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Research paper

Estimate of genetic variability components via quantitative traits in coffee (*coffeaarabica* L.) germplasm in Ethiopia

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Detail identification and quantification of genetic variability in the base population is an important for a successful conservation and utilization of genetic resources in coffee improvement work. The study was undertaken at Metu Agricultural Research Sub Center to estimate the extent of genetic variability of coffee. Sixty two Coffee germplasms along with two check varieties (74110 and 74112) were used for this study. The experiment was superimposed during 2018 cropping seasons on six years old coffee trees which was laid down in 8x8 simple lattice designs. The accessions were established under uniform temporary shade trees of Sesbaniasesban and other managed practices were applied as per the coffee agronomic production practice to the orchard. Data on 25 quantitative traits were recorded from four representative trees per row. Analysis of variance revealed the presence of significant (P<0.05) difference among the tested accessions for most of the traits. The maximum tree yield (0.58kg) was recorded on the accession Y105, while the minimum (0.20kg) was obtained from Y73. The high yielding accession (Y105) exhibited a yield advantage of 107.14% and 61.11% relative to check varieties (74110 and 74112), respectively. High phenotypic (PCV) and moderate genotypic coefficients of variations (GCV) were recorded for yield per tree and number of secondary branches; while high PCV and GCV values were recorded for coffee berry disease and coffee leaf rust reactions. However, the differences between PCV and GCV for these traits were higher except for number of secondary branches. High heritability coupled with high expected genetic advance as percent of mean was obtained for secondary branches, suggesting that this trait was under the control of additive gene action. Therefore, this trait can be improved through selection easier than other traits. Generally, the present study revealed the existence of immense genetic variability among coffee germplasm for important morphological traits.

Key words: *Coffeaarabica* L., GCV, PCV, Heritability, GA

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INTRODUCTION

Coffee (*Coffea Arabica* L.) belongs to the genus Coffea, in the family *Rubiaceae.* The genus coffea comprises nearly 124 well identified species; however *Coffeaarabica* L.and *Coffeacanephora* P. are the two commercially important species (Davis *et al.,* 2006; Gray*et al*., 2013). *Coffeaarabica* is by far the most important commercial species because of its best cup quality as well as wide choice of flavor and contribute to more than 70% of the world coffee production (Gray et al.,2013).The Arabica coffee is known as allopolyploidy and self –fertile species (2n=4x=44) will others are diploid and self-infertile (Lashermes *et al*., 2000; Silvarolla *et al*., 2004).

Coffee is one of the most widely drunk beverages and important source of foreign exchange income for many countries in the world. It is grown in about 80 countries straddling over 10.2 million hectares of land in tropical and subtropical regions of the world, especially in Africa, Asia, and Latin America. More than 125 million people in the coffee growing areas worldwide derive their income directly or indirectly from its product (Mishra and Slater, 2012). It ranks second after oil in international trade and has several million jobs in producer and consumer countries where more than nine tons of green beans are produced annually (ICO, 2016; USDIA, 2017).

Ethiopia is the fifth major exporter of Arabica coffee in the glob next to Brazil, Vietnam, Colombia and Indonesia; while it is the highest producer in Africa(Davis *et al*.,2012, ICO,2014).coffee contributes about 24% of the country's foreign currency earnings(Minten*et al*., 2014). Ethiopian coffee cultivation plays a vital role in both cultural and socio-economic life of the nation. Hence, more than 15 million populations (>15%) depend on coffee value chain for their income and employment (Gray *et al*., 2013)**.**The crop is mainly produced in Southern, Southwestern, and Eastern part of the country. Its total area coverage is estimated to be around 700,474.69 hectares; which is 9.94% of all the total crop production areas covered in the country, where as the estimated annual national production is about 469,091.10tons (CSA,2017), of which about 95% is produced by 4 million small scale farmers with average landholdings below two hectares (Francom and Tefera, 2016)**.**Fifty percent of its production is locally consumed, reflecting the commodity's cultural importance in the country (USAID, 2012;Berhanu*et al*., 2015).

