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Variability of Coffee (*Coffeaarabica* L.) Germplasm Collections Based on Morphological Quantitative Characters

Meseret Degefa[1, *], Sentayehu Alamerew[2], Ali Mohammed[2], Adeba Gemechu[2]

[1]Awada Agricultural Research Sub-Centre, Yirgalema, Ethiopia

[2]Colleges of Agriculture and Veterinary Medicine (JUCAVM), Jimma University, Jimma, Ethiopia

Email address:

meseret.deg2008@gmail.com (M. Degefa)

[*]Corresponding author

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Abstract: Ethiopia is the center of genetic diversity of Arabica coffee (*Coffeaarabica* L., Rubiaceae). In receipt of more information on genetic variability is a must for additional enhancement of coffee (*Coffeaarabica* L.). An experiment was carried out at Awada Agricultural Research Sub Center, Ethiopia, to study the amount of phenotypic diversity between southern coffee (*Coffeaarabica* L.) germplasm accessions on a quantitative character. Entirety 104 entries consisting of 100 accessions from southern parts of Ethiopia and four standard cultivars were evaluated using augmented design. The key goal of the study was to assessphenotypic and genotypic variances, the broad sense heritability, genetic advance and estimate the principal component among various quantitative characters. Data on 22 quantitative traits were recorded from five envoy trees per row for each accession. One hundred and four Arabica coffee accessions were grouped into four distinct groups by cluster analysis indicating a wide genetic diversity of coffee genotypes. Cluster I, II, III and IV contained 04 (3.85%), 29 (27.89%), 66 (63.46%) and 05 (4.81%) of the accessions, respectively. The X^2 test show that inter cluster squared distances were significant at $p<0.01$ and $p<0.05$. Highest inter-cluster distance (D^2) was found among cluster I and IV (D^2 =102.61), even as the minimum inter-cluster distance (D^2) was obtained between cluster II and III (13.26). First 8 principal components with Eigen values more than one were dependable for about 76.34% of the total variation among the germplasmaccessions. Normally, the present study revealed the existence of immense genetic variability among coffee germplasm for various important morphological traits. Consequently, there is a possibility to make use of these traits to expand genotypes that do superior than the existing varieties for the upcoming coffee enhancement plan.

Keywords: *Coffeaarabica,* Genetic Variability, the Broad Sense Heritability, Genetic Advance, Principal Component, Yield and Yield Components, Germplasm

1. Introduction

Coffee is a permanent field crop which belongs to the genus *Coffea*in the *Rubiacea*family and is mostly grown in the tropical and subtropical areas [5]. The genus *Coffea*consist of almost 124 familiar species [12] of which just two species, *Coffea Arabica* Linnaeus (Arabica coffee) and *Coffeacanephora* Pierre (Robusta coffee) are the two commercially imperative species. Arabica coffee is certainly the key commercial species and give to above 70% of globe coffee production [19]. *Coffeaarabica* is a self-fertile allotetraploid (2n=4x=44), whereas others are diploid (2n=2x=22) and self-infertile [3, 24].

Arabica coffee is the well favorite non-alcoholic global drink, and is a crucial basis of foreign exchange income for a lot of countries. Several expected that the whole coffee supply chain offers a livelihood for 125 million people globally [9] and is the next mainly exported product after oil

universally [12]. Ethiopia is the top producer of coffee in Africa and the fifth key exporter in the world subsequently to Brazil, Vietnam, Colombia and Indonesia, contributory to 4.2% of the whole globe coffee production [20]. Ethiopia is not just the leading producer plus exporter of Arabica coffee, as well the origin and center of genetic diversity in the southwestern highlands of the country. Such being of genetic diversity offer huge chance for coffee enhancement [23]. In spite of, the enormous area of cultivation, wealth of great genetic diversity and value to the national economy, the productivity of coffee is extremely low (about 669.6 Kgha-1) [10]. Different researchers have an explanation for main causal reasons for such low yields, such as the utilizes of unimproved coffee landraces, conventional husbandry, processing performance and the direct and indirect impacts of climatic unevenness [18, 36]. Moreover, in spite of the availability of coffee genetic diversity in the country, coffee genetic resources are under grave pressure of loss, mostly due to deforestation, substitute of traditionally grown landrace by a small number of new released enhanced varieties, environmental degradation and vary in land utilize [39]. Thus, it is relevant and necessitate of the coffee breeders' to collect, pick and develop coffee varieties which are high yielder, disease resistant and most excellent cup quality which can meet up the clients command. About 5731 accessions are preserved at Institute of Biodiversity Conservation [36] and 6721 accessions at Jimma Agricultural Research Center field gene bank [35].

Information concerning genetic diversity amongst genotypes of every crop is primary to approximate the potential of genetic get in a breeding agenda and for efficient maintenance and exploitation of available genetic wealth, which aid in picking hopeful parental lines in hybrid variety enlargement [5, 15, 30, 40] reported the existence of genetic variability with the coffee germplasm for mainly of the traits considered. In addition, in spite of great coffee genetic resources in the crop species, the country has not so far been completely make use of its coffee genetic resources as likely in terms of improving coffee output and comprehensive information on the degree of genetic diversity is not so far accessible. Keep this in outlook, this present study expected to approximation phenotypic and genotypic variances, the broad sense heritability, genetic advance and assess the principal component along with coffee germplasm accession based on numerous quantitative traits.

