



International Journal of  
**Plant Breeding  
and Genetics**

ISSN 1819-3595



Academic  
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## Variability and Association of Quantitative Traits in Anchote (*Coccinia abyssinica* (Lam.) Cogn.) in Ethiopia

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### ABSTRACT

Forty nine anchote (*Coccinia abyssinica* (Lam.) Cogn.) accessions were planted in simple lattice design at Bako Agricultural Research Center in 2011 to estimate components of variability, heritability, genetic advance and association among quantitative traits. Highly significant difference ( $p \leq 0.01$ ) and wider range of variations were observed for most of the characters. High genotypic coefficient of variation along with high heritability and genetic advance was obtained from hundred seed weight, number of seeds per fruit, number of fruits per plant, root yield per plant, total root yield, marketable root yield and average fruit yield, showing the possibility of anchote yield improvement through selection. However, the rest characters showed low genetic variability, heritability and genetic advance under selection. Average root yield was positively and significantly ( $p < 0.01$ ) associated at genotypic and phenotypic level with root diameter ( $r_g = 0.858$  and  $r_p = 0.593$ ) and it also showed positive and highly significant association with root length ( $r_g = 0.482$  and  $r_p = 0.345$ ) signifying that indirect improvement would be very effective. Further evaluation including more accessions at different locations is suggested for having appropriate information.

**Key words:** *Coccinia abyssinica*, genetic variability, heritability, genetic advance, correlation

### INTRODUCTION

Anchote (*Coccinia abyssinica*) is an endemic perennial trailing plant cultivated for its tuberous root in the south and western parts of Ethiopia, an area where other root crops also grown (Schippers, 2000). The crop has high nutritional values as well as great potential for medicinal, economic and socio-cultural make use of (Hora, 1995). It is rich in carbohydrate, vitamins, minerals, protein and calcium as compared to other root crops (Fekadu, 2011). The roots basically represent a source of energy and leaves with vines are a source of protein (Fikadu, 2011). Traditional medicinal practitioners use anchote to treat different type of diseases such as diabetes, gonorrhoea, tuberculosis, asthma and cholesterol lowering (Getahun, 1985). Furthermore, it is a potential root crop that can tolerate drought, poor soil conditions and termites attack (Sisay *et al.*, 2009). Well adapted to an elevations varying from 1300 to 2800 m.a.s.l. where the rainfall ranges from 762-1016 mm. The mean minimum and mean maximum temperature required for proper anchote growth and development is 12 and 28°C, respectively and it prefers soil pH ranges from 4.5 to 7.5 (Getahun, 1985).

The first step in any plant breeding program is to identify plants that exhibit variation for the traits of interest. Desirable traits of combination should be sought among plants in existing populations such as recommended cultivars, breeding lines and landrace cultivars. Information on the extent and nature of variability in a population is very essential for further improvement in a given crop. Though anchote has been in cultivation for many years and an important crop to small holder farmers so far, apart from some observations made in nutritional contents of the crop, the extent and nature of variability for yield and other desirable traits is not yet systematically assessed. Effective utilization of anchote germplasm for selection requires information on the genetic variability as an essential prerequisite for further improvement of anchote. Therefore, the present study was designed and was undertaken to generate such information using 49 anchote accessions.

## MATERIALS AND METHODS

Forty nine anchote accessions obtained from Debre Zeit Agricultural Research Center were used in this study (Table 1). The study was conducted at Bako Agricultural Research Center (at 1650 meters above sea level) in western Ethiopian agro ecologies on nitosols under rain fed conditions of 2011 cropping season. The experiment was laid out in 7×7 Simple Lattice Design (Yates, 1936). The plot size was five rows of 2 m length and 40 cm between rows (4 m<sup>2</sup>) and 20 cm between plants within a row. Trials were hand planted on flat bed (plot) with two seeds per hill at depth of five centimeter and it was thinned to one seedling per hill after a month of planting to get 125, 000 plant

