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Genetic Variability and Correlation of Traits among Progenies of Potato Crosses in Ethiopia

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Abstract

Background: Investigating the causes and magnitude of genetic variation in segregating potato population that derived from crossing is vital to know the genetic consequences of hybridization and improve potato varieties. However, very little effort has been carried in creating local population through crossing and genetic information on created potato population.
Objective: The study was conducted to assess genetic variability and correlation among traits in locally created potato crosses population.
Materials and Methods: A total of 81 genotypes were evaluated for 18 traits in a 9 x 9 simple lattice design. Data collection and analysis was done from sixteen plants or central rows.
Results: The results revealed highly significant variations for all traits except proportion of medium tuber size and specific gravity of tubers indicating the existence of genetic variability among population. Marketable and total tuber yields variability of tested genotypes ranged from 2.51 to 55.62 t ha $^{-1}$ and 10.82 to 58.31 t ha $^{-1}$, respectively. The phenotypic and genotypic coefficients of variation ranged between 4.67 to 92.88% and 3.25 to 73.5%, respectively. Heritability in broad sense and genetic advance as percent of mean also ranged from 28.81 to 91.64% and 4.65 to 90.33%, respectively with less influence of environmental fluctuations. Total tuber yield had positive and significant phenotypic and genotypic correlations with stem height, tuber yield per plant, tuber number per plant, average tuber weight and marketable tuber yield. This indicated that the traits are heritable with governing of additive gens for effective selection.
Conclusion: The range and mean values of the variables obtained suggest the existence of sufficient variability among the tested and possibility of wide genetic base creation for improving potato population using locally created genotypes. Hence, promising genotypes with desirable traits could be recommended to produce new variety or use as parental lines for future breeding program.

Keywords: Broad sense heritability; Correlations; Genetic advance; Genotypes; Tuber yield

1. Introduction

Potato (*Solanum tuberosum* L.) is a highly heterozygous tetraploid plant, originating in South America. It is a tuber bearing crop belonging to the family Solanaceous and has 48 chromosomes. Potato is the world's third most important food crop in overall production after rice and wheat, and is a food security crop in Ethiopia (Devaux *et al.* 2014). It is mainly used as vegetable and available in the market throughout the year with reasonable price and has great importance in rural economy of the country as compared to other vegetables crops in Ethiopia.

In Ethiopia, potatoes are mostly cultivated in the central, north western, southern, and eastern parts of the country (Semagn Asredie *et al.,* 2016). The crop has potential for improving the livelihoods of millions of smallholder farmers in the high lands area of the country. The potential for higher yield per unit area, early maturity, and excellent food value give the potato crop greater potential for improving food security, increasing household income, and reducing poverty than other crops (Semahagn Asredie *et al.*, 2015). In 2018/19, the area under potato production of Maher season in the country was about 73,677.64 hectares with an average tuber yield of 14.18 t ha^{-1} (CSA, 2019*).* This is relatively low, especially when considering the favorable climate at higher elevations, soils, and irrigation potential in Ethiopia. The main production constraints are related to narrow genetic basis and susceptibility to diseases among varieties. Ethiopia's tremendous variation in altitude, temperature, rain fall, soil type and ecological settings also give rise to the need for a wide range of varieties, which are not likely to be provided by existing breeding programs (Semahagn Asredie *et al*., 2015). So, continuously developing new cultivars through crossing is needed for a sustainable increase in potato variability and production under the present environmental change and high human population growth (Bradshaw, 2006).

Ethiopia has more than 36 potato varieties that are approved for cultivation to address the production problems in the country (MoA, 2016). These improved varieties were developed from introduced germplasms mainly from International Potato Center

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(CIP) either in the form of true potato seeds or clones and varieties imported to the country through technology shopping programs for adaptation trials and subsequent registration as a variety (Gebremedhin Woldegiorgis *et al.,* 2013).

Creating genetic variability in tetraploid potato crop through hybridization in the country is limited due to too much dependence on CIP materials (Getachew Assefa *et al*., 2016). Because of this constraint most smallholder farmers are still growing old varieties that are low yielding and disease susceptible. Improving productivity of the crop through hybridization is necessary to develop varieties which are adaptable to a wide range of environments (Semahagn Asredie *et al*., 2015). Ethiopian local potato varieties are more heterozygous than the CIP genotypes that are cultivated in Ethiopia (Semahagn Asredie *et al*., 2016). Varieties developed from crossing of existing local varieties are more likely to be adapted to local growing conditions. Therefore, creating genetic diversity by conventional breeding using locally adapted genotypes (existing local land races and released varieties) in the country is required to reduce dependency on foreign materials and develop climate smart potato varieties which are widely adaptable and fulfill growers' preferential traits.

Studying the causes and magnitude of variation from segregating population or genotypes derived from conventional crossing is vital in understanding the genetic consequences of hybridization to develop better potato varieties (Mehboob *et al.,* 2016). Evaluating crossing products in different generations of selection can also help to estimate genetic parameters such as heritability to identify the best breeding strategy (Antonio *et al.,* 2012).

Genetic variability in potato genotypes that were introduced from CIP has been studied and variability in segregation was reported by many researchers like Addisu Fekadu *et al.* (2013); Abraham Lamboro (2014); Getachew Assefa *et al.* (2016); Wassu Mohammed (2015) and Tesfaye Abebe et *al.* (2012). But not much effort has been made in a country to study the genetic variability and improve varieties by generating genotypes through crossing. Hence, the present investigation was conducted to evaluate the extent of variability, heritability, genetic advance, and correlation of traits in populations of cross Jalene x AterAbaba, Belete x Aterababa and Gera x Shenkola varieties for different yield and its related traits.