Table 1. *Description of the genotypes.*

Genotype	Districts	Specificlocation	Altitude (m.a.s.l)	Total no collected
Aw 05/06, Aw 59/06, Aw 94/06, Aw 111/06	Bensa	Tibiro	1750 - 1800	4
Aw 64/06, Aw 103/06	Bensa	Silinga	1740 - 1770	2
Aw 81/06, Aw 66/06, Aw 12/06, Aw 99/06	Bensa	Ware	1850 - 1210	4
Aw 92/06, Aw 96/06, Aw 106/06	Bensa	Bensha	1700 – 1930	3
Aw 79/06	Bensa	Hedamo	1800	1
Aw 58/06, Aw 29/06, Aw 107/06	Bensa	Segera	1750 – 1930	3
Aw 97/06, Aw 100/06, Aw 67/06, Aw 108/06, Aw 04/06	Bensa	Setamo	1790 – 2015	5
Aw 30/06, Aw 93/06, Aw 104/06	Bensa	Golisa	1800	3
Aw 71/06, Aw 98/06, Aw 89/06, Aw 78/06, Aw 73/06	Bensa	Shemalega	1790 - 2020	5
Aw 10/06, Aw 62/06, Aw 91/06, Aw 84/06, Aw 28/06, Aw 95/06	Bensa	Gungvma	1720 – 1790	6
Aw 27/06, Aw 68/06, Aw 83/06, Aw 72/06	Bensa	Hatese	1750 – 1810	4
Aw 02/06, Aw 88/06, Aw 90/06	Bensa	Micharo-2	1720 – 1800	3
Aw 67/06, Aw 112/06	Bensa	Mulke	1750 – 1760	2
Aw 60/06, Aw 61/06, Aw 109/06	Bensa	Abaye	1740 – 1750	3
Aw 08/06, Aw 22/06, Aw 26/06, Aw 74/06, Aw 76/06	Bensa	Leleno	1750 – 1830	5
Aw 14/06	Bensa	Mike	1780	1
Aw 105/06	Bensa	Agensa	1980	1
Aw 34/06, Aw 65/06	Dara	Chire	1800	2
Aw 16/06, Aw 75/06, Aw 80/06	Dara	Kisho	1770	3
Aw 01/06, Aw 07/06, Aw 41/06, Aw 51/06	Dara	Wachi cha	1800	4
Aw 24/06	Dara	Boreta	1750	1
Aw 21/06	Dara	Doke	1750	1
Aw 23/06	Dara	Olone	1750	1
Aw 19/06, Aw 57/06, Aw 85/06	Dara	HalelaDaka	1750	3
Aw 49/06, Aw 54/06, Aw 87/06	Dara	Buna Tawaba	1740	3
Aw 53/06, Aw 56/06, Aw 63/06, Aw 77/06	Dara	Loya	1750	4
Aw 11/06, Aw 25/06, Aw 42/06, Aw 55/06	Dara	Chiro	1800	4
Aw 06/06, Aw 39/06, Aw 52/06, Aw 70/06	Dara	Shilicho	180 – 1810	4
Aw 32/06, Aw 40/06, Aw 43/06	Dara	Babe Kombolcha	1830	3
Aw 31/06, Aw 38/06, Aw 46/06	Dara	AlemeKancha	1750 - 1800	3
Aw 17/06, Aw 18/06, Aw 45/06, Aw 82/06	Dara	BangoMarkos	1750 – 1875	4
Aw 03/06, Aw 09/06	Dara	Dubancho	1760 - 1800	2
Aw 15/06, Aw 20/06, Aw 86/06,	Dara	Megenecho	1740 - 1760	3
Checks				
744, 7440, 75227, 1377				

2. Materials and Methods

2.1. Description of the Experimental Area

The study was carried out at Awada Agricultural Research Sub Center. It is established at 315 km from Addis Ababa in southern Ethiopia near Yirgalem town. The sub-center is situated in the moderate to cool semi-arid mid highland agro-ecology of southern Ethiopia. Geographically, it is located at 6°3'N latitude and 38°E longitude at an altitude at an elevation of about 1740 m.a.s.l. The area has a semi-bimodal rainfall distribution characterized by double wet and dry seasons with an average precipitation of 1342 mm per annum. The average yearly smallest and highest air temperatures are 11 and 28.4°C, respectively whereas the annual mean least and highest rainfall are 858.1 and 1676.3 mm [28].

2.2. Genotypes

The study was carried out on the established 100°C. *arabica* genotypes together with four standard checks. The coffee genotypes were collected from the potential and in lieu of areas in the southern coffee growing part of Ethiopia. Details of geographical origin of the collected genotypes were given in Table 1.

2.3. Treatments and Experimental Design

Treatments consisted of 100 coffee accessions and four released varieties (75227, 744, 7440 and 1377) were incorporated as standard checks. The experiment was planted using an augmented design, which is used with replicated controls (checks) to evaluate the performance of non-replicated accession in complete block designs in five blocks in a single row (plot) consisting of ten trees per plot. The plant-to plant spacing used was two meters by two meters, while spacing between blocks were four meters. All the suggested agronomic practices were applied evenly to all the plots [13].

