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Genetic Variability of Sidama Coffee (*Coffea Arabica* L.) Landrace for Agro-morphological Traits at Awada, Southern Ethiopia

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Getting more information on genetic variability is a prerequisite for further improvement of coffee (*Coffea arabica L.*). Although Ethiopia is known as a primary diversity for *Coffea arabica* the knowledge on nature and extent of variation of the coffee accessions has one of the major problems in coffee improvement program. Hence, to assess the nature and extent of variability on agro-morphological traits, test trial was conducted at Awada, Southern Ethiopia. The trial was consisted one hundred twenty Sidama land race Arabica coffee and four standard checks and arranged in augmented design with four replications of the checks. Analysis of variance showed significant difference among the tested genotypes for most of the quantitative traits considered in the study, indicating the existence of sufficient genotypic variation among the coffee accessions. Phenotypic coefficients of variation ranged from 4.52 (fruit length) to 60.89 (coffee berry disease) while, genotypic coefficients of variance ranged from 3.92 (bean width) to 56.52 (coffee berry disease). Likewise, high broad sense heritability coupled with high genetic advance as percent of the 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 confirming that genotypic variance has contributed substantially to the total phenotypic variance.

Keywords: Coffea arabica, coffee accession, genetic variability, genotypic variation, broad sense heritability, genetic advance

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INTRODUCTION

Coffee (*Coffea arabica*) is the most important commercial coffee species and is the only allopolyploid (2n = 4x = 44) coffee species. It is self-fertile at approximately above 95% (Lashermes et al., 2000; Silvarolla et al., 2004). *Coffea arabica* is cultivated in most parts of the tropics, accounting for 80 % of the world coffee market, and about 70% being produced by smallholder farmers (Gole et al., 2002). It is the only coffee species occurring in Ethiopia and is geographically isolated from the rest of the *Coffea* species in the world (Lashermes et al., 2000; Anthony et al., 2001; Wintgens, 2004). The phenotypic variation of *Coffea arabica* and its adaptation under

different environmental conditions show the presence of high arabica coffee genetic diversity in Ethiopia (Paulos and Teketay, 2000). This led botanists and scientists to agree that Ethiopia is the center of origin and diversification of arabica coffee (Bayetta and Labouisse, 2006).

The availability of such diverse agro-ecological and arabica coffee in Ethiopia is an opportunity for the country. However, there are many biotic and abiotic factors contributing to challenging coffee production and yield per unit area in the country, predominant use of local coffee variety, use of conventional production and processing practices. These in turn seriously decreases the overall national coffee production and productivity (Taye, 2010). Beside this, the ample coffee genetic resource is under threat mostly due to the increasing population pressure, deforestation, expansion of large-scale farms and the replacement of the traditional production systems by expansion of large scale farms and the farmers' varieties by a high yielding and disease resistant varieties, and climate change (Paulos and Teketay, 2000; Taye, 2013). To reduce such threats, considerable efforts have been made by the national coffee collection program to collect, conserve and utilize the Ethiopian coffee germplasm.

In order to exploit the available coffee genetic resources characterization and evaluation of germplasm is the crucial step in the improvement process following different methods. By using morphological traits (Mesfin and Bayetta, 2008, Ermias, 2005; Olika et al., 2011) characterized arabica coffee collections and have indicated the presence of high genetic diversity in Ethiopian coffee.

Similarly, genetic diversity analyses of cup quality and biochemical characteristics of Arabica coffee conducted in Ethiopia by Yigzaw (2005), Abeyot et al. (2011), Olika et al. (2011) and in Kenya by Kathurima et al. (2009) has confirmed the existence of rich genetic diversity. Based on molecular markers (Anthony et al., 2002; Essayas, 2005; Yigzaw, 2005; Alemayehu et al., 2010) have reported the existence of genetic diversity among coffee arabica genotypes of Ethiopia. Such works on coffee plant are still considered as a vital benefits and base for future breeding program. The present study was, therefore, carried out with the objectives to assess agro-morphological diversity among coffee accession and estimate the magnitude of phenotypic or genotypic variance, heritability and expected genetic advance in different agro-morphological traits.

MATERIALS AND METHODES

Experimental site

The field experiment was conducted at Awada Agricultural Research Sub-Center (AARSC), in 2013 cropping season. AARSC is found 45 km South of Hawassa in Sidama Zone and is located at 6°3'N Latitude and 38°E Longitude at an altitude of 1750 m.a.s.l. The area receives an annual minimum and maximum rainfall 858.1 and 1676.3 mm, respectively. The annual average minimum and maximum air temperatures are 11.0^{0}C and 28.4^{0}C, respectively. The major soil types of the center are eutric-nitosol and chromotic-cambisols that are highly suitable for coffee production (Mesfin and Bayetta, 2008).

Treatments and Experimental design

The treatments consisted of 120 coffee land race collected from Sidama Zone (Dale and Aleta Wondo Woredas) and field established in 2006 at the AARSC. These coffee land races collected from different agro-ecologies of Dale and Aleta Wondo Woredas since, 2005. Moreover, four released varieties (75227, 744, 7440 and 1377) were included as standard checks for the study.

