analysis:

The collected data were subjected to analysis of variance (ANOVA) using SAS statistical software 9.0 (SAS, 2000).

Genetic Divergence and Clustering of Clones:

Genetic distance of clones was estimated using Euclidean distance (ED) calculated from 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 = $\sqrt{\sum_{i=1}^{n}\left(Xij-Xik\right)}^{\frac{2}{2}}$ (Sneath and Sokal, 1973), Where EDjk = distance between clones j and k; xij and xik = phenotype traits values of the i^{th} character for clones j and k, respectively; and n = number of phenotype traits used to calculate the distance. The distance matrix from phenotype traits was used to construct dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrogram.

Principal Component Analysis:

Before computing principal component analysis, the data was standardized to mean of zero and variance of one. The principal component based on correlation matrix was calculated using SAS software version 9.0 (SAS, 2000). According to Gutten's lower bound principle, that Eigen values <1 should be ignored (Kumar et al., 2011).

RESULTS

Analysis of Variance:

The analysis of variance (ANOVA) due to treatments were highly significant for all traits except medium sized tubers (%) and specific gravity (g.cm^3) of tubers indicating the presence of notable genetic variability among them. The presence of significant differences among clones obtained from crossing suggested the chance of obtaining clones that perform than their parents and standard check variety for different traits.

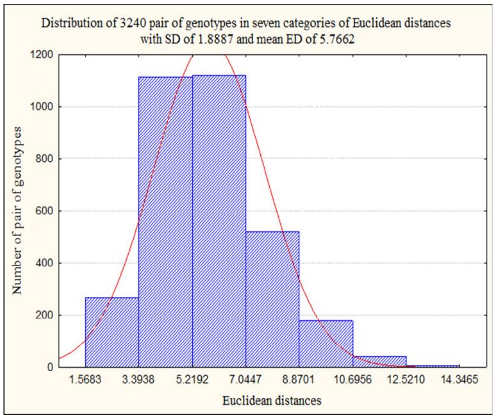

Fig.1: Distribution of 3240 pair of clones into seven categories of Euclidean distance for progenies.

Genetic Divergence and Clustering:

Euclidean Distance of Clones and Parental Varieties

The Euclidean distance (ED) of 3240 pairs of clones with their parents ranged from 1.57 to 14.35 with the mean, standard deviation, and coefficient of variation of 5.77, 1.89, and 32.77% respectively (Table 2 and Fig .1). A total of 486 (15%) pair of clones had ED significantly lower (3.88, overall mean-SD) than overall mean ED of pair clones and 507 (15.65%) pair clones had ED significantly higher (>7.66, overall mean + SD) than overall mean ED of pair clones. From total of 3240 pairs of clones about 1428 (44.07%) pairs of clones had the higher ED than over all mean ED of all clones. The ED of parent varieties, *Belete* and *Ater Ababa* was 7.64 which is higher than over all mean ED of clones, but Jalene and Ater Ababa showed ED of 2.9 and between *Gera* and *Shenkola* was also 3.1 which were lower than overall mean ED of clones.

Among the 81 tested clones, only forty-five percent exhibited higher Euclidean distance than overall mean ED of clones. The highest genetic distance was computed between B x A.164 and B x A.248 (14.35) followed by Ge x Sh.206 and B x A.248 (13.7) and between *Shenkola* and B x A.248 (13.07) indicating their less relatedness to other clones studied. Whereas the shortest genetic distances were noted between J x A.42 and J x A.34 (1.57) and J x A.266 (1.74). Genetic distance between parental varieties such as *Shenkola* and *Aterababa* was 7.26, *Shenkola* and *Jalene* (6.67), *Gera* and *Aterababa* (6.47), *Belete* and *Dagim* (6.42) *Gera* and *Jalene* (5.49), Gera and *Dagim* (5.19), *Belete* and *Gera* (4.64), *Shenkola* and *Dagim* (4.53) and *Belete* and *Shenkola* (3.05).