2.4. Methods of Data Collection

In the path of this study, data on 22 quantitative character, namely: total plant height (cm), Height up to first primary branch (cm), main stem diameter (cm), canopy diameter (cm), number of primary branches (no), percentage of bearing primary branches (%), number of secondary branches (no), average length of primary branches (cm), number of nodes of primary branches (no), leaf length (cm), leaf width (cm), leaf area (cm^2), fruit length (mm), fruit width (mm), fruit thickness (mm), bean length (mm), bean width (mm), bean thickness (mm), hundred bean weight (gm), yield per tree (g), coffee berry disease (%) and rust incidence (%), were collected from each accession using the standard procedures of IPGRI [21]. Yield per tree was taken for four successive years.

2.5. Methods of Data Analysis

2.5.1. Cluster Analysis (CA)

Clustering analysis is a multivariate statistical analysis procedure linking the partitioning a set of objects into groups so that objects within a group are related and objects in different groups are disparate [11]. The 104 coffee accessions for 22 quantitative characters were clustered using the proc cluster of SAS with average linkage technique of clustering approach [32]. The number of clusters was determined by looking into three statistics specifically pseudo F, pseudo t^2 and the cubic clustering criteria (CCC). The number of clusters is determined where the CCC and pseudo F statistics combined with a small value of the pseudo t^2 statistics and a large pseudo t^2 statistics for the next cluster fusion.

2.5.2. Divergence Analysis

Compute for a set distance based on multiple characters was given by generalized [26] for the 22 quantitative characters and was analyzed using the method procdiscrim of SAS [32]. D^2 statistics is by:

$$D^2 ij = (\bar{A}i - \bar{A}j) S^{-1} (\bar{A}i - \bar{A}j)$$

Where, D^2ij = total generalized distance among class i and j; (Āi−Āj) are the difference in the mean vectors of $i^{th}$and j^{th}germplasm accessions; S^{-1} is the variance- covariance matrix of pooled error.

Testing the significance of D^2 values attained for a pair of population was in use as the calculated value of x^2 (chi-square) and tested against the tabulated value of x^2 for P degrees of freedom, at right probability level where P is the number of quantitative characters measured [34].

2.5.3. Principal Component Analysis (PCA)

Principal component analysis is a multivariate method for investigative relationships among some quantitative variables. Data of quantitative traits were standardized for principal component analysis and cluster analysis to decrease the pressure of outliers and differences in scale of measurements by subtracting the mean from each value and then divided by the standard deviation in order to scale to zero mean and unit variance [11].

Principal component analysis was executed using a correlation matrix by employing process princompcorr of SAS in organize to examine the relationships among quantitative traits that are associated between each other by changing into uncorrelated traits called principal components.

3. Results and Discussion

3.1. Divergence/Distance Analysis (D^2)

The details of the genetic diversity and relationships existing in *C. arabica* collections are vital for setting up breeding approach and germplasm conservation. Analysis of inter-and intra-cluster distances for 22 quantitative traits by employing the discrim method of pair wise generalized squared distance revealed significant and highly significant ($P<0.05$, and $P<0.01$) genetic distances among best part of

clusters and non-significant variation within accessions set in the similar cluster (Table 2).

In the inter-cluster distance analysis, clusters that are divergent are helpful sources of genotypes that could be used in the hybridization plan to obtain an ample choice of difference between the isolation and to exploiting heterosis from genetically diverse parental lines. The present study revealed the likely utilization of such information and the presence of such crowd of distantly related genotypes that can be immediately employed in the hybridization for hybrid variety progress. The highest inter-cluster distance was between cluster I and IV (D^2=102.61) go after in between cluster II and IV (D^2=60.86) and cluster I and III (D^2=41.32). The least inter cluster distance was observed between cluster II and III (D^2=13.26) followed by cluster I and II (D^2=16.98**)** and cluster III and IV (D^2=19.59)**.** The highest value of inter-cluster distance indicated that the accessions fit in with these clusters were varied. On the other hand, the lowest cluster distance specifies a close relationship between the accessions. Therefore from the study of the above result coffee accessions from cluster IV and clusters I and II as well as cluster III and cluster I could be potential parental lines for exploitation heterotic value through crossing. [31], reported that crossing germplasm accessions belonging to different clusters of wide Mahalanobis distance (D^2) could exploit opportunities for transgressive segregation as there is a high probability that distinct genotypes would contribute unique desirable alleles at different loci. The degree of heterosis amid populations which reflect differences in gene frequencies is really associated with their genetic divergence [14]. In arabica coffee [6] and [7] reported genetic yield upgrading is most likely to succeed in the use of genetically diverse elite parental lines in the breeding planned that are distinctly different in their morphological characteristics. [38], on the other hand, reported that better performance of coffee hybrid for yield and for most of yield related traits in crosses linking diverse parents with respect to geographical origin balance to crosses having parents of comparable geographical origin. [34], also reported divergence analysis is performed to see the diverse genotypes for hybridization purpose so that genotypes set together are less divergent than genotypes which fall into different clusters, mainly clusters divided by the largest numerical distance (D^2) show the utmost difference.