Ethiopia is not only major producer and exporter of Arabica coffee, but also origin and center of genetic diversity for this valuable crop species. The entire genetic diversity of indigenous (wild) Arabica is confined mainly in the Afromontane rain forest located in the West and East of Great Rift Valley (Kassahun *et al*., 2013; Taye and Jurgen, 2008). Different research findings illustrated the importance of Ethiopian coffee genetic materials in breeding program for high productivity and disease resistance (Girma, 2005; Labouisse *et al*., 2008). Ethiopian Arabica materials were used as parents and crossed with commercial varieties to obtain strong hybrid vigor, resulting in over 30% higher productivity of the F1 hybrids in Central America (Bertrand *et al*., 1997).The other evidence in the existence of genetic diversity in coffee in Ethiopia is the damage caused to coffee production in Eastern Africa by the outbreak of the coffee berry disease in the 1970s and 1980s. In Ethiopia the disease does not affect coffee production significantly, chiefly due to the availability of high genetic diversity, which helped to develop cultivars resistant to the disease in a very short time using materials from wild type coffee gene pool (Mesfin and Bayetta,1984). Moreover, the diversity of coffee, soil and climate, production and processing methods, among others enabled the country to produce and supply the de facto organic coffee (Taye and Tesfaye, 2002). Hence there is no doubt in the existence of gene pool in wild genetic variability that can safeguard coffee production from dangers posed by possible stresses.

Despite its importance as invaluable genetic resource for long term crop improvement work, the Ethiopian Arabica coffee gene pool is threatened by genetic erosion mostly attributed to deforestation of its natural habitat, establishment and expansion of modern plantation with new released variety and illegal and legal settlements (Woldemariam *et al*., 2002). To mitigate such risks, starting from 1973 considerable coffee germplasm collection have been made during the national coffee collection program to capture the available coffee genetic variability for the purpose of selecting and developing adaptable coffee varieties. Hence, a total of about 12,452indigenous and exotic coffee germplasm were collected and *ex-situ* conserved at the Institute of Biodiversity Conservation (5731 accessions) (Taye, 2010) and Jimma Agricultural Research Center (6721 accessions) field gene banks (Tadesse, 2017).

However, some germplasm died in their maintenance fields due to climate change and adaptation problem, as they are forced to be grown outside of their original environment. It has been well understood that genotypes belonging to one region adapt differently when grown in another region (Bayetta *et al*., 1993). To alleviate such barrier, the conservation program was designed according to their area of origin and specific adaptation to minimize the risk of genetic erosion that may occur due to natural selection (Fikadu *et al*., 2008). Having such fact, location specific coffee technology generation and promotion under diverse coffee growing agro ecologies with different research projects has been the main breeding strategy of the National coffee genetic improvement program. Accordingly, to date it has developed and released 40 new coffee cultivars (34 pure lines and 6hybrids) for different localities (Tadesse,

2017).

Detail identification and quantification of genetic variability in crop species is important for a successful conservation and utilization of genetic resources in plant breeding. Such knowledge and visualization can be achieved through the study of morphological, structural and functional attributes of germplasm as the carrier of all hereditary characteristics of any given species (Jaramillo and Baena, 2000). Morphological markers in coffee are vital to distinguish variation based on external observation differences (De Vienne *et al*., 2003). So far, genetic variability study in some Arabica coffee geremplasm has been conducted in different years by different authors in Ethiopia (Ermias, 2005; Mesfin and Bayetta, 2005;Yigzaw, 2005; Olika *et al*., 2011; Getachew *et al*., 2017; Lemi and Ashenafi, 2016) who reported existence of genetic variability among the coffee germplasm for most of the traits studied.

Yayu forest is one of the remained parts of Afromontane rainforest in southwestern highlands of Ethiopian and globally designated as UNESCO Biosphere Reserves in June, 2010, primarily as a gene reserve for *in situ* conservation of wild *Coffeaarabica* (Beyene, 2014). Some diversity assessment studies at population level suggested the existence of genetic variability in Yayu coffee gene pool (Gole, 2008; Taye 2006). However, there is no detailed diversity study at individual level in Yayu coffee germlasm with considerable number of accessions, which in fact is crucial to design conservation strategy and for efficient exploitation of its germplasm in coffee improvement program. Consequently, the study was undertaken to estimate the extent of genetic variability of Yayu coffee germplasm.

MATERIALS AND METHODS

The experiment was conducted at Metu Agricultural Research Sub Center using Sixty-four *Coffeaarabica* L. germplasm including two standard check varieties (Table 1). The study was superimposed during the 2018 cropping seasons on six years old coffee trees. Experiment was laid down in an 8X8 simple lattice design with eight accessions per each incomplete block. Each accession was planted in a single row of six trees using spacing of 2m by 2m. Accessions were established under uniform *Sesbaniasesban* temporary shade trees and all other management practices were also uniformly applied for the orchard as per the coffee agronomic production practices.