Table 1: Lists of anchote germplasm accessions used in this study

Accessions	Woreda/district	Altitude (m.a.s.l.)	Accessions	Woreda	Altitude (m.a.s.l.)
207984	Asosa	1400	90802-1	A/Chomen	1980
DD	Gidda gebo	2359	90801	A/Chomen	1780
DD-1	Gidda gebo	2359	90802	A/Chomen	1780
223085	Digga leka	2200	223108	Ale	2150
223086	Digga leka	2200	223109	Ale	2150
223092	Sibu sire	1900	223110	Ale	2150
223093	Sibu sire	1900	223112	Bedelle	1980
223094	Sibu sire	1900	223108-1	Ale	1920
223096	Guto wayu	2100	223109-1	Ale	2050
223097	Guto wayu	2100	223104	Dedo	1800
223098	Guto wayu	2100	223105	Dedo	1800
223099	Jimma arjo	2560	223113	Manna	1980
223100	Jimma arjo	2560	240407G	Dacha	2150
223101	Jimma arjo	2560	240407B	Decha	2000
DIGGA	Digga	2123	229702-1	Hulet Iju Enese	1890
KICHI	Gute	1821	220563	Bako Tibe	1780
KUWE	Sibu sire	1987	220563-1	Bako Tibe	1750
SODDU	Sibu sire	1823	223087	Gimbi	2300
DIGGA-1	Digga	2123	223088	Gimbi	2300
223096-1	Guto wayu	2320	223090	Gimbi	2300
223086-1	Digga leka	2180	GM	Gimbi/A/Sena	2400
KICHI-1	Gute	1821	230566	Gimbi	1820
KUWE-1	Sibu sire	1987	223090-1	Gimbi	2112
223097-1	Guto wayu	2230	223087-1	Gimbi	2165
DIGGA-2	Digga	2123			

population per hectare. Fertilizer were applied as Diammonium Phosphate (DAP) and urea at the rate of 46 kg N and 20 kg P<sub>2</sub>O<sub>5</sub> (Girma and Gudeta, 2007). All recommended rate of P<sub>2</sub>O<sub>5</sub> were applied at the time of planting while N was applied in split, half at the time of planting and the remaining half at the start of vine development. Crop management practices such as weeding, cultivation etc., were performed as per recommendation (Girma and Gudeta, 2007).

Data on 22 quantitative traits were recorded on plant basis with 10 plants from each accession by random sampling method from the middle rows and marked at early stage before the vines development. Data were recorded for quantitative traits by adopting descriptors of cucurbits (ECPGR, 2008) and descriptors of sweet potato (Huaman, 1991). The data were collected on vine number, flower width (cm), days to 50% emergence, number of fruits per plant, fruit yield per plant (kg), total root yield (t ha<sup>-1</sup>), hundred seeds weight (g), root yield per plant (kg), marketable root yield (t ha<sup>-1</sup>), root length(cm), fruit weight (g), fruit diameter (cm), fruit length (cm), number of seeds per fruit, flower length (cm), maturity date , root diameter (cm), internodes length (cm), leaf length (cm), vine length (cm), petiole length (cm) and internodes diameter (mm).

The relative efficiency of simple lattice design obtained was better than randomized complete block design (Table 2). Therefore, data of all traits were subjected to Analysis of Variance (ANOVA) based on simple lattice design using SAS (2008) computer software. The difference between treatments mean was compared using LSD at 5% probability level. The phenotypic and genotypic variances and coefficient of variations were estimated as per the procedure suggested by Burton and DeVane (1953). Heritability in the broad sense for quantitative characters was computed using the formula suggested by Singh and Chaudhary (1985). Genetic Advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1999). The character associations presented by correlation coefficient between different pairs of characters at the genotypic and phenotypic level were calculated from the genotypic, phenotypic and environmental covariance obtained by covariance analysis.

## RESULTS AND DISCUSSIONS

The analysis of variance showed highly significant ( $p \leq 0.01$ ) differences among the tested accessions for most characters except days to maturity, flower length and width (Table 2). The economic traits like root length, root diameter, root yield per plant, marketable root yield and total root yield showed highly significant differences among anchote accessions. These significant variations among tested materials for the characters indicated the existence of variability to have an effective selection. In view of this it is reasonable to state that there is a good chance to improve anchote through selection breeding. The variation observed for measured quantitative traits in this study were in agreement with the earlier findings of Desta (2011) who reported the significant difference among 36 anchote accessions; Tsegaye *et al.* (2007) on 30 sweet potato genotypes and AbdEl-Salam *et al.* (2010) six snake cucumber genotypes.

The mean storage root yield of anchote accessions ranged from 25.00 to 65.63 t ha<sup>-1</sup> of which 40.82% of the accessions gave root yield exceeding grand mean (40.740 t ha<sup>-1</sup> meanwhile, >79.50% of the accessions showed highest mean root yield values than accessions collected from Bako area indicating its greatest role to the total variability observed among anchote accessions (Table 3). Of all tested materials the highest storage root yield (65.63 t ha<sup>-1</sup>) was obtained for accession Kichi which was collected from mid altitude (1821 m.a.s.l.) of Gute Woreda (Oromia) while, the lowest storage root yield (25.00 t ha<sup>-1</sup>) for accession 223090 which was collected from the mid altitude (2300 m.a.s.l.) of Gimbi Woreda (Oromia). On the other hand, of all tested materials based on mean

Table 2: Analysis of variance (mean squares) for 22 characters of 49 anchote accessions grown at BARC (2011/12)

