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Genetic Diversity Analysis for Quality Attributes of Some Promising *Coffea arabica* Germplasm Collections in Southwestern Ethiopia

¹Abeyot Tessema, ²Sentayehu Alamerew, ³Taye Kufa and ²Weyessa Garedew

¹SNNPRT, Bonga Zone Agriculture, Bonga, Ethiopia

²College of Agriculture and Veterinary Medicine, Jimma University, P.O. Box 307, Jimma, Ethiopia

³Jimma Research Center, Ethiopian Institute of Agricultural Research, P.O. Box 192, Jimma, Ethiopia

Abstract: The study was carried out to determine the magnitude of genetic diversity among *Coffea arabica* germplasm accessions. For this, twenty-one native coffee germplasm collections of six geographical areas were used for the study. The coffee genotypes were field, established in 2002 at the Jimma Agricultural Research Center, southwestern using a randomized complete block design of three replications. Ripe red coffee cherries were handpicked and prepared for laboratory determinations on quality and biochemical attributes. Analysis of variance, clusters, principal component and divergence analyses were computed. The results indicated significant ($p < 0.01$) variations for the most coffee quality and biochemical attributes due to coffee genotypes. Cluster analysis grouped the entries into 4 different clusters. The clusters also demonstrated maximum inter- and minimum intra-variances for all the quality attributes. Moreover, the distances among the clusters were highly significant, indicating the possible superiority of heterosis from the highly divergent parents. The analysis of principal component showed four PC1, PC2, PC3 and PC4 with the respective eigenvalue of 5.11, 1.92, 1.73 and 1.16, explaining 84.41% of the total variance. This underlines that coffee breeding strategy within and among geographical areas may provide quality improvement with known origin quality profile. It can be concluded that the promising coffee germplasm collections were diverse in terms of most quality traits and biochemical constituents due to genetic factors. Thus, selection of superior coffee cultivars requires careful evaluations and characterizations for quality attributes and other desirable traits under various field management and processing techniques across locations.

Key words: Physical quality, biochemical composition, organoleptic quality, coffee genetic diversity, cluster analysis, principal component analysis, quality traits in coffee

INTRODUCTION

Ethiopia is believed to be the primary centre of origin and genetic diversity for Arabica coffee (*Coffea arabica* L.). The total area of land devoted to coffee production is estimated at 662,000 ha, of which 496,000 ha are estimated to be productive. The majority of coffee production (90%) comes from the smallholders while the rest is produced by large-scale producers (state farms and investors) (FAO, 2002). In Ethiopia, coffee can grow in a wide range of agroecology from 550 to 2000 m.a.s.l (Paulos and Teketay, 2000). The diversity of coffee, soil and climate, production and processing methods, among others, enable the country to produce and supply the de facto organic coffees (Taye and Tesfaye, 2002). Ethiopian coffee is processed and exported in two processing techniques, namely, natural sun-dried (70%) and washed (30%) coffees (Senbet *et al.*, 2008).

About 5175 germplasm accessions have been collected from the different coffee growing areas of the country through the national coffee collection program and maintained at the Jimma Agricultural Research Center and its sub-centers (Bayetta and Labouisse, 2006). In addition, the Biodiversity Conservation Institute of Ethiopia preserved over 4000 accessions in *ex-situ* coffee gene bank at Choche biodiversity unit in Jimma Zone, Southwest Ethiopia (Paulos and Teketay, 2000). Now this increased to a total of 11691 arabica coffee germplasm accessions which have been collected and *ex-situ* conserved at the Jimma Research Centers (5960 accessions) and Institute of Biodiversity Conservation (5731 accessions) field gene banks (Kufa, 2010). At the Jimma Research Center the multidisciplinary research team has developed and released 37 coffee cultivars (34 pure lines and 3 hybrids) which are high yielding, resistant to diseases and possess unique quality profile. This include

Corresponding Author: Sentayehu Alamerew, Department of Horticulture and Plant Sciences,
College of Agriculture and Veterinary Medicine, Jimma University, P.O. Box 307, Jimma, Ethiopia
Tel: +0251(0)471110102 Fax: +0251(0)471110934

the known Ethiopian coffee brands (Sidama, Yirgacheffe and Harar) and other identified potential areas (Wellega/Gimbi, Kaffa, Illu Aba Bora, Bebeke/Tepi and others) with unique specialty coffee types in the country. Hence, coffee research has played a pivotal role in safeguarding the coffee sub-sector and improving coffee productivity and foreign exchange earnings in the country (Girma *et al.*, 2008).