3.2. Cluster Analysis

Average linkage cluster analysis was calculated for quantitative traits to classify coffee accessions in to like groups that are useful for the description and assessment of coffee genotypes. The phenotypic similarity of 104 coffee germplasm accessions was assessed by cluster analysis. Coffee genotypes well thought-out in the present study were classified into seven clusters based on the proc cluster of SAS with average linkage method of clustering strategy using 22 quantitative traits (Table 3). The number of genotypes classified in each cluster varied from 04, 29, 66 and 05 in cluster I, II, III and IV, respectively. Furthermore, among 104 coffee genotypes 3.85%, 27.89%, 63.46% and 4.80%, where coffee genotypes clustered in cluster I, II, III and IV, respectively (Table 3). The genotypes used as checks, 1377, 744, 75227 and 7440 were grouped in cluster II.

The greater part of accessions (95 or 91.35%) was classified in to two clusters (27 and 66 genotypes) in clusters II and III, respectively. Others clusters had from 4 up to 5 members. These accessions were grouped in to cluster III were the largest with 66 accessions (63.46%) followed by cluster II with 29 accessions (27.89%), cluster IV with 05 accessions (4.80%), cluster I with 04 accessions (3.85%) of the total population, indicative of that coffee accessions of the same cluster group were at least morphologically similar. The clustering pattern of the accessions revealed the existence of genetic diversity in the coffee accessions of the characters considered. From previous work, [30] has made cluster analysis based on 22 quantitative traits grouped 49 Limmu coffee genotypes in to four clusters.

Also, substantial disparity in cluster means was observed for 22 quantitative traits (Table 4). Accessions in cluster-I the highest fruit width, fruit thickness, coffee leaf rust and the lowest mean value of green bean yield per tree, leaf area, bean length, bean thickness, total plant height, hundred bean weight, stem diameter, canopy diameter, number of primary branches, percentage of bearing primary branches, average length of primary branches and number of nodes of primary branches. Accessions in cluster-II showed the highest mean values for leaf length, bean length, handered bean weight, the total plant height, average length of primary branches, coffee berry disease and the lowest in fruit thikness, leaf width and number of secondary branch. In the same way, the highest cluster mean was found for fruit length, leaf area, bean thickness and height up to first primary branches in cluster-VII whereas, fruit thickness and bean length and coffee berry disease which had the lowest mean value. Lastly, accessions in cluster-IV illustrated highest leaf width, bean thickness, stem diameter, canopy diameter, number of primary branches, number of secondary branches, green bean yield per tree and also the lowest mean value of fruit length, fruit width, fruit thickness, leaf length, height up to first primary branches and coffee leaf rust. The present study more or less in harmony with the finding of [17] reported clustering of 124 coffee genotypes with 19 quantitative characters. This point out that dissimilar clusters have different breeding values that enable breeders to improve different traits and parental selection should be made based on the relative pro of each cluster for each trait depending on the objective of the breeding program.

Table 2. *Inter (bottom) and intra (bold and diagonal) cluster distance among 104 arabica coffee accessions for 22 quantitative characters.*

Cluster	I	II	III	IV
I	0			
II	16.98	0		
III	41.32**	13.26	0	
IV	102.61**	60.86**	19.59	0

* Significant at p<0.05 for X^2=33.92; ** Significant at p<0.01 for X^2=40.29, ns= Significant.

Table 3. *Clustering patterns of 104 coffee accessions based on 22 coffee morphological characters.*

Cluster	No. of accessions	% of genotypes	Name of accessions in each cluster
I	04	3.85	AW-05, AW-21, AW-45, AW-74
II	29	27.89	AW-77, AW-83, AW-100, AW-104, AW-54, AW-63, AW-79, AW-90, AW-11, AW-60, AW-86, AW-99, AW-53, AW-71, AW-80, AW-59, AW-82, AW-50, AW-62, AW-52, AW-24, AW-46, AW-89, AW-101, AW-81, AW-92, AW-93, AW-88, AW-87
III	66	63.46	AW-97, AW-98, AW-57, AW-58, AW-36, AW-94, AW-09, AW-13, AW-95, AW-67, AW-68, AW-33, AW-72, AW-27, AW-47, AW-26, AW-102, AW-08, AW-76, AW-38, AW-61, AW-64, AW-66, AW-48, AW-73, AW-34, AW-42, AW-25, AW-51, AW-69, AW-28, AW-31, AW-19, AW-49, AW-56, AW-40, AW-78, AW-65, AW-41, AW-103, AW-06, AW-55, AW-17, AW-23, AW-39, AW-12, AW-22, AW-96, AW-29, AW-43, AW-15, AW-16, AW-20, AW-85, AW-91, AW-44, AW-14, AW-07, AW-84, AW-35, AW-70, AW-75, 75227, 744, 7440, 1377
IV	05	4.80	AW-18, AW-37, AW-10, AW-32, AW-30
Total	104	100	

Table 4. *Mean values of 22 morphological traits for four clusters of 104 coffee germplasm evaluated.*