Sources of variation	Mean squares							Efficiency relative to RCBD
	Replication	Treatment		Block within replication	Error		R <sup>2</sup> %	
		Unadjusted	Adjusted		Interablock	RCBD		
df	1	48	48	12	36	48	-	-
RD (cm)	1.760	1.770	1.610**	0.130	0.230	0.210	91.280	88.760
INL (cm)	6.230	3.490	3.000**	0.680	0.980	2.280	82.360	90.740
FRYPP (kg)	0.000	0.020	0.010**	0.000	0.000	0.006	96.910	91.020
FRWt (g)	0.090	181.620	165.720**	14.390	15.320	15.090	94.150	98.480
HSWt (g)	0.010	1.890	1.520**	0.050	0.050	0.050	97.890	98.960
VN (cm)	0.010	0.930	0.800**	0.010	0.010	0.460	99.180	100.000
FW	0.010	0.150	0.140ns	0.140	0.130	0.130	65.780	100.230
DM	2450.000	257.870	253.380ns	210.710	172.920	238.430	75.040	101.770
TRY (t ha <sup>-1</sup> )	91.410	216.640	197.360**	18.790	14.250	15.380	95.430	101.820
RYPP (kg)	0.010	0.010	0.010**	0.000	0.001	0.000	95.370	102.030
MRY (t ha <sup>-1</sup> )	77.130	208.700	191.640**	19.850	14.630	15.930	95.150	102.200
RL (cm)	9.900	1.590	1.480**	0.800	0.570	0.630	82.350	102.600
DE	34.330	5.420	4.420**	2.140	1.500	3.860	85.560	102.930
NFRPP	0.000	6.230	5.020**	0.120	0.070	0.080	99.150	106.060
PEL (cm)	20.030	10.170	8.800**	1.880	1.300	5.880	92.990	106.370
FRD (cm)	0.030	0.070	0.050**	0.040	0.020	0.030	82.810	106.660
FRL (cm)	0.190	0.120	0.110**	0.050	0.030	0.030	86.580	107.630
FL (cm)	0.020	0.040	0.040ns	0.050	0.030	0.030	72.630	107.820
NSPF	110.370	468.660	364.560**	14.190	6.820	8.660	98.930	112.440
IND (mm)	0.000	0.010	0.010**	0.000	0.002	0.000	91.850	117.040
VL (cm)	135.580	2558.520	2048.220**	1075.880	424.270	587.170	89.890	120.200
LL (cm)	16.160	6.520	6.150**	2.630	0.900	1.330	91.760	127.260

\*\*Highly significant at 0.01 probability level, ns: Non significant RCBD: Randomized complete block design, R<sup>2</sup>: Reliability of model df: Degree of freedom, VN: Vine No., FW: Flower width, DE: Days to 50% emergence, NFRPP: No. of Fruits plant<sup>-1</sup>, FRYPP: Average fruit yield plant<sup>-1</sup>, TRY: Total root yield, HSWt: Hundred seeds weight, RYPP: Average root yield plant<sup>-1</sup>, MRY: Marketable root yield, RL: Root length, FRWt: Average fruit weight, FRD: Fruit diameter, FRL: Fruit length, NSPF: No. of seeds fruit<sup>-1</sup>, FL: Flower length, MD: Maturity date, RD: Root diameter, INL: Internodes length, LL: Leaf length, VL: Vine length, PEL: Petiole length and IND: Internodes diameter

values, the highest fruit yield per plant (0.44 kg) was noted for the accession 223101 which was collected from the high land (2400 m.a.s.l.) of Jimma Arjo Woreda (Oromia) whereas, the lowest fruit yield per plant (0.03 kg) was noted for accession 207984 which was collected from the low land (1400 m.a.s.l.) of Asosa zone (Benishangul Gumuz). The high storage root yielding anchote accession (Kichi followed by GM) has medium maturity period.

Genotypic and phenotypic variance ranging from 0.002 to 811.980 and 0.006 to 1236.250, respectively, were estimated for the traits considered in this study (Table 3). Thus, high phenotypic variance values 1236.25, 185.69, 105.80, 103.14 and 90.40 were noted for characters like vine length, number of seeds per fruit, total root yield, marketable root yield and average fruit weight, respectively. In addition, high genotypic variance values of 811.98, 178.87, 91.56, 88.51 and 75.31 were noted for same characters.