The existences of genetically diverse strains of this crop plant in this country led botanists and scientists to agree that Ethiopia is the center for origin, diversification and dissemination of the coffee plant (Bayetta and Labouisse, 2006). However, the country is not yet fully utilizing its coffee genetic resources in terms of improving coffee production and productivity which is mainly attributed to genetic erosion. The increasing population pressure, deforestation, expansion of large-scale farms, settlement programmers, climate change, etc., led to genetic erosion of coffee in Ethiopia (Paulos and Teketay, 2000; Gole *et al.*, 2000).

Though quality is an inherent factor, environment and genetic diversity can play the major roles in determining coffee physical, organoleptic and bean biochemical quality attributes expression (Leroy *et al.*, 2006). Despite this, little effort has been made on quality of *Coffea arabica* L. development through selection and breeding with high yielding cultivars. Much work has not been done to characterize germplasm on basis of their quality characters especially based on biochemical and organoleptic characters, largely due to limited capacity. Currently, it is crucial to focus on environmental sustainability and coffee diversity (Kufa, 2010) to mitigate the risks of genetic erosion at their country of origin. This would promote effective and efficient utilization of Arabica coffee genetic resources and improve the livelihoods of million rural people in Ethiopia and elsewhere. It is therefore imperative to compare the patterns and magnitudes of genetic diversity and identify suitable coffee genotypes with desirable traits, including quality attributes and profile mapping. This study was carried out to evaluate and characterize some arabica coffee germplasm collections with regard to bean physical quality, biochemical compositions and organoleptic characteristics.

MATERIALS AND METHODS

Description of study site: The experiment was carried out from 2002 to 2010 at the Jimma Agricultural Research Center (JARC) (7°46' N latitude and 36°0' E longitude, 1753 m), southwest Ethiopia. The center is located at 350 km away from Addis Ababa, 8 km away from the

Jimma town in the direction of south western part. The center is located within the Tepid to cool humid highlands agro-ecological zone of the country. The area receives adequate amount of rainfall with the total mean annual rainfall of about 1529 mm. The mean maximum and minimum air temperatures of the research site are 26.3 and 11.6°C, respectively (Paulos and Teketay, 2000). The driest season lasts between December and January. The soil type of the center is dominated by Nitosol or Eutric *nitosol*, reddish-brown or darkish-brown, clay or clay loam texture and slightly acidic (Paulos and Teketay, 2000).

Experimental materials: Twenty-one *Coffea arabica* germplasm genotypes have been collected from the major coffee growing areas in southwestern Ethiopia (Table 1). This batch was selected based on promising performances with regard to coffee berry disease resistance, quality and yield as compared to other national collections between 1977 and 1997. The selected promising coffee accessions were advanced to variety trial and reestablished at the Jimma Agricultural Research Center field gene banks in 2002. Therefore, this experiment was superimposed on these established accessions.

Experimental design and sampling: A randomized complete block design of three replications was used for field planting of coffee trees. Each genotype was planted in a single row of eight trees per plot using a spacing of 2×2 m. All pre-and post-field management practices were uniformly applied as per recommendations of the center (IAR, 1996). For this study, healthy and ripe red coffee cherries were selectively handpicked from 7-year-old