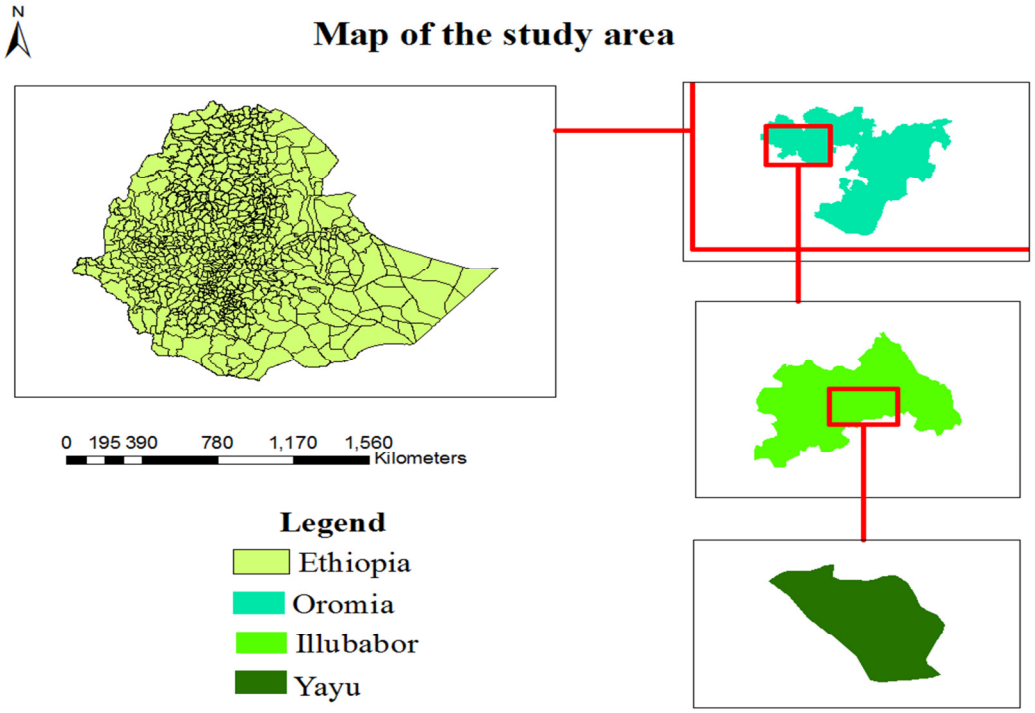

Figure 1. Mapof Arabica coffee collection site (Yayu) and study area(Metu in Illubabor zone).

Data Collected

According to the International Plant Genetic Resources Institute (IPGRI, 1996) coffee descriptor, data of 25 quantitative traits were randomly measured from four trees per row on each accessions as described below.

Table 1. Description of *Coffea Arabica* L. germplasm used in the study

Accessions	District	peasant association	Specific collection site	Accessions	District	Specific collection site
Y63	Yayu	Gechi	Dogi	Y95	Yayu	Geri geba
Y64	Yayu	Gechi	Dogi	Y96	Yayu	Geri geba
Y65	Yayu	Gechi	Dogi	Y97	Yayu	Geri geba
Y66	Yayu	Gechi	Dogi	Y98	Yayu	Geri geba
Y67	Yayu	Gechi	Dogi	Y99	Yayu	Geri geba
Y68	Yayu	Achebo	Sembo	Y100	Yayu	Geri geba
Y69	Yayu	Achebo	Sembo	Y101	Yayu	Geri geba
Y70	Yayu	Achebo	Sembo	Y102	Yayu	Geri geba
Y71	Yayu	Achebo	Sembo	Y103	Yayu	Geri geba
Y72	Yayu	Achebo	Sembo	Y104	Yayu	Geri geba
Y73	Yayu	Achebo	Sembo	Y105	Yayu	Gordeya
Y74	Yayu	Achebo	Sembo	Y106	Yayu	Gordeya
Y75	Yayu	Achebo	Sembo	Y107	Yayu	Gordeya
Y76	Yayu	Achebo	Sembo	Y108	Yayu	Gordeya
Y77	Yayu	Achebo	Sembo	Y109	Yayu	Gordeya
Y78	Yayu	Achebo	Sembo	Y110	Yayu	Gordeya
Y79	Yayu	Achebo	Sembo	Y111	Yayu	Gordeya
Y80	Yayu	Achebo	Sembo	Y112	Yayu	Gordeya
Y81	Yayu	Achebo	Geba	Y113	Yayu	Degitu
Y82	Yayu	Achebo	Geba	Y114	Yayu	Degitu
Y83	Yayu	Achebo	Geba	Y115	Yayu	Degitu
Y84	Yayu	Achebo	Geba	Y116	Yayu	Degitu
Y85	Yayu	Achebo	Geba	Y117	Yayu	Degitu
Y86	Yayu	Achebo	Geba	Y118	Yayu	Degitu
Y87	Yayu	Yayu	Achebo	Y119	Yayu	Degitu
Y88	Yayu	Yayu	Achebo	Y120	Yayu	Degitu
Y89	Yayu	Yayu	Achebo	Y121	Yayu	Degitu
Y90	Yayu	Yayu	Achebo	Y122	Yayu	Degitu
Y91	Yayu	Yayu	Achebo	Y123	Yayu	Degitu
Y92	Yayu	Yayu	Achebo	Y124	Yayu	Degitu
Y93	Yayu	Yayu	Achebo	74110	Metu	Bishari
Y94	Yayu	Yayu	Achebo	74112	Metu	Bishari