2. Material and Methods

2.1. 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 the longitude ranging from 37° 28' 38" to 37° 29' 50" E and latitude ranging from 11° 16' 19" to 11° 17' 28" N in northwestern highlands of Ethiopia with an average altitude of 2240 meters above sea level (Andualem Wolie *et al.,* 2013). The mean annual total rainfall during the growing season was 1432 mm with the average minimum and maximum temperatures of 10.81 and 25.55 ℃, respectively.

2.2. Description of the Experimental Materials and Design

The experimental materials comprised 81 genotypes. From this, seventy-five genotypes were offspring produced from biparental crossing of Ethiopian potato varieties by Adet Agricultural Research Center in 2015. In addition, five high yielding parent varieties, namely, Belete, Aterababa, Gera, Shenkola and Jalene and Dagim (the latest registered variety) was included as a standard check for comparison in this experiment (Table 2).

The experiment was laid out as a 9 x 9 simple lattice design. Each genotype was planted in a gross and net plot size of 1.5 m x 3m which contained two rows in plot and twenty plants per plot. Medium-sized and well sprouted potato tubers were planted at the spacing of 75 cm between rows and 30 cm between plants. The recommended dose of fertilizer was applied at a rate of 81/69 N/P_2O_5 per hectare. The whole phosphors fertilizer was applied during planting, but N source applied in split at planting, 2 weeks after emergence and at flowering at equal $\frac{1}{3}$ rate. Earthing up was executed two times throughout the entire growing period, one at 30 days and another one at 60 days after planting. Fungicide chemical (Ridomil) was applied once when symptom occurred on experiment to control potato late blight disease.

Table 1. Description of parental varieties for different traits.

S/N	Parent	Released	Characteristics
1	Belete CIP-393371.58	2009	Strong stems, high yield and dry matter, excellent stew quality, late blight tolerance, early bulking, early maturing and good for French fries, large tuber, white flower, and tuber skin color, very susceptible for bacterial wilt, hollow heart, sometimes its shape become amorphous, bitter taste than others
2	Jalene CIP-37792.5	2002	Good dry matter and boiling quality, early maturing, early flowering, white tuber skin and flower color, late blight susceptible shallow eye depth, good taste
3	Gera KP-90134.2	2003	Long storage life, strong stems, high yield, late blight tolerant and well adapted to dry areas, very high deep tuber eye, white flower and tuber skin, round tuber shape
4	Shenkola KP-90134.5	2005	Good taste and boiling quality, white flower and tuber skin color, good yield, oval tuber shape, shallow eye depth, good taste, has tall stem
5	Aterababa	Local	Good canopy cover, stew quality, taste, early maturing, round shape, high dry matter, good market demand and storage quality, late blight susceptible, bacterial wilt resistant than others, pink tuber skin and flower color, round tuber shape

Note: *Descriptions are organized from Tesfaye Abebe et al. (2013) and Semahagn Asredie et al. (2015).*

Table 2. List of potato offspring and parents with standard check variety used in the experiment.

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

Note: Trt = Treatment, J x A = Jalene cross Ater abab, B x A = Belete cross Ater ababa, Ge x Sh = Gera cross Shenkola, Dagim = Standard check variety and numbers followed crosses indicated the code of genotype (experimental material).

2.3. Data Collection and Analysis

2.3.1. Data collection

Observations were recorded on different traits such as days to emergency (DE), days to flowering (DF), days to maturity (DMA), main stem number (SN), plant height (PH), tuber number per plant (TNP), tuber yield per plant (TYP), very small tuber numbers (VSN), medium sized tubers (MDN), large sized tubers (LTN), tuber dry matter content (DM), tuber starch content (SC), tuber specific gravity, average tuber weight (AW), marketable tuber number (MTN), marketable yield (MY), unmarketable tuber yield (UNMY) and total tuber yield (TY). Some of morphological qualitative traits like, flower color, plant growth habit type, predominant tuber skin color and flesh color, tuber skin type, eye depth and number per tuber were recorded in all the entries as per the standards and codes specified in potato descriptors of AICRP on potato, Huaman *et al.* (1977) during the peak of crop growth.

2.3.2. Data Analysis

The quantitative data were subjected to analysis of variance (ANOVA), but descriptive statistics was used to describe qualitative data by taking samples from five plants for each trait. Means for significant treatments were compared using Fisher 's protected least significant differences (LSD) at 5% ($P<0.05$) level of significance. The traits that exhibited significant mean squares in ANOVA were further subjected to genetic analyses. The phenotypic (σ^2_p), genotypic (σ^2_g) variances, environmental variance (σ^2_e) and the corresponding phenotypic (PCV) and genotypic (GCV) coefficients of variation for each trait were estimated following the method described by Burton and Devane (1953). Genotypic variance (σ^2_g) = $\frac{GMS-MSE}{r}$, Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$. where, MSE =Mean square of error and GMS=genotypic mean square. Broad sense heritability estimates and genetic advance were also calculated using the formula of Burton (1952) and Johnson *et al.* (1955), respectively: h^2_b (Broad sense heritability) (%) $=\frac{\sigma^2 g}{\sigma^2 p}$x100, where σ^2_g= genotypic variance and σ^2_p=Phenotypic variance. Genetic advance (GA) for each trait was computed using the formula adopted by Johnson *et al.* (1955) as: GA= $GA=k.\sigma_p.h^2_b$.Where, k= selection differential (k=2.06 at 5% selection intensity), σ_p= Phenotypic standard deviation of the trait, h^2_b= broad sense heritability of the character.