Table 1: Geographical origin of the coffee genotype used for the study

Genotype	Region	Zone	Wereda	Site	Altitude
23000	SNNP	Benchmaji	Dizi	Garro	1326
23002	SNNP	Benchmaji	Sheko	Aybera	1634
23004	Oromia	Jimma	Goma	Choche	1634
23006	SNNP	Benchmaji	Meanit	Shasha	1324
23008	Oromia	Jimma	Goma	Choche	1771
23011	SNNP	Benchmaji	Dizi	Bero	1349
23013	SNNP	Benchmaji	Dizi	Bai	1439
23015	SNNP	Kaffa	Gimbo	Boka	1711
23017	SNNP	Benchmaji	Dizi	Bero	1349
23019	Oromia	Jimma	Goma	Choche	1735
23022	SNNP	Benchmaji	Dizi	Bai	1443
23024	SNNP	Benchmaji	Dizi	Bai	1552
23026	SNNP	Benchmaji	Sheko	Sanka	1677
23028	SNNP	Benchmaji	Dizi	Bero	1347
23030	Oromia	Jimma	Goma	Choche	1769
23041	SNNP	Benchmaji	Dizi	Garro	1336
23042	SNNP	Benchmaji	Sheko	Aybera	1667
23045	Oromia	Jimma	Seka Chekorsa	Melko	1751
23046	SNNP	Benchmaji	Sheko	Gizmeret	1613
23047	SNNP	Keffa	Gimbo	Boka	1712
23050	SNNP	Benchmaji	Sheko	Gacheb	1679

coffee trees during a peak harvesting season. The fresh coffee samples were carefully prepared using the washed processing method (pulping, fermentation and drying) as described by Clark (2005).

Data collection: Data on physical parameters (seed moisture content, average bean weight, green bean size and shape and make) and organoleptic quality (using 0-5 scale) were determined from the prepared coffee samples. More over, The biochemical analysis of green arabica coffee was used to determine caffeine, crude protein, sucrose, fat, dry matter and crude minerals by wet methods (AOAC, 1990).

Data analysis: The number of cluster was decided where the cubic clustering criteria (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. A measure of a group distance based on multiple characters was given by generalized (Mahalanobis, 1936) D^2 statistics for the characters.

Principal component analysis is a multivariate technique for examining relationships among several quantitative variables (Crossa, 1990). Principal component analysis was performed using correlation matrix by employing procedure of SAS version 9.2 (SAS, 2001) in order to examine the relationships among the quantitative according to ISO (1992). Further, uniform coffee beans were prepared from each accession by passing through a sieve size of 14 inch. Then, the standard procedures (ISO, 1992) were followed for organoleptic quality analyses (aromatic intensity, aromatic quality, acidity, body, bitterness, flavour and overall standard). Moreover, the samples were prepared and chemical compositions of green arabica coffee beans (caffeine, crude protein, sucrose, fat, dry matter and crude mineral) were determined according to AOAC (1990).

The 21-coffee genotypes were clustered using the proc cluster of SAS with average linkage method of clustering strategy which grouped and sorted the accession into clusters to form dendrogram using the SAS, 2001). The number of clusters was determined by following the approach suggested by Copper and Milligan (1988) by looking into three statistics, namely pseudo F, pseudo t^2 and the Cubic Clustering Criteria (CCC) for characters that were correlated among each others by converting into uncorrelated characters called principal components

The collected data for physical, organoleptic quality and biochemical were subjected to analysis of variance (ANOVA) in a randomized complete block design with three replications using SAS version 9.2 (SAS, 2001).

Divergence analysis was done using the procedure proc disc rim of SAS version 9.2 (SAS, 2001). Testing the significance of D^2 values for a pair of clusters was taken as the calculated value of χ^2 (chi-square) and tested against the tabulated value of chi-square for P degrees of freedom at appropriate probability level, where P is the number of quantitative characters (Singh and Chaundhary, 1977).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) results revealed highly significant difference ($p < 0.01$) among the genotypes for all the physical quality, organoleptic attributes and biochemical compositions, except overall standard, body and sucrose content, respectively (Table 2). Similar finding were reported by several authors (Silvarolla *et al.*, 2000; Clifford, 1985; Yigzaw *et al.*, 2007) in arabica coffee.

Clustering of genotypes and genetic divergence: The means of cluster are depicted in Table 3, 5 and 7 for physical quality, organoleptic and biochemical composition quality attributes. The genetic divergence results for physical quality, organoleptic and biochemical composition quality are presented in Table 4, 6 and 8, respectively. Accordingly, cluster classification for bean physical quality attributes depicted that the genotypes were clustered into four groups with intra and inter cluster variance of 37.97 and 62.03%, respectively (Table 3).

