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Research Article

Genetic Variability, Heritability and Character Association in Anchote *(Coccinia abyssinica (Lam.) Cogn.)* Genotype for Yield Improvement in Kellem Wollega Zone, Oromia, Ethiopia

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Abstract

Anchote is an indigenous Ethiopian root crop with considerable potential for improving food and nutritional security. However, limited information on genetic variability, heritability, and character associations constrains the effective utilization of its germplasm in breeding programs. This study was conducted to assess genetic variability, heritability, character associations, and genetic divergence among 36 anchote accessions. The experiment was conducted under rainfed conditions at Haro Sabu Agricultural Research Center during the 2013/14 cropping season using a simple lattice design with two replications. Data on 13 quantitative agro-morphological, yield-related, and disease-response traits were analyzed using analysis of variance, genetic parameter estimation, phenotypic and genotypic correlation analysis, principal component analysis (PCA), and cluster analysis. Analysis of variance revealed significant differences among accessions for days to flowering, vine length, root length, root diameter, root weight, marketable yield, unmarketable yield, total yield, and powdery mildew. The genotypic coefficient of variation was highest for unmarketable yield (62.40%), followed by root weight (27.77%), powdery mildew (28.68%), marketable yield (22.17%), and total yield (21.70%). Marketable yield and total yield exhibited broad-sense heritability estimates of 60.18% and 59.36%, respectively, with corresponding genetic advances as percentages of the mean of 35.48% and 34.49%, indicating promising potential for selection. Phenotypic and genotypic correlation analyses revealed strong positive associations between root diameter and root weight (0.874 and 0.866, respectively), while root weight was positively associated with marketable and total yield. The first four principal components explained 69.55% of the total variation, with root weight, root diameter, marketable yield, and total yield contributing substantially to the first component. Cluster analysis grouped the accessions into three clusters comprising 13, 20, and three accessions. Cluster II exhibited the highest mean marketable yield (20.55) and total yield (20.63), while the greatest inter-cluster divergence occurred between Clusters II and III ($D^2 = 116.82$, $p < 0.01$). Based on individual accession performance, Acc-37, Acc-101, Acc-95, Acc-54, and Acc-47 were identified as promising candidates for further yield evaluation. These findings demonstrate useful agro-morphological diversity among the evaluated anchote accessions and provide a basis for selection and parental identification. Further multi-location and multi-season evaluations are required to confirm the yield performance, stability, and adaptability of promising accessions before their use in variety development.

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Keywords

Anchote, Variability, Heritability, Character Association, Genetic Divergence, Yield

1. Introduction

Anchote *(Coccinia abyssinica (Lam.) Cogn.)* is a diploid (2x = 20) species that belongs to the Cucurbitaceae family and genus Coccinia [21]. This genus comprises 27 species confined to sub-Saharan Africa [11]. It is domesticated and remains indigenously grown in large portions of South, Southwest, and Western Ethiopia. Anchote has edible tubers varying in shape that have spherical to conical shapes at maturity [21]. The crop grows in varying ecological niches with altitudinal ranges from 1300 to 2800 m above sea level and average annual rainfall ranging from 762 to 1016 mm [1, 10]. This is indicative of the presence of varying adaptability and diversity in the anchote germplasm.

Anchote has high nutritional values as well as great potential for medicinal, economic and socio-cultural make use of [12]. It is rich in carbohydrate, vitamins, minerals, protein and calcium as compared to other root crops [7]. The roots basically represent a source of energy and leaves with vines are a source of protein [7]. Traditional medicinal practitioners use anchote to treat different type of diseases such as diabetes, gonorrhea, tuberculosis, asthma and cholesterol lowering [8]. Furthermore, it is a potential root crop that can tolerate drought, poor soil conditions and termites attack [18].

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 undertaken to generate such information using 36 anchote genotypes.

2. Materials and Methods

2.1. Description of Study Site

The study was conducted at Haro Sabu Agricultural Research Center main station in Kellem Wollega Zone of western Oromia, Ethiopia during 2014/15 EC. Haro Sabu Agricultural Research Center is located west of 540 km away from Addis Ababa, Ethiopia. It lies between 8°53′50.60″N latitude and 35°13′37.60″E longitude, at an altitude of 1,550 m.a.s.l. The amount of rain fall the area received ranging from 1,100 to 1,800 mm and a hot, humid temperature ranging from 16.30°C to 30°C. The dominant soil type is clay and pH is 5.7. Cereals, pulses, oil seeds, coffee, vegetables, fruits, spice, root and tuber crops are the major component of crop production in the study area. This location has favorable agro-ecological condition for anchoter growing area in western Ethiopia.

2.2. Experimental Materials

Thirty six (36) anchote accessions collected from West and Kellem Wollega Zones were used in this study assessed genetic variability, heritability and characters association with standard check (Desta-01) (Table 1). Nationally recommended rate of fertilizers: DAP at the rate of 200kg/ha (at sown) and Urea at the rates of 150Kg/ha (50% at sown and 50% at vine development) were applied.

Table 1. *Lists of anchote accessions used in this trial and passport.*

Acc.ession Name	Woreda	Zone	Altitude(m asl)	Latitude(N)	Longitude€	Topography (hilly, plane, level, swampy)	Sample (pure line, clone, population, mixture	Source of collection (field, back yard, store, market)	Nature of sample (seed, finger, pod, bulb, other	Genetics status (wild, weed, landrace, breeding line
Acc-6	S/Chanqa	Kellem Wollega	1551	8º 53.594 '	35 º 04.401 '	Plane	Pureline	Backyard	Fruit	Landrace

Acc.ession Name	Woreda	Zone	Altitude(masl)	Latitude(N)	Longitude€	Topography (hilly, plane, level, swampy)	Sample (pure line, clone, population, mixture	Source of collection (field, back yard, store, market)	Nature of sample (seed, finger, pod, bulb, other	Genetics status (wild, weed, landrace, breeding line
Acc-10	H/ Galan	Kellem Wollega	1713	8º 43.683 '	34 º 54.171'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-11	H/ Galan	Kellem Wollega	1956	8º 41.923 '	34 º 51.49 8'	Hilly	Pureline	Backyard	Fruit	Landrace
Acc-12	H/ Galan	Kellem Wollega	1922	8º 39.099 '	34 º 50.891'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-18	Sayo	Kellem Wollega	1984	8º 32.87 '	34 º 44.89'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-28	Sayo	Kellem Wollega	2042	8º 34.825 ' '	34 º 44.612'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-32	Sayo	Kellem Wollega	2115	8º 33.927 '	34 º 43.097'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-37	H/Galan	Kellem Wollega	2052	8º 41.722 '	34 º 49.385'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-44	D/Sedi	Kellem Wollega	1517	8º 51.157 '	35 º 12.357'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-46	D/Sedi	Kellem Wollega	1523	8º 52.394 '	35 º 11.117'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-47	D/Sedi	Kellem Wollega	1523	8º 52.499 '	35 º 11.048'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-48	D/Sedi	Kellem Wollega	1533	8º 52.643 '	35 º 13.769'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-53	D/Sedi	Kellem Wollega	1603	8º 56.026 '	35 º 15.17'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-54	L/Qile	Kellem Wollega	1636	8º 54.702 '	35 º 18.309'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-55	L/Qile	Kellem Wollega	1639	8º 57.22 '	35 º 18.668'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-57	L/Qile	Kellem Wollega	1703	8º 58.992 '	35 º 19.786'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-58	L/Qile	Kellem Wollega	1686	8º 56.243 '	35. º 20.740'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-61	Yubdo	West Wollega	1706	9º 00.268 '	35 º 20.856'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-62	Yubdo	West Wollega	1704	9º 00.268 '	35 º 20.901'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-64	Yubdo	West Wollega	1710	8º 59.471 '	35 º 21.806'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-71	Yubdo	West Wollega	1789	8º 57.988 '	35 º 33.818'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-73	Ganji	West Wollega	1807	8º 59.096 '	35 º 34.698'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-74	Ganji	West Wollega	1682	9º 03.73 '	35 º 38.235'	Plane	Pureline	Backyard	Fruit	Landrace