The dendrograms from UPGMA cluster analysis based on ED matrixes presented in Fig. 2, showed comparatively low similarity among the 81 potato populations. Dendrogram depicting dissimilarity of each biparental crosses were also analyzed separately to see cluster pattern of clones which produced from hybridization of two parent varieties (Fig. 3, 4, 5). This showed most of *Jalene* and *AterAbaba* offsprings that exhibited higher dissimilarity and genetic distances than their parents and standard check variety (Table 2 and Fig. 3). Whereas in family of *Belete* and *AterAbaba* offsprings, showed less similarity and some clones were higher than female parent (*Belete*), but most showed high genetic distance than their male parent (*AterAbaba* variety) and standard check variety (Fig. 4). In crosses of *Gera* and *Shenkola*, only two clones showed higher genetic distance than parents and others had lower distance or high similarity (Fig.5). Hence, the

Table 2: List of 75 clones and 5 parents with one standard check variety used in the experiment

No	Clone	Min	Max	Mean	SD	CV (%)
1	J x A.277	2.1	10.69	5.35	1.73	32.29
2	B x A.153	3.82	10.12	6.06	1.17	19.37
3	J x A.296	2.87	10.88	5.71	1.71	30
4	B x A.174	2.12	9.31	5.36	1.53	28.55
5	J x A.94	2.3	10.55	5.78	1.75	30.19
6	B x A.225	2.59	9.37	5.04	1.39	27.59
7	GE xSH.65	2.73	9.25	4.78	1.26	26.36
8	*Belete*	3.05	12.75	7.26	1.79	24.6
9	J x A.140	1.81	9.29	4.85	1.69	34.73
10	B x A.74	2.21	10.13	4.44	1.38	31.04
11	J x A.170	2.5	11.55	6.69	1.77	26.46
12	B x A.112	3.44	10.44	6.14	1.51	24.59
13	J x A.21	2.5	10.69	5.79	1.74	29.99
14	B x A.184	2.65	9.52	5.37	1.32	24.68
15	B x A.164	4.22	14.35	8.00	1.99	24.89
16	J x A.120	3.04	10.26	5.94	1.44	24.26
17	J x A.187	2.99	9.93	5.56	1.4	25.14
18	B x A.44	2.72	11.86	6.39	1.74	27.23
19	J x A.39	2.24	9.91	4.4	1.38	31.49
20	B x A.198	2.43	10.95	5.75	1.59	27.68
21	GE x SH.29	6.7	12.37	9.2	1.1	11.98
22	J x A.42	1.57	10.72	4.47	1.51	33.79
23	B x A.15	2.36	11.07	5.07	1.3	25.69
24	J x A.49	1.92	11.28	4.94	1.68	33.99
25	B x A.60	3.2	11.24	6.18	1.45	23.48
26	J x A.77	2.69	11.85	6.44	1.85	28.69
27	Gera	3.06	11.99	6.37	1.48	23.17