1. **Height up to first primary Branch (cm):** height from the ground up to first primary branch was measured using tape meter per tree
2. Total tree height (cm): height from the ground level to the tip of the tree was measured using tape meterper tree
3. Number of main stem node: this was counted from bottom to the top of the tree
4. Average Inter-node length on orthotropic branch (cm): was computed per tree as (TH–HFPB)/TNN-1, where TH = total plant height, HFPB =height up to first primary branch, TNN = total number of main stem nodes.

5. **Main stem diameter (mm):** was measured as a diameter of the main stem at five cm above the ground using caliper.
6. Canopy Diameter (cm):average length of tree canopy was measured twice, east-west and north- south direction.
7. Number of primary branches: total number of primary branches was counted per tree
8. Number of secondary branches: total number of secondary branches was counted per tree
9. Percentage of bearing primary branches (%): was computed per tree as (NBPB/Npb) * 100, where NBPB = number of bearing primary branches per tree, Npb = total number of primary branches per tree.
10. Number of nodes on primary branches:numbers of nodes of six selected primary branches (from bottom, middle and top of the tree) were counted.
11. Length of primary branches (cm): the average lengths of six selected primary branches (from bottom, middle and top of the tree) were measured using tape meter.
12. Average Inter-node length on primary branches (cm): the average internodes length of primary branches was calculated by dividing the average length of primary branch to the average number of nodes on primary branch.
13. Leaf length (cm): average of five normal (> node 3 from the terminal bud) leaves measured from petiole end to apex per tree.
14.Leaf width (cm): average of five normal (> node 3 from the terminal bud) leaves measured at the widest part
15. **Leaf area (cm^2**): was calculated by multiplying leaf length and width by constant 0.66
16. Fruit length (mm): average of 10 normal and mature green fruits of each tree measured at the longest part using digital caliper
17. Fruit width (mm): average of 10 normal and mature green fruits of each tree measured at the widest part using digital caliper
18. Fruit thickness (mm): average of 10 normal and mature green fruits of each tree measured at the thickest part using digital caliper
19. Bean length (mm): average of 10 normal beans of each tree measured at the longest part
20.Bean width (mm): average of 10 normal beans of each tree measured at the widest part
21. Bean thickness (mm): average of 10 normal beans of each tree measured at the thickest part
22.**Hundred Bean weight:** hundred beans per accession were dried with oven and calculated at 11% moisture content as follows: ("bean weight at 0% moisture content" x 100) / ("bean number" x 0.89)
23. Green bean yield per tree (kg): weight of fresh cherries per tree recorded and converted in to clean coffee per tree
24. Coffee berry disease severity (CBD):- severity was directly estimated as the percentage of diseased berries (damaged berries over on all barriers of bearing branch) from each of the trees assessed. It was rated using standard disease scales (0-6) adopted from Phiri*et al*.(2001); where, 0= no disease, 1= trace to 5%, 2= 6-10% showing infected berries, 3= 11-30% of infection, 4=31-50% of infection, 5=51-75% of infection and 6=maximum black lesion girdling the stem top killed and Highest yield lose.
25. Coffee leaf rust severity (CLR):-severity percentage of leaves per tree were also directlyestimated as the percentage of diseased leaves (damaged leaves over on all the top, middle and bottom part of the tree) and it was estimated by using a rating scale 0 to 6points (Bigirimana*et al*., 2012), as follows: 0 = no chlorosis; 1 = trace up to 5% showing infected leaves; 2 = 6 – 10% of infection, 3 = 11 – 30% infection; 4 = 31 – 50% of infection; 5 =51-75% of infection and 6=intense lesions associated with leaf shedding. The percentage of severity index (PSI) for each disease was calculated using the formula suggested by Shrestha and Mishra (1994) and the result was transformed using arc sin transformation method for statistical analysis.

$$\text{PSI} = \frac{\text{Sum of all numerical rating}}{\text{Total numberof plants rated x maximum score of scale}} \text{x}100$$

Based on the disease severity level for each respective diseases, 0-10 % of infection were considered as resistant, 11-20% infection as moderately resistant, 21-30% of infection as moderately susceptible, and 31-50% infection as susceptible and >51% infection as higly susceptible response.