Acc.ession Name	Woreda	Zone	Altitude(m asl)	Latitude(N)	Longitude€	Topography (hilly, plane, level, swampy)	Sample (pure line, clone, population, mixture	Source of collection (field, back yard, store, market)	Nature of sample (seed, finger, pod, bulb, other	Genetics status (wild, weed, landrace, breeding line
Acc-77	Homa	West Wollega	1619	9º 04.929 '	35 º 44.398'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-80	Homa	West Wollega	1608	9º 04.225 '	35 º 41.849'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-89	Gimbi	West Wollega	1711	9º 09.368 '	35 º 46.566'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-95	Nedjo	West Wollega	1879	9º 31.12 '	35 º 29.161'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-101	M/Sibu	West Wollega	1755	9º 49.753 '	35 º 04.51'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-105	M/Sibu	West Wollega	1652	9º 45.105 '	35 º 09.325'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-106	M/Sibu	West Wollega	1616	9º 44.145 '	35 º 20.072'	Plane	Pureline	Backyard	Fruit	Landrace
ACC-111	B/Dirmaji	West Wollega	1971	9º 20.863 '	35 º 35.081'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-114	B/Coqorsa	West Wollega	1612	9º 15.664 '	35 º 31.652'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-115	B/Coqorsa	West Wollega	1669	9º 13.369 '	35 º 32.145'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-117	Guliso	West Wollega	1557	9º 11.044 '	35 º 30.142'	Plane	Pureline	Backyard	Fruit	Landrace
Acc-120	L/Asabi	West Wollega	1538	9º 09.932 '	35 º 33.422'	Plane	Pureline	Backyard	Fruit	Landrace

2.3. Experimental Design

Simple lattice design with two replications was used. The experimental area was divided into two homogenous replications and treatments was assigned to each plot randomly. A total of 36 genotypes were grouped into six (6) blocks, each block containing six (6) genotypes. The spacing between rows and plants was 50 cm and 20 cm, respectively. Four rows per plot and ten plants per row, a totally of 400 plants per plot were used in a gross plot size of 2m x 2m = $4m^2$. The distance between block, replication and plot was 1.3m, 1.5m and 1m, respectively.

2.4. Experimental Procedures and Managements

The field experiment was conducted under rainfed conditions **at** Haro Sabu Agricultural Research Center (main station) during the main cropping season (June to October) of the experimental year. Before planted, the experimental field was selected and cleared of unwanted materials such as stones, crop residues, weeds, and other foreign materials. The land was prepared by ploughing at least three times using oxen in order to obtain a fine seedbed (plot) suitable for sown seed. After land preparation, the experimental field layout was marked and plots were laid out using the 3 m × 4 m × 5 m triangular method to ensure proper plot arrangement and right-angle alignment.

Anchote seeds of each accessions were sown on well-prepared plots. Fertilizer was applied following the recommendation for anchote production in the area. Di-ammonium phosphate (DAP) was applied at the rate of 200 kg ha^{-1} at the time of sown and Nitrogen fertilizer was applied at the rate of 150 kg ha^{-1} in the form of urea in two splits: 50% at sown and 50% at vine development. All fertilizer applications was made uniformly to all experimental plots. All other field management practices were carried out uniformly for all experimental units as required, following the national anchote production

recommendations.

2.5. Data Collected

Data were collected from the two middle rows of each plot by leaving the border rows. Days to flowering, Days to maturity, vine length, internode length, root length, root diameter, root weight, marketable fresh root yield, unmarketable fresh root yield, total fresh root yield and disease reaction were recorded.

2.6. Statistical Data Analysis

2.6.1. Analysis of Variance

Data was analyzed followed procedures appropriate to the simple lattice design [9]. Analysis of variance (ANOVA) for all quantitative characters were carried out using R software. Mean separation among genotype means was performed using the Least Significant Difference (LSD) test at the 5% probability level.

2.6.2. Estimation of Variance Components

Genetic variance, phenotypic variance, and environmental variance were analyzed by the formula indicated below [17]. Using R, version 4.4.0 software:

$$Environmental\ variance\ (\delta 2e) = MSe,$$

$$Genotypic\ variance\ (\delta 2g) = (MSg - MSE)/r$$

$$Phenotypic\ variance\ (\delta 2p) = (2g + \delta 2e),$$

Where, Mse = Mean square error, r= replication,

$$\text{Phenotypic coefficients of variation PCV} = \frac{\sqrt{\delta p2}}{Y} \text{ x } 100$$

$$\text{Genotypic coefficients of variation GCV} = \frac{\sqrt{\delta g2}}{Y} \text{ x } 100$$

δp^2 =phenotypic variance, δg^2 = genotypic variance,

$\bar{Y}$= grand mean of a character.

Where; PCV and GCV values was categorized as low (0-10%), moderate (10-20%) and high (>20%) [19].

2.6.3. Heritability, Genetic Advance and Genetic Advance as Percent of Mean

Expressed as the percentage of the ratio of the genotypic variance ($\delta^2 g$) to the phenotypic variance ($\delta^2 p$) and estimated on genotype mean [2]. Using R, version 4.4.0 software:

$$H^2 = \delta 2g\ /\delta 2p\ *\ 100$$

Where, H^2 =Heritability in Broad sense, $\delta^2 p$= phenotypic variance,

$\delta^2 g$= genotypic variance.

The heritability percentage was categorized as low (0-40%), Moderate (40-60%), high (60-80%) and very high (>80%).

Genetic advance as percent of mean (GAM) was calculated for each character using the formula given [13]:

$$GA = H2\ *\ K\delta p\ /\bar{Y}\ *\ 100$$

Where: H^2 is the heritability estimate, k is the selection differential (2.06) at 5% selection Intensity, σ p is the phenotypic standard deviation and $\bar{Y}$ is mean of the trait. Genetic advance as percent of mean was estimated as follows:

$$\text{GAM} = \frac{GA}{Y} \text{ x } 100$$

Where, GAM = Genetic advance as percent of mean, GA = Genetic advance, $\bar{Y}$ = Population mean of the character being evaluate as low (0-10%); moderate (10-20%) and high (>20%).

2.6.4. Correlation Analysis

Phenotypic and genotypic correlation coefficients was estimated using the standard procedure from corresponding variance and covariance [14]. Using R, version 4.4.0 software as:

$$\text{rp} = \frac{\sqrt{\text{Pcov x.y}}}{\delta\text{px.}\delta\text{py}} \text{ x } 100$$

$$\text{rg} = \frac{\sqrt{\text{gcov x.y}}}{\delta\text{gx.}\delta\text{gy}} \text{ x } 100$$

Where,

r_p = phenotypic correlation coefficient and

r_g = genotypic correlation coefficient between characters x and y Pcovxy = phenotypic covariance and

Gcovxy = genotypic covariance between characters x and y δp_x = Phenotypic variance of variable x

δg_x = Genotypic variance of variable x δp_y = Phenotypic variance of variable y δg_y = Genotypic variance of variable y

The calculated phenotypic correlation value was test for its significance using t-test: t = rph /SE (rp)

where

Where, rp = Phenotypic correlation; SE (rp) = Standard error of phenotypic correlation obtained using the following formula [16].

$$SE(Rp) = \frac{\sqrt{1-\text{r2p}}}{\text{n}-1}$$

Where, n is the number of genotypes tested, $r^2 p$ is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels will be tested for their significance by the formula indicated below [15]:

$$t = r_{gxy} / SEr_{gxy}2$$

the calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at a 5% level of significance. Where n is a number of genotypes.

2.6.5. Path Coefficient Analysis

Based on genotypic and phenotypic correlations, path coefficient analysis which refers to the estimation of direct and indirect effects of the root yield attributing characters (independent character) on root yield (dependent character) were calculated based on the following formula [4]. Using R-software as follows:

$$rij = Pij + \Sigma rikpkj$$

Where, r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic and phenotypic correlation coefficients.

P_{ij} = direct effects of the independent character (i) on the dependent variable (j) as measured by the genotypic path coefficients, and

Σrikpkj = Summation of components of indirect effects of a given independent character

(i) on a given dependent character (j) via all other independent characters (k).

The residual effect, which determines how best the causal factors account for the variability of the dependent factor seed yield, was computed using the formula;

$$1 = p2R + \Sigma\ p\ ijrij$$

Where, p2R is the residual effect.

$\Sigma\ p\ ijrij$ = the product of direct effect of any variable and its correlation coefficient with yield.

2.6.6. Principal Component Analysis

Principal component analysis (PCA) was performed to identify the characters that contribute most to the total variation among anchote accessions. Prior to analysis, the data was standardized to a mean of zero and a variance of one in order to remove the effect of differences in measurement scales among traits. PCA was then be computed based on the correlation matrix using R software**.**

The number of principal components to be retained was determined using the Kaiser criterion, whereby only components with eigenvalues greater than 1.0 was retained for interpretation. In addition, the percentage of total variation explained by each principal component and the cumulative proportion of variance was examined. Traits with high loading values in the retained components was considered as the major contributors to genetic divergence among the genotypes.

2.6.7. Genetic Distance and Clustering

Genetic divergence among the 36 anchote accessions was assessed using *Euclidean distance (ED)* computed from standardized quantitative traits. Prior to analysis, the data for each trait was standardized by subtracting the mean and dividing by the standard deviation so that all traits contribute equally to the analysis regardless of their measurement scale. The Euclidean distance between the *j*th and *k*th genotypes was calculated [20]:

$$EDjk = \sqrt{[\Sigma(i=1 \text{ to } n)\ (Xij - Xik)^2]}$$

Where, EDjk = distance between genotypes j and k; xij and xik = phenotype traits values of the i^{th} character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance.