According to Deshmukh *et al.* (1986) PCV and GCV value is higher if it is = 20%, medium (10-20%) and lower = 10%. Accordingly, high phenotypic coefficient of variation were noted for

Table 3: Estimates of range, mean, phenotypic ( $\sigma^2_p$ ) and genotypic ( $\sigma^2_g$ ) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability ( $H^2$ ), expected genetic advance (GAM) and genetic advance as a percentage of mean (GA%) for 19 characters of 49 anchote accessions at BARC (2011/2012)

Characters	Range		Mean	$\sigma^2_g$	$\sigma^2_p$	GCV (%)	PCV (%)	$H^2$ (%)	GA	GAM (%)
	Minimum	Maximum								
DE	9.000	14.000	11.450	1.460	2.960	10.560	15.030	49.310	1.750	15.270
PEL (cm)	8.550	18.810	12.360	3.750	5.050	15.670	18.180	74.220	3.440	27.800
LL (cm)	9.390	20.000	12.600	2.630	3.530	12.860	14.900	74.510	2.880	22.880
INL (cm)	8.780	15.750	11.710	0.360	2.640	5.120	13.880	13.620	0.460	3.890
IND (cm)	0.330	0.850	0.430	0.004	0.006	14.800	17.939	68.067	0.108	25.152
VL (cm)	163.240	332.490	229.710	811.980	1236.250	12.400	15.310	65.680	47.570	20.710
VN	1.000	4.000	2.970	0.170	0.630	13.860	26.780	26.790	0.440	14.780
FRL (cm)	1.470	2.790	2.480	0.040	0.070	7.970	10.490	57.650	0.310	12.460
FRD (cm)	1.270	2.790	2.000	0.020	0.040	6.180	9.690	40.640	0.160	8.110
NFRPP	1.000	10.000	5.730	2.470	2.540	27.430	27.820	97.190	3.190	55.700
FRWt (g)	22.140	62.410	43.080	75.310	90.400	20.140	22.070	83.310	16.320	37.880
NSPF	20.000	85.000	47.040	178.870	185.690	28.430	28.970	96.330	27.040	57.480
HSWt	1.350	5.650	2.870	0.730	0.790	29.850	30.930	93.160	1.700	59.350
FRYPP (kg)	0.030	0.440	0.250	0.002	0.008	17.889	35.777	25.000	0.046	18.425
RL (cm)	7.620	11.710	9.730	0.450	1.030	6.930	10.410	44.360	0.930	9.510
RD (cm)	4.130	8.890	6.430	0.700	0.910	13.010	14.820	77.060	1.510	23.520
RYPP (kg)	0.200	0.520	0.330	0.005	0.006	20.328	22.473	81.818	0.125	37.878
MRY (t ha <sup>-1</sup> )	24.820	64.750	40.050	88.510	103.140	23.490	25.360	85.810	17.950	44.830
TRY (t ha <sup>-1</sup> )	25.000	65.620	40.740	91.560	105.800	23.490	25.250	86.540	18.340	45.010

CH: Character, GV: Genotypic variance, PV: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation,  $H^2$ : Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as a percentage of mean, VN: Vine number, DE: Days to 50% emergence, NFRPP: No. of fruits plant<sup>-1</sup>, FRYPP: Fruit yield plant<sup>-1</sup>, TRY: Total root yield, HSWt: Hundred seeds weight, RYPP: Root yield plant<sup>-1</sup>, MRY: Marketable root yield, RL: Root length, FRWt: Fruit weight, FRD: Fruit diameter, FRL: Fruit length, NSPF: No. of seeds fruit<sup>-1</sup>, RD: Root diameter, INL: Internodes length, LL: Leaf length, VL: Vine length, PEL: Petiole length and IND: Internodes diameter

characters like average fruit yield per plant (35.777%), hundred seed weight (30.930%), number of seeds per fruit (28.790%), number of fruits per plant (27.820%), vine number (26.720%), marketable root yield (25.360%), average root yield per plant (22.470%), total root yield (25.350%) and average fruit weight (22.070%). Same characters showed high genotypic coefficients of variation, except vine number and average fruit yield per plant which showed medium genotypic coefficients of variation. In addition, medium (10-20%) phenotypic and genotypic coefficients of variation were obtained for the characters like petiole length (18.180 and 15.670%), internodes diameter (17.930 and 14.800%), vine length (15.310 and 12.400%), days to 50% emergence (15.030 and 10.560%), leaf length (14.900 and 12.860%), root diameter (14.820 and 13.010%). Internodes length (13.880%), fruit length (10.490%) and root length (10.410%) showed medium values of PCV level only and vine number (13.86%), vine length (12.40) genotypic values signifying the existence of high genetic variability among anchote accessions.