Prior to statistical analysis normality testof the data was performed and thenall the 25 quantitative traits considered were subjected to analysis of variance using the SAS software. ANOVAof 8 X8 simple lattice design was done using the mean of sample data for each trait. The simple lattice design analysis of variance as structured in Table 2 (Cochran and Cox, 1957) was used to derive variance components such as phenotypic and genotypic variances, phenotypic and genotypic coefficient of variations, heritability and genetic advance under selection.

Table 1. Analysis of variance (ANOVA) for simple lattice design.

Source of variations	Df	SS	MS	F-valus
Replications	(r-1)	SS_r	MS_r	MS_r/MSe
Genotype (adjusted)	(k^2-1)	SS_g	MS_g	MS_g / MSe
Blocks with in replication (adj.)	r (k-1)	SS_b	MS_b	MS_b/MSe
Intra block error	(k-1)(rk-k-1)	Sse	MSe	

r = Number of replication, g=Number of genotypes, Df= degree of freedom, k= block sizes, SS= Sum squares, MS= Mean squares, SSr= Sum squares of replication,SSg = Sum square of genotypes,SSb= sum square of block,SSe= Sum square of error, MSr = mean of square due to replication, MSg = mean of square due to genotypes, MSb= mean square of block within replication, MSe = mean of square due to error.

Simple lattice design ANOVA was computed using the following model:

$Y_{ijk=} \mu + t_i+\beta_j+ \chi_{k(j)} +\Sigma_{ijk}$

Where, $Y_{ijk=}$ response of Y trait from the**i^{th}**Genotype under**j^{th}** replication and K^{th} level of incomplete blocks within replications, **μ**= overall mean effects, **t_i**= effects of i^{th} level of Genotypes, **β_j**= effects of j^{th} level of replication, **$\chi_{k(j)}$**= effects of K^{th} level of incomplete blocks within replications,**Σ_{ijk}**= the residual or random error component.

Estimation of genetic parameters

Different genetic parameters including genotypic variance (σ^2g), phenotypic variance (σ^2p), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula, adopted from Burton and De Vane (1953).

Phenotypic variance $(\sigma^2_{p)} = \sigma^2_g + \sigma^2_e$

Where, $\boldsymbol{\sigma}^2_g$ = genotypic variance, σ^2_e= environmental variance= Error Mean Squares.

$$\text{Genotypic variation } (\sigma^2 g) = \frac{(MSg - MSe)}{r}$$

Where, $MSg_=$ mean square of genotype, MSe = mean square of error, r=replications

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\bar{\mathbf{X}}} x100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\boldsymbol{\sigma}^2 g}}{\bar{\mathbf{X}}} x100$$

Where: σ^2p =Phenotypic variance, σ^2g= Genotypic variance, $\bar{x} =$ Grand mean

Estimation of heritability and genetic advance: Broad sense heritability (H) values were computed based on the formula of Falconer and Mackay (1996) below***:***

$$\text{Heritability in broad sense (H)} = \frac{\sigma^2 g}{\sigma^2 p} x100$$

Where, H =heritability in broad sense, σ^2p =Phenotypic variance, σ^2g= Genotypic variance.

Genetic advance under selection (GA): The genetic advance was estimated by the following formula **(**Allard, 1960).

$$\mathbf{GA} = K^{*}\sigma p^{*}H = k.\sqrt{\sigma^{2}p}\,\frac{\sigma^{2}g}{\sigma^{2}p} = k^{*}H\sqrt{\sigma^{2}p}$$

Where, H = Heritability in broad sense;σp = Phenotypic standard deviation on mean basis of each trait;GA=Expected genetic advance;k = the selection differential at 5% selection intensity (K = 2.063).

Genetic advance as percent of mean (GAM) was computed to compare the extent of predicted advance of different traits under selectionusing the following formula (Falconer and Mackey, 1996).

$$\mathrm{GAM} = \frac{\mathbf{GA}}{\bar{\mathbf{X}}}\mathrm{X}100$$

Where, GAM=Genetic advance as percent of mean; GA=Genetic advance under selection and

$\bar{\mathbf{X}}$ =Grand mean of the respective trait.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) revealed the existence of significant ($p<0.05$) variation among coffee germplasm for most of the quantitative traits studied except forheight up to first primary branch, number of main stem nodes, percentage of bearing primary branches, leaf width, leaf area and fruit length (Table 3). The existences of sufficient variability among the evaluated materials create immense opportunity to bring considerable improvement through selection and cross breeding in the future coffee improvement program.