The resulting distance matrix was then be used for *cluster analysis* to group the genotypes according to their similarity. A dendrogram was constructed using the *Unweighted Pair-Group Method with Arithmetic Mean (UPGMA)* in *R software*. The clustering results was presented in the form of a dendrogram, which was helped to identify genetically divergent groups of accessions and support the selection of parents for future breeding and hybridization programs.

3. Results and Discussions

3.1. Analysis of Variances

The analysis of variance revealed significant differences ($p \leq 0.01$ or $p \leq 0.05$) among the 36 anchote accessions for most quantitative traits, including days to flowering (DF), vine length (VL), root length (RL), root diameter (RD), root weight (RW), weight of marketable yield (WMY), weight of unmarketable yield (WUMY), total yield (TY), and powdery mildew (PM) (Table 2). However, days to maturity (DM), stand count at harvest (SCAH), internode length (IL), and leaf blight (LB) showed no significant differences among the tested accessions. The significant variation observed in important root and yield-related traits suggests the presence of useful variability among the accessions and indicates opportunities for improving anchote through selection or This significant genetic variation among genotypes suggested that the genotypes were genetically diverse and it could be a good opportunity for breeders to select genotypes for trait of interest for variety development. There was highly significant differences among anchote accessions for most quantitative traits, particularly root length, root diameter, root yield per plant, marketable root yield, and total root yield [25]. Similarly, highly significant differences among 30 sweet potato genotypes for all the characters studied, demonstrating the importance of genetic variability in improving root and tuber crops [23]. More recently, a study of 282 anchote accessions also demonstrated substantial agro-morphological diversity among accessions, further supporting the potential of anchote germplasm for crop improvement [6]. These findings collectively indicate that the variation observed in the present study is consistent with previous research

and provides a basis for identifying promising anchote accessions for further evaluation and breeding.

The relative efficiency of the simple lattice design compared with the randomized complete block design (RCBD) ranged from 96.13% for DM to 139.48% for WUMY (Table 2). Relative efficiencies greater than 100% for most traits indicate that the simple lattice design improved experimental precision compared with RCBD, particularly for WUMY, powdery mildew, root weight, and other yield-related traits. This demonstrates the usefulness of the lattice design for evaluating a relatively large number of accessions when field variability needs to be controlled. The coefficient of determination (R^2) ranged from 73.60% for SCAH to 87.22% for RW, indicating that the fitted models accounted for a substantial proportion of the observed variation.

Table 2. *Analysis of variance for 13 quantitative characters of 36 anchote accessions grown at HSARC (2013/14 EC).*

Trait	G. Mean	Mean squares						R^2 (%)	Relative Efficiency % to RCBD	Lattice CV %
		Replication	Treatment		Blocks within Replication	Intra block Error	RCBD Error			
			Unadjusted	Adjusted						
DF	78.25	16.06	32.59	29.09***	19.64	7.63	7.57	86.58	99.17	3.53
DM	174.94	102.72	33.94	24.20ns	49.57	17.93	17.24	76.33	96.13	2.42
SCAH	15.10	3.13	8.31	8.16ns	8.70	5.39	6.18	73.60	114.72	15.38
VL	406.65	6216.12	4626.23	4531.12*	4544.15	2251.17	2811.19	78.88	124.88	11.67
IL	15.73	9.39	3.56	2.75ns	6.75	2.39	2.82	74.32	118.00	9.83
RL	12.79	1.39	5.20	5.03***	3.13	1.41	1.74	85.55	123.02	9.29
RD	20.04	120.13	22.80	23.03**	8.65	9.10	9.20	81.66	101.13	15.06
RW	0.23	0.07	0.01	0.01***	0.01	0.00	0.00	87.22	130.55	25.43
WMY	17.18	556.87	51.82	43.52*	55.93	19.95	21.93	84.11	109.94	26.00
WUMY	0.12	0.01	0.03	0.03*	0.03	0.01	0.02	78.93	139.48	101.38
TY	17.29	552.04	51.02	43.04*	55.69	19.86	22.12	84.04	111.35	25.78
LB	1.36	0.22	0.45	0.43ns	0.37	0.23	0.25	76.52	108.50	35.32
PM	1.68	3.13	1.03	0.84*	1.64	0.43	0.58	81.79	133.99	39.22

**=Highly significant at $p<0.01$; *=significant at $p<0.05$; ns=Non significant; G.Mean=Grand mean; RCBD=Randomized complete block design; R^2=Reliability of model; DF= Days to flowering; DM=Days to maturity; SCAH=stand count at harvest; VL=Vine length; Internodes length= LL; RL=Root length; RD=Root diameter; RW=Root weight; WMY=Weight of marketable yield; WUMY=Weight of unmarketable yield; TY=Total yield; LB=Leaf blight; PM=Powdery mildew.

3.2. Mean Performance of Genotypes

The mean values of the 13 anchote traits showed considerable variation among the evaluated genotypes (Table 3). Days to flowering (DF) ranged from 67 to 89 days, with a mean of 78.25 days, while days to maturity (DM) ranged from 166 to 187 days, with a mean of 174.94 days. Stand count at harvest (SCAH) ranged from 7 to 19, averaging 15.10. Vine length (VL) varied from 275.40 to 545.20, with a mean of 406.65, whereas internode length (IL) ranged from 11.60 to 20.60, with a mean of 15.73. Root length (RL) ranged from 9.20 to 19.40, averaging 12.79, while root diameter (RD) varied from 10.40 to 32.20, with a mean of 20.04. Root weight (RW) ranged from 0.067 to 0.584, with a mean of 0.23.

The mean total yield (TY) ranged from 3.187 to 33.51, with a grand mean of 17.29, while weight of marketable yield (WMY) ranged from 2.76 to 33.51, averaging 17.18. Weight of Unmarketable yield (WUMY) varied from 0 to 0.715, with a mean of 0.12. Leaf number (LB) ranged from 1 to 3, averaging 1.36, whereas powdery mildew (PM) ranged from 1 to 4, with a mean of 1.68. These differences indicate the presence of substantial phenotypic variation among the evaluated anchote genotypes, particularly for root diameter, root weight, marketable yield, and total yield, providing opportunities for selection of desirable genotypes.

3.3. Genetic Variability and Genetic Parameters

The estimation of genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance as a percentage of the mean (GAM) provides important information for assessing genetic variability and identifying promising traits for selection in anchote. The results indicated considerable variation among the evaluated traits. The observed ranges were 67–89 days for days to flowering (DF), 166–187 days for days to maturity (DM), 9.2–19.4 for root length (RL), 10.4–32.2 for root diameter (RD), and 2.76–33.51 for marketable yield (WMY). These differences suggest that the evaluated genotypes may offer opportunities for selecting desirable morphological and yield-related characteristics. Based on the reported GCV estimates, high genotypic variability was observed for unmarketable yield (62.40%), podery mildew (28.68%), root weight (27.77%), leaf blight (23.03%), weight of marketable yield (22.17%) and total yield (21.70%). Moderate GCV values were recorded for RD (13.01%) and RL (10.37%), whereas DF (4.52%), DM (1.46%), SCAH (6.87%), vine length (7.83%) and internode length (3.61%) exhibited low reported values. Using the commonly applied classification of GCV and PCV values below 10% are low, values from 10 to 20% are moderate, and values above 20% are high [3]. The relatively high GCV values for WMY and TY suggest useful genetic variability for improving anchote productivity. There was considerable genetic variability and selection potential for root yield and related traits among anchote accessions in Ethiopia [25]. Similarly, agro-morphological diversity among 282 anchote accessions, demonstrating the importance of evaluating diverse germplasm to identify superior genotypes for breeding [6].

3.3.1. Comparison of Phenotypic and Genotypic Coefficients of Variation

The PCV estimates were higher than the corresponding GCV estimates for all evaluated traits, indicating that the observed phenotypic variation was generally greater than the estimated genotypic variation. The differences between PCV and GCV ranged from 0.62 percentage points for DF to 38.32 percentage points for WUMY. Relatively small differences were observed for DF (0.62), DM (0.70), RL (2.20), VL (3.85) and RD (3.84), suggesting comparatively limited environmental influence on the expression of these traits relative to traits with larger differences. In contrast, larger differences were observed for WUMY (38.32), LB (11.57), PM (11.31), RW (6.77), TY (6.46), SCAH (6.45) and WMY (6.41), suggesting that environmental or experimental factors may contribute substantially to their observed phenotypic variation. However, the PCV–GCV difference is an indicator of the relative contribution of non-genetic variation, not a direct estimate of environmental variance. The importance of evaluating genotypic and phenotypic variability together when identifying selection opportunities [13]. Similarly, considerable variation among 282 anchote accessions for several agro-morphological and physiological traits, including root yield, vine length and leaf area index, demonstrating the importance of assessing both genetic variation and environmental influences during anchote improvement [6].