Table 2: Analysis of variance (mean squares) for physical, organoleptic and biochemical quality attributes in Arabica coffee genotypes

Analysis	Physical block (df = 2)	Genotype (df = 20)	Error (df = 40)
SM	0.01	20.57**	0.11
OVS	0.19	1.21ns	0.29
ABW	0.03	7.44**	0.05
Organoleptic			
AI	0.19	1.44**	0.09
AQ	0.19	1.21**	0.11
BO	0.30	1.45ns	0.24
AC	0.19	1.21**	0.11
FL	0.01	4.11**	0.03
BT	0.02	2.58**	0.02
OVAS	0.19	1.21**	0.11
Biochemical			
DM	0.02	4.94**	0.02
CAF	0.01	0.07**	0.01
PRO	0.01	0.67**	0.0001
ASH	0.11	1.42**	0.07
SUC	0.19	1.21ns	0.11
FAT	0.03	7.45**	0.05

**Significant at $p < 0.01$ probability level. ns: Non significant ($p > 0.05$). DM: Dry matter; CAF: Caffeine; SUC: Sucrose; PRO: Protein, AI: Aromatic intensity; AQ: Aromatic quality; AC: Acidity; BO: Body, BT: Bitterness; FL: Flavour; OVAS: Overall standard; SM: Shape and make; OVS: Over screen; ABW: Average bean weight

Table 3: Clustering of the 21-coffee genotypes for the bean physical quality attributes

Clusters	Physical quality characters		
	SM	OVS	ABW
I	13.50**	96.79**	15.48**
II	9.33*	89.87	13.53
III	12.00	67.60*	16.10**
IV	12.00	74.20	13.10*

Inter cluster variance (%): 62.03; Intra cluster variance (%): 37.79; SM: Shape and make; OVS: Over screen, ABW: Average bean weight, ** High mean value, * Low mean value

Hence, cluster I was characterized by relatively high mean value of shape and make (13.50) and over screen (96.79) and average bean weight (15.48). Cluster II was characterized by low shape and make (9.33). Cluster III was characterized by low over screen (67.60) and high average bean weight (16.10). Cluster IV included coffees with low average bean weight (13.10) (Table 3). The present findings are in line with Crossa (1990) who reported objects within the group are more similar and objects in different group are more dissimilar.

With regard to the percent contribution of geographical origins over clusters for physical quality attributes, the twenty-one genotypes collected from six weredas wordas were grouped into four clusters (Fig. 1). Consequently, the contributions per cluster varied from 16.67 to 50%. In this regard, large (50%) amounts of genotypes were contributed to cluster I by Sheko worda, Cluster II by Sheko and Dizi (40%) each, Cluster III and Cluster IV by Dizi (50%). Except one genotype from Goma (20%) all the genotypes in cluster II were contributed by Sheko and Dizi (data not shown). In most cases it was difficult to see the genotypes that were collected from one geographical origin in the same cluster. That means, they were clustered in mixture of geographical origin this could be attributed to gene flow among geographical origins. The present result supports the finding of Ayana and Bekele (1999). This could be explained as gene flow in coffee could be further attributed to human interference (Gole *et al.*, 2000). Further, based on molecular markers analysis Esayas (2005) clustered coffee population on the bases of their geographic origin. But the same workers failed to cluster coffee population according to their respective populations due to the presence of substantial gene flow between local populations in the form of seedling coffee plant. Further, Esayas (2005) reported based on molecular markers analysis clustering of coffee population on the bases of their geographic origin but failed to cluster according to their respective populations due to the presence of substantial gene flow between local populations in the form of young (seedling) coffee plant. According to him the inter regional clustering of some coffee tree samples from different regions could be

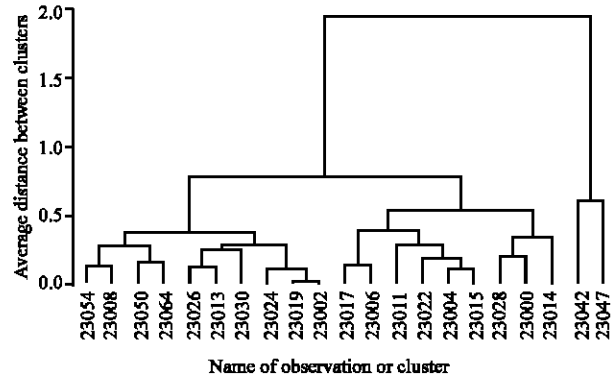


Fig. 1: Denderogram of 21 *Coffea arabica* L. genotypes for bean physical quality attributes