Table 2. Analysis of variance (Mean squares) for 25quantitative traits of 64 coffee germplam studied at Metu

Traits	Mean squares				RE (%)	CV (%)
	Replication (1)	Treatment (adjusted)(63)	Blocks within rep.(adj.)(14)	Error (49)		
HUP	162.00	12.23 ^{ns}	13.97	9.35	103.38	11.46
TPH	182.41	603.20*	287.13	321.80	97.60	8.61
NMSN	328.64	8.00 ^{ns}	7.28	6.40	100.29	7.84
AILM	7.41	0.48**	0.52	0.17	111.01	7.12
SD	582.68	17.05**	9.24	2.15	101.24	3.10
CD	264.21	212.84**	350.75	63.65	135.14	4.80
NPB	498.49	25.12**	27.02	9.45	123.49	6.44
NSB	506.02	1469.03**	671.90	155.13	100.23	8.65
PBPB	2195.53	164.22^{ns}	133.71	130.6	100.01	34.75
NNPB	14.99	3.03**	5.68	0.34	145.75	3.27
ALPB	834.36	66.18*	173.39	39.57	149.5	8.21
AILPB	8.30	0.38**	0.49	0.04	122.00	4.48
LL	2.95	0.52**	0.46	0.18	105.44	3.47
LW	5.61	0.15 ^{ns}	0.44	0.10	151.16	5.37
LA	690.99	23.41 ^{ns}	35.72	17.13	111.25	8.70
FL	28.69	0.90 ^{ns}	1.54	0.58	120.16	4.57
FW	23.14	0.70**	1.31	0.36	136.86	4.14
FT	24.61	0.50**	1.24	0.28	150.11	4.30

Table 3. continues

BL	2.91	0.56**	0.24	0.13	98.46	3.31
BW	0.66	0.09**	0.07	0.03	109.27	3.00
BT	0.13	0.04**	0.03	0.02	100.78	3.70
HBW	20.08	4.34**	1.93	0.98	101.56	5.60
CBD	45.55	165.48**	153.72	86.54	106.87	89.45
CLR	129.38	61.14**	49.25	26.21	108.29	49.21
YLD	0.045	0.010*	0.007	0.006	100.420	21.00

*=highly significant (p<0.01), *= significant (p<0.05), ns= non significant, HUP= height up to first primary branches, TPH= total plant height, NMSN= number of main stem nodes, AILMS= average inter-node length of main stem, 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, FT= fruit thickness, BL= bean length, BW= bean width, bean thickness, HBW= hundred bean weight, CBD =coffee berry disease, CLR =coffee leaf rust, DF= YLD = yield per tree, RE= relative Efficiency, CV= coefficient of variation.

It is generally agreed that *Coffeaarabica* is predominantly self-pollinated species; hence a high degree of genetic uniformity is expected (Lashermes *et al*., 1996a). However, in contrast with the widely accepted perception, Meyer (1965) has observed and reported the existence of 40% to 60% out crossing rate in wild Arabica coffee populations in Ethiopia. This finding has been confirmed by Gezahegn *et al*. (2014) who did the first formal mating system analysis of *C. Arabica* populations based on the inheritance of genetic marker and found an overall multilocus out crossing rate as high as 76% in its native range. Therefore, the possible reason for the existence of considerable genetic diversity in the present study will be attributed to either out crossing nature of the crop through different pollinators (Meyer, 1965; Gezahegn *et al*., 2014), or to the gene flow through dissemination of seeds and seedlings from place to place by means of wild animal and human being (Esayas *et al*. 2005; Senbeta 2006).The significant difference observed for measured quantitative traits in this study were in agreement with the finding of earlier authors who reported considerable genetic variability within the Arabica coffee population for yield, disease resistance and growth characters (Bayetta, 1997; Olika *et al*., 2011; Getachew *et al*., 2017; Ermias, 2005; Yigzaw, 2005; Lemi and ashenafi, 2016).

Range and mean value of different traits

The performance of the accessions ranged widely for number of secondary branches (85.7-209.35), total plant height (159.3-253.55 cm), CBD severity (0.00-60.87%), yield per tree (0.20-0.58 kg clean coffee), canopy diameter (145.2-185.19cm), average length of primary branches (63.36-95.48 cm), CLR severity (0.07-23.95%), number of primary branches (37.00-58.71) and hundred bean weight (14.25-21.80 g). Out of these important traits, highest ranges were obtained for number of secondary branches, total plant height, CBD severity, and average yield per tree, which played important role in the total variability of coffee germplasm. The mean performance showed that the average mean value was almost doubled of the minimum mean value for the above important agronomic traits. This result was more or less in harmony with the finding of Yigzaw (2005), Olika *et al*. (2011) and Getachew *et al*. (2017).