Cluster / No.	FL	FW	FT	LL	LW	LA	BL	BW	BT	HBW	TPH
I	1.5	1.19**	1.15**	11.86	4.57	36.18*	0.95*	0.61	0.35	14.78	207.80*
II	1.52	1.17	1.11*	12.33**	4.50*	37.02	1.00**	0.62	0.37	16.22	245.76**
III	1.53**	1.18	1.11*	12.15	4.72	38.27**	0.99	0.62	0.38**	15.74	238.82
IV	1.47*	1.16	1.11*	11.69*	4.73**	36.93	0.96	0.63**	0.38**	14.85	225.72
Mean	1.5	1.17	1.12	12.01	4.63	37.1	0.97	0.62	0.37	15.4	229.52

Cluster / No.	SG	CD	HUF	NOP	PBP	ALPB	NNPB	NSB	CBD	CLR	GBY
I	3.16*	178.99*	18.24	78.20*	61.50*	87.10*	24.93*	116.2	23.18	19.53	158.90*
II	3.21	180.3	20.67	84.31	71.85	103.22**	26.3	114.78*	26.62**	17.17	263.46
III	3.41	191.6	21.63	84.76	69.4	97.62	26.65	115.52	16.39*	13.94	445.23
IV	3.68**	200.85**	17.75*	84.77**	75.02**	89.9	27.72**	121.45**	19.85	9.37*	632.88**
Mean	3.36	187.93	19.57	83.01	69.44	94.46	26.4	116.99	21.51	15	375.12

**,* represents maximum and minimum values respectively, HUP= height up to first primary branches, TPH= total plant height, NMSN= number of main stem nodes, SD= stem diameter, CD= canopy diameter, NPB= number of primary branches, NSB=number of secondary branches, PBPB= percentage of bearing primary branches, NNPB= number of nodes of primary branches, ALPB= average length of primary branches, AILPB= average inter node length of primary branches, LL= leaf length, LW= leaf width, LA=leaf area, FL= fruit length, FW= fruit width, BL= bean length, BW= bean width, BT= bean thickness, HBW= hundred bean weight, PL= petiole length, CBD =coffee berry disease, CLR =coffee leaf rust, GBY = Green bean yield per tree.

3.3. Estimation of Genetic Parameters

3.3.1. Phenotypic and Genotypic Coefficients of Variation

Genotypic coefficients of variation (GCV) ranged with the least value for number of secondary branch (2.877%) to the highest value for coffee berry disease (47.838%) while phenotypic coefficients of variation (PCV) vary from (3.371%) for fruit width to (47.9273%) for coffee berry disease (Table 5). Phenotypic and genotypic coefficient of variation values larger than 20% are measured as high, whereas values less than 10% are to be low and values between 10 and 20% as medium. According to this explanation, High phenotypic (47.927% and 31.553%) and high genotypic (47.838% and 21.894%) coefficients of variation were recorded for traits coffee berry disease and coffee leaf rust, respectively. Whereas, handered bean weight and yield per tree had medium PCV (13.777% and 14.400%) and GCV medium (12.703% and 12.344%) values, respectively. While, leaf area and height up to first primary branches had medium PCV (10.485%, 10.846% and 10.843%) values, respectively. The traits of high PCV and medium to high GCV recommended that, the genotype could be reflected by the phenotype, suggesting the success of selection based on the phenotypic performance for these traits. Medium phenotypic (10.485% and 10.846%) and low genotypic (9.614% and 9.070%) values, respectively for leaf area and height up to first primary branches. Yet, low PCV and low GCV were recorded for total plant height, stem diameter, canopy diameter, fruit length, fruit width, fruit thickness, leaf length, leaf width, bean length, bean width, bean thickness, number of primary branches, number of secondary branches, percentage of bearing primary branches, number of nodes of primary branches and average length of primary branches. Comparable results were reported by [40, 33, 16, 2, 27] in arabica coffee studies for different morphological characters.

3.3.2. Estimates of Heritability

Broad sense heritability estimates for the 22 quantitative traits ranged from 22.80% average length of primary branch to 99.00% for coffee berry disease (Table 5). [37], generally classified heritability estimates as low (<20%), medium (20-50%) and high (>50%). Based on this categorization, heritability estimates of larger than 50% was recorded for traits such as coffee berry disease (99%), bean width (90.30%), bean thickness (87.90%), fruit width (86.00%),

handered bean weight (85.00%), leaf area (84.10%), leaf length (81.60%), fruit thickness (80.00%), leaf width (78.80%), bean length (73.70%), yield per tree (73.50%), fruit length (70.50%), stem diameter (70.10%), height up to first primary branches (69.90%), number of primary branches (67.80%), canopy diameter (54.00%), indicating the minimum effect of environment on the phenotypic expression of these characters and efficiency of selection in the advancement of these traits.