3. Results and Discussion

3.1. Analysis of Variance and Mean Performance of Genotypes

Results of the analysis of variance (ANOVA) of 18 quantitative traits for the 81 genotypes showed significant ($P \leq 0.01$) differences among the tested potato populations for all traits except proportion of medium tuber size (%) and specific gravity (g/cm^3) of tubers (Table 3). The presence of significant differences among the genotypes obtained from three biparental crosses and their parents suggested the chance of obtaining better performing offsprings/genotypes than their parents for the different important yield and its related traits. The genotypes are expected to be highly heterozygous in which additive and non-additive gene actions and in most case, both operate (Ross, 1986), (Arndt and Peloquin, 1990). Therefore, the observed variations among the potato genotypes could be exploited through vegetative propagation.

The present findings agree with findings of Hajam *et al.* (2018) who reported significant variations among 38 genotypes for days to flowering, plant height, tuber number per plant, tuber yield per plant and average tuber weight. Hirut Betaw *et al.* (2017) reported highly significant differences among 60 progenies of 32 families, 12 twelve parents and check varieties for growth, physiological and tuber yield related traits. Melito *et al.* (2017) also reported highly significant difference for total tuber yield from genotypes obtained biparental crosses. Zakerhamid (2014) showed significant differences among 166 hybrids and two parents for plant height, main stem number per plant, tuber weight per plant, average tuber weight and tuber yield. Nickmanesh and Hassanpanah (2014) evaluated 127 hybrids with their two parents and reported significant differences for days to flowering, plant height, tuber weight per plant, and total tuber yield.

The genotypes/offsprings, parents and the check variety observed 16 to 24, 42 to 60 and 88 to 102 days of 50% emergence, 50% flowering and 90% maturity, respectively (Table 4). The 41 potato offsprings of Jalene x Ater Ababa had lowest mean days to 50% emergency. The 24 potato progenies of Belete x Ater Ababa also showed lowest mean days to 50% flowering. While the 10 potato offsprings of Gera x Shenkola manifested lowest mean days to maturity. However, the individual genotypes, J x A.277, J x A.296, J x A.187, J x A.135, J x A.201, J x A.122, J x A.196, J x A.246 and J x A.165 showed early emergency of plants than their parents, standard check variety and other genotypes. Similarly, J x A.23 and J xA.130 genotypes observed early maturity (88 days) than other progenies, parents, and check variety. A total of nine potato progenies showed early maturity than the standard check variety in this study.

The main stem number and stem height ranged between 2 and 9; and 32.27 and 73.33 cm, respectively (Table 4). Potato offspring of Jalene and Ater Ababa exhibited the highest mean of main stem numbers whereas the maximum mean stem height recorded for progenies of Gera and Shenkola. Genotype B x A.164 showed maximum stem height (73.33 cm) followed by Ge x Sh.319 (71.64 cm) but more stem numbers recorded for genotype J x A.9. These genotypes which had more main stems and tall stem height can produce high tuber yield.

Other authors also found the performance of crosses and parental varieties for phenological and growth traits. Hajianfar *et al.* (2017) recorded main stem numbers ranging between 3.33 and 4.29 and stem height ranging between 52.33 and 64.77cm for potato hybrids. Parmar *et al.* (2015) found plant height ranging from 37.16 to 54.80 cm with a mean of 42.29 cm and main stem number per hill ranging from 1.93 to 3.93 with a mean 2.91 in potato genotype. Biswas (2010) showed the range of plant height from 15.0 to 57.0 cm with a mean 37.9 cm for and 1 to 6 with a mean 2.1 for main stem numbers for potato progenies.

Table 3. Mean squares from the simple lattice ANOVA for traits of 81 potato genotypes.

Trait	Rep df =1	Blocks (adj.) df =16	Genotype (unadj.) df = 80	Genotype (adj.) df = 80	Error (RCBD) df = 80	Intra block (Error) df = 64	RE of SL Over RCBD	CV (%)
DE	32	3.49	8.14**	7.74**	2.5	2.25	103.61	8.36
DF	9.88	4.2	77.32**	73.56**	3.54	3.37	100.92	3.97
DMA	52.25	6.50	28.89**	28.76**	9.36	10.07	92.91	3.24
SN	2.47	0.82	3.12**	2.96**	0.93	0.96	96.99	25.78
SH	99.25	37.69	168.85**	150.79**	25.51	22.47	105.06	10.03
TNP	0.5	3.74	30.17**	25.12**	4.58	4.78	95.65	16.3
TYP	0.0005	0.007	0.09**	0.08**	0.008	0.008	96.79	14.21
AW	30.33	53.52	587.04**	565.85**	61.58	63.59	96.83	16.7
MTN	54267	1562.95	3916.31**	3360.49**	1185.46	1091.09	102.46	25.04
MY	210.12	12.72	200.13**	192.04**	16.4	17.33	94.68	16.55
UNMY	286.56	3.75	20.86**	18.77**	3.83	3.86	99.42	31.3
TY	5.89	10.92	189.95**	177.46**	14.97	15.99	93.66	16.69
VSN	17515	139.8	275.23**	265.25*	142.08	142.66	99.6	32.63
MDN	19781	190.98	210.36^{ns}	191.5^{ns}	155.2	146.26	101.37	24.43
LTN	50.72	48.9	335.45**	327.70**	52.12	52.92	98.48	31.36
DM	37.07	3.88	20.70**	19.61**	5.4	5.78	93.43	11.05
SG	0.14	0.0009	0.001ns	0.001^{ns}	0.002	0.002	89.13	3.53
SC	34.86	3.25	16.43**	15.52**	4.68	5.04	92.89	14.48