More than 50% of the tested coffee accessions (32) and 86% of the tested coffee accessions (55) had mean yield exceeding the mean yield of standard check varieties (74112 and 74110), respectively. The maximum yield per tree was recorded on the accession Y105 (0.58kg) followed by Y86 (0.57kg) and Y74 (0.55kg). The high yielding accession (Y105) had a yield advantage of 61.11% and 107.14% compared with the standard checks (74112 and 74110), respectively.

According to this visual field observation, the coffee accession also showed significantly different reaction against coffee berry disease (CBD) and coffee leaf rust (CLR).The highest CBD severity value (60.87 %) was recorded onaccessionY118 which washighly susceptible to CBD, whereas susceptible to moderately susceptible response was found on accession Y120 (33.14%) and Y65 (21.23%), respectively. Most of the tested materials (52%) i.e., 34 accession had CBD severity below the grand mean values (10.40%). Among these, 26% of the accessions (17) scored less than 5% CBD severity level. Likewise, the maximum CLR severity value was recorded on accession Y120 (23.95 %) followed by Y97 (21.49%) and Y115 (21.25%). Half of these accessions (32) had CLR severity level below ten present. Accessions Y82, Y112, Y85, Y86, Y99, and Y94 had CLR severity level less than the standard check (74110) severity level (3.61%).

Generally, the range and mean performance of the

traits studied confirmed the presence of an enormous genetic variability between the tested accessions. Hence, there is an opportunity to find genotypes having disease resistance and high yielding potential among the tested entries that perform better than the existing varieties to utilize for the future coffee improvement program.

Estimation of genotypic and phenotypic coefficients of variation

Table 4 presents means, the estimates of genotypic and phenotypic variance, genotypic (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance expressed as percent of mean(GAM). The ranges for phenotypic and genotypic coefficients of variation were (3.67%-107.81%) and (2.44%-60.34%), respectively. As stated by Deshamukh *et al.(*1986), phenotypic and genotypic coefficient of variation values greater than 20% are considered as high, whereas values less than 10% are to be low and values between 10 and 20% as medium. According to this description, High phenotypic (24.18% and 20.00%) and medium genotypic (12.09% and 17.79%) coefficients of variation were recorded for traits like yield per tree and number of secondary branch, respectively. Whereas, CBD and CLR had high PCV (107.81% and 63.55%) and GCV (60.34%and 40.18%) values, respectively. The traits with high PCV and moderate to high GCV suggested that, the genotype could be reflected by the phenotype, suggesting the effectiveness of selection based on the phenotypic performance for these traits. However, the differences between PCV and GCV for these traits were higher except for number of secondary branches, indicating the influence of environment on them.

Moderate phenotypic (10.32% and 10.24%) and low genotypic (5.69 % and 9.34 %) coefficients of variation were recorded for total plant height and average inter node length of primary branches, respectively. However, low PCV and GCV were recorded for average inter-node length of main stem node, stem diameter, canopy diameter, and number of nodes of primary branches, average length of primary branches, leaf length, fruit width, fruit thickness, bean length, bean width, bean thickness and hundred beans weight.

The present finding illustrated that, PCV was higher than GCV for all studied quantitative traits, suggesting the observed variation in the coffee accessions were both the combination of genotypic and environment effect. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflected high environmental influence; while small differences reveal high genetic influence (Akinwale *et al*., 2011). Accordingly, the difference between PCV with the corresponding GCV values was relatively higher for yield per tree, average length of primary branches, CBD and CLR reaction, indicating the higher influence of the environment on these traits. However, this difference was comparatively low for stem diameter, number of nodes of primary branches, bean width, bean length, bean thickness, canopy diameter, hundred bean weight and number of secondary branches. The small difference indicating that there is a minimal influence of environment on the expression of these traits. Therefore, selection based on phenotypic performance would be effective to bring considerable improvement in these traits.

The current finding is in agreement with Seyum and Bayetta (2007) and Olika *et al*. (2011) who reported high PCV and GCV values for yield and number of secondary branch and moderate PCV and GCV values for height up to first primary branch and hundred beans weight. This finding is further in line with Getachew *et al*.(2017) who noted high PCV and GCV values for CBD reaction and yield per tree and high PCV and moderate GCV values for number of secondary branches as well as narrow gap between PCV and GCV values for hundred bean weight, number of nodes of primary branches, stem diameter, bean length, though wider gap between PCV and GCV for yield per tree, coffee berry disease severity, number of primary branches, number of secondary branches and number of main stem node.