28	J x A.31	1.84	10.75	4.9	1.64	33.51
29	GexSh.101	1.86	8.95	4.55	1.61	35.46
30	J x A.333	3.26	12.61	7.92	1.95	24.62
31	B x A.228	2.93	10.44	5.2	1.4	26.84
32	J x A.266	1.74	11.51	5.97	1.59	26.65
33	J x A.143	3.26	11.07	6.54	1.75	26.8
34	J x A.326	2.54	10.76	5.3	1.63	30.82
35	*Dagim*	2.55	9.66	5.06	1.41	27.94
36	J x A.188	3.51	10.39	6.27	1.53	24.44
37	J x A.60	3.05	10.49	6.03	1.74	28.88
38	B x J.16	2.73	11.32	5.86	1.58	26.92
39	J x A.34	1.57	10.36	4.5	1.55	34.38
40	Ge xSh.319	2.69	11.42	6.01	1.77	29.5
41	B x A.140	3.62	11.13	7.09	1.54	21.68
42	J x A.23	2.16	9.44	5.32	1.56	29.29
43	J x A.27	1.89	8.87	4.76	1.55	32.55
44	Ge x Sh.186	3.67	10.51	6.93	1.63	23.45
45	J x A.130	2.64	10.23	5.25	1.54	29.37
46	B x A.163	3.15	10.92	5.54	1.29	23.2
47	J x A.67	2.64	10.06	5.43	1.45	26.75
48	Shenkola	3.05	13.08	6.97	1.71	24.56
49	Ge x Sh.206	4.45	13.7	7.88	1.53	19.4
50	J x A.146	2.3	10.4	5.69	1.81	31.8
51	B x A.8	3.22	10.91	6.27	1.79	28.54
52	J x A.102	3.22	11.17	5.91	1.49	25.15
53	B x A.213	2.27	10.94	5.45	1.59	29.08
54	J x A.245	2.43	11.83	5.78	1.87	32.36
55	J x A.345	2.33	9.26	4.75	1.44	30.31
56	B x A.201	2.37	8.86	4.81	1.46	30.43
57	*Aterababa*	1.86	8.87	4.55	1.56	34.39
58	J x A.135	3.44	11.23	6.66	1.76	26.41
59	B x A.603	2.31	11.14	5.22	1.58	30.21
60	J x A.201	2.63	11.69	5.82	1.7	29.17
61	B x A.55	1.74	11.94	5.96	1.76	29.58
62	J x A.9	5.05	11.17	6.85	1.27	18.57
63	Ge x Sh.100	1.84	10.56	4.91	1.69	34.35
64	B x A.248	7.95	14.35	10.31	1.29	12.52
65	J x A.18	3.63	11.83	6.48	1.61	24.8
66	J x A.123	2.62	9.51	5.42	1.54	28.38
67	B x A.207	2.27	10.6	5.91	1.52	25.78
68	J x A.186	2.16	9.48	5.55	1.57	28.28
69	B x A.129	2.91	9.98	5.36	1.62	30.26
70	J x A.122	2.16	9.31	5.42	1.48	27.28
71	J x A.243	2.25	9.04	4.7	1.54	32.63
72	Ge x Sh.90	2.56	10.12	4.67	1.41	30.14
73	Ge x Sh.317	1.88	9.42	5.05	1.5	29.71
74	J x A.196	3.41	11.73	6.67	1.84	27.61
75	J x A.250	1.81	9.28	4.73	1.66	35.04
76	J x A.119	2.75	11.64	6.22	1.86	29.92
77	J x A.246	1.92	8.94	4.93	1.48	29.95
78	J x A.165	2.27	9.54	4.92	1.43	29.04
79	*Jalene*	2.56	10.02	4.69	1.41	30
80	B x A.97	3.63	10.9	6.11	1.48	24.23
81	Ge x Sh.96	1.92	10.56	4.65	1.59	34.3
	Overall	1.57	14.35	5.77	1.89	32.77