Table 4: Squared Mahalanobis distance between clusters for physical quality attributes in the studied arabica coffee genotypes

Cluster	I	II	III	IV
I				
II	19.68***			
III	32.11***	13.87***		
IV	13.99***	32.47***	26.92***	

χ^2 : 5.99*; X^2 : 9.21** and χ^2 : 13.82*** where *, ** and *** are at 5, 1 and 0.1% probability level, respectively

due to the transport of coffee seeds across regions and their subsequent planting. Moreover, Seyoum *et al.* (2004) reported the absence of association between geographic origin and classification. On the contrary, Mesfin and Bayetta (2007) analyzed preliminary phenotypic data and reported variability for each character and certain relationship between this variability and the geographical origin of the accessions.

Distance between clusters for physical quality: Mahalanobis Squared distance between clusters of bean physical quality attributes was found to be very highly and significantly ($p < 0.001$) divergent (Table 4). The smallest cluster distance ($D^2 = 13.87$) was observed between cluster II and III while the maximum cluster distance ($D^2 = 32.47$) was observed between II and IV. The second most divergent clusters were I and III ($D^2 = 32.11$). The rest of the clusters were also very highly and significantly divergent. Since maximum genetic recombination and variation in the subsequent generation is expected from crosses that involve parents from the clusters characterized by maximum distance. Thus, crosses between genotypes selected from cluster II with IV, I with III and cluster III with IV are expected to produce relatively better genetic recombination and segregation for physical quality attributes. Similarly,

Arunachalam *et al.* (1984) reported the magnitude of the resulting heterosis that largely dependent on the degree of genetic divergence in the parental lines. Peeters and Martinelli (1989) also observed that crossing germplasm accessions from significantly divergent clusters could maximize opportunities for transgressive segregation as there is a high probability that unrelated genotypes would contribute unique desirable alleles at different loci. Therefore, crossing of genotypes as parent from clusters that are highly and significantly distant clusters such as cluster II and IV will provide maximum segregation and recombination hence, maximum heterosis vigor can be achieved with due attention of our specific objectives.

Genotypes of cluster classification for sensorial quality attributes were clustered into four groups with intra and inter cluster variances of 26.87 and 73.13%, respectively (Table 5). The variance decomposition for optimal classification for lower intra cluster variance showed that almost homogenous individuals were grouped together. In this study, cluster means for sensorial quality attributes indicated different results among the clusters. Accordingly, cluster I was characterized by the highest mean values of aromatic intensity (4.00), aromatic quality (4.00), flavour (3.64), overall standard (4.00) but by the lowest values of bitterness (0.00), body (3.10) and astringency (0.00). Cluster II was characterize by the highest mean values of flavour (3.87), acidity (3.04), astringency (1.00) and body (3.89) in contrast to lowest values of bitterness (0.87) aromatic intensity (2.87), aromatic quality (2.96) and overall standard (2.96). Whereas, cluster III was characterized by the highest mean values of bitterness (1.75) and astringency (1.00) but by the lowest mean values of flavour (1.75)(2.75). Cluster IV was characterized by high mean value of aromatic intensity (5.00), aromatic quality (4.85) and overall standard (4.85) but by low mean value of acidity (1.15) and astringency (0.00). Hence, the average values for most quality traits were observed to differ among the clusters. Similarly, Wamatu *et al.* (2003) clustered 21 genotypes for organoleptic quality attributes and found different results for organoleptic quality attributes among the clusters.

Contribution of geographical origins over clusters for organoleptic quality attributes, the results of the 21-genotypes showed the presence of variation within the

same location of collection (Fig. 2). Accordingly, the genotypes from Sheko woreda were distributed into two clusters (I and IV). The divergence analysis depicted very highly significant ($p < 0.001$) variations with the distance (15.89) found between cluster I and IV- this sentence is deleted. It can be understood that these genotypes are quite different for organoleptic quality attributes, though they were from the same geographic origin. Therefore, there is no need to go for geographic origins to collect genetically diverse plants in breeding for such quality traits. The possible explanation for this could be the wide genetic divergence in the features created within each geographic origin through selection and genetic drift. This corroborates with earlier findings of other authors such as Murthy *et al.* (1965) in brassica, Murthy and Ananda (1966) in linseed, Arunachalam and Ram (2006) in sorghum, Singh and Bains (1968) in cotton, Gupta and Singh (1970) and Malhotra *et al.* (1974) in mung bean.