3.3.2. Broad-sense Heritability, Genetic Advance and Genetic Advance as a Percentage of the Mean (GAM)

The reported broad-sense heritability estimates ranged from 22.04% for IL to 77.23% for DF. Using the commonly applied classification, heritability was high for DF (77.23%), RL (68.07%) and RW (64.63%); moderate for DM (46.12%), VL (44.90%), RD (59.64%), WMY (60.18%), WUMY (38.38%), TY (59.36%), LB (44.32%) and PM (51.44%); and low for SCAH (26.55%) and IL (22.04%). These results suggest differences among traits in their potential response to selection, although heritability estimates depend on the experimental design and the environment in which the genotypes were evaluated. The reported GAM values were highest for WUMY (79.75%), RW (46.05%), PM (42.44%), WMY (35.48%), TY (34.49%), LB (31.63%), RD (20.73%) and RL (17.65%). The combination of relatively high GCV, heritability and GAM for WMY and TY suggests promising potential for improving anchote yield through selection. Wondimu et al. (2014), in their study of 49 anchote accessions at Bako Agricultural Research Center, reported useful genetic variability and selection potential for root yield and related traits. More recently, reported high heritability and genetic advance for important traits, including root yield, vine length and leaf area index, among 282 anchote accessions [6]. The importance of considering heritability and genetic advance jointly when assessing the expected response to selection [13]. Nevertheless, broad-sense heritability includes additive and non-additive genetic effects; therefore, high heritability combined with high GAM suggests selection potential but does not, by itself, prove predominantly additive gene action.

The results identify WMY, TY, RL and RD as potentially useful traits for anchote improvement. Weight of marketable yield and total yield are particularly important because their reported GCV values exceeded 20%, their heritability estimates were approximately 60%, and their GAM values exceeded 34%. Root length and root diameter may also be useful selection criteria because of their moderate GCV and relatively high heritability estimates. However, the high reported GAM for WUMY and PM should not automatically be interpreted as desirable. Selection should generally aim to reduce them. Furthermore, WUMY has a mean close to zero, making its coefficient of variation particularly sensitive to small changes in the mean and the precision of the variance estimates. The RW variance is also rounded to 0.00, so its unrounded value.

Table 3. Estimates of range, mean, phenotypic (σ^2p) and genotypic (σ^2g) 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 36 anchote accessions at HSARC (2013/2014).

Trait	Minimum	Maximum	Mean	Vg	Vp	GCV(%)	PCV(%)	PCV and GCV differences	H^2 (%)	GA	GAM(%)
DF	67	89	78.25	12.50	16.19	4.52	5.14	0.62	77.23	6.41	8.19
DM	166	187	174.94	6.57	14.24	1.46	2.16	0.7	46.12	3.59	2.05
SCAH	7	19	15.10	1.07	4.05	6.87	13.32	6.45	26.55	1.10	7.30
VL	275.4	545.2	406.65	1012.96	2255.86	7.83	11.68	3.85	44.90	44.00	10.82
IL	11.6	20.6	15.73	0.32	1.46	3.61	7.68	4.07	22.04	0.55	3.49
RL	9.2	19.4	12.79	1.76	2.58	10.37	12.57	2.2	68.07	2.26	17.65
RD	10.4	32.2	20.04	6.80	11.40	13.01	16.85	3.84	59.64	4.15	20.73
RW	0.06708	0.58434	0.23	0.00	0.01	27.77	34.54	6.77	64.63	0.11	46.05
WMY	2.76	33.5055	17.18	14.50	24.09	22.17	28.58	6.41	60.18	6.09	35.48
WUMY	0	0.7145	0.12	0.01	0.01	62.40	100.72	38.32	38.38	0.09	79.75
TY	3.187	33.5055	17.29	14.08	23.72	21.70	28.16	6.46	59.36	5.96	34.49
LB	1	3	1.36	0.10	0.22	23.03	34.60	11.57	44.32	0.43	31.63
PM	1	4	1.68	0.23	0.45	28.68	39.99	11.31	51.44	0.71	42.44

vg= Genotypic variance; vp= 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; DF= Days to flowering; DM=Days to maturity; SCAH=stand count at harvest; VL=Vine length; Internodes length= LL; RL=Root length; RD=Root diameter; RW=Root weight; WMY=Weight of marketable yield; WUMY=Weight of unmarketable yield; TY=Total yield; LB=Leaf blight; PM=Powdery mildew.

3.4. Character Association

3.4.1. Phenotypic Correlation Among Anchote Traits

The phenotypic correlation analysis revealed varying positive and negative relationships among the 13 anchote (Coccinia abyssinica) traits (Table 4). The strongest positive and highly significant correlation was observed between root diameter (RD) and root weight (RW) (r=0.874), followed by root length (RL) and RW (r=0.579), RD and marketable yield (WMY; (r=0.570), and RD and total yield (r=0.568). Root weight was also positively correlated with WMY and TY (r=0.555 for both). These results suggest that root size and weight are important indicators of anchote productivity. Similarly, Wondimu et al. (2014) reported significant positive phenotypic correlations of average root yield with root diameter (r=0.593) and root length (r=0.345), supporting the potential use of root traits as indirect selection criteria. Moreover, a 2025 study of 282 anchote accessions found significant associations between root yield and root diameter, leaf area, and root weight per plot, further supporting the importance of root and canopy traits in anchote improvement.

Other significant associations included positive correlations between days to flowering (DF) and RD (r=0.288) and RW (r=0.314); internode length (IL) and RD (r=0.287) and RW (r=0.276); and shoot canopy height (SCAH) with WMY (r=0.250) and TY (r=0.251). Conversely, SCAH was negatively correlated with IL (r=-0.323), RD (r=-0.278), and RW (r=-0.319). Days to maturity (DM) also showed negative correlations with WMY (r=-0.278) and TY (r=-0.282), suggesting that earlier-maturing accessions tended to have higher yields in this experiment. Unmarketable yield (WUMY) was positively associated with leaf blight (r=0.333) and powdery mildew (r=0.283), while LB and PM were strongly positively correlated (r=0.504). These relationships may indicate associations between vegetative characteristics, disease incidence, and yield components, but they do not establish causal effects. Overall, root diameter, root weight, and root length appear to be promising traits for selection to improve anchote productivity. However, because phenotypic correlations reflect both genetic and environmental influences, genotypic correlation and path coefficient analyses are needed to identify the direct and indirect effects of these traits on yield.

Table 4. Phenotypic correlation coefficient of the 13 characters in 36 anchote accessions grown at HSARC (2013/14).

Character	DF	DM	SCAH	VL	IL	RL	RD	RW	WMY	WUMY	TY	LB	PM
DF	1	0.041	-0.111	-0.026	0.186	0.137	0.288*	0.314**	0.170	-0.030	0.170	-0.061	-0.090
DM		1	-0.104	0.108	0.017	-0.159	-0.059	-0.147	-0.278*	-0.110	-0.282*	-0.049	-0.153
SCAH			1	-0.146	-0.323**	-0.098	-0.278*	-0.319**	0.250*	0.003	0.251*	-0.031	0.047
VL				1	0.250*	-0.077	0.128	0.078	-0.084	-0.150	-0.088	-0.166	-0.230
IL					1	0.062	0.287*	0.276*	0.048	-0.139	0.045	0.073	0.050
RL						1	0.253*	0.579***	0.246*	0.182	0.251*	0.143	0.091
RD							1	0.874***	0.570***	-0.208	0.568***	-0.001	-0.185
RW								1	0.555***	-0.133	0.555***	0.027	-0.133
WMY									1	-0.192	1***	-0.001	-0.102
WUMY										1	-0.169	0.333**	0.283*
TY											1	0.007	-0.096
LB												1	0.504***
PM													1

**=Highly significant at p<0.01; *=significant at p<0.05; ns=Non significant; DF= Days to flowering; DM=Days to maturity; SCAH=stand count at harvest; VL=Vine length; Internodes length= LL; RL=Root length; RD=Root diameter; RW=Root weight; WMY=Weight of marketable yield; WUMY=Weight of unmarketable yield; TY=Total yield; LB=Leaf blight; PM=Powdery mildew.