pair clones between1.57 to 3.46 were (306), 3.47 to 5.35 (1183), 7.25 to 9.13 (465), 9.15 to 11.02 (153), 11.07 to 12.84 (30) and 13.08 to 14.35(3) (Fig.1).

Based on the mean Euclidean distance, only five clones and one parental variety such as B x A.248 (10.31), Ge x Sh.29 (9.2), B x A.164 (8.0), J xA.33 (7. 92), Ge x Sh.206 (7.88) and *Belete* variety (7.26) were exhibited significantly highest mean genetic distance of >7.66 (over all mean distances of clones + standard deviation) (Table 2).

Clustering of Clones:

The result of genetic distance analysis among clones for all possible pair of characters showed that, seventy-five offsprings, five parents and one standard check variety were grouped into sixteen different clusters using non-hierarchical clustering (Table 3).

Generally, the 81 potato clones grouped into 16 clusters ranged from 0 to 12.0 (Fig. 2). It was

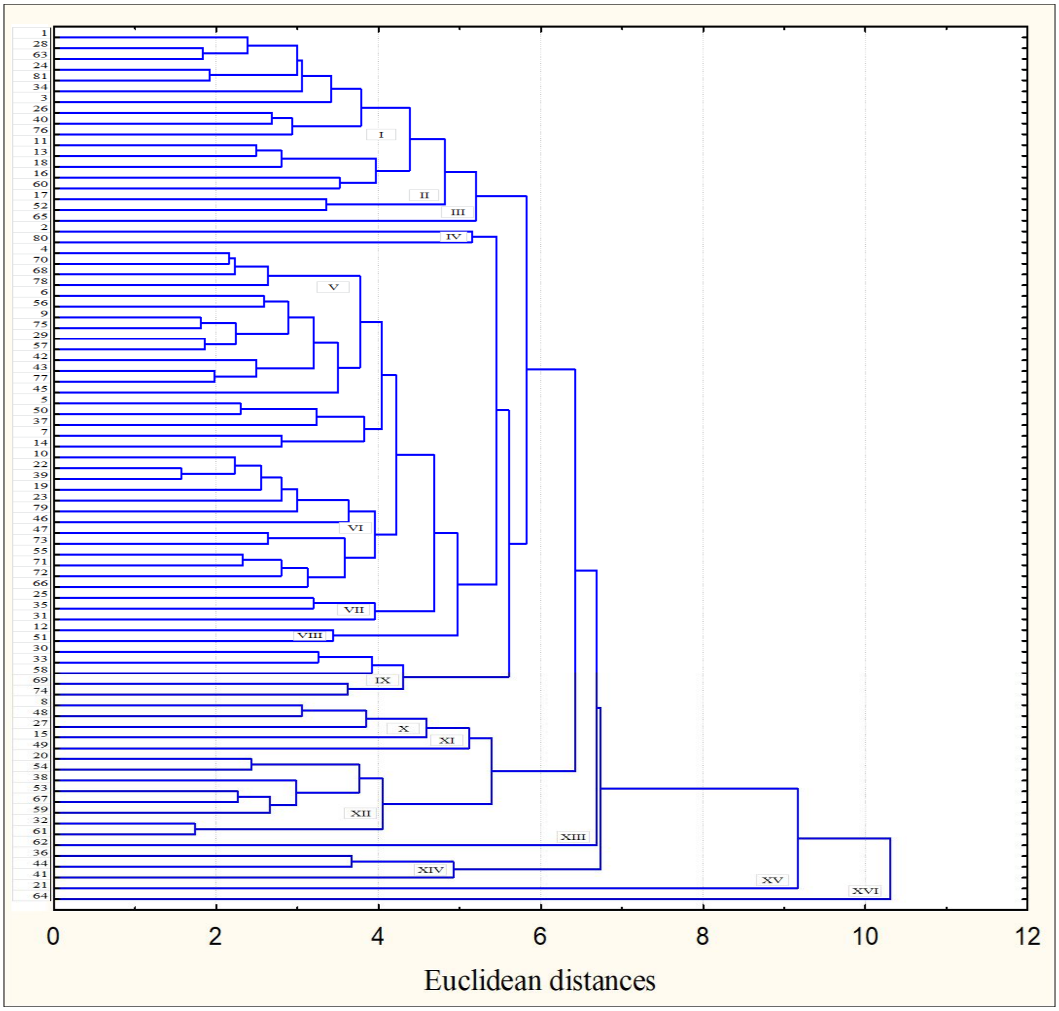

Fig. 2: Dendrogram depicting dissimilarity of 81 clones by Unweighted Pair group Method with Arithmetic Means clustering method from Euclidean distances matrix estimated from 16 Agro-morphology traits

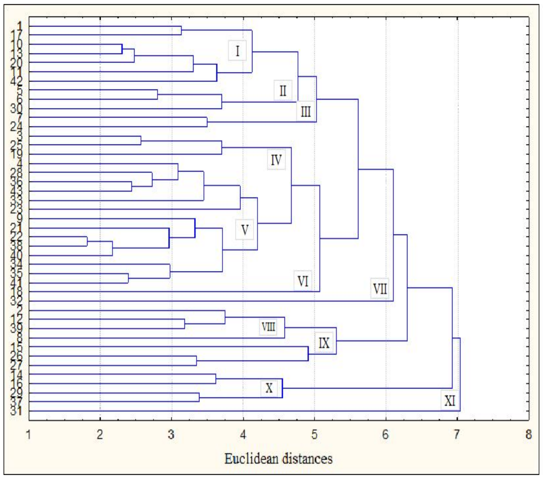

Fig. 3: Dendrogram depicting dissimilarity of 41 clones obtained from crossing of *Jalene* and *Aterababa* by Unweighted Pair group Method estimated from 16 Agro-morphology traits

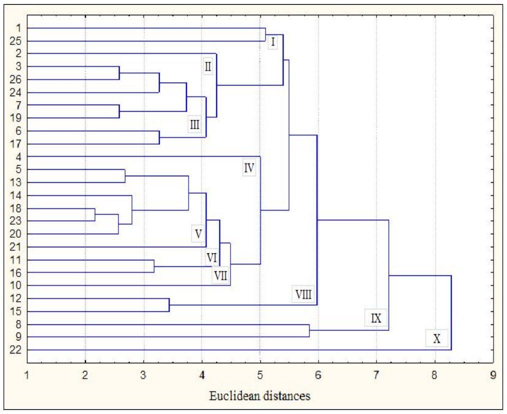

Fig. 4: Dendrogram depicting dissimilarity of 24 clones obtained from crossing of *Belete* and *Aterababa* by Unweighted Pair group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 16 Agro-morphology traits