The experiment was laid down in the field using augmented design, which is used with replicated checks to assess the performance of non-replicated accession in complete block designs (Petersen, 1994; Sharma, 2006) in four blocks. A single row consisting of ten trees per plot and plant-to-plant spacing used was two meters by two meters, while spacing between blocks was four meter. The recommended agronomic practices for coffee were uniformly and properly applied for nursery and field operations.

Data collection and Statistical analysis

During the time of this study, data on 26 quantitative characters, namely : plant height (cm), stem diameter (cm), number of main stem nodes (no), angle of primary branches (degrees), canopy diameter (cm), average inter node length of main stem (cm), average length of primary branches (cm), average girth of primary branches (cm), average inter node length of longest primary branches (cm), number of primary branches(no), number of secondary branches (no), percentage of coffee bearing primary branches (%), height up to first primary branches (cm), leaf length (cm), Leaf width (cm), leaf area (cm^2), fruit length (mm), fruit width (mm), fruit thickness (mm),hundred green bean weights (g), green bean yield per tree (g), bean length (mm), bean width (mm), bean thickness (mm), coffee berry disease (%) and coffee leaf rust (%) and 7 qualitative characters, namely: growth habit, stem habit, branching habit, leaf shape, young leaf color, fruit shape and fruit color, were recorded from each accession using the standard procedures of (IPGRI, 1996).

Variability among accessions was estimated using phenotypic and genotypic variance and coefficient of variability according to Burton and Devane (1953). Analysis of variance of the traits was computed using SAS computer program (SAS, 2002). Broad sense heritability, genetic advance and genetic advance as percent of the mean were analyzed according to Robinson et al. (1949) and Johnson et al. (1955). The Clustering of coffee genotypes was done to separate genotypes into different groups using proc cluster of SAS, average linkage option was used and based on agglomerative hierarchical clustering procedure.

RESULT AND DISSCUSIONS

Analysis of quantitative traits

Significant differences were observed ($P<0.05$) between the tested 124 coffee genotypes (checks and accessions) for average green bean yield per tree in the five consecutive years harvests from 2009 to 2013 indicated in Table 1. In addition, the one-degree freedom contrast that compared the 120-tested coffee germplasm with the 4-standard checks was significant for all years except for the 2010 harvesting season. These results agree with the statements of renowned coffee breeders (Antonio et al., 2010), who suggested that the high yield years are best suited for selection for bean yield in arabica coffee progenies.

Likewise, the results of ANOVA for 25 yield contributing traits showed significant differences ($P<0.05$) among the studied coffee accessions and checks for all the traits except for 11 traits (Table 2). Overall, the variations observed for measured quantitative characters in this study are in agreement with the earlier findings of Bayetta (1991) who reported the presence of significant variation in coffee growth characters. Similarly, Mesfin and Bayetta (2008) who reported significant difference among the 100 Hararge coffee accessions in 14 quantitative characters. The variability for important traits in the present study clearly proved the possibility to bring considerable improvement mainly in coffee yield and disease resistance through selection and hybridization. In addition, many researchers for example, Abdi, 2009; Ermias, 2005; Yigzaw, 2005; Olika et al., 2011 have confirmed significant differences among coffee germplasm accessions collected from major growing region of Ethiopia.

Phenotypic and Genotypic variation

Estimates of environmental (EV), genotypic (GV) and phenotypic variability (PV) are presented in Table 4. According to Deshmukh et al. (1986), phenotypic and genotypic coefficients of variation values greater than 20% are considered as high, whereas values less than 10% are considered to be low and values between 10 and 20% are considered as medium. Accordingly fruit length and bean width had the lowest PCV and GCV, respectively, while the highest PCV and the highest GCV were recorded for CBD. For both PCV and GCV low values were observed for CANDIA, LL, FL, BW traits. All other traits had moderate PCV and GCV values for most of the traits genotypic coefficients of variation were very close to their corresponding estimates of phenotypic coefficient of variation, suggesting the greater role of the genotype in the expression of these traits. PCV was much higher than GCV for CBD and CLR indicating the higher influence the environment has on these traits. The findings of the present study are comparable with the results of Mesfin and Bayetta (2008) who reported that the estimates of PCV and GCV in 100 Harrerge coffee accessions for the 14 quantitative characters ranged from 5.9 to 54.8% and 3.2 to 37.5%, respectively.