Note: **and **Significant at $P\leq 0.05$ and $P\leq 0.01$ probability levels, respectively. DE = days to emergency, DF = days to 50% flowering, df=degree of freedom, DMA = days to 90% maturity, SN = main stem number, SH (cm) = stem height, TNP = tuber number per plant, TYP (g) = tuber yield per plant, AW (g) = average tuber weight, MTN = marketable tuber number, MY = marketable yield t ha^{-1}, UNMY = unmarketable yield t ha^{-1}, TY = total yield t ha^{-1}, VSN = very small tuber size in percentage, MDN = medium tuber size percentage, LTN = large size tuber percentage, DM = tuber dry matter content(%), SG = specific gravity of tuber, SC = tuber starch content (%), CV (%) = coefficient of variation.*

Tested genotypes showed 6 to 25 tuber number per plant, 0.23 to 1.025kg tuber yield per plant,16.61 to 106.83g average tuber weight, 11 to 310 marketable tuber number per net plot, 2.51 to 55.62 marketable tuber yield, 0.33 to 24.9 unmarketable and 10.82 to 58.31ha^{-1} total tuber yield (Table 4). The result of range and mean of marketable and total tuber yield were greater than the findings reported by Getachew Assefa *et al.* (2016), Wassu Mohammed (2014), Wassu Mohammed and Simret Burga (2015), Addisu Fekadu *et al.* (2013) and Tesfaye Abebe *et al.* (2012) from tested Ethiopian cultivated varieties and non-registered CIP genotypes. The greater number of tubers per plant and marketable tuber number per plot were 25 and 246.5 for genotypes J x A.170 and J x A.18. On the other hand, the highest and significantly different tuber yield per plant, marketable tuber yield and total tuber yield noted from genotype B x A.164, followed by J x A.119. In contrast, the highest significant unmarketable tuber yield 24.9 t ha^{-1} was recorded for genotype Ge x Sh.29, followed by Ge x Sh.206 13.59 t ha^{-1} due to very deep eye depth and cracking of tubers. This may show dominance of maternal inheritance traits which Gera variety (female parent) imparts very deep eye on tubers.

Generally, in the current study, about 40% potato offspring exhibited significantly higher total tuber yields than the standard check Ethiopian variety. Single genotype B x A.164 and J x A.119 showed total tuber yield advantage of 209.17% and 133.96%, respectively, over the standard check and about 36.7% and 3.5% yield advantage over Belete (high yielding registered variety) so far in Ethiopia. In a similar kind of study, Melito *et al.* (2017) found that 48% of the genotypes from a total of 27 populations which produced from seven biparental crosses/families that showed higher total tuber yield compared to the standard check.

The highest mean tuber number per plant and marketable tuber number recorded from biparental crosses of Jalene and Ater ababa whereas the maximum mean of tuber yield per plant, average tuber weight and unmarketable tuber yield found in crosses of Gera x Shenkola variety (Table 4). In addition, potato genotypes (offsprings) produced from Belete cross with Ater Ababa manifested highest mean for marketable tuber yield and total tuber yield. This may be due to over dominance of maternal effect which Belete (female parent) is high yielder variety in the country.

Tuber size distribution such as proportion of small tubers, medium tubers and large tubers ranged from 5.86 to 59.07; 26.8 to 81.08; and 0.6 to 55.67%, respectively (Table 4). The maximum mean percentage of small tubers and large tubers were noted from progenies of Jalene and Ater Ababa (41) and Gera and Shenkola accordingly. The maximum proportion of small tubers (59.07%) showed by genotype J x A.333 whereas, genotype Ge x Sh.206 and parental varieties such as shenkola and belete variety exhibited significantly highest percentages of large tubers.

Proportion of quality traits (tuber dry matter and starch content) ranged from 13.78 to 29 and 8.28-21.84% (Table 4). These results agree with the findings of Garnica *et al.* (2012) who reported tuber dry matter and starch content (%) that ranged from 22.1 to 28.06 and 15.86 to 21.51%, respectively. But higher than explained by Tesfaye Abebe *et al.* (2012) who evaluated 25 released potato varieties and the varieties overall values ranged from 17.65 to 26.70% dry matter content and 9.75 to 17.82% for total starch content under Adet environment. Potato offsprings of Belete and Ater Ababa produced higher mean tuber dry matter yield and tuber starch content (%) than other biparental crosses. Significantly lower tuber dry matter and starch content (%) were recorded from crosses of Gera and Shenkola variety by genotype Ge x Sh.186. Individual genotypes B x A.97 and J x A.266 showed higher tuber dry matter yield and starch content than all other clones. The results may be due to positive correlation of dry matter content with total starch content (r=1**) as observed in this study and suggests that continuous evaluation of these crosses may result in a higher chance of obtaining genotypes with high tuber quality traits. A total of forty (40) potato offsprings and four parental varieties produced the maximum percentages of tuber dry matter yield and starch content than the standard check variety.