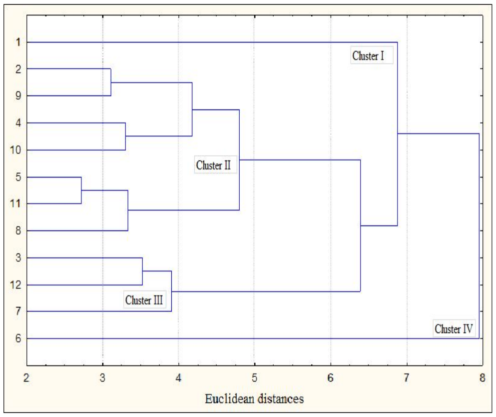

Fig. 5: Dendrogram depicting dissimilarity of 12 clones with two parents (*Gera* and *Shenkola*) by UPGMA clustering method from Euclidean distances matrix estimated from 18 agromorphology trait.

and starch content (20.91) were computed from cluster IV. Cluster X showed the highest mean stem height (64.67cm), marketable tuber yield (42.42t ha^{-1}), total tuber yield (44.46 t ha^{-1}) and dry matter (23.65%). Cluster XI had also maximum tuber yield per plant^{-1} (1.03kg), average tuber weight (103.3 gm), total tuber yield (45.71t ha^{-1}) and proportion of large sized tubers.

Principal Component Analysis:

The PCA result are presented in four principal components with Eigen values ranged from 1.91 to 6.078 and percentage of total variance ranged from 10.6 to 33.8% (Table 5).

The first two PCs: PC1 and PC2 with values of 33.8% and 16.6% respectively, contributed to a total of 50.4% gross variation among evaluated clones for 16 morpho-agronomic traits. The cumulative contribution of PC1 was due to the contribution (>0.5) of total tuber yield, tuber yield per plant, marketable tuber yield and stem height, tuber dry matter, starch content%, marketable tuber number, proportion of small sized tubers and average tuber weight.

DISCUSSIONS

In the current study, all the clones revealed high range of Euclidean distance (ED) than reported by Berhan et al. (2018), Namugga et al. (2017), Panigrahi et al. (2014), Wassu (2014) and Tesfaye et al. (2013). Manosh et al. (2008) suggested that higher heterosis can be achieved by using crosses obtained from parents that have moderate dissimilarity or genetic distance. Hence, selecting parents based on their genetic distance can generate heterotic crosses (Sandhu et al., 2001).

Table 3: Clustering pattern of 75 clones and 5 parents with standard check in 16 clusters

Cluster	No of clone	Offspring and parents in different clusters
I	15	JxA.120, J x A.277, J xA.31, Ge x Sh.100, JxA.49, Ge x Sh.96, JxA.326, JxA.296, JxA.77, Ge x Sh.319, J x A.119, J x A.170, JxA.21, B x A.44, J x A.201
II	2	JxA.187, JxA.102
III	1	JxA.18
IV	2	B xA.153, B xA.97
V	19	B x A.174, JxA.122,JxA.186, JxA.165, BxA.225, BxA.201, JxA.140, JxA.250, Ge x Sh.101, Ater Ababa, JxA.23, JxA.27, JxA.246,JxA.130, JxA.94, J xA.146, JxA.60, Ge x Sh.65, BxA.184
VI	13	Bx A.74, JxA.42, J x A.34, JxA.39, B x A.15, Jalene, B x A.163, JxA.67, Ge x Sh.317, J xA.345, J xA.243, Ge x Sh.90, JxA.123
VII	3	B x A.60, Dagim, BxA.228
VIII	2	B xA.112, BxA.8
IX	5	J xA.333, J xA.143, JxA.135, B xA.129, JxA.196
X	4	Belete, Shenkola, Gera, B x A.164
XI	1	Ge x Sh.206
XII	8	B xA.198, J x A.245, B xA.16, B xA.213, B xA.207, B xA.603 J x A.266, B xA.55
XIII	1	J x A.9
XIV	3	JxA.188, Ge x Sh.186, BxA.140
XV	1	Ge x Sh.29
XVI	1	B x A.248

The dendrograms from UPGMA cluster analysis showed some of the clones that have a common parent were not in the same cluster and most progenies were not close to their parents. This could be because of the random reassortment of alleles in the biparental cross (Yada et al., 2015). In biparental crosses of *Jalene* with *AterAbaba*, most clones grouped in cluster V and I and others were clustered in remaining clusters, but their parents were distributed in different clusters. So, grouping of materials of same origin into different clusters indicates broad genetic base of the clones belonging to that origin (Shanmugam et al., 1982). Hence, this result indicated that there is a high level of variation between the parents and the resultant clones, which suggests the presence of greater chance for improving the required traits in tetraploid potato through local crossing and