Similarly, a previous research conducted on 16 coffee genotypes for 18 quantitative characters revealed that the PCV and GCV ranged from 4.5 to 53.4% and 3.3 to 51.7%, respectively (Yigzaw, 2005). Getachew (2012) also reported high PCV (91.5 and 41.7%) and GCV (62.8 and 22.1%) values for CBD reaction and yield per tree, respectively. Unlike in this result the author reported high PCV (30%) and moderate GCV (18.03%) for number of secondary branches. The slight difference in the ranges of these previous studies and this could be due to the differences in the number of genotype studied, age of coffee and environmental conditions under which the genotypes were tested. From the high GCV values in our study it can be deduced that coffee berry disease reaction, coffee leaf rust reaction and average green bean yield have high amount of exploitable genetic variability. It also signifies that there is greater potential for favorable advance in selection in these attributes when compared to other characters. The present finding is agreement with the findings of Olika et al. (2011) and Getachew (2012) who have reported high PCV and GCV values for coffee berry disease reaction and yield per tree; moderate PCV and GCV values for height up to first primary branch and hundred bean weights.

Heritability and Genetic advance

The estimate of the broad sense heritability for various characters of coffee ranged from 50.47% for coffee leaf rust reaction to 90.30% for leaf length (Table 3). The recorded estimates of heritability are high (>50%) 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

Table 1. Analysis of variance for green bean yields across five consecutive years (2009-2013) and overall mean yield for coffee germplasm accessions used for the study

Coffee green bean yield in years	Mean Squares for different Sources of variation and their significance						
	Blocks (d.f=3)	All entries (d.f=123)	Tested Accessions (d.f=119)	Checks (d.f=3)	Checks vs Accessions (d.f=1)	Error (d.f=9)	CV (%)
GBYT09	6116.74^{ns}	25884.89**	4462.0820**	151792.51**	182406.52**	4498	26.9
GBYT10	680.83^{ns}	2005.19*	1970.50*	3644.63*	1215.18^{ns}	596.2	64.75
GBYT11	2410.36^{ns}	172117.34**	173917.92**	53335.83^{ns}	314191.86*	39012	31.5
GBYT12	14527.80^{ns}	35974.15*	34507.37*	18580.53^{ns}	262701.59**	9970	36.7
GBYT13	22749.98^{ns}	79247.29*	75474.80 *	396.24^{ns}	764726.69**	28200	29.6
AvGBYT	2730.74^{ns}	22786.84**	21246.21**	18498.41*	218986.16**	4578	19.3

ns = not significant, * and ** significant at 0.05 and 0.01 level of probability, respectively. d.f = degree of freedom, CV = coefficient of variation, GBYT09, GBYT10, GBYT11, GBYT12 and GBYT13 = Green bean yield per tree (g) in 2009, 2011, 2012 and 2013, respectively and AvGBYT= Average green bean yield per tree over the five years.

primary branches (83.80%), plant height (83.70%), number of primary branches (82.83%), percent of bearing primary branches (76.91%), angle of primary branches (76.28%), 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%). These results are in agreement with the results of Olika et al. (2011) who observed high heritability values ranged from 50.08% (average inter node length of primary branches) to 81.13% (hundred bean weight).

Similarly, Bayetta (2001) reported heritability estimates between 71.43 and 97.32% for all characters measured in his study, and suggested greater effectiveness of selection and improvement to be expected for these characters in the future breeding program. Yigzaw (2005) has also observed high heritability for hundred green bean weight, number of secondary branches and canopy diameter. However, Getachew (2012) indicated the moderately low heritability for fruit length (48.08%), coffee berry disease severity (47.15%), plant height (47.05%), average inter node of main stem (41.38%), leaf length (41.28%), number of primary branches (39.40%),

Table 2 Analysis of variance for yield components for the coffee germplasm accessions at Awada, 2013/14

Plant characters	Mean Squares for different Sources of variation and their significance						
	Blocks (d.f=3)	All entries (d.f=123)	Test Accessions (d.f=119)	Checks (d.f=3)	Checks vs Accessions (d.f=1)	Error (d.f=9)	CV (%)
PH	1869.95^{ns}	5124.86*	4462.08*	7837.23*	75857.74**	1167.4	11.45
STDIA	2.11*	2.25**	2.05**	0.49^{ns}	30.79**	0.38	12.31
NMSTN	3.70^{ns}	46.38**	35.24**	218.25**	856.95**	7.69	9.18
APBR	86.46^{ns}	198.26*	184.25*	173.65^{ns}	1938.53**	56.64	10.87
CANDIA	235.80^{ns}	1121.70**	949.84**	1638.07**	20023.91**	187.4	7.17
AvILMST	1.09*	1.32**	1.25**	1.79**	7.98**	0.23	9.51
AvLPB	255.96^{ns}	425.09**	402.88**	290.05^{ns}	3473.52**	78.68	10.94
AvGPB	0.01^{ns}	0.02^{ns}	0.02^{ns}	0.06^{ns}	0.27**	0.02	15.43
AvILPB	0.51^{ns}	0.60^{ns}	0.58^{ns}	0.80^{ns}	1.46^{ns}	0.5	27
NPB	291.91^{ns}	532.41*	498.91*	899.21*	3418.72**	133	13.62
NSB	1656.40^{ns}	5060.91^{ns}	4844.23^{ns}	2985.53^{ns}	37071.84**	2629.5	22.48
PBPB	12.41^{ns}	132.95**	116.51**	116.00*	2140.45**	19.12	5.38
HUFPB	9.95^{ns}	58.41^{ns}	59.60^{ns}	21.57^{ns}	27.30^{ns}	75.82	4.58
LL	2.88*	3.77**	3.77**	0.14^{ns}	13.94**	0.45	5.89
LW	1.05^{ns}	0.75^{ns}	0.74^{ns}	0.79^{ns}	2.63*	0.34	12.45