Furthermore, the current finding revealed that, for all characters, estimates of phenotypic coefficients of variation were higher than genotypic coefficient of variation (Table 3), indicating the apparent variations in the accessions were not only genotypic but also environmental influence. This observation agrees with the earlier finding of Aina *et al.* (2007) in cassava. However,

phenotypic coefficients of variation and genotypic coefficients of variation in this study were close to one another for most characters, indicating the high contribution of genotypic variance to the expression of these characters than environmental variance and favors greater possibilities of improvement through selection. These high proportions of phenotypic and genetic variation along with high GCV and PCV indicating, genotype could be reflected by the phenotype and the effectiveness of selection based on phenotypic performance for these characters. Meaning, genetic variation can play important role in the inheritance of yield attributes in anchote and is an indication of high response to selection. The present finding is in line with the finding of Tsegaye *et al.* (2007) in 30 sweet potato genotypes. The present study is in agreement with the findings of AbdEl-Salam *et al.* (2010) in snake cucumber genotypes, Afangideh and Uyoh (2007) cucumber genotypes, Akinwale *et al.* (2010) in cassava genotypes, Desta (2011) in anchote accessions, Tsegaye *et al.* (2007) in sweet potato genotypes.

According to Singh (2001) heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40-59% are medium and values less than 40% are low. Accordingly, very high heritability values were noted for quantitative characters like number of fruits per plant (97.190%), number of seeds per fruit (96.330%), hundred seed weight (93.160%), total root yield (86.540%), marketable root yield (85.810%) and fruit weight (83.310%) (Table 3). Root yield per plant (81.818%), root diameter (77.060%), leaf length (74.510%), petiole length (74.220%), internodes diameter (68.670%) and vine length (65.68%) showed moderately high heritability. Subsequently, medium heritability were recorded for the characters such as fruit length (57.65%), days to 50% emergence (49.31%), root length (44.36%) and fruit diameter (40.64%) suggesting such characters were least affected by environmental modifications so that, selection based on phenotypic performance would be reliable. On the other hand, low heritability were recorded for traits like vine number (26.790%), fruit yield per plant (25.000%) and internodes length (13.620%) indicating environmental effect constitutes a major portion of the total phenotypic variation. This finding is in line with the finding of Akinwale *et al.* (2010) in 43 cassava genotypes and sweet potato genotypes Tsegaye *et al.* (2007) and Jones (1986). Afangideh and Uyoh (2007) also, reported very high heritability values for the traits like vine length, average fruit number and fruit yield while medium heritability value for trait fruit length in cucumber. As opposed to this finding AbdEl-Salam *et al.* (2010) found low heritability values for fruit yield per plant. He also found moderately high heritability values for number of fruits per plant, fruit diameter and fruit length in snake cucumber genotypes collected from different regions of Egypt.

Genetic advance (GAM%) as percent of mean was ranged from 3.89% (for internodes length) to 59.35% (for hundred seed weight) (Table 3). Within these range, a relatively high genetic advance was observed for hundred seed weight (59.35%), number of seeds per fruit (57.48%) and number of fruits per plant (55.70%). Fruit diameter, root length and internodes length showed lowest genetic advance. Selection based on those traits with a relatively high GAM will result in the improvement of performance of genotypes for the traits. This low GAM arises from low estimate of phenotypic variance and heritability. This result is in line with the work of Tsegaye *et al.* (2007) in 30 sweet potato genotypes, Afangideh and Uyoh (2007) in cucumber and AbdEl-Salam *et al.* (2010) in snake cucumber.

Estimate of genetic advance is more useful as a selection tool when considered jointly with high genotypic coefficients of variation and heritability values (Johnson *et al.*, 1955). Accordingly, characters like hundred seed weight, number of seeds per fruit, number of fruits per plant, total

Table 4: Phenotypic ( $r_p$ ) correlation coefficient of the 17 characters in 49 anchote accessions grown at BARC (2011/12)

Characters	AFRYPP	PEL	LL	INL	IND	VL	VN	FRL	FRD	NFRPP	AFRW	NSPF	HSWT	RL	RD	ARYPP
DE	0.070	-0.213	0.071	0.031	0.260	-0.036	0.120	0.009	0.206	0.042	-0.011	-0.032	0.019	0.055	0.017	-0.009
AFRYPP	-	0.079	0.316*	0.255	0.004	-0.045	0.141	0.096	0.191	0.678**	0.619**	-0.071	0.166	-0.124	-0.048	0.099
PEL		-	0.226	0.071	-0.002	-0.058	-0.007	0.268	-0.022	-0.008	0.145	-0.066	0.159	-0.122	-0.114	0.064
LL			-	0.177	0.025	-0.196	-0.127	0.266	0.072	0.255	0.127	-0.342*	0.325*	-0.095	-0.074	-0.067
INL				-	-0.161	0.205	-0.026	0.090	-0.091	0.029	0.206	-0.202	0.033	0.175	-0.069	0.053
IND					-	0.025	0.131	-0.266	-0.144	0.104	-0.080	-0.213	-0.152	0.145	0.057	0.020
VL						-	-0.231	-0.095	-0.178	-0.024	-0.057	0.097	-0.196	0.159	0.042	0.250
VN							-	-0.199	-0.025	-0.109	0.334*	-0.176	0.171	0.159	-0.090	0.001
FRL								-	0.473**	-0.027	0.119	0.123	0.232	-0.204	-0.212	-0.219
FRD									-	0.068	0.167	0.115	0.171	-0.034	-0.178	-0.222
NFRPP										-	-0.036	0.019	0.169	-0.165	0.105	0.218
AFRW											-	-0.043	0.052	-0.144	-0.214	-0.181
NSPF												-	-0.032	-0.172	-0.223	-0.167
HSWt													-	-0.077	-0.346*	-0.159
RL														-	0.037	0.345*
RD															-	0.593**