The present findings are also supported by results of previous workers. Addisu Fekadu *et al.* (2013) reported availability in tuber size distribution that ranged from 4.6 to 56.67% for small sized tubers, 27.80 to 49.00% for medium sized tubers and 0.5 to 65.7% for large sized tubers. Melito *et al.* (2017) also reported the possibility of obtaining many genotypes with better tuber yield from bi-parental crosses. Similarly, Hajianfar *et al.* (2017) reported as high as 11.96, 41.22 and 37.19 t ha^{-1} tuber number per plant, total tuber yield, and marketable yield, respectively, and tuber dry matter up to 26.7% in hybrids of potato genotypes. In addition, Luthra *et al.* (2017) observed the range from 6.23 to 10.34 for tuber number per plant, 20.2 to 36.6 for marketable yield, 23.7 to 38.8 for total yield t ha^{-1} and 13.9 to 18.5% for dry matter from potato progenies. Additionally, Parmar *et a l.* (2015) showed tuber yield per plant 249.15 to 511.07gm and average tuber weight 48.53 to 98.2gm among 32 potato progenies. Furthermore, Nizamuddin *et al.* (2010); Zakerhamidi (2014) and Nickmanesh and Hassanpanah (2014) reported a wide range of tuber yield in progenies of two varietal crosses. Feltran *et al.* (2004) reported high dry matter and starch content ranged from 15.7 to 22.4% and 56.7 to 71.4%, respectively, in 18 potato cultivars.

In family base, the maximum proportion in 41 potato offspring obtained from crossing Jalene with AterAbaba showed semi-erect growth habit (39.02%), light pink flower color (80.49%), brown tuber skin color (29.27%), yellow tuber flesh color (44.34%), medium tuber eye depth (39.02%), smooth skin type

(58.54%), oval tuber shape (39.02%) and intermediate (5≤20) eye numbers(39%). On other hand, most proportion of potato offsprings/genotypes derived from Belete and Ater Ababa contained decumbent growth habit (45.83%), light pink flower (58.33%), brown tuber skin color (37.5%), yellow tuber flesh color (41.67%, medium tuber eye depth (54.16%), smooth tuber skin type (70.8%), round and long tuber shape (60%) and inter mediate tuber eye number (91.67%). However, the proportion of the genotypes generated from Gera cross Shenkola observed decumbent (45.83%) growth habit, light, and intense purple flower color (100%), light brown (30%) and white tuber skin color (50%), light yellow tuber flesh color (40%), light yellow tuber flesh color (40%) for each) and oval tuber shape (70%) in this study.

According to Kumar *et al.* (2018) white-flesh-colored potatoes are low in carotenoids (<100µg/100 g fresh weight) whereas the carotenoids content of yellow-fleshed varieties is higher (about 560µg/100 g FW). Intense yellow to near orange flesh color is associated with carotenoid concentrations >2000µg/100g. Based on this information, about 33 from a total of 75 potato progenies showed white and cream flesh color which is low in carotenoids, while other genotypes contained yellow and different flesh color which had high carotenoid content. Cultivars which possess either shallow or medium eye depths are perfect to reduce losses during peeling and trimming. Therefore, the results of crossing Belete and Ater Ababa produced large proportion of skin type highly desired for any French frying or processing industries and as such considering these parental materials seems essential to producing clonal population targeting processing industries. Hence, genotypes in this study showed difference by morphological qualitative traits not only among all families but also with in biparental crosses.

3.2. Genetic Variability Components

3.2.1. Phenotypic and genotypic coefficients of variations

The variability components (phenotypic and genotypic variances and coefficient of variations, heritability in broad sense and genetic advances as percent of mean) were estimated for agro morphological traits (Table 5). The estimates of genotypic and phenotypic coefficient of variations were computed in the range between 3.25 to 51.41 and 4.67 to 60.28%, respectively. The lowest and the highest values were computed for days to maturity and number of large tubers, respectively. According to Siva Subramanian and Menon (1973), PCV and GCV values roughly more than 20% are high, whereas values less than 10% are low and values between 10 and 20% to be medium. Correspondingly, days to flowering, plant stem height, average tuber weight, marketable tuber number, marketable tuber yield and total tuber yield exhibited high phenotype and genotypic variance indicating greater scope of selection for the improvement of these characters. Similarly, Haydar (2009) reported the maximum genotypic and phenotypic variance for plant height. Hajam *et al.* (2018) also observed highest GV and PV for average tuber weight, tuber yield per plant and total tuber yield, and in addition, Benavente and Pinto (2012) found high genotypic variance for total tuber yield from among families and within families in 30 potato genotypes which produced by biparental crossing.

Maximum phenotypic coefficients of variation (PCV) was computed for main stem number, tuber number per plant, average tuber weight, tuber yield per plant, marketable tuber number, marketable yield, total tuber yield, tuber starch content and percentages of small tubers and large tubers whereas highest genotypic coefficients of variation (GCV) had observed for traits such as main stem number, tuber number per plant, average tuber weight, tuber yield per plant, marketable tuber number, marketable yield, total tuber yield, percentages of small tubers and large tubers. In line with this study, Ozturk and Yildirim (2014) reported high genetic coefficient of variation (GCV) for total yield (26.2 %), plant height (21.2 %) and average tuber weight (20.4 %) for genotypes. The characters having high GCV indicate high potential for effective selection (Burton, 1957). Characters with high genetic variability and genetic advance are also important for selecting the desirable parents (Biswas *et al.*, 2005).

High estimates of phenotypic (PCV) and genotypic coefficients of variation (GCV) were observed for main stem number, tuber number per plant, average tuber weight, tuber yield per plant, marketable tuber number, marketable tuber yield, total tuber yield, small tuber, and large tuber percentage. The result was agreed with authors such as Hajam *et al.* (2018), noted highest GCV and PCV for traits number of main stems, total tuber yield and tuber yield per plant. The traits which exhibited high estimates of genotypic and phenotypic coefficient of variations had high probability of improvement through selection to develop new variety (Singh, 1990). Moderately high phenotypic (PCV) and genotypic coefficients of variation (GCV) were computed for plant stem height, days to 50% flowering and tuber dry matter. Moderate phenotypic coefficients of variation (PCV) were also noted for days to 50% emergency. Abraham Lamboro (2014) reported moderately high PCV and GCV for plant stem height, percentage of small tubers and days to emergence. Low estimates of PCV and GCV were obtained for days to maturity. This agrees with Kameshwari (2015) who reported the lowest GCV and PCV for days to maturity. The lowest GCV and PCV suggested that selection for the desired character based on phenotypic expression of genotypes might not be effective in attaining the desired genotypes due to the highest masking of factors to express these traits. Singh (1990) also reported low GCV and PCV values for dry matter content.