Table 2 Analysis of variance for yield components for the coffee germplasm accessions at Awada, 2013/14 continued

Plant characters	Mean Squares for different Sources of variation and their significance						
	Blocks (d.f=3)	All entries (d.f=123)	Test Accessions (d.f=119)	Checks (d.f=3)	Checks vs Accessions (d.f=1)	Error (d.f=9)	CV (%)
LA	63.59^{ns}	105.44^{ns}	102.76^{ns}	52.86^{ns}	581.74**	52.36	19.67
FL	2.93*	1.87*	1.88*	1.55^{ns}	2.49*	0.44	4.45
FW	1.86^{ns}	0.98^{ns}	0.96^{ns}	1.40^{ns}	2.62^{ns}	0.6	7.35
FT	0.41^{ns}	0.97^{ns}	0.98^{ns}	0.73^{ns}	0.20^{ns}	1.11	10.47
BL	1.08^{ns}	1.12^{ns}	1.10^{ns}	2.26^{ns}	0.10^{ns}	0.9	10.71
BW	0.08^{ns}	0.31*	0.30*	0.42*	0.67*	0.1	5.46
BT	0.28^{ns}	0.23^{ns}	0.22^{ns}	0.45^{ns}	0.84^{ns}	0.22	12.5
HGBW	7.27^{ns}	19.60*	19.84*	5.06^{ns}	34.34*	6.22	14.55
CBD	300.47 ^{ns}	707.26 *	658.02*	306.78^{ns}	7767.55**	198.14	37.69
CLR	182.31^{ns}	273.55 ^{ns}	252.65 ^{ns}	270.26 ^{ns}	2770.54 *	286.71	51.53

*, ** significant at 0.05 and 0.01 level of probability, respectively. ns=non-significant, d.f=degree of freedom; CV=coefficient of variation; PH=Plant height (cm); STDIA=Stem diameter (cm); NMSTN=Number of main stem nodes; APBR=Angle of primaries branches (degree); CANDIA=Canopy diameter (cm); AvILMST=Average inter node length of main stem (cm); AvLPB=Average length of primary branches (cm); AvGPB=Average girth primary branches (cm); AvILPB=Average inter node length of primary branches (cm); NPB=Number of primary branches; NSB=Number of secondary branches; PBPB =Percentage of bearing primaries branches; HUFPB=Height up to first primary branches (cm); LL=Leaf length (cm); LW=Leaf width (cm); LA=Leaf area (cm^2); FL=Fruit length (mm); FW=Fruit width (mm); FT=Fruit thickness (mm); HGBW=Hundred (100) green bean weights (gm); BL=Bean length (mm); BW=Bean width (mm); BT =Bean thickness (mm); CBD =Coffee berry disease (%) and CLR= Coffee leaf rust (%) reaction

average length of primary branches (36.91%) and clean coffee yield per tree (28.00%). Ermias (2005) has revealed low heritability for percent of bearing primary branches (13%). In this study, results are generally in agreement with most of the findings of previous studies. Some of discrepancies with some previous findings may attribute to the differences in number and type of genotypes studied and number of seasons and locations from which the data were collected.

The estimates of genetic advance as percent of mean (GAM) that could be expected from selecting the top 5% of the coffee genotypes is presented in Table 3. Accordingly, the value of GAM were high for CBD (108.08%), CLR (45.07%), average green bean yield (35.62%), stem diameter (29.82%), average inter node length of stem (26.02%), number of primary branches (25.60%), plant height (24.45%) and average length of primary branches (23.46%). Similarly, Abdi (2005) reported that the GAM was higher for green bean yield per plant (111.4), leaf area (56.4), number of secondary branches (35.0), leaf width (34.7), leaf length (27.9) and 100 green bean weights (23.8%). The author reported moderate GAM for number of main stem nodes (19.92%), number of secondary branches

Table 3. Estimates of components of Variance, PCV, GCV, Heritability and Genetic Advance for 19 quantitative characters for 124 arabica coffee genotypes