3.4.2. Genotypic Correlation Among Anchote Traits

The genotypic correlation coefficients indicated positive and negative relationships among the evaluated anchote traits, reflecting potential genetic associations that may influence selection efficiency. The strongest positive and highly significant correlation was observed between root diameter (RD) and root weight (RW) (r_g=0.866), followed by root weight (RW) and weight of marketable yield (WMY) (r_g=0.574), root weight and total yield (r_g=0.573), and root length (RL) and root weight (RW) (r_g=0.567). Root diameter was also positively correlated with weight of marketable yield (WMY) (r_g=0.517) and total yield (TY) (r_g=0.512). These results suggest that genetic improvement of root size and weight could contribute to improved anchote productivity. They are consistent with Wondimu et al. (2014), who reported positive associations of anchote root yield with root diameter (r=0.858) and root length (r=0.482).

Other notable relationships included positive correlations between days to flowering (DF) and RD (r_g=0.390) and RW (r_g=0.378), indicating that later-flowering accessions tended to have larger and heavier roots. Stand count at harvest (SCAH) was negatively correlated with RD (r_g=-0.523) and RW (r_g=-0.479), potentially reflecting competition among plants for available resources. Root diameter was negatively correlated with unmarketable yield (WUMY) (r_g=-0.404), while WMY was also negatively correlated with WUMY (r_g=-0.345). These associations may indicate that accessions with greater root diameter and marketable yield tend to have lower unmarketable yield. Furthermore, leaf blight (LB) was positively correlated with powdery mildew (PM) (r_g=0.581) and WUMY (r_g=0.485), suggesting an association between disease levels and unmarketable production. Overall, root diameter, root weight, and weight of marketable yield appear to be promising selection traits for anchote improvement.

Table 5. Genotypic correlation coefficient of the 13 characters in 36 anchote accessions grown at HSARC (2013/14).

Traits	DF	DM	SCAH	VL	IL	RL	RD	RW	WMY	WUMY	TY	LB	PM
DF	1	0.039	-0.1836	-0.034	0.216	0.145	0.390*	0.378*	0.216	-0.100	0.215	-0.007	-0.117
DM		1	-0.1593	0.071	0.156	-0.151	0.114	-0.021	-0.170	-0.055	-0.173	-0.004	-0.288
SCAH			1	-0.239	-0.182	-0.067	-0.523**	-0.479**	0.141	-0.098	0.140	0.118	0.231

Traits	DF	DM	SCAH	VL	IL	RL	RD	RW	WMY	WUMY	TY	LB	PM
VL				1	0.290	-0.197	0.183	0.062	-0.039	-0.257	-0.045	-0.333*	-0.306
IL					1	0.022	0.325	0.260	0.056	-0.288	0.049	-0.020	0.187
RL						1	0.127	0.567***	0.287	0.190	0.294	0.140	0.114
RD							1	0.866***	0.517**	-0.404*	0.512**	-0.102	-0.156
RW								1	0.574***	-0.238	0.573***	-0.024	-0.068
WMY									1	-0.345*	1***	-0.001	0.004
WUMY										1	-0.324	0.485**	0.200
TY											1	0.010	0.009
LB												1	0.581***
PM													1

**=Highly significant at p<0.01; *=significant at p<0.05; ns=Non significant; DF= Days to flowering; DM=Days to maturity; SCAH=stand count at harvest; VL=Vine length; Internodes length= LL; RL=Root length; RD=Root diameter; RW=Root weight; WMY=Weight of marketable yield; WUMY=Weight of unmarketable yield; TY=Total yield; LB=Leaf blight; PM=Powdery mildew.

3.5. Multivariate Analysis of Genetic Diversity

3.5.1. Principal Component Analysis (PCA) for Quantitative Traits

Principal component analysis (PCA) was used to examine the variability among the 36 anchote genotypes. Principal component analysis (PCA) of 13 growth, yield, and yield-related traits in 36 anchote genotypes revealed that the first four principal components had eigenvalues greater than 1 and collectively explained 69.55% of the total variation. PC1 contributed the largest proportion (28.40%), followed by PC2 (18.28%), PC3 (13.11%), and PC4 (9.76%), while the first two components together accounted for 46.68% of the variation. PC1 was primarily associated with root weight (0.469), root diameter (0.457), weight of marketable yield (0.402), and total yield (0.399), indicating that root size and productivity were major sources of variation among the genotypes. PC2 was characterized by leaf blight (−0.431), powdery mildew (−0.428), and vine length (0.405), reflecting differences in plant architecture and disease-related traits. PC3 was mainly associated with stand count at harvest (−0.518), weight of unmarketable yield (0.403), leaf blight (0.321), weight of marketable yield (−0.317), and total yield (−0.310), whereas PC4 was characterized by internode length (−0.658) and powdery mildew (−0.513). These findings indicate that variation among the evaluated anchote genotypes was influenced by several distinct trait combinations rather than a single characteristic. Similar diversity in quantitative and agro-morphological traits among Ethiopian anchote accessions was reported [24], supporting the value of multivariate analysis for characterizing anchote germplasm.

The remaining components explained relatively smaller proportions of variation: PC5 (7.65%), PC6 (6.34%), PC7 (5.68%), PC8 (4.91%), PC9 (2.70%), PC10 (1.81%), PC11 (1.22%), and PC12 (0.14%), while PC13 explained virtually no additional variation. These components were associated mainly with phenological traits, including days to maturity and flowering, root length, vine length, and disease responses. Based on the eigenvalue-greater-than-one criterion, the first four components are the most appropriate for emphasizing the major patterns of variation. From a breeding perspective, the strong contributions of root weight, root diameter, and yield-related traits to PC1 suggest that these characteristics should receive particular attention when identifying promising genotypes for root-yield improvement. Nevertheless, component coefficients indicate directions of variation rather than desirability, so genotype scores and actual trait means should be considered before selecting parents.

Table 6. *Eigen vectors, proportion and cumulative percentage of variation explained by principal components (PC) for quantitative characters of 36 anchote genotypes evaluated at HSARC in, 2013/2014.*

Principal components													
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**	**PC12**	**PC13**
DF	0.245	0.007	0.196	0.015	-0.308	0.803	-0.109	-0.316	-0.132	0.167	-0.064	0.005	0.000

Principal components													
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**	**PC12**	**PC13**
DM	-0.004	0.275	0.207	-0.045	-0.728	-0.382	0.309	-0.046	-0.066	0.318	0.009	0.029	0.000
SCAH	-0.175	-0.262	-0.518	-0.179	-0.213	0.124	0.306	-0.183	-0.212	-0.191	0.573	0.045	0.000
VL	0.093	0.405	-0.044	-0.192	0.404	-0.211	-0.002	-0.668	-0.328	0.161	0.030	-0.003	0.000
IL	0.180	0.138	0.206	-0.658	0.073	0.113	0.346	-0.024	0.508	-0.277	0.003	0.010	0.000
RL	0.193	-0.314	0.214	0.289	0.230	0.013	0.710	-0.031	-0.200	0.015	-0.150	-0.339	0.000
RD	0.457	0.100	0.166	-0.044	-0.050	-0.115	-0.290	0.193	-0.135	-0.128	0.497	-0.577	0.000
RW	0.469	-0.073	0.229	0.113	0.107	-0.090	0.061	0.147	-0.183	-0.079	0.275	0.741	0.000
WMY	0.402	-0.250	-0.317	0.016	-0.098	-0.162	-0.081	-0.181	0.238	0.119	-0.160	-0.016	0.710
WUMY	-0.251	-0.248	0.403	0.285	0.059	-0.090	-0.086	-0.415	0.481	0.128	0.439	0.006	0.016
TY	0.399	-0.257	-0.310	0.023	-0.097	-0.165	-0.083	-0.192	0.251	0.123	-0.151	-0.016	-0.704
LB	-0.096	-0.431	0.321	-0.228	-0.214	-0.230	-0.241	-0.267	-0.312	-0.499	-0.276	0.002	0.000
PM	-0.091	-0.428	0.135	-0.513	0.163	-0.015	-0.089	0.211	-0.170	0.644	0.070	-0.007	0.000
Eigenvalue	3.692	2.377	1.704	1.268	0.995	0.824	0.739	0.639	0.351	0.236	0.158	0.018	0.000
Variance Percent	28.399	18.282	13.109	9.757	7.651	6.341	5.682	4.912	2.698	1.814	1.216	0.137	0.000
Cumulative Percent	28.399	46.682	59.791	69.548	77.199	83.540	89.222	94.134	96.833	98.646	99.863	100.000	100.000

3.5.2. Cluster Analysis

(i). Cluster Mean Analysis for Quantitative Traits

The cluster mean analysis of 36 anchote genotypes revealed considerable variation in maturity, vegetative growth, root characteristics, and yield-related traits. The genotypes were grouped into three clusters, comprising 13 accessions in Cluster I (36.11%), 20 in Cluster II (55.56%), and three in Cluster III (8.33%). The unequal distribution of accessions among clusters suggests that the evaluated genotypes differed in their overall quantitative characteristics. However, cluster size alone cannot establish the degree of genetic diversity or the breeding value of a group. This observation agrees with, 49 anchote accessions into five clusters using 17 quantitative traits and identified variation among the groups in root yield, vine characteristics, and other agronomic traits [24]. Similarly, characterized 282 anchote accessions using 26 quantitative agro-morphological and physiological traits and identified three clusters with different trait combinations [6]. These studies confirm that multivariate analysis can distinguish anchote germplasm according to its phenotypic characteristics and help identify promising material for crop improvement.