\*\*\*Significant at probability level of 0.05 ( $r = 0.281$ ) and 0.01 values ( $r = 0.362$ ), respectively, DE: Days to 50% emergence, AFRYPP: Average fruit yield plant<sup>-1</sup>, PEL: Petiole length, LL: Leaf length, INL: Internodes length, VL: Vine length, VN: Vine number, FRL: Fruit length, FRD: Fruit diameter, NFRPP: No. of fruits plant<sup>-1</sup>, AFRWt: Average fruit weight, NSPF: No. of seeds fruit<sup>-1</sup>, HSWt: Hundred seeds weight, RL: Root length, RD: Root diameter, ARYPP: Average root yield plant<sup>-1</sup>

root yield, marketable root yield, average fruit weight and average root yield per plant showed high genotypic coefficients of variation, heritability values and genetic gain indicating these characters are principally under genetic control (due to high additive gene effect) and selection for them can be achieved through their phenotypic performance. For traits with high heritability value but moderate value of genetic advance needs careful selection for such traits. Similarly, characters with high heritability values but low value of genetic advance may be governed by non additive gene action or high genotype by environmental interaction and used for development of hybrid varieties. Lower heritability values and genetic advance for internodes length implies most of the variations for these traits were environmental and such traits requires management practice than selection to improve the traits performance.

A trait with high heritability value but low GCV implies its improvement through early generation selection does not give the desired results. Under low GCV and heritability values direct selection for the trait may not be possible but through indirect selection of other secondary traits. Generally, the high value for heritability and genetic advance of the characters in current study provide information for the existence of wider genetic diversity among anchote accessions and this offers high chances for improving several traits of the crop through simple selection.

Phenotypic ( $r_p$ ) and genotypic ( $r_g$ ) correlation estimates of average root and fruit yield per plant as well as various characters were presented in Table 4 and 5, respectively. Average root yield per plant was positively and significantly ( $p < 0.01$ ) correlated both at phenotypic and genotypic level with root diameter and root length. Indicating accessions producing more root diameter and root length are high yielder. Conversely, average root yield per plant showed negative and highly significant correlation with fruit length ( $r_g = 0.387$ ) and fruit diameter ( $r_g = 0.473$ ) only at genotypic level indicating simultaneous improvement for root yield and fruit yield is ineffective. Similarly, average fruit yield per plant were positively and significantly correlated with number of fruits per plant and average fruit weight both at phenotypic and genotypic levels. Moreover, average root



Table 5: Genotypic ( $g_s$ ) correlation coefficient of the 17 characters in 49 anchote accessions grown at BARC (2011/12)

Characters	DE	AFRYPP	PEL	LL	INL	IND	VL	VN	FRL	FRD	NFRPP	AFRW	NSPF	HSWT	RL	RD	ARYPP
DE	1	0.074	-0.253	0.077	-0.078	0.416**	-0.258	0.215	-0.061	0.094	0.090	-0.085	-0.080	0.020	0.366**	-0.010	0.004
AFRYPP		1	0.084	0.335*	0.316*	-0.002	-0.100	0.149	0.030	0.147	0.720**	0.601**	-0.059	0.168	-0.245	-0.021	0.088
PEL			1	0.226	0.091	-0.084	0.031	-0.002	0.303*	-0.159	-0.038	0.157	-0.076	0.166	-0.259*	-0.187	0.026
LL				1	0.309*	-0.143	-0.354*	-0.132	0.429**	0.118	0.312*	0.075	-0.394**	0.430**	-0.387**	-0.028	-0.170
INL					1	-0.313*	0.289*	-0.043	0.066	-0.292*	0.044	0.296*	-0.265	0.047	0.339*	-0.117	0.108
IND						1	-0.086	0.162	-0.532**	-0.256	0.106	-0.117	-0.248	-0.186	0.120	0.052	0.031
VL							1	-0.304*	-0.230	-0.218	-0.017	-0.120	0.074	-0.277	0.199	0.266	0.321*
VN								1	-0.268	-0.020	-0.136	0.387**	-0.181	0.178	0.214	-0.128	-0.002
FRL									1	0.308*	-0.087	0.046	0.175	0.271	-0.583**	-0.296*	-0.387**
FRD										1	0.041	0.056	0.135	0.193	-0.075	-0.297*	-0.473**
NFRPP											1	-0.055	0.013	0.169	-0.187	0.102	0.209
AFRW												1	-0.025	0.046	-0.227	-0.284*	-0.236
NSPF													1	-0.054	-0.207	-0.303*	-0.220
HSWt														1	-0.109	-0.484**	-0.165
RL															1	0.470**	0.482**
RD																1	0.858**
ARYPP																	1