Characters	GV	EV	PV	PCV	GCV	H^2 (%)	GA	GAM
GBYT13	14322.00	7050.11	21372.11	25.80	21.12	67.01	201.81	35.62
HGBW	3.63	1.56	5.18	13.28	11.11	69.98	3.28	19.14
PH	1498.42	291.84	1790.26	14.18	12.97	83.70	72.95	24.45
STDIA	0.60	0.09	0.70	16.74	15.57	86.46	1.49	29.82
NMSTN	10.17	1.92	12.09	11.50	10.55	84.09	6.02	19.92
APBR	45.55	14.16	59.71	11.16	9.75	76.28	12.14	17.54
CANDIA	264.47	46.85	311.32	9.24	8.52	84.95	30.88	16.17
AvILMST	0.46	0.06	0.51	14.23	13.41	88.78	1.31	26.02
AvLPB	101.77	19.67	121.44	13.59	12.44	83.80	19.02	23.46
NPB	133.57	27.68	161.24	15.00	13.66	82.83	21.67	25.60
NSB	799.76	640.20	1439.96	17.06	12.72	55.54	43.42	19.52
PBPB	65.30	19.61	84.91	10.69	9.38	76.91	14.60	16.94
LL	1.04	0.11	1.15	9.45	8.98	90.30	1.99	17.58
LW	0.13	0.08	0.21	9.91	7.70	60.47	0.57	12.34
LA	13.46	13.09	26.55	14.01	9.97	50.69	5.38	14.63
FL	0.35	0.11	0.46	4.52	3.94	75.80	1.06	7.06
BW	0.05	0.03	0.08	4.78	3.92	67.27	0.39	6.62
CBD	92.19	14.81	106.99	60.89	56.52	86.16	18.36	108.08
CLR	14.61	14.34	28.94	43.35	30.79	50.47	5.59	45.07

GBYT13= Green bean yield per tree (g) in 2013; PH= Plant height (cm); STDIA=Stem diameter (cm); NMSTN= Number of main stem nodes; APBR= Angle of primaries branches (degree); CANDIA = Canopy diameter (cm); AvILMST =Average Internode length of main stem (cm); AvLPB= Average length of primary branches (cm); NPB=Number of primary branches; NSB=Number of secondary branches; PBPB =Percentage of bearing primaries branches; LL =Leaf length (cm); LW =Leaf width (cm); LA=Leaf area (cm^2); FL =Fruit length (mm); BW =Bean width (mm); HGBW=Hundred green bean weights (gm);CBD =Coffee berry disease (%) and CLR = Coffee leaf rust (%) reaction

(19.52%), hundred green bean weight (19.14%), leaf length (17.58%), angle of primary branches (17.54%), percent of bearing primary branches (16.94%), canopy diameter (16.17%), leaf area (14.63%) and leaf width (12.34%) and low GMA for fruit length (7.06%) and bean width (6.62%). In addition, Yigzaw (2005) observed relatively high values of genotypic coefficient of variation, broad sense heritability and genetic advance for characters.

Furthermore, the combined use of genetic coefficient of variation, heritability and genetic advance seems vital for effective improvement of a particular trait in a population (Yigzaw, 2005). In this study, high estimates of heritability coupled with high genetic advance as percent of mean were observed for characters such as coffee berry disease, coffee leaf rust, average green bean yield, stem diameter, average inter node length of stem, plant height, number of primary branches and average length of primary branches which revealed that most likely the high heritability are due to additive gene effects and improvement through selection based on phenotypic performance can be effective. Similar results in coffee were also reported by several researchers (Ermias, 2005; Yigzaw, 2005; Abdi, 2009; Olika et al., 2011; Getachew, 2012). According to Olika et al. (2011), expected genetic advance as percent of the mean from selecting the top 5% of the genotype varied between 0.11 to 77.64% for height up to first primary branches, number of secondary branches, hundred green coffee bean weight and yield of clean green coffee per tree in arabica coffee accessions showed higher heritability and genetic advance.

Table 4. Clustering patterns of 124 coffee accessions based on 19 quantitative traits

Cluster	No. of accessions in each cluster	% of genotypes in cluster	Serial number	Name of accessions in each cluster
I	30	24.19	1,5,13,16,17,22,24,25,28,29,42,45,47, 48,55,69,88,90,91,93,96,100,102,104, 105,106,108,110,111,114	AW-87,AW-24,AW-77,AW-43,AW-07,AW-76,AW-68,AW-73,AW-09,AW-11,AW-66,AW-12,AW-62,AW-64,AW-67,AW-71,AW-21,AW-79,AW-61,AW-114,AW-122,AW-10,AW-90,AW-27,AW-45,AW-123,AW-30,AW-100,AW-120,AW-101
II	47	37.90	18,27,31,33,34,35,36,37,39,43,44,46,49,50,51,53,54,57,59,61,62,63,64,66,68,70,71,72,73,75,76,77,78,79,80,81,82, 83,84,86,87,94,95,99,101,107,123	AW-115,AW-78,AW-01,AW-05,AW-65,AW-59,AW-33,AW-81,AW-18,AW-34,AW-26,AW-75,AW-46,AW-70,AW-58,AW-47,AW-63,AW-102,AW-31,AW-99,AW-105,AW-20,AW-94,AW-85,AW-98,AW-79,AW-104,AW-15,AW-36,AW-74,AW-103,AW-37,AW-108,AW-60,AW-125,AW-88,AW-03,AW-57,AW-28,AW-84,AW-38,AW-16,AW-55,AW-106,AW-116,AW-41,AW-02,1377
III	23	18.55	4,12,15,20,21,26,30,32,67,89,92,97,103,109,112,113,115,116,117,118,121,122,124	AW-92,AW-22,AW-14,AW-53,AW-29,AW-25,AW-69,AW-39,AW-17,AW-112,AW-121,AW-40,AW-117,AW-50,AW-110,AW-107,AW-124,AW-118,AW-32,AW-109,744,75227,7440
IV	14	11.29	7,10,11,14,23,40,41,52,56,58,65,74,85,98	AW-96,AW-06,AW-48,AW-91,AW-113,AW-83,AW-82,AW-54,AW-52,AW-51,AW-19,AW-72,AW-84,AW-80
V	2	1.61	119,120	AW-119,AW-111
VI	2	1.61	8,38	AW-23,AW-86
VII	2	1.61	3,6	AW-95,AW-13
VIII	2	1.61	9,19	AW-35,AW-93
XI	1	0.81	2	AW-04
X	1	0.81	60	AW-97