The cluster means showed contrasting patterns for flowering and maturity. Cluster I had the lowest mean days to flowering (76.77 days), followed by Cluster II (79.05 days) and Cluster III (79.33 days). Thus, Cluster I flowered approximately 2.56 days earlier than Cluster III. In contrast, Cluster III had the lowest mean days to maturity (172.83 days), whereas Cluster I had the highest (176.19 days). This indicates that earlier flowering did not necessarily correspond to earlier maturity among the three groups. The difference between flowering and maturity may reflect variation in developmental patterns among the evaluated genotypes, although further analysis would be needed to determine the underlying relationships. Wide ranges in quantitative characteristics among a much larger collection [6]. These findings support evaluating flowering and maturity as separate selection criteria because their relative importance may differ according to the target production environment and breeding objective.

Differences in vegetative and root morphological traits further distinguished the three clusters. Cluster I recorded the highest mean vine length (426.98), followed by Cluster II (403.07) and Cluster III (342.40). Conversely, Cluster III recorded the highest mean root length (14.47), followed by Cluster II (13.13) and Cluster I (11.88). Cluster II had the highest mean values for SCAH (15.55), internode length (15.95), root diameter (21.33), and root weight (0.26). These contrasting patterns indicate that no cluster was superior for all measured characteristics. Instead, each cluster displayed a different combination of vegetative and root traits. There was differences in root diameter, root yield, vine characteristics, and

other quantitative traits among anchote accessions [24]. In addition, extensive variation in vine length, internode length, root length, root diameter, and root yield among 282 anchote accessions [6]. The agreement between these studies supports the conclusion that Ethiopian anchote germplasm contains substantial phenotypic variation that could be exploited to develop varieties with desirable combinations of above-ground growth and storage-root characteristics.

The differences in yield-related traits were particularly important for identifying potentially valuable germplasm. Cluster II recorded the highest mean weight of marketable yield (WMY = 20.55) and total yield (TY = 20.63), followed by Cluster III (WMY = 15.25; TY = 15.62) and Cluster I (WMY = 12.43; TY = 12.54). Relative to Cluster I, Cluster II had approximately 64.5% higher mean total yield and 65.3% higher mean weight of marketable yield. These differences identify Cluster II as the most promising group for preliminary yield-oriented selection in the present study. This interpretation is supported by Wondimu et al. (2012), who found that root diameter exerted the largest positive direct effect on average root yield per plant, with a path coefficient of 0.478. Their results indicate that root diameter could be a useful indirect selection criterion for improving anchote yield. However, the superiority of Cluster II in the present study should be confirmed using appropriate statistical comparisons and additional environments before it is released to study area.

Cluster III, despite comprising only three accessions, recorded the highest mean root length (14.47), LB (2.67), PM (2.83), and weight of unmarketable yield (WUMY = 0.37). In contrast, Cluster I was characterized by the earliest flowering and greatest vine length, while Cluster II had the highest total yield and weight of marketable yields. These differences indicate that the value of each cluster depends on the breeding objective and the desirability of individual traits. For example, Cluster II may provide promising accessions for yield improvement, whereas selected accessions from Cluster III could be useful if longer roots are desirable for the intended production system or market. Conversely, the higher unmarketable yield of Cluster III may be undesirable if the objective is to maximize marketable production. Anchote accessions differ in combinations of root, vine, and yield characteristics [6, 24]. Therefore, breeding decisions should be based on individual accession performance and the relationships among traits rather than on cluster membership alone.

Table 7. *Cluster mean analysis for quantitative characters of 36 anchote genotypes evaluated at HSARC in, 2013/2014.*

Trais	Cluster I	Cluster II	Cluster III
DF	76.77	79.05	79.33
DM	176.19	174.45	172.83
SCAH	14.35	15.55	15.33
VL	426.98	403.07	342.40
IL	15.62	15.95	14.77
RL	11.88	13.13	14.47
RD	18.64	21.33	17.50
RW	0.18	0.26	0.23
WMY	12.43	20.55	15.25
WUMY	0.12	0.08	0.37
TY	12.54	20.63	15.62
LB	1.23	1.25	2.67
PM	1.42	1.68	2.83
Number_of_Accessions	13	20	3

(ii). Aaverage Intra-Cluster Genetic Divergence (D^2) for Quantitative Traits

Table 8 presents the average intra-cluster genetic divergence among 36 anchote accessions evaluated at cropping season. The accessions were grouped into three clusters, comprising 13, 20, and 3 accessions in clusters I, II, and III, respectively. The average intra-cluster D^2 values were 22.59, 25.07, and 22.30 for clusters I, II, and III, respectively. Cluster II exhibited the highest average intra-cluster divergence (25.07), followed by cluster I (22.59), while cluster III showed the lowest value (22.30). These results suggest that the accessions in cluster II exhibited comparatively greater variability in their multivariate quantitative trait profiles than those in the other clusters. The relatively high intra-cluster divergence in cluster II may be associated with differences among its 20 accessions in traits such as root yield, root dimensions, vine growth, and other morphological and agronomic characteristics measured in the study. In contrast, the lower average divergence in cluster III suggests that its three accessions were comparatively similar in their overall trait profiles. Nevertheless, because cluster III contained only three accessions, its estimated average divergence should be interpreted cautiously; a small cluster size limits the number of accession pairs available for evaluating within-cluster variability.

The minimum and maximum pairwise D^2 values further demonstrate the variation within each cluster. In cluster I, pairwise divergence ranged from 7.18 to 47.40, while cluster II showed a range of 7.45 to 50.65. Cluster III had a minimum pairwise D^2 of 18.06 and a maximum of 29.31. The largest maximum pairwise divergence was therefore observed in cluster II (50.65), followed by cluster I (47.40), indicating that these clusters each contained accession pairs with substantial differences in their multivariate trait profiles. The comparatively narrow range in cluster III suggests less variation among its three accessions, although its minimum pairwise

distance was higher than those of clusters I and II. Thus, the results indicate that accessions within the same cluster were not completely homogeneous. Hierarchical clustering groups accessions according to their overall similarity, but appreciable differences may remain among individual accessions within each group. Consequently, breeders should not assume that all accessions belonging to a particular cluster have identical characteristics.

This finding is broadly consistent with the agro-morphological diversity study of 49 anchote accessions using 17 phenotypic and agronomic traits and grouped them into five clusters [24]. This findings demonstrated the existence of variability among anchote accessions and highlighted the importance of multivariate analysis for classifying germplasm and identifying promising materials for crop improvement. Although this study emphasized inter-cluster divergence rather than the exact intra-cluster values reported here, it supports the interpretation that anchote accessions can differ considerably in their quantitative characteristics. Similarly, 30 anchote accessions using newly developed EST-SSR markers and reported variation in genetic diversity among accessions, with expected heterozygosity ranging from 0.15 to 0.44 [22]. Their analysis of molecular variance showed that 84.7% of the variation occurred within accessions and 15.3% among accessions, demonstrating the importance of examining diversity at both individual and group levels. Although molecular-marker diversity is not directly equivalent to Mahalanobis D^2 calculated from phenotypic traits, both studies emphasize the presence of useful diversity within anchote germplasm.

From a plant-breeding perspective, the intra-cluster divergence results provide useful information for identifying accessions for further evaluation and conservation. Cluster II deserves particular attention because it contained the largest number of accessions (20) and had the highest average intra-cluster D^2 (25.07), as well as the largest maximum pairwise distance (50.65). Therefore, selecting accessions from this cluster based on their individual performance could help identify contrasting parents or promising materials for direct selection. Cluster I also contained substantial diversity, with an average D^2 of 22.59 and a maximum pairwise distance of 47.40. Although cluster III had the lowest average intra-cluster D^2 (22.30), its three accessions showed a minimum pairwise distance of 18.06, indicating that even the most similar pair in this cluster was relatively distinct according to the reported distance measure. Nevertheless, the usefulness of any accession for breeding should be determined by its desirable agronomic characteristics, particularly total root yield, root diameter, root weight, and other traits relevant to the breeding objective. The value of genetic-diversity information for conservation and breeding [22]. Consequently, the combined interpretation of intra-cluster divergence, inter-cluster divergence, and cluster means can provide a stronger basis for parent selection than any single measure alone.