Table 4. Average family mean values (range) of evaluated genotypes for quantitative traits.

Family	No. of clone	Range	DF	MA	SN	SH	TNP	TYP	ATW	MTN	MY	UNM	TY	VSN	LTN	DM	SC
J x A	41	Min	44	88	3	33.1	7	0.23	16.61	66	6.58	0.33	10.8	6.25	0.6	14.13	8.59
		Max	53	101	9	66	25	0.97	71.38	247	43.8	8.19	44.1	59.1	40.29	27.68	20.67
		Mean	48	95	5	49.2	14	0.59	42.27	144	23.3	3.7	27.0	30	18.14	21.18	14.88
B x A	24	Min	42	88	2	32.3	6	0.27	26.45	75	8.73	1.05	11.7	5.86	3.2	15.63	9.93
		Max	55	102	6	73.3	23	1.03	78.1	226	55.6	7.65	58.3	42.5	49.78	29.00	21.84
		Mean	46	95	4	46.6	12	0.62	53.55	130	26.9	3.4	30.3	23.3	27.23	21.73	15.36
Ge x Sh	10	Min	46	90	3	41.3	8	0.3	35.11	13.5	2.51	0.58	16.8	13.2	12.6	13.78	8.28
		Max	60	99	7	71.6	17	1.03	103.3	193	33.9	24.9	45.7	52.2	55.47	25.48	18.7
		Mean	50	94	5	53.9	12	0.63	56.49	118	21.7	7.51	29.2	27.2	27.61	21.57	15.22
Jalene	1	Mean	54	93	4	50.2	15	0.6	40.96	135	23.0	4.41	27.4	36.3	17.81	18.15	12.18
Aterababa	1	Mean	45	91	4	48.1	13	0.49	39.32	108	17.1	5.34	22.4	34.9	13.19	22.18	15.76
Belete	1	Mean	48	99	2	52.9	8	0.88	106.8	111	41.0	1.66	42.6	13.2	55.67	24.3	17.66
Gera	1	Mean	52	99	2	65.8	13	0.89	72.87	157	37.1	2.23	39.3	14.3	41.31	20.98	14.69
Shenkola	1	Mean	55	101	2	66.6	10	0.82	82.11	127	36.0	1.6	37.6	16.9	55.59	23.75	17.17
Dagim	1	Mean	48	92	2	57.4	10	0.43	48.94	105	16.4	2.47	18.9	20.4	31.86	21.3	14.99
		G.mean	48	95	4	49.3	13	0.6	48.74	135	24.5	3.9	28.0	27.0	23.0	21.47	15.14

Note: *J x A = Jalene cross with Ater ababa, B x A = Belete cross with Ater ababa, Ge x Sh= Gera cross with Shenkola, Dagim = standard check variety, Min=minimum, Max = maximum, G.mean=Grand mean, DE = days to emergency, DF = days to 50% flowering, DMA = days to 90% maturity, SN = main stem number, SH (cm) = stem height, TNP = tuber number per plant, TYP (g) = tuber yield per plant, AW (g) = average tuber weight, MTN = marketable tuber number, MY = marketable yield(t* ha^{-1}*), UNMY = unmarketable yield (t* ha^{-1}*), TY = total yield(t* ha^{-1}*),VSN = very small tuber size percentage, MDN = medium tuber size percentage, LTN = large size tuber percentage, DM=tuber dry matter content (%), SG = specific gravity of tuber, and SC = tuber starch content (%).*

On this study, the PCV values were slightly higher than their corresponding GCV values for all the characters considered which reflect a little influence of environment on the expression of characters. This agrees with Getachew Assefa *et al.* (2016) and Biswas (2005) reported high phenotypic variances than genotypic variances for growth and yield traits in genotypes.

3.2.2. Heritability and genetic advance

Estimate of heritability in broad sense ranged from 28.81 to 91.64% for percentages of small sized tubers and days to flowering, respectively (Table 5). As suggested by Pramoda (2002), h^2b estimates is categorized as low < 40%, medium 40-59%, moderately high (60-79) and very high (≥80%). Based on this category, very high heritability estimate was noted for days to flowering (91.64%), tuber yield per plant (80%) and average tuber weight (80.45%) indicating the selection of genotypes for such characters could be easy and may lead to the improvement of the mean values in selected genotypes for those traits. Presence of high heritability indicated that these traits are less influenced by environmental fluctuations and governed by the additive gene effects that are substantially contributing towards the expression of traits. Similarly, Ozturk and Yildirim (2014) reported the highest board sense heritability's for average tuber weight, Moussa (2013) noted high estimates of heritability for tuber yield per plant from 17 potato genotypes comprising seven parents and their ten crosses, and Haydar (2009) also reported high heritability for tuber yield per plant and tuber numbers per plant respectively from seven potato parent and hybrids.

High heritability coupled with high genetic advances was computed for average tuber weight indicating the influence of additive gene effect on the trait. Hence, these traits can be improved through simple selection. Effectiveness of selection is considered more reliable when heritability is coupled with genetic advance. The result was in close agreement with the findings of Moussa (2013) and Biswas (2005) who reported that high heritability value along with high genetic advance for average tuber weight in potato hybrids.