Cluster analysis of genotypes using quantitative traits

The phenotypic similarity of 124 coffee genotypes was also assessed by cluster analysis using 19 quantitative characters. Cluster analysis confirmed the presence some variation among genotypes. The 124 coffee genotypes were grouped into ten clusters (Table 4 and Figure 1). The genotypes used as checks, 1377 were grouped in cluster II while 744, 75227 and 7440 were grouped in cluster III.

The majority of accessions (114 or 91.93%) were classified in to four clusters (47, 30, 23 and 14 genotypes) in clusters I, II, III and IV, respectively. Others clusters had from 1 up to 2 members. These accessions were grouped in to Cluster II were the largest with 47 accessions (37.90%) followed by cluster I with 30 accessions (24.19%), cluster III with 23 accessions (18.55%), cluster IV with 14 accessions (11.29%) of the total. Clusters V, VI, VII and VIII for each had 2 accessions (1.61%) of the total population and clusters VX and X also had one accession (0.08%) for each in the total population, indicating that coffee accessions of the same cluster group were at least morphologically similar. The

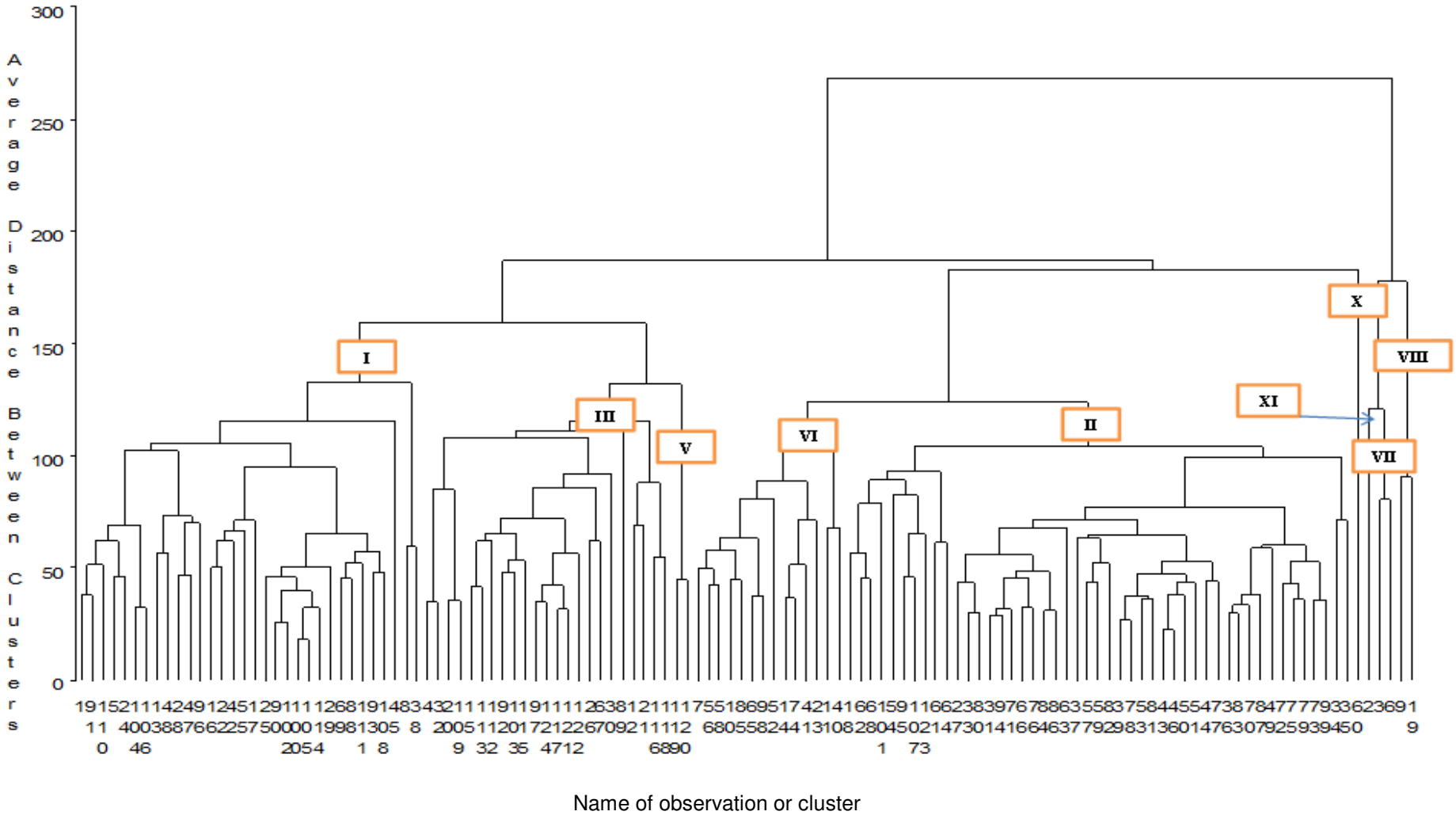

Figure 1. Dendrogram showing hierarchical clustering patterns of 124 coffee accessions for 19 quantitative traits

Table 5. Clustering patterns of 124 coffee accessions based on qualitative characters

Cluster	No. of accessions in each cluster	% of genotypes in cluster	Serial number	Name of accessions in each cluster
I	21	16.94	4,5,7,8,9,15,23,27,28,37,40,44, 49,50,64,79,81,89,96,109,119	AW-92,AW-24,AW-96,AW-23,AW-35,AW-14,AW-113,AW-78,AW- 09,AW-81,AW-83,AW-26,AW-46,AW-70,AW-94, AW-60, AW-88, AW-112, AW-122, AW-50 AW-119
II	17	13.71	6,11,13,17,19,29,32,33, 47,55,61,62,63,90,99,104,123	AW-13, AW-48, AW-77,AW-07,AW-93,AW-11,AW-39,AW-05,AW-62,AW-67,AW-99,AW-105,AW-20,AW-79,AW-116,AW-27,1377
III	14	11.29	3,12,14,16,22,30,34, 38,46,83,87,112,115,124	AW-95,AW-22,AW-91,AW-43,AW-76,AW-69,AW-65,AW-86,AW 75,AW-57,AW-16,AW-110,AW-124,7440