Table 8. *Average intra cluster divergence (D^2) value in 36 anchote accessions tested at at HSARC in 2013/2014.*

Cluster	Number_of_Accessions	Average_Intra_Cluster_D2	Minimum_Pairwise_D2	Maximum_Pairwise_D2
Cluster 1	13	22.59	7.18	47.40
Cluster 2	20	25.07	7.45	50.65
Cluster 3	3	22.30	18.06	29.31

(iii). Aaverage Inter-Cluster Genetic Divergence (D^2) for Quantitative Traits

Table 9 presents the average inter-cluster genetic divergence among three clusters of 36 anchote accessions evaluated. The results revealed considerable differences in genetic divergence among the clusters, with D^2 values of 14.61 (non-significant) between clusters I and II, 106.68 (highly significant) between clusters I and III, and 116.82 (highly significant) between clusters II and III. The highest inter-cluster divergence was observed between clusters II and III (D^2 = 116.82**), followed by clusters I and III (D^2 = 106.68**), whereas the lowest divergence was recorded between clusters I and II (D^2 = 14.61 ns). These findings indicate that clusters II and III were the most genetically divergent groups based on the quantitative traits included in the analysis, while clusters I and II exhibited comparatively greater similarity. The highly significant differences between clusters II and III and between clusters I and III suggest that the accessions grouped into these clusters differ substantially in their overall multivariate trait profiles. In contrast, the non-significant difference between clusters I and II suggests that the observed separation between these two groups was not statistically supported at the significance level used in the study. However, a non-significant D^2 value does not necessarily mean that the two clusters are genetically identical; rather, it indicates insufficient statistical evidence to conclude that their multivariate means differ under the applied test.

The present findings are consistent with the earlier study of Wondimu et al. (2014), who evaluated 49 anchote accessions

for 17 morphological and agronomic traits at Bako Agricultural Research Center and identified five clusters with varying levels of inter-cluster divergence. Their study reported a maximum D^2 value of 273.968 between clusters IV and V and a minimum, non-significant value of 14.224 between clusters II and III, demonstrating that anchote germplasm contains groups with markedly different levels of divergence. Although the numerical values and cluster identities differ from those of the present study, both investigations demonstrate the usefulness of Mahalanobis D^2 analysis for identifying relatively similar and highly divergent anchote groups. The assessment of 282 anchote accessions using agro-morphological and physiological traits, reported substantial phenotypic variability among accessions for root yield, vine length, leaf area, and other important characteristics [6]. Molecular evidence from anchote germplasm also supports the existence of genetic differentiation among accessions, although much of the total diversity can occur within populations [5].

From a plant-breeding perspective, the high and significant divergence between clusters II and III (D^2 = 116.82**) makes these groups the first candidates for selecting contrasting parents for future hybridization, followed by clusters I and III (D^2 = 106.68**). Crosses between carefully selected accessions from these divergent clusters may broaden the genetic combinations available to breeders and increase the opportunity to recover desirable recombinants with improved root yield, root size, and other economically important traits. However, high genetic divergence alone does not guarantee superior hybrid performance or heterosis; parental selection should also consider cluster means, individual accession performance, heritability, and the breeding objectives. Divergent anchote groups could provide opportunities to obtain transgressive segregants [24]. Therefore, accessions from clusters II and III should be prioritized for further evaluation, while accessions from clusters I and II may be more useful when the breeding objective involves combining complementary traits between comparatively similar groups. Overall, the results confirm that substantial multivariate divergence exists among the 36 anchote accessions evaluated at HSARC and that this diversity can support the selection of promising parents for anchote improvement.

Table 9. *Average inter cluster divergence (D^2) value in 36 anchote accessions tested at at HSARC in 2013/2014.*

Cluster	II	III
I	14.61ns	106.68**
II		116.82**
III		

*=Significant at p<0.05, **=highly significant at p<0.01, ns=non significant at p>0.05

(iv). Hierarchical Clustering of 36 Anchote Accessions

Figure 1 showed the hierarchical clustering dendrogram grouped the 36 anchote accessions into three clusters based on their quantitative agro-morphological traits. Cluster I contained 13 accessions (36.1%), cluster II contained 20 (55.6%), and cluster III contained three (8.3%). Cluster II was the largest, indicating that more than half of the evaluated accessions shared relatively similar overall trait profiles, whereas cluster III represented a smaller, distinct group. The different branch heights indicate varying degrees of similarity among accessions within and between clusters. There were 49 anchote accessions into five clusters based on 17 morphological and agronomic traits, confirming substantial phenotypic diversity in Ethiopian anchote germplasm [24].

From a plant-breeding perspective, the three clusters provide a useful basis for identifying candidate parents for anchote improvement. When considered alongside the inter-cluster divergence results, the greatest divergence occurred between clusters II and III (D^2 = 116.82**), followed by clusters I and III (D^2 = 106.68**), suggesting that crosses between carefully selected accessions from these groups may offer opportunities to combine complementary traits and generate useful variation in subsequent generations. The potential of divergent anchote populations for breeding and selection [24], and with molecular diversity studies highlighting the value of anchote germplasm characterization for conservation and improvement [22]. However, the final choice of parents should also consider cluster means, individual accession performance, and desirable traits such as total root yield, root diameter, and root weight. Because the dendrogram is based on quantitative phenotypic traits, its clusters should be interpreted as groups of multivariate similarity rather than definitive molecular genetic groups.

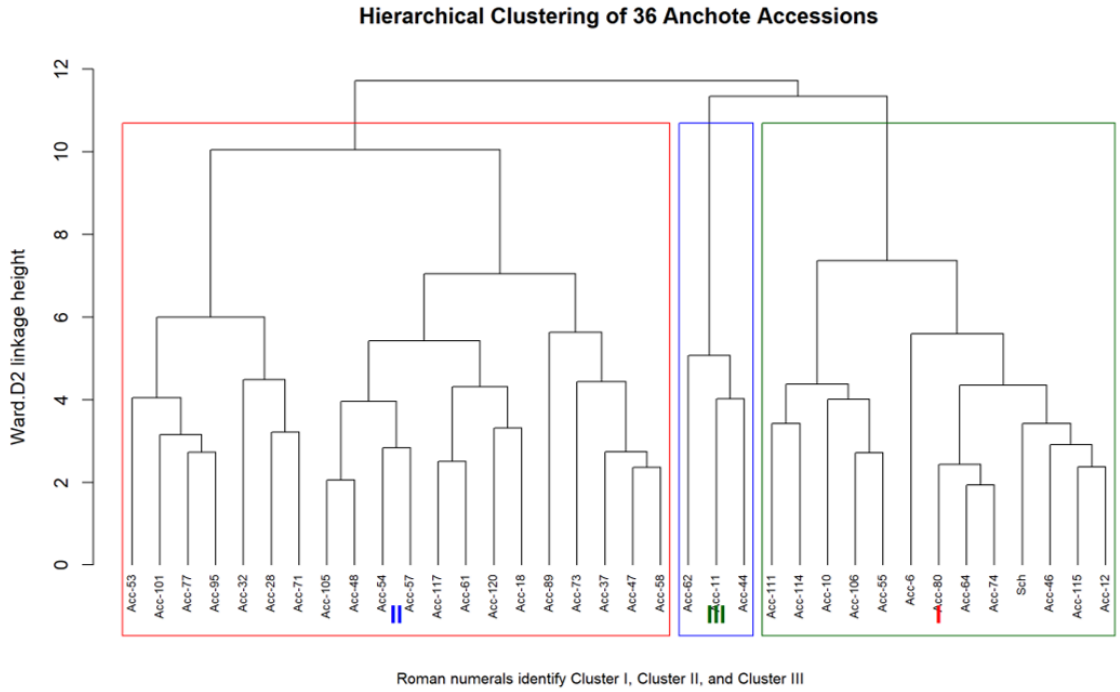


Figure 1. *Dendrogram of 36 anchote accessions into 3 clusters based on 13 quantitative characters.*

4. Conclusion and Recommendations

4.1. Conclusion

The present study demonstrated considerable agro-morphological variability among 36 anchote accessions. Significant differences among accessions for several important agronomic, root-related, yield, and disease-response traits indicate the availability of useful genetic resources for anchote improvement. The variation observed in root diameter, root weight, marketable yield, and total yield is particularly important for identifying accessions with desirable characteristics for productivity improvement.

Estimates of genetic parameters indicated differences among traits in their potential response to selection. Marketable yield and total yield were particularly promising, with genotypic coefficients of variation of 22.17% and 21.70%, broad-sense heritability estimates of 60.18% and 59.36%, and genetic advances as percentages of the mean of 35.48% and 34.49%, respectively. These results suggest that selection for improved yield could be effective within the evaluated germplasm. However, broad-sense heritability includes both additive and non-additive genetic effects, and the estimates obtained under a single location and season should be interpreted within the limits of the experimental conditions.