\*\*Significant at probability level of 0.05 ( $r = 0.281$ ) and 0.01 values ( $r = 0.362$ ), respectively, DE: Days to 50% emergence, AFRYPP: Average fruit yield plant<sup>-1</sup>, PEL: Petiole length, LL: Leaf length, INL: Internodes length, VL: Vine length, VN: Vine No., FRL: Fruit length, FRD: Fruit diameter, NFRPP: No. of fruits plant<sup>-1</sup>, AFRWt: Average fruit weight, NSPF: No. of seeds fruit<sup>-1</sup>, HSWt: Hundred seeds weight, RL: Root length, RD: Root diameter, ARYPP: Average root yield plant<sup>-1</sup>

yield per plant had positive and significant association with vine length at genotypic level while, average fruit yield per plant had positive and significant association with leaf length (both at phenotypic and genotypic levels) and internodes length. This result is in agreement with work of Tsegaye *et al.* (2006) and Hossain *et al.* (2010) in sweet potato genotypes.

Average fruit yield per plant had positive significant correlation with leaf length, number of fruits per plant and average fruit weight. Positive and highly significant correlation was noted between fruit length and fruit diameter. Average root yield per plant showed positive and highly significant correlation with root length and root diameter suggesting that, improvement aimed at any one of the character would lead to improvement in root yield. It is in line with the report of Afangideh and Uyoh (2007) in cucumber; AbdEl-Salam *et al.* (2010) in snake cucumber.

Estimates of genotypic correlation coefficients between each pair of characters are presented in Table 5. Accordingly, positive and highly significant genotypic correlations were observed between days to 50% emergence and internodes diameter ( $r_g = 0.416$ ) and days to 50% emergence and root length ( $r_g = 0.366$ ) while, it had no significant correlation with the rest of characters.

The vegetative characters like any other non vegetative characters had either positive or negative association with each other or with other characters. Cogent of this, petiole length showed positive and significant correlation with fruit length ( $r_g = 0.303$ ) and negative significant correlation with root length ( $r_g = 0.299$ ) whereas, it had no significant correlation with the rest of characters.

Positive and highly significant correlations were observed between leaf length and fruit length ( $r_g = 0.429$ ), leaf length and hundred seed weight ( $r_g = 0.430$ ). Besides, positive and significant correlation were observed between leaf length and internodes length ( $r_g = 0.309$ ) and leaf length and number of fruits per plant ( $r_g = 0.312$ ). Negative and highly significant correlation observed between leaf length and number of seeds per fruit ( $r_g = 0.394$ ) and root length ( $r_g = 0.387$ ). In addition, negatively significant correlation were observed between leaf length and vine length ( $r_g = 0.334$ ) while it had no significant correlation with the rest of characters studied.

Positive and significant correlation were observed between internodes length and root length ( $r_g = 0.339$ ), internodes length and average fruit weight ( $r_g = 0.296$ ), internodes length and vine length ( $r_g = 0.289$ ). Negative and significant correlation were observed between internodes length and internodes diameter ( $r_g = 0.313$ ) and fruit diameter ( $r_g = 0.292$ ). Similarly, Negative and highly significant correlation were observed between internodes diameter and fruit diameter ( $r_g = 0.532$ ) while, it had no significant correlation with other characters studied. Positive and significant correlation were observed between vine length and average root yield per plant ( $r_g = 0.321$ ) also, negative and significant correlation were observed between vine length and number of vine ( $r_g = 0.304$ ) but it had no significant associations with the rest of characters. Similarly, vine number had positive and highly significant correlation with average fruit weight ( $r_g = 0.387$ ) but, it had no significant correlation with the rest of the characters.

Anchote fruit characters as well showed positive and negative genotypic correlation with the rest of the characters studied. Accordingly, negative and highly significant association were observed between fruit length and root length ( $r_g = 0.583$ ), negative and highly significant correlation with average root yield per plant ( $r_g = 0.378$ ), negative and significant correlation with root diameter ( $r_g = 0.296$ ) and positive and significant correlation with fruit diameter ( $r_g = 0.308$ ) but, it had no significant association with the rest of characters. Similarly, negative and highly significant correlation observed between fruit diameter and average root yield per plant ( $r_g = 0.473$ ), negative and significant correlation with root diameter ( $r_g = 0.296$ ) but it had no significant association with the rest of characters.