Moderately high heritability was also ranged between 72.75 and 77.86% for stem height, tuber number per plant, marketable tuber yield, total tuber yield and proportions of large sized tubers while medium heritability showed for days to emergency, days to maturity, marketable tuber number, tuber dry matter and tuber starch content percentage. In line with this study, Mishra *et al.* (2017) obtained moderately high heritability for marketable yield (77.1%), total tuber yield (76.8%) and tuber dry matter from hybrids. Low heritability value noted for small tuber size (28.81%). This indicates that selection may be considerably difficult or virtually impractical due to the masking effect of the environment. High heritability accompanied with low genetic advances was recorded for tuber yield per plant. This suggested that the character was influenced due to favorable influence of environment or predominant effects of non-additive gene rather than genotypes. Panse (1957) reported that low heritability accompanied with genetic advance is due to non-additive gene effects for the particular trait. As stated, Panes and Sukhatme (1964), high heritability values associated with equally high genetic advance is chiefly due to dominance and epistasis.

The genetic advance as percent mean was categorized as low (≤10%), moderate, (10-20%) and high (≥20%) by Johnson *et al.* (1955). Based on these categories, the highest genetic advance for tested genotypes expressed as percentage of the mean (GAM) showed for all traits ranging from 25.08 to 90.33% except for days to emergency, days to maturity, percentages of tuber dry matter and tuber starch content (Table 5). Traits which showed high values of genetic advance might be due to additive gene action. Similarly, Kameshwari (2015) reported high genetic advance in percentage of mean for average tuber weight and tuber yield per plant.

Table 5. Variability components for 16 traits of evaluated 81 genotypes and parental varieties.

Trait	Range	Mean	σ^2g	σ^2p	GCV (%)	PCV (%)	Hb (%)	GA (5%)	GAM (5%)
Days to emergence	16-24	18.12	2.95	5.20	9.47	12.58	56.65	2.66	14.68
Days to flowering	42-60	61.00	36.97	40.35	12.72	13.28	91.64	11.99	25.08
Days to maturity	88-102	94.51	9.41	19.48	3.25	4.67	48.3	4.39	4.65
Stem height(cm)	32.27-73.33	49.34	73.19	95.66	17.34	19.82	76.51	15.42	31.24
Main stem number	2.0-9.0	3.80	1.08	2.04	27.23	37.43	52.9	1.56	40.79
Tuber number/plant	6.0-25.0	12.93	12.69	17.48	27.55	32.33	72.63	6.26	48.37
Average tuber weight(g)	16.61-106.83	48.74	261.72	325.32	33.20	37.01	80.45	29.89	61.33
Tuber yield /plant(kg)	0.23-1.03	0.60	0.04	0.05	32.63	35.79	80.00	0.37	61.26
Marketable tuber number	11-310	134.5	1412.61	2503.7	27.94	37.19	56.42	58.16	43.23
Marketable yield t ha^{-1}	2.51-55.62	24.46	87.61	112.52	38.26	43.36	77.86	17.01	69.55
Total yield t ha^{-1}	10.82-58.31	28.32	81.94	108.01	31.97	36.7	75.87	16.24	57.36
Tuber dry matter	13.78-29	21.47	6.23	14.47	11.62	17.72	43.02	3.37	15.7
Tuber Starch content	8.28-21.84	15.14	4.94	11.49	14.69	22.39	43.04	3.01	19.85
Small tuber	5.86-59.07	26.89	61.36	212.99	29.13	54.27	28.81	8.66	32.2
Large tuber	0.6-55.67	49.99	141.26	194.18	51.41	60.28	72.75	20.88	90.33

Note: *σ^2g = genotypic variance, σ^2p = phenotypic variance, PCV (%) = phenotypic coefficient of variation (%) = genotypic coefficient of variation, Hb (%) = heritability in broad sense, GA = genetic advance, and GAM = genetic advance as percent of mean.*

3.2.3. Phenotypic and genotypic correlations

The estimates of genotypic and phenotypic correlation coefficients between total tuber yield and all possible pairs of yield components are presented in Table 6. Phenotypic and genotypic association of days to emergency with days to flowering was positive. This indicates that selection for this trait may lead to early mature genotypes. Days to emergency was negatively correlated with main stem number, tuber number per plant and marketable tuber number at phenotypic and genotypic levels but, positively correlated with proportion of large tuber size at both levels. Plant stem height positively correlated with tuber yield per plant, tuber number plant, average tuber weight, marketable tuber number, marketable tuber yield, total tuber yield, tuber dry matter, tuber starch content and proportion of large tuber sized tubers at both correlations level but, it correlated negatively with proportion of small tuber size at genotypic level.

Total tuber yield showed positive genotypic and phenotypic association with days to maturity, tuber number per plant, average tuber weight, marketable tuber number, tuber dry matter, tuber starch content and proportion large tuber size but showed negative association with proportion of small tuber sizes. Both marketable tuber yield and total tuber yield were positively correlated with plant stem height, tuber yield per plant, tuber number per plant, marketable tuber number and average tuber weight, tuber dry matter, tuber starch content and proportion of large tuber numbers at phenotypic level. These positive correlations indicating that selection for improving one character will lead to increase the other one which is positively correlated with that character. In contrast, marketable tuber yield and total tuber yield were negatively correlated with proportion of small tuber sizes. In similarly with Abraham Lamboro *et al.* (2014) and Addisu Fekadu *et al.* (2013) who reported highly significant negative correlation of total tuber yield with proportion of small sized tubers at genotypic and phenotypic level. Negative correlation between two traits implies selection for improving one character will likely cause decrease in the other traits.