Table 4: Mean values of 16 clusters for 75 clonal progenies and 5 parents with their standard checks tested at Adet 2018/2019

Cluster	DE	DF	DMA	SN	SH	TNP	TYP	ATW	MTN	MY	UNMY	TY	VSN	LTN	DM	SC
I	17.20	47.27	94.27	5.33	56.61	18.53	0.79	44.75	193.73	32.22	4.08	36.30	25.31	19.53	24.02	17.41
II	16.00	46.00	95.00	5.00	62.76	14.00	0.84	60.56	173.75	34.45	3.07	37.51	18.17	31.13	17.38	11.49
III	17.00	49.00	93.00	4.00	50.31	19.00	0.51	27.14	246.50	22.40	0.82	23.22	14.13	4.79	23.43	16.88
IV	21.50	47.00	94.50	3.00	43.98	12.50	0.52	44.04	143.00	25.15	3.78	28.93	20.90	18.70	27.95	20.91
V	18.16	47.89	95.00	3.95	43.36	10.47	0.44	42.96	104.63	17.29	3.10	20.39	27.63	19.23	20.01	13.83
VI	18.62	49.08	93.46	4.08	50.01	14.46	0.59	42.63	134.35	24.06	4.99	29.05	33.24	20.29	22.04	15.64
VII	19.67	48.67	90.00	2.67	55.88	9.00	0.56	65.07	108.83	23.75	2.09	25.83	16.30	35.81	20.72	14.47
VIII	23.00	52.00	93.50	3.50	35.44	10.00	0.33	34.97	91.50	13.38	3.02	16.40	31.42	10.70	20.59	14.35
IX	16.40	49.60	95.00	4.20	41.97	14.00	0.34	25.17	97.20	10.48	5.01	15.50	50.61	4.08	16.59	10.79
X	20.75	52.00	99.75	2.25	64.67	11.75	0.90	81.71	147.50	42.42	2.05	44.46	14.77	50.59	23.65	17.08
XI	19.00	53.00	98.00	3.00	61.95	11.00	1.03	103.30	93.50	32.13	13.59	45.71	17.73	55.47	23.48	16.92
XII	17.88	46.63	94.63	3.38	50.25	11.50	0.79	69.44	141.38	34.36	2.19	36.55	17.74	38.35	23.73	17.15
XIII	21.00	52.00	99.00	9.00	44.42	18.00	0.63	36.31	158.50	23.22	5.73	28.95	37.59	13.33	21.43	15.10
XIV	20.67	55.00	95.67	3.33	37.01	7.67	0.39	52.73	99.83	18.01	0.92	18.92	15.08	32.67	14.96	9.33
XV	19.00	49.00	97.00	4.00	50.63	9.00	0.62	72.04	13.50	2.51	24.90	27.40	52.20	17.68	21.73	15.36
XVI	19.00	0.00	102.00	4.00	32.33	10.00	0.27	26.45	95.50	8.73	2.97	11.69	30.82	3.20	16.05	10.31
Mean	19.05	46.51	95.61	4.04	48.85	12.56	0.60	51.83	127.70	22.78	5.14	27.92	26.48	23.47	21.11	14.81

Note: DE = Days to 50% emergency, DF = Days to 50% flowering, DF = Days to 50% flowering, DMA = Days to 90% maturity, SN = main stem number per plant, SH = stem height, TNP = Tuber number per plant, TYP = tuber per plant, ATW = Average tuber weight (kg), MTN = main stem number, TY = Total yield (t ha^{-1}).