On the other hand, moderate heritability were recorded for coffee leaf rust (48.10%), number of secondary branches (43.30%), percentage of bearing primary branches (24.00%), number of nodes of primary branches (24.00%), total plant height (23.90%), average length of primary branches (22.80%), which implies the prospect of using these traits in coffee enhancement plan, because of acceptable level of correspondence between genotype and phenotype. This finding is in accordance with estimates of heritability obtained for arabica coffee by [22]. [7, 33], reported high broad sense heritability for 15 of the 18 morphological characters studied on six elite parental lines and their 15 F1 crosses for characters like stem diameter, number of leaves, height, shoot fresh weight, root dry weight and number of nodes which ranged from 71.43% to 97.32%. This result recommended that cause of environment on the phenotypic expression of the characters is low; therefore, development during selection could be effective. Similarly, high heritability estimates for hundred bean weight, number of secondary branches and canopy diameter and medium heritability of bean thickness were also reported by [40]. Like high heritability values have also been reported by [30] for bean length, bean width, number of secondary branches, number of primary branches, average inter-node length of primary branches and hundred bean weight, and medium heritability values for stem diameter, leaf length, yield of green bean and fruit thickness. Further, the finding of [15] has been more or less similar to the current study for most of the traits considered. [16] reported broad sense heritability for leaf length (90.30%), average inter node length of main stem (88.78%), stem diameter (86.46%), coffee berry disease reaction (86.16%), canopy diameter (84.95%), number of main stem nodes (84.09%), average length of primary branches (83.80%), plant height (83.70%), number of primary branches (82.83%), percent of bearing primary branches (76.91%), fruit length (75.80%), hundred green bean weight (69.98%), bean weight (67.27%), average green bean yield (67.01%), leaf width (60.47%), leaf area (50.69%) and coffee leaf rust reaction (50.47%). In the same way, [1] has also reported high heritability values for leaf area (99.99%), leaf length (99.98%), leaf width (99.86%), hundred green bean weight (95.93%), and green bean yield (94.13%), inter node length of main stem (83.50%), stem diameter (76.98%), canopy diameter (68.31%), number of secondary branches (64.06%) and plant height (61.14%).

3.3.3. Genetic Advanceas Percent of Means

Genetic gain (GA) that could be estimated from selecting the top 5% of the genotypes as percent of mean different from 4.377% for the number of nodes of the primary branches to 167.43% for coffee berry disease (Table 5). As measure by [22] the genetic advance as percent of mean was classified as low (0-10%), medium (10-20%) and high (≥20%). As per this idea, the highest (≥20%) GAM was observed for coffee berry disease severity (167.43%), coffee leaf rust severity (51.419%), yield per tree (42.530%), height up to first primary branches (28.975%), stem diameter (23.324%) and hundred bean weight (22.783%). Moderate GAM (10-20%) was attaining for leaf area (17.435%), leaf width (12.642%), bean thickness (12.479%), bean length (11.123%), canopy diameter (10.533%). On the contrary, fruit length, fruit width, fruit thickness, leaf length, bean width, total plant height, number of secondary branch, percentage of bearing primary branches, number of nodes of primary branches and average length of primary branches illustrate lower estimates of GAM (<10%) value.

The low GCV and low GAM observed for these traits shows that the characters were under high environmental influence; hence selection based on these traits would be less effective. Larger genotypic coefficients of variation along with high heritability and genetic advance provide better information than each parameter alone. Therefore, characters that exhibited high genotypic coefficients of variation, heritability and genetic advance would be useful as a basis for selection [40, 22], reported that estimates of heritability show only the effectiveness with which the selection of genotypes could be based on phenotypes but its efficacy increased when used along with estimates of genetic advance. In the present study, characters such as coffee berry disease severity (167.43%), coffee leaf rust severity (51.419%), yield per tree (42.530%), height up to first primary branches (28.975%), stem diameter (23.324%) and hundred bean weight (22.783%) showed relatively larger values for genetic advance for these characters suggesting the effectiveness of selection to improve these traits.

Accordingly, high heritability together with high genetic advance as percent of mean was acquire for coffee berry disease severity, yield per tree, stem diameter, hundred bean weight and height up to first primary branches, even as high heritability with moderate GAM was achieve for leaf width, leaf area, bean length, bean thickness and canopy diameter. Later, pooled high GCV, high heritability and high GAM were recorded for CBD reaction (47.838, 99.00, and 167.43%) and CLR reaction high GCV (21.894%), moderate heritability (48.10%) and high GAM (51.419%) in the order of magnitude; whereas moderate GCV (12.344%), high heritability (73.50%) and high GAM (42.53%) were recorded from yield per tree, telling that yield is complex in nature chiefly because of its quantitative inheritance.

Also, fruit length, fruit width, fruit thickness, leaf length and bean width showed moderate heritability along with low genetic advance. Moderate to high heritability with low genetic advance suggests that the traits are unfair by environmental things [16], this would make complicated to improve these traits through simple selection, as concerns

cross breeding is the best option for improvement of such kind of traits. The present finding is partly in agreement with [30] who studied on Limu coffee collections and reported as height up to first primary branches, number of secondary branches, hundred beans weight and yield per tree showed higher heritability and genetic advance. [15] found high heritability together with high genetic advance as percent of mean (GAM) for hundred bean weight and height up to first primary branch and high GCV, moderate heritability and high GAM for CBD severity, while stem diameter, number of nodes of primary branches, and average inter node length of primary branches showed high heritability with moderate GAM. Moreover, [38] found high heritability with high GAM for a number of main stem nodes, stem diameter and internodes length, whereas, yield per tree recorded moderate heritability and high GAM on Lemu coffee collections. Likewise, [16] found high broad sense heritability coupled with high genetic advance as percent of mean were observed for coffee berry disease, average green bean yield, stem diameter, average inter node length of stem, plant height, number of primary branches and average length of primary branches verify that genotypic variance has give to a large extent to the total phenotypic variance.