In present study the tuber dry matter had exhibited strong phenotypic and genotypic correlation ($r = 1$) with tuber starch content. This suggested that the simple selection to improve one trait simultaneously increase the second character. Similarly, highly significant correlation was reported for dry matter and tuber starch content by Wassu Mohmmad (2016) who observed the correlation was near to perfect ($r = 0.97$ to 0.99) and Khayatnezhad *et al.* (2011) that reported stronger positive and significant correlations between starch content and dry matter content. Generally, in most of traits genotypic correlation was higher than phenotypic correlation indicating an inherent association between various characters. This agrees with Addisu Fekadu *et al.* (2013) who reported higher genotypic correlation than phenotypic correlation. The main genetic cause of such correlation is pleiotropy, which refers to manifold effects of a gene (Falconer, 1989).

Above results were similarly reported by Tripura *et al.* (2016) who found tuber number per plant have positive and significant association with total tuber yield. Panigrahi *et al.* (2017) reported that total tuber yield showed positive and significant correlation with marketable tuber yield at both phenotypic as well as at genotypic levels. Sattar *et al.* (2007) reported tuber yield per plant was positively and significantly correlated with number of tubers per plant, average tuber weight and dry matter content of tuber. He also showed the significant positive genotypic correlation of average weight of tubers with number of tubers per plant, yield of tuber per plant and tuber dry matter percentages.

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for different pairs of traits in potato.

Trait	DE	DF	DMA	SH	SN	TYP	TNP	AW	MTN	MY	TY	DM	SC	SMN	LSN
DE	1	0.24*	0.14	-0.21	-0.4**	-0.15	-0.26*	0.1	-0.24*	-0.09	-0.09	0.07	0.07	-0.09	0.14
DF	0.21*	1	-0.07	0.1	-0.15	0.11	0.01	0.15	0.00	0.12	0.14	0.05	0.05	-0.014	0.23*
DMA	0.04	-0.03	1	0.02	0.02	-0.03	0.07	0.02	0.04	0.07*	0.11*	-0.03	-0.03	0.09	0.07
SH	-0.17*	0.07	-0.02	1	0.1	0.102	0.73**	0.36**	0.43**	0.67**	0.71 **	0.41**	0.41**	-0.30*	0.43**
SN	-0.29*	-0.13	-0.04	0.07	1	0.13	0.53**	-0.36**	0.42**	0.08	0.1	0.04	0.04	0.19	-0.39**
TYP	-0.12	0.09	0.02	0.69**	0.11	1	0.5**	0.49 **	0.61**	0.91**	0.97**	0.54**	0.54**	-0.4**	0.54**
TNP	-0.2*	-0.00	-0.02	0.35**	0.45**	0.5**	1	-0.35*	0.8**	0.39*	0.47**	0.38*	0.38*	0.23*	-0.35*
AW	0.08	0.13	0.03	0.38**	-0.3**	0.59**	-0.36**	1	-0.03	0.35*	0.59**	0.25*	0.25*	-0.58**	0.90**
MTN	-0.23*	-0.02	-0.23*	0.38**	0.34**	0.57**	0.71**	-0.05	1	0.7**	0.64**	0.47**	0.47**	-0.36*	-0.01
MY	-0.10	0.10	0.05*	0.61**	0.06	0.89**	0.41**	0.54**	0.67**	1	0.95**	0.52**	0.52**	-0.56**	0.61**
TY	-0.08	0.11	0.06*	0.68**	0.07	0.95**	0.49**	0.54**	0.54**	0.93**	1	0.56**	0.56**	-0.40*	0.57**
DM	-0.06	0.04	0.03*	0.31**	0.05	0.45**	0.3**	0.21*	0.38**	0.44**	0.45**	1	1.00**	-0.21	0.18
SC	-0.06	0.04	0.03*	0.31**	0.05	0.45**	0.3**	0.21*	0.38**	0.44**	0.45**	1.0**	1	-0.21	0.18
SMN	0.08	0.01	-0.04	-0.14	0.08	-0.23*	0.16*	-0.39**	-0.52**	-0.4**	-0.20*	-0.21*	-0.21*	1	-0.64**
LSN	0.1	0.21*	0.05	0.39**	-0.35	0.51**	-0.34**	0.87**	-0.03	0.57**	0.53**	0.14	0.14	0.14	1

Note: **and **, significant at P<0.05 and P<0.01, respectively, DE = days to emergency, DF = days to flowering, DMA = days to maturity, SH = plant stem height, SN = main stem number, TYP = tuber yield per plant, TNP=tuber number per plant, AW = average tuber weight, MTN = marketable tuber number, MY = marketable yield, UNMY = unmarketable yield, TY = total tuber yield, SMN = very small tuber size percentage, LSN = large size tuber percentage, DM = tuber dry matter content (%) and SC = tuber starch content (%).*

4. Conclusions

Genetic variability is the base for the crop improvement. The availability of more diverse current materials obtained from local crossing indicated the chance of getting desirable genes to improve the potato crop. Hence, potato offspring generated from hybridization of cultivated potato varieties showed genetically variability in yield and its related traits and morphological traits in the current study. The high range and mean values of the evaluated parental varieties and progenies also suggest that the existence of enough variability correlations of traits. Biparental crosses of Jalene with Aterababa and Belete with Aterababa varieties produced more promising/better genotypes than the crosses of Gera and Shenkola, and standard check variety in yield and yield related traits. So, the result of this study also indicated the continuously producing more diverse clones by local crossing can reduce dependency on international potato center materials in the country. Therefore, additional experiments will be carried out to evaluate the most promising genotypes for desirable traits, with the purpose to either produce new variety or select parental lines for further breeding.

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