Table 5: The results of principal component analysis (PCA) for 16 quantitative traits

Trait	Eigen vectors			
	PCA1	**PCA2**	**PCA3**	**PCA4**
Days to 50% emergency	-0.08	-0.303	-0.218	-0.269
Days to 50% flowering	0.159	-0.22	-0.313	-0.001
Days to maturity	-0.139	-0.312	0.585	0.708
Main stem number	-0.139	-0.312	0.585	0.708
Stem height(cm)	0.757	0.054	-0.052	0.143
Tuber number per plant	0.392	0.812	-0.066	0.262
Tuber yield per plant(kg/plant)	0.947	0.046	-0.076	0.105
Average tuber weight(gm/tuber)	0.635	-0.685	-0.111	-0.095
Marketable tuber number	0.672	0.603	0.32	-0.083
Marketable yield (t ha ^{1})	0.945	-0.024	0.138	-0.047
Unmarketable yield (t ha ^{1})	-0.057	0.114	-0.666	0.516
Total yield (t ha ^{1})	0.951	0.013	-0.079	0.123
Very small tuber%	-0.539	0.342	-0.532	0.468
Large tuber%	0.62	-0.746	-0.017	-0.114
Tuber dry matter%	0.686	0.26	-0.08	0.104
Starch content%	0.686	0.261	-0.08	0.104
Eigen value	6.078	2.979	2.107	1.91
Difference	3.099	0.873	0.197	0.519
Variance (%)	33.8	16.6	11.7	10.6
Cumulative variation (%)	33.8	50.4	62	72.7

Note: PCA1= principal component analysis 1, PCA2 = principal component analysis 2, PCA3 = principal component analysis 3, PCA4 = principal component analysis 4

selection activities. Because crossing between the members of a diverse cluster could produce a superior hybrid (Biswas et al., 2010). So, forty-one clones generated from crosses of these varieties were distributed in 9 clusters among a total of 16 clusters.

Inter-mating parents based on genetic divergence is expected to produce heterotic progenies having reasonably high yield (Luthra, 2005). Clonal progenies derived from crossing of *Gera* and *Shenkola* varieties were also dispersed in five clusters and none of the clones clustered with their parents, but parental varieties clustered in same cluster (X); due to same origin or pedigree suggesting the narrow genetic bases between parents. Hence, genetic diversity study for the five parents and their progenies revealed that most of the progenies did not group with their parents, indicating the existence of high level of genetic distance among the studied clones. This could be created due to the random assortment of alleles in the biparental cross (Yada et al., 2015).

The total contribution of the four principal component axes of current study result was higher than the result (70.5%) reported by Meaza (2015). de Lange and Labuschagne (1999) have considered all variables with loadings of 0.50 - 0.99 as major factors. In this study, the variables that have loadings within this range would be the ones that are emphasized as priority traits in the future breeding program in these clones. The first four components were retained in analysis, having Eigen values of >1. The rest factors having Eigen value < 1 were ignored according to Gutten's lower bound principle (Kumar et al., 2011). According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero.

Similarly, Mondal et al. (2007) applied non-hierarchical clustering using a co-variance matrix for 31 clones with their parents by grouping into five different clusters and Arslanoğlu et al. (2011) classified 146 potato clones, based on 15 variables in to 27 clusters. Ebrahim (2021) reported highest contribution of percentage of very small tuber sizes, marketable tuber yield, average tuber weight, percentage of larger tuber sizes and total tuber yield to PCA1.Verma and Singh (2016) noted the first vector with high positive weight to tuber yield per plant. Afshari et al. (2017) recorded the maximum contribution of variation by total yield in the first PC and plant height and tuber number per plant in PC2 and tuber dry matter in PC4 from five PCs. Sepideh (2014) reported the total variation of 81% from the first four principal components in 166 clonal progenies with two parents and found high diversity from main stem number per plant, plant height and total tuber yield among one family. Nickmanesh (2014) also showed PC1 which accounted for about 41.28% of the variation for tuber number per plant, tuber weight per plant and tuber yield. He also reported the second group that accounted for about 21.55% of the variation named a "plant structural" factor which consisted of the main stem number per plant and plant height from 127 clonal progenies obtained from crossing of two potato varieties.

In conclusion, the dendrogram constructed based on the Euclidean distance matrix showed dissimilarity of clones not only for aggregated families but also biparental crosses (potato offsprings produced from two parental varieties).The crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and wide variability in genetic architecture. The most distant offsprings were observed in crosses of *Belete* and *Aterababa* followed *Jalene* and *Aterababa* potato varieties. In crosses of *Gera* and *Shenkola*, most clones showed low genetic distance than parents due to same pedigree in which improving could not be considered. So, crosses among the clones of clusters I, II, X, XI and XII would results in high heterosis. Hence, the current study results showed that the presence of exploitable genetic distance among potato clones that were produced from local crossing. Therefore, additional experiments will be carried out to evaluate the most promising and genetically distant clones for desirable traits, with the purpose to either produce new variety or select parental lines for future breeding.

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