Conversely, Gimbo woreda contributed all genotype into cluster II for organoleptic quality attributes. Based on this result Shako woreda has wider genetic variability as compared to Gimbo woreda. Because, Gimbo woreda's genotypes fall in the same cluster (II) which means they were similar for organoleptic quality attributes since, genotypes within the clusters are similar (Crossa *et al.*, 1990). The collections from Bench Maji Zone (Sheko, Meamt and Dizi) were grouped in cluster I, II and IV. There is no genotype that was grouped in cluster IV

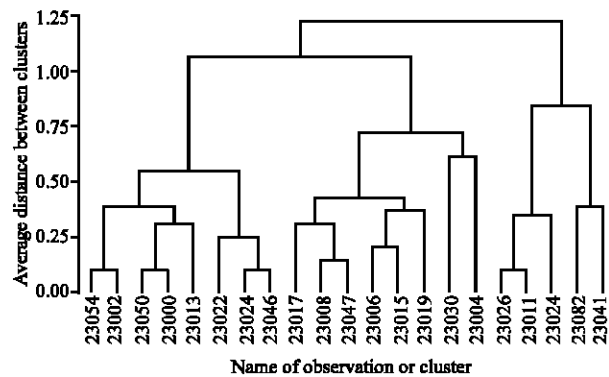


Fig. 2: Denderogram of 21 *Coffea arabica* genotypes for organoleptic quality attributes

Table 5: Organoleptic quality attributes of clusters for the arabica coffee genotypes

Cluster	Organoleptic character								
	BT	FL	AI	AQ	AC	AS	BO	OVAS	
I	0.00*	3.64**	4.00**	4.00**	2.00	0.00*	3.10*	4.00**	
II	0.87*	3.87**	2.87*	2.96*	3.04**	1.00**	3.89**	2.96*	
III	1.75**	1.75*	3.16	3.20	2.80	1.00**	3.59	3.20	
IV	1.00	2.50	5.00**	4.85**	1.15*	0.00*	3.30	4.85**	

Intra cluster variance (%): 26.87% Inter cluster variance (%): 73.13% BT: Bitterness; FL: Flavour; AI: Aromatic intensity; AQ: Aromatic quality; AC: Acidity; AS: Astringency; BO: Body; OVAS: Overall standard; ** Highest value and * Lowest value

other than those from Maji zone. The findings indicated that the coffee arabica germplasm collections were diverse in organoleptic quality attributes. There were coffee genotypes with different organoleptic quality attributes spread over the clusters and crossing of clusters would give positive response to quality improvement. This supports the work done by Getu (2009) that reported within and between geographical origins variations in arabica coffee accessions. This is great opportunity in selection and breeding program to improve location specific varieties and promote production of known coffee quality profile. According to Bayetta (1997), diallel crossing of parents with different clusters in coffee resulted in better heterosis than within cluster crosses. Therefore, apart from selection improvement further progress in variety development program can be achieved through crossing of genotypes clustered in different groups.

The distance between clusters for organoleptic quality estimated using Squared Mahalanobis distance was found to be very highly significant ($p < 0.001$) (Table 6). The highest distance ($D^2 = 44.54$) was found between clusters III and IV while the lowest cluster distance ($D^2 = 24.40$) was found between cluster I and III. In fact maximum genetic recombination and variation in the subsequent generation is expected from crosses that involve parents from the clusters characterized by maximum distances. Hence, crosses between genotypes selected from cluster III and IV is expected to produce relatively better genetic recombination and segregation in their progenies. However, the selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on the specific objective of hybridization program. This agrees with Gemechu (2006) and Reddy (1988) who found that hybrids between genotypes with maximum genetic divergence generally display a greater recombination and segregation than those between closely related strains. Moreover, Singh (2003) described that the increased magnitude of hybrid vigor with the increase of genetic distance.