Alternatively, positive and highly significant correlation were observed between average fruit yield and number of fruits per plant ( $r_g = 0.720$ ) and average fruit weight ( $r_g = 0.601$ ), positive and significant correlation with leaf length ( $r_g = 0.335$ ) and internodes length ( $r_g = 0.316$ ). Other fruit traits such as average fruit weight and number of seeds per fruit showed negative and significant association with root diameter ( $r_g = 0.284$  and  $0.303$ , respectively) and the correlation between hundred seed weight and root diameter ( $r_g = 0.484$ ) were a little bit strong negative and highly significant. All storage root traits under studies were showed positive and significant correlation with each other. For instance, positive and highly significant correlation were observed between average root yield per plant and root diameter ( $r_g = 0.858$ ) whereas, positive and significant correlation were observed between average root yield per plant and root length ( $r_g = 0.482$ ) and between root length and root diameter ( $r_g = 0.470$ ).

Similarly, Aina *et al.* (2007) noted that root parameters such as medium-sized roots, number of roots and small sized roots were highly significantly correlated with root yield in cassava genotypes. Generally, average root yield per plant had positive and highly significant association with root diameter ( $r_g = 0.858$ ) and root length ( $r_g = 0.482$ ) and positive and significant correlation with vine length ( $r_g = 0.321$ ) indicating root yield can be improved by improving root length and root diameter. Conversely, average root yield per plant showed negative and highly significant correlation with fruit yield traits such as fruit length ( $r_g = 0.387$ ) and fruit diameter ( $r_g = 0.473$ ) indicating simultaneous improvement for root yield and fruit yield is ineffective.

From the estimate of genotypic correlation, about 28.35% of the total traits association showed significant, out of which 55% of them associated positively. This positive association could be resulted from the presence of common genetic elements or microenvironment (or both) that controls the characters to the same direction. Positive significant association due to the effect of genes can be the result of the presence of strong coupling linkage between their genes or the character may be the result of pleiotropic genes that could control these characters in with the same direction (Kearsey and Pooni, 1996). Yet again, from the studies some characters showed negative and significant association among each other. Such negative correlation might be because of different genes or pleiotrophic genes that have dominance on the character may control the character in different direction (Kearsey and Pooni, 1996).

Therefore, selection for characters based on its close association (positive and negative) with other characters is very useful for simultaneous improvement of all the associated characters. On the other hand, for characters, manifesting negative association, simultaneous improvement of characters could be difficult and independent selection may have to be carried out to improve such characters. This finding is in line the work of Tsegaye *et al.* (2006) in sweet potato, Akinwale *et al.* (2010) in 43 Cassava genotypes; Afangideh and Uyoh (2007) in cucumber and AbdEl-Salam *et al.* (2010) in snake cucumber.

From this finding, it is possible to infer that most of root yield and its related traits were negatively significantly correlated with fruit yield and its related traits indicating genotype that possesses high fruit yield tends to produce less root yield and the vice versa. This may also indicate the presence of competition between the shoot and storage root for photosynthate (as anchote storage root bulking overlap with anchote fruit setting stages) were make assimilate competition sever. Consistent with this finding Tsegaye *et al.* (2006) reported the accumulation of assimilates in shoots results in reduction of accumulation of assimilates in sweet potato root storage. Similarly, in some sweet potato cultivars the shoot system served as an alternative sink for assimilate during early growth period and resulted in delayed storage root bulking (Wilson, 1982).

In addition, even though it is a year trial in single location, there is an implication to combat lower storage root yielding accessions through breeding program by improving average root yield per plant, root length and root diameter since this traits have significant and positive correlation with each other. Likewise, there is an implication to combat lower fruit yielding accessions through breeding program by improving number of fruits per plant, average fruit weight and leaf length given that this traits have significant and positive correlation with each other. In line with this, Tsegaye *et al.* (2006) noted the same on 30 sweet potato genotypes. Therefore, selection for characters based on its close association (positive and negative) with other characters is very useful for simultaneous improvement of all the associated characters. On the other hand, for characters, manifesting negative association, simultaneous improvement of characters could be difficult and independent selection may have to be carried out to improve such characters.

#### ACKNOWLEDGMENT

I the authors acknowledge Oromia Agricultural Research institute and Bako agricultural Research center for the source of Budget for the research and Jimma University College of agriculture and veterinary medicine for the support they render for the accomplishment of the research.

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