Table 5. *Estimates of phenotypic and genotypic coefficient of variability, broad sense heritability and genetic advance as percent of mean for 22 quantitative traits of 104 coffee germplasm accessions.*

Characters	GV	PV	HRT (%)	PCV (%)	GCV (%)	GAD	GAM (%)
FL	0.00526	0.00746	70.50	5.700	4.786	0.105	6.930
FW	0.00136	0.00158	86.00	3.371	3.127	0.066	5.571
FT	0.00229	0.00286	80.00	4.795	4.290	0.086	7.701
LL	0.37754	0.46284	81.60	5.571	5.032	1.054	8.635
LW	0.09204	0.11684	78.80	7.353	6.526	0.588	12.642
LA	13.2639	15.7771	84.10	10.485	9.614	6.605	17.435
BL	0.00504	0.00684	73.70	8.434	7.240	0.109	11.123
BW	0.00084	0.00093	90.30	4.901	4.658	0.054	8.626
BT	0.00069	0.00079	87.90	7.445	6.980	0.047	12.479
HBW	4.02828	4.73788	85.00	13.777	12.703	3.600	22.783
TPH	70.889	296.144	23.90	7.175	3.510	11.950	4.982
SD	0.05382	0.07682	70.10	8.197	6.861	0.789	23.324
CD	46.4793	86.086	54.00	4.936	3.627	19.800	10.533
HUP	3.65814	5.23144	69.90	10.846	9.070	6.110	28.975
NPB	25.7882	38.0469	67.80	7.354	6.054	15.915	18.973
PBP	8.6786	36.1453	24.00	8.550	4.190	4.744	6.747
ALPB	9.21116	40.4571	22.80	6.552	3.126	5.049	5.201
NNPB	0.69972	2.90952	24.00	6.482	3.179	1.152	4.377
NSB	10.8728	24.5606	44.30	4.324	2.877	7.402	6.458
CBD	68.0789	68.3313	99.60	47.927	47.838	28.880	167.43
CLR	10.2393	21.2657	48.10	31.553	21.894	7.515	51.419
GBY	2493.89	3394.04	73.50	14.400	12.344	172.064	42.530

HUP= height up to first primary branches, TPH= total plant height, SD= stem diameter, CD= canopy diameter, NPB= number of primary branches, NSB=number of secondary branches, PBP= percentage of bearing primary branches, NNPB= number of nodes of primary branches, ALPB= average length of primary branches, LL= leaf length, LW= leaf width, LA=leaf area, FL= fruit length, FW= fruit width, FT= fruit thickness, BL= bean length, BW= bean width, BT= bean thickness, HBW= hundred bean weight, CBD =coffee berry disease, CLR =coffee leaf rust, GBY = green bean yield per tree, GA =Genetic advance, GAM= Genetic advance as percent of means, GCV= Genotypic coefficient of variation, GV = Genotypic variance, H= Broad sense heritability, PCV= Phenotypic coefficient of variation, PV= Phenotypic variation.

3.4. Principal Component Analysis (PCA)

Principal component analysis was prepared using 22 quantitative traits with the aim of minimizing the dimensionality of large number of unified traits in a given data set and retaining utmost information about the genetic variation (Table 6). As a result, the first eight principal components with Eigen values more than one were dependable for about 76.34% of the total variation among the germplasm accessions. The primary principal component which accounted for 19.23% of the variability among accessions were qualified to discriminatory traits such as fruit length, fruit width, fruit thickness, leaf length, leaf area, bean length, bean width, bean thickness, hundred bean weight, percentage of bearing primary branches and green bean yield per tree. Besides, 14.71% of the total variability among the tested accessions accounted for the second principal component initiated from variation in fruit length, leaf length, leaf width, leaf area, bean length, total plant height, stem diameter, canopy diameter, height up to first primary branches, number of primary branches, number of secondary branches, coffee berry disease and green bean yield per tree. Correspondingly, the third principal component, which clarify 9.99% of the total variation get from the variation of the fruit length, bean length, hundred bean weight, total plant height, height up to first primary branches, length of primary branches, number of nodes of primary branches, number of secondary branches, coffee berry disease and coffee leaf rust. Quantitative traits which had ample part to the fourth principal component that accounted for 8.34% total variation was fruit width, fruit thickness, total plant height, stem diameter, height up to first primary branches, number of

primary branches, percentage of bearing primary branches and green bean yield per tree. The dissimilarity in the fifth principal component (7.18%) was also recognized to traits like leaf length, leaf area, total plant height, number of primary branches, percentage of bearing primary branches, length of primary branches and number of nodes of primary branches, By the magnitude of eigenvector loading, bean width, hundred bean weight, percentage of bearing primary branches, number of nodes of primary branches, number of secondary branches, coffee berry disease and green bean yield per tree were majorly loaded on principal component sixth (6.03%). On the other hand, bean thickness, total plant height, number of primary branches, coffee berry disease and coffee leaf rust mainly unfair the variation in the seventh principal component (5.87%). Lastly, quantitative traits, such as leaf width, bean length, bean width, bean thickness, hundred bean weight, height up to first primary branches, coffee leaf rust and green bean yield per tree contributed mainly to the variation of the eight principal components, which elucidate the lasting 5.00% of the variations. Consistent with this finding many investigators also found similar result from different Arabica coffee germplasm [15, 25, 30]. Of all quantitative characters evaluated only bean yield per tree give to the variations in five principal components out of the eight principal components and also total plant height, bean length, height up to first primary branches and coffee berry disease offer to the variations in four principal components out of the eight principal components (Table 6). The present study confirmed that arabica coffee accessions displayed large amount of variations for the traits studied. This broad trait diversity evident among the arabica accessions advocates ample opportunities for genetic enhancement through selection directly from the accessions and/or selection of diverse parents for hybridization programs and conservation of the germplasm for upcoming consumption. The existence of wide morphological diversity among arabica coffee is reliable with the earlier work of [2, 16, 27, 28, 40].