Cluster characterization for bean biochemical attributes is presented in Table 7. According to the results of cluster classification for bean biochemical attributes, the genotypes were clustered into four groups with intra and inter cluster variances of 22.47 and 77.53%, respectively for biochemical quality attributes. Cluster I was characterized by relatively high mean value of fat (13.13) but low for sucrose (7.35). Cluster II was characterized by low mean value of dry matter (91.04), ash (2.60) protein (4.37) and caffeine (1.26). Cluster III was characterized by high value (3.87) of ash and low value

Table 6: Squared Mahalanobis distance between clusters for organoleptic quality attributes for the studied arabica coffee genotypes

Cluster	I	II	III	IV
I				
II	25.14***			
III	24.40***	24.51***		
IV	36.98***	35.10***	44.54***	

χ^2 : 14.07*, χ^2 : 18.48** and χ^2 : 24.32*** where *, ** and *** are at 5, 1 and 0.1% probability level, respectively

Table 7: Cluster classification for biochemical quality attributes of arabica coffee genotypes

Cluster	Characters					
	DM	ASH	PRO	CAF	SUC	FAT
I	92.11	3.54	4.43	1.27	7.35*	13.13**
II	91.04*	2.60*	4.37*	1.26*	7.62	12.98
III	93.53	3.87**	4.37*	1.27	7.54	12.56
IV	95.00**	3.80	4.65**	1.35**	7.75**	12.19*

Intra cluster variance: 22.47%, Inter cluster variance: 77.53%; DM: Dry matter; PRO: Protein; CAF: Caffeine; ** High and * Low mean values, respectively

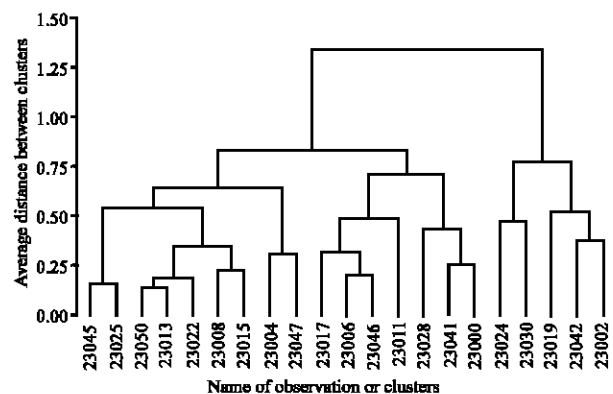


Fig. 3: Denderogram of the 21-*Coffea arabica* genotypes based on biochemical attributes

(4.37) protein. Cluster IV was exceptionally characterized by high values of dry matter, protein, sucrose and caffeine with the respective values of 95.00, 4.65, 7.75 and 1.35 but with low fat content. The variance decomposition for optimal classification with lower intra cluster variance and indicates good quality classification where almost homogenous individuals were grouped together.

The results of the percentage contribution of geographic origin over clusters for biochemical attributes revealed the possibility of obtaining dissimilar genotypes from the same geographical origin (Fig. 3). Accordingly, collections from the three districts (Sheko, Dizi and Meanit) of Benchmaji zone were found to contribute to all clusters, except cluster II. The highest contributions were noted for cluster I, III and IV was 57.50, 100 and 60%, respectively (data not shown). Arabica coffee collections of varied geographical origins were diverse for bean biochemical compositions. This is in harmony with

Table 8: Squared Mahalanobis distance between clusters for biochemical quality attributes for the studied arabica coffee genotypes

Cluster	I	II	III	IV
I	0			
II	28.69***	0		
III	29.15***	29.61***	0	
IV	20.62***	23.81***	21.22***	0

χ^2 : 11.07 *, χ^2 : 15.09 ** and χ^2 : 20.52 *** where *, ** and *** are at 5, 1 and 0.1% probability level

Mawardi and Hulupi (2005) and Getu (2009) who reported genetic diversity for biochemical compositions among arabica coffee genotypes, indicating the existing potentials for quality improvements.