IV	32	25.81	2,10,20,21,24,25,31,35,36,39,42,43,48, 57,58,66,67, 71,73,85, 86,95,98, 101,103,105,106,108,111,114,120	AW-04,AW-06,AW-53,AW-29,AW-68,AW-73,AW-01,AW-59,AW-33,AW-18,AW-66,AW-34,AW-64,AW-102,AW-51,AW-85,AW-17,AW-104,AW-15,AW-36,AW-84,AW-38,AW-106,AW-80,AW-41,AW 117,AW-45,AW-123, AW-30,AW-120,AW-101,AW-111
V	14	11.29	18,41,51,52,53,59,65 ,74, 76,91,94,102,110,116	AW-115,AW-82,AW-58,AW-54,AW-47,AW-31,AW-19,AW-72,AW-103,AW-61,AW-55,AW-90,AW-100,AW-118
VI	16	12.90	26,45,54,60,68,69,77,78, 82,84, 88, 92,100,107,117,118	AW-25,AW-12,AW-63,AW-97,AW-98,AW-71,AW-37,AW-108,AW-03,AW-28,AW-21,AW-121,AW-10, AW-02,AW-32,AW-109
VII	3	2.43	70,75,93	AW-89,AW-74,AW-114
VIII	4	3.23	1,56,97,113	AW-87,AW-52,AW-40,AW-107
XI	2	1.61	121,122	744,75225
X	1	0.81	80	AW-125

clustering pattern of the accessions revealed the existence of genetic diversity in the coffee accessions for the characters studied. From previous work, Abdi (2009) who studied phenotypic diversity among 49 Harerge coffee accessions for 16 quantitative characters reported that the accessions were grouped into 6 clusters. Similarly, Olika et al. (2011) has made cluster analysis based on 22 quantitative traits grouped 49 Limmu coffee genotypes in to four clusters.

Cluster analysis genotypes based on qualitative characters

The 124 coffee accessions were clustered into 10 distinct groups based on seven qualitative characters (Table 5 and Figure 2). Cluster-IV was the largest and consisted of 32 accessions (25.81%) followed by cluster-I (16.94%), cluster-II (13.71%), cluster VI (12.90%), cluster-III and cluster V (11.29% for each), cluster VIII (3.23%), cluster VII (2.43%) and cluster XI (0.81%). Accessions grouped under cluster VI have predominately intermediate growth habit, strong stem, and many primary branches with many secondary branches, lanceolate leaf shape, brownish-tipped young leaves, obovate fruit shape and light red fruit color. Cluster XI on the other hand, comprised 2 accessions. Accessions falling in to cluster XI were characterized by open with spreading branch, very few primary branches,