Correlation analysis revealed strong positive relationships between root diameter and root weight at both phenotypic and genotypic levels. Root weight and root diameter were also positively associated with marketable and total yield, suggesting that these traits could complement direct yield measurements during selection. PCA further demonstrated that root weight, root diameter, marketable yield, and total yield were major contributors to the variation among accessions. Collectively, this finding support the use of root morphological characteristics alongside direct yield measurements when identifying promising anchote germplasm.

Cluster analysis grouped the accessions into three clusters containing 13, 20, and three accessions, respectively. Cluster II recorded the highest mean marketable yield (20.55) and total yield (20.63), making it the most promising cluster for preliminary yield-oriented selection. The greatest inter-cluster divergence was observed between Clusters II and III (D^2 = 116.82, $p < 0.01$), followed by Clusters I and III (D^2 = 106.68, $p < 0.01$). These divergent groups may provide useful candidates for parental selection, provided that individual accession performance and complementary agronomic characteristics are also considered.

Based on the reported individual accession means, Acc-37, Acc-101, Acc-95, Acc-54, and Acc-47 were identified as promising candidates for further evaluation because of their comparatively high marketable and total yields. Acc-28 and Acc-32 also showed potential for further assessment of root diameter and root weight. Nevertheless, these accessions should be considered preliminary candidates rather than confirmed superior varieties because their performance has not yet been validated across multiple environments. Overall, the study provides useful baseline information for anchote germplasm characterization, selection, conservation, and breeding. Further multi-location and multi-season evaluation is essential to establish the yield stability, adaptability, and

suitability of the promising accessions for variety development in western Ethiopia.

4.2. Recommendations

Based on the findings of this study, marketable and total root yield should be prioritized as the main selection criteria for anchote improvement, supported by root diameter, root weight, and root length. Promising accessions (Acc-37, Acc-101, Acc-95, Acc-54, and Acc-47) should be further evaluated for yield performance, while Acc-28 and Acc-32 should be considered for improving root characteristics. Parental selection should consider both genetic divergence and agronomic performance, with particular attention to accessions from Clusters II and III, which showed the greatest genetic divergence. Breeding efforts should also focus on improving marketable root yield, root quality, and resistance to major diseases, particularly powdery mildew and leaf blight.

Furthermore, promising accessions should be evaluated through replicated multi-location and multi-season trials across representative anchote-growing environments to assess genotype-by-environment interactions, adaptability, and yield stability before wider recommendation. Further research should investigate the genetic basis of important yield traits, validate associations between root characteristics and yield, and assess the combining ability of selected parents. Molecular characterization should also be integrated with agro-morphological evaluation to enhance the conservation and effective utilization of anchote genetic resources.

Abbreviations

ANOVA	Analysis of Variance
DAP	Diammonium Phosphate
GA	Genetic Advance
GAM	Genetic Advance as Percentage of Mean
GCV	Genotypic Coefficient of Variation
H^2	Broad-sense Heritability
LSD	Least Significant Difference
MS	Mean Square
OARI	Oromia Agricultural Research Institute
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
RCBD	Randomized Complete Block Design
RE	Relative Efficiency
UPGMA	Unweighted Pair-Group Method with Arithmetic Mean

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Author Contributions

Alemayehu Latera: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Project administration, Software, Visualization, Writing – original draft

Kibiru Kena: Investigation, Resources, Validation, Supervision

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Conflicts of Interest

The authors declare no conflicts of interest.

Appendix

Table 10. Mean value of anchote genotypes.

Genotype	DF	DM	SCAH	VL	IL	RL	RD	RW	WMY	WUMY	TY	LB	PM
Acc-10	76.5	169	13.5	482.8	17.5	14	19.3	0.24	12.81	0.09	12.90	1	1.5
Acc-101	87.5	173	15.5	368.2	14.7	12.7	23.9	0.30	25.43	0.00	25.43	1	1
Acc-105	78	172	16	446	13.7	11	21	0.22	19.21	0.21	19.42	1	1.5
Acc-106	75.5	176	10.5	437	15.9	11.8	21.2	0.24	16.30	0.10	16.40	1	1
Acc-11	80.5	175	16	302.9	15.4	11.9	20	0.22	16.00	0.21	16.21	3	3.5
Acc-111	81.5	175.5	10.5	425.8	15.7	12.7	22.3	0.29	18.52	0.31	18.83	1.5	1.5
Acc-114	82.5	181	11.5	418.5	17.2	11.7	20.9	0.21	12.78	0.09	12.87	1.5	1

Genotype	DF	DM	SCAH	VL	IL	RL	RD	RW	WMY	WUMY	TY	LB	PM
Acc-115	78.5	176.5	15	372.7	15	12	20	0.20	9.88	0.06	9.94	1	2
Acc-117	80.5	176	17	343.6	16	12.2	17.9	0.21	17.30	0.08	17.38	1	2
Acc-12	74.5	171.5	16	375	14.9	12	15.3	0.13	11.00	0.09	11.09	1	2
Acc-120	70.5	171.5	15	371	16.3	12.8	19.8	0.22	16.94	0.09	17.03	1.5	3
Acc-18	75.5	168.5	14.5	336.4	14.9	12.6	21.5	0.24	17.40	0.23	17.63	1	1.5
Acc-28	75	177	11	417.7	15.3	13.7	26.3	0.38	19.59	0.09	19.68	1	1
Acc-32	88	172	12	511	18.4	13.5	27.5	0.42	18.58	0.07	18.65	1	1.5
Acc-37	75.5	172.5	16.5	473.2	14.9	12.7	21.3	0.27	26.55	0.00	26.55	1.5	2
Acc-44	81.5	172	15	372.8	14.4	13.3	15.1	0.15	12.42	0.47	12.89	2.5	2.5
Acc-46	74.5	175.5	16.5	380	15.5	11.3	20.4	0.21	14.55	0.10	14.65	1.5	1
Acc-47	73.5	172	17.5	403.5	15.9	15	19.6	0.28	24.03	0.00	24.03	1.5	2
Acc-48	78	173.5	17.5	454.7	14.7	11.9	19.4	0.17	17.78	0.14	17.92	1.5	1
Acc-53	78	183.5	14.5	347.9	15.6	13.9	23.5	0.30	20.86	0.19	21.05	1.5	2
Acc-54	76.5	171	17.5	428.3	15.2	13.6	17.3	0.20	25.09	0.09	25.17	1	1
Acc-55	74.5	176	13	469	13.2	11.5	19.4	0.20	14.82	0.06	14.88	1	1.5
Acc-57	81.5	171.5	17.5	336.4	14.5	11.8	15.5	0.15	22.59	0.06	22.65	1	1
Acc-58	77	177.5	16.5	399.5	16.3	13.1	20.6	0.25	21.02	0.00	21.02	1.5	2.5
Acc-6	73	181.5	16.5	418.7	15	13.2	10.7	0.07	5.42	0.30	5.73	1	1
Acc-61	84	172	16.5	356.9	15.3	14.9	16.9	0.19	13.69	0.14	13.83	1	2
Acc-62	76	171.5	15	351.5	14.5	18.2	17.4	0.32	17.32	0.44	17.77	2.5	2.5
Acc-64	79.5	178	15.5	450.3	15.8	10.7	18.8	0.16	9.52	0.07	9.59	1.5	1
Acc-71	83	177.5	12.5	392.8	17.6	15.7	25	0.40	17.68	0.00	17.68	1	1
Acc-73	81.5	168.5	16.5	438.4	18.7	13.5	21	0.26	21.67	0.00	21.67	1.5	3.5
Acc-74	78	179	15.5	445.4	16.2	11.2	19.3	0.17	13.58	0.04	13.63	1.5	2
Acc-77	82	179	14	408.3	16.2	12.4	24.8	0.29	20.45	0.00	20.45	1.5	1
Acc-80	78	181	16.5	461.4	15.1	12.9	18	0.17	12.66	0.07	12.73	1	1
Acc-89	76.5	183.5	16.5	443.5	19.5	10.9	19.9	0.17	19.92	0.17	20.09	1.5	2
Acc-95	79	177	16.5	384	15.3	14.6	23.8	0.36	25.27	0.00	25.27	1.5	1
Sch	71.5	170	16	414.2	16.1	9.5	16.7	0.10	9.70	0.12	9.82	1.5	2

Where: DF= Days to flowering; DM=Days to maturity; SCAH=stand count at harvest; VL=Vine length; Internodes length= LL; RL=Root length; RD=Root diameter; RW=Root weight; WMY=Weight of marketable yield; WUMY=Weight of unmarketable yield; TY=Total yield; LB=Leaf blight; PM=Powdery mildew.

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