Mahalanobis squared distance between clusters for biochemical composition was found to be very highly significantly divergent (Table 8). The maximum cluster distance was found between cluster (II and III ($D^2 = 29.61$) followed by I and III ($D^2 = 29.15$) (Table 8). The rest of the clusters were also very highly significantly divergent. Since the magnitude of heterosis largely depends upon the degree of genetic diversity among the parental lines, the germplasm accessions belonging to the pairs of distant clusters could be very useful in hybridization program to obtain a wide spectrum of variation among the segregates and to maximize heterosis. Similarly, Bayetta (2001) reported that heterosis largely depends upon the degree of genetic diversity among the parental lines. Moreover, Senbet *et al.* (2008) reported that better performance of coffee in crosses involving diverse parents with respect to genetic distance. Thus, it is possible to say that the accessions from cluster II and cluster III could offer potential parental lines for maximizing heterotic value.

Principal component (PC): The analysis of PC showed four PC1, PC2, PC3 and PC4 with the respective eigenvalue of 5.11, 1.92, 1.73 and 1.16, explaining 84.41% of the total variance (Table 9). The first principal component explained about 43.69% of the total variance, the second principal component explained 17.05% of the total variance, the third principal component explained 12.16% of the total variance and the fourth principal component explained 11.51% of the total variance. In addition, the eigenvalue indicated four components provide a good summary of the data, two components accounting for 60.74% of the total variance, three components explaining 72.90% and four components explaining 84.41% of the total variance. The subsequent components contribute less than 16%. The contribution of a trait can be determined by considering the absolute value of a trait coefficient (eigenvector) that is greater than half when divided by the square root of the variance of the eigenvalue of the respective principal component

Table 9: Eigenvalue, variance and eigenvectors for quality attributes of coffee genotypes

Analysis	Principal component			
	PC1	PC2	PC3	PC4
SM	0.31	0.04	-0.29	-0.18
ABW	0.31	0.05	-0.43	0.19
OVS	0.27	0.15	-0.03	-0.02
Organoleptic				
AI	0.31	-0.25	-0.55	0.01
AQ	0.38	0.29	0.06	0.01
BO	0.28	0.11	0.12	0.21
AC	0.39	-0.39	0.11	0.05
FL	0.23	-0.54	-0.06	-0.11
AS	-0.30	0.09	0.01	-0.21
BT	-0.19	0.27	0.23	-0.55
OVAS	0.39	-0.05	0.16	-0.23
Biochemical				
DM	0.19	0.09	0.56	0.51
CAF	-0.30	-0.29	0.18	-0.17
ASH	0.20	-0.39	-0.12	0.13
PRO	-0.41	0.11	-0.30	0.33
SUC	0.22	-0.12	0.07	-0.18
FAT	0.33	-0.55	-0.04	-0.37
Eigenvalue	5.11	1.92	1.73	1.16
Proportion of variance (%)	43.69	17.05	12.16	11.51
Cumulative variance (%)	43.69	60.74	72.90	84.41

DM: Dry matter; CAF: Caffeine; SUC: Sucrose; PRO: Protein; AI: Aromatic intensity; AQ: Aromatic quality; AC: Acidity; BO: Body; AS: Astringency; BT: Bitterness; FL: Flavour; OVAS: Overall standard; SM: Shape and make; ABW: Average bean weight

(Copper and Milligan, 1988). This criterion was to decide the importance of characters in the different principal components. Accordingly, shape and make, average bean weight, aromatic intensity, aromatic quality, acidity, astringency, overall standard, caffeine, protein and fat contributed much for variability in the first component. Aromatic intensity, aromatic quality, acidity, flavour, caffeine, ash and fat were the quality attributes contributed much for variation in the second principal component. Shape and make, average bean weight, aromatic intensity, dry matter and protein were the quality attributes that contributed much for variations in the third principal component. The quality attributes that contributed much for variation in principal component four were bitterness, dry matter, protein and fat content (Table 9).

CONCLUSION

The findings of the study demonstrate the existence of diversity among the Ethiopian coffee germplasm collections in bean physical, organoleptic and biochemical quality attributes. The influence of geographical origin on these traits was also evident, strengthening our current local landrace coffee research and development strategy. Hence, sustainable production and export of superior quality coffees demand, *inter alia*, identification of the

right cultivars with desirable traits including low caffeine under specific environments, field management and processing techniques. Moreover, molecular, physiological, quality and biochemical analyses should be undertaken to further characterize the germplasm and develop quality profile mappings with the views to ensure effective utilization, conservation and traceability of the great coffee genetic wealth in the country.

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