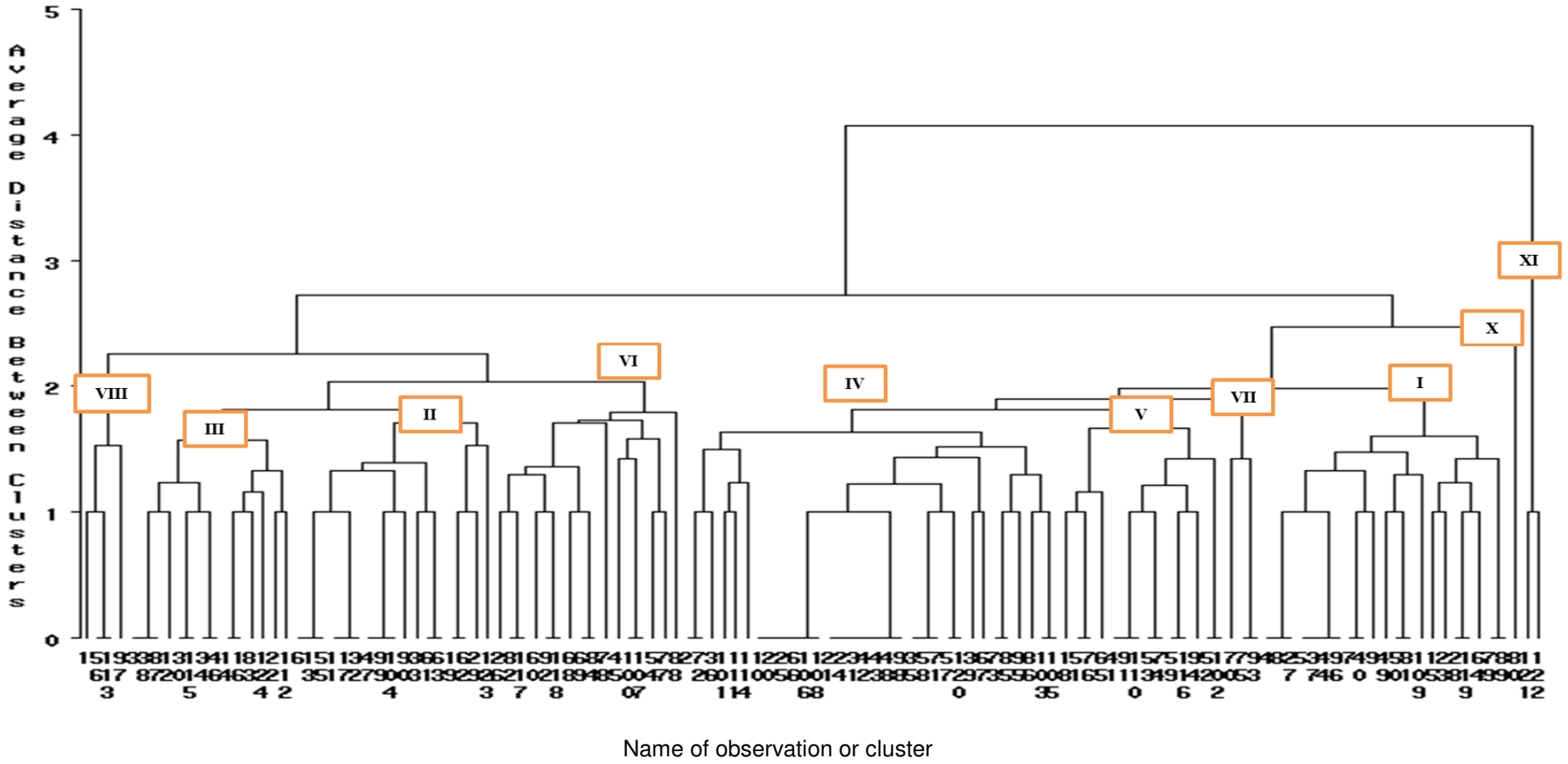

Figure 2. Dendrogram showing hierarchical clustering patterns of 124 coffee accessions for 7 qualitative traits

greenish young leaf tip color, obovate leaf shape, round and light red fruit shape and color. In addition, 17 accessions were grouped under cluster II. These accessions typically possess predominantly open with spreading branch, strong stem, many primary branches with many secondary and tertiary branches, bronze young leaf tip color, ovate leaf shape, obovate fruit shape, and dark red fruit color. One accession is grouped in cluster X (AW-125) was characterized under cluster X. It had open with spreading branch, strong stem, many primary branches with many secondary branches, bronze young leaf tip color, round fruit shape and dark red fruit color.

Finally, the agro-morphological characters among evaluated Sidama arabica coffee genotypes have been confirmed the presence of diversity. Hence, the existence of genetic diversity is potential resource for improvement of coffee through selection and hybridization. The coffee germplasm should be properly conserved and could serve as raw material for the in future coffee genetic improvement program. In addition of the observed variability for very important traits in coffee quality attributes and disease resistance related significantly should be exploited in order to improve the productivity of coffee. The morphological diversity observed in this study should be further addressed using the molecular techniques (using DNA markers) characterization.

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