Table 6. *Eigen values, total variance, cumulative variance and eigenvectors for 22 quantitative traits studied on 104 coffee germplasm accessions.*

Traits	Eigenvectors							
	PC I	PC II	PC III	PC IV	PC V	PC VI	PC VII	PC VIII
FL	0.278	0.222	0.209	0.078	-0.182	-0.013	-0.169	-0.013
FW	0.311	0.098	0.034	0.166	-0.317	0.0250	0.044	-0.307
FT	0.300	-0.037	0.061	0.115	-0.258	-0.074	0.039	-0.451
LL	0.223	0.116	0.011	-0.301	0.426	-0.213	0.028	-0.212
LW	-0.002	0.403	-0.048	-0.417	-0.122	-0.007	0.001	0.132
LA	0.114	0.373	-0.032	-0.480	0.128	-0.110	0.016	-0.004
BL	0.348	0.114	0.250	0.001	0.044	0.026	-0.173	0.119
BW	0.370	0.009	0.008	0.072	0.088	0.269	0.049	0.146
BT	0.287	0.0369	-0.164	0.031	0.066	0.070	0.428	0.301
HBW	0.410	0.007	0.159	0.053	-0.022	0.112	-0.019	0.164
TPH	-0.052	0.265	0.207	0.372	0.268	-0.305	0.137	-0.008
SG	-0.050	0.390	-0.202	0.232	0.051	0.002	0.097	-0.275
CD	-0.165	0.400	-0.147	0.078	-0.017	0.121	-0.065	-0.102
HUF	-0.012	0.128	0.117	0.226	-0.191	-0.200	-0.248	0.509
NOP	-0.142	0.288	0.081	0.373	0.181	-0.116	0.213	0.074
PBP	0.127	-0.156	0.010	0.147	0.487	0.290	0.081	-0.121
ALPB	-0.008	-0.029	0.377	-0.016	0.267	-0.251	-0.402	-0.041
NNPB	-0.098	0.054	0.160	0.008	0.270	0.519	-0.245	0.012
NSB	-0.192	0.226	0.148	0.025	-0.160	0.395	-0.203	-0.033
CBD	-0.153	0.127	0.433	-0.101	-0.112	0.274	0.284	-0.170
CLR	-0.102	-0.011	0.387	-0.120	-0.070	0.041	0.501	0.224
GBY	0.126	0.182	-0.426	0.120	0.066	0.189	-0.104	0.202
Eigenvalue	4.23	3.24	2.20	1.83	1.58	1.33	1.29	1.10
% of total variation	19.23	14.71	9.99	8.34	7.18	6.03	5.87	5.00
% of Cumulative variation	19.23	33.94	43.93	52.27	59.44	65.48	71.34	76.34

LL= leaf length, LW= leaf width, LA=leaf area, FL= fruit length, FW= fruit width, FT= fruit thickness, BL= bean length, BW= bean width, BT= bean thickness, HBW= hundred bean weight, HUP= height up to first primary branches, TPH= total plant height, SD= stem diameter, CD= canopy diameter, NPB= number of primary branches, NSB=number of secondary branches, PBP= percentage of bearing primary branches, NNPB= number of nodes of primary branches, ALPB= average length of primary branches, CBD =coffee berry disease, CLR =coffee leaf rust, GBY = green bean yield per tree, PC= principal component.

4. Conclusion

Classification of germplasm accessions based on 22 quantitative traits using the linkage system of hierarchical cluster analysis resulted in grouping of the germplasm accessions into 4 groups. Most of the inter-cluster distances were extremely dissimilar indicative of the occurrence of inconsistency which can be exploited during selection and hybridization. In the meantime, greatest inter-cluster distance (D^2) was observed among cluster I and IV. Hence crossing coffee accession amid these clusters will result in good heterosis. The principal component analysis discloses that the first eight principal components accounted for 76.34% of the total variation. As a result, information obtained from cluster and principal component analysis in

this study will be useful for coffee breeders to design breeding program for future use.

The present study revealed that the occurrence of high levels of diversity for some agro-morphological characters among evaluated arabica coffee genotypes. These genotypes should be well conserved and could serve as raw material for the genetic advance of distinctive characters of the crop throughout selection and hybridization. To sum up, the existence of genetic variability and association among traits in the base population is an important resource to exploit during selection and cross breeding in crop development plan. The current study established the existence of huge genetic variability amongst coffee genotypes germplasm for various key morphological traits. Hence there is a chance to exploit these traits in order to develop genotypes that perform superior than the existing varieties for the forthcoming coffee development plan.

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