Heritability and genetic advance

Broad sense heritability estimates for the 19 quantitative traits ranged from 25.00% for yield per tree to 83.16% for average inter-node length of primary branches (Table 4). Verma and Agarwal (1982) generally classified estimates as low (<20%), medium (20-50%) and high (<50%). Based on this classification, average inter-node length of primary branches (83.16%), number of secondary branches (80.90%), number of nodes of primary branches (79.80%), stem diameter (77.60%), hundred bean weight (63.16%), bean length (62.49%), bean width (55.21%) and canopy diameter (53.96%) exhibited high heritability estimates. A high heritability value implies these traits were less influenced by the environment in their expression. Hence, selection based on phenotypic traits will be effective. On the other hand, medium broad sense heritability estimates were observed for leaf length (49.06%), average inter-node length of main stem(46.59%), number of primary branches(45.33%), coffee leaf rust severity(39.99%), total plant height (30.42%), bean thickness(33.31%), fruit width(32.28), coffee berry disease severity (31.32), fruit thickness(28.02%), average length of primary branches(25.16%) and yield per tree(25.00 %), which implies the possibility of using these traits in coffee improvement programs, because of acceptable level of correspondence between genotype and phenotype.

The current result has been partially in agreement with Bayetta *et al.* (2001) who noted high heritability estimates for all characters studied. Similarly, high heritability estimates for hundred bean weight, number of secondary branches and canopy diameter and medium heritability for bean thickness were also reported by Yigzaw (2005). Comparable high heritability values have also been reported by Olika *et al*. (2011) for bean length, bean width, number of secondary branches, and 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 Getachew *et al*. (2017) has been more or less similar to the current study for most of the traits considered.

Table 4. Estimates of range, mean, genotypic (σ^2g) and phenotypic (σ^2p) variances , genotypic (GCV) and phenotypic(PCV) coefficient of variations, broad Sense heritability (H), expected genetic advance (GA) and expected genetic advance as percentage of mean(GAM) for 19 characters of 64 coffee germplasm studied at Metu.

Traits	range		mean	(σ^2g)	(σ^2p)	H (%)	GCV (%)	PCV (%)	GA	GAM (%)
	Min	Max								
TPH	159.30	253.55	208.44	140.70	462.50	30.42	5.69	10.32	13.50	6.48
AILMS	4.16	7.21	5.87	0.15	0.33	46.59	6.65	10.00	0.55	9.36
SD	43.50	58.80	48.96	7.45	9.60	77.60	5.57	6.33	4.96	10.13
CD	145.23	185.19	166.77	74.59	138.4	53.96	5.18	7.05	13.09	7.85
NPB	37.00	58.71	47.71	7.84	17.29	45.33	5.87	8.71	3.89	8.15
NSB	85.70	209.35	144.06	656.95	812.8	80.90	17.79	20.00	47.56	33.01
NNPB	15.09	21.11	17.83	1.35	1.69	79.80	6.51	7.29	2.14	11.99
ALPB	63.36	95.48	76.60	13.30	52.88	25.16	4.76	9.49	3.77	4.93
AILPB	3.52	5.55	4.46	0.17	0.21	83.16	9.34	10.24	0.78	17.56
LL	10.97	13.43	12.22	0.17	0.35	49.06	3.39	4.84	0.60	4.90
FW	13.03	15.99	14.45	0.17	0.53	32.28	2.86	5.04	0.48	3.35
FT	11.22	13.47	12.29	0.11	0.39	28.02	2.69	5.08	0.36	2.94
BL	9.84	12.13	10.89	0.21	0.34	62.49	4.25	5.37	0.75	6.93
BW	6.10	6.89	6.54	0.03	0.06	55.21	2.73	3.67	0.27	4.18
BT	3.66	4.23	3.94	0.01	0.03	33.31	2.44	4.23	0.11	2.91
HBW	14.25	21.80	17.66	1.68	2.66	63.16	7.34	9.23	2.12	12.03
CBD	0.00	60.87	10.40	39.47	126.0	31.32	60.34	107.81	7.25	69.67
CLR	0.07	23.95	10.40	17.47	43.68	39.99	40.18	63.55	5.45	52.42
YLD	0.20	0.58	0.370	0.0020	0.008	25.00	12.092	24.184	0.050	12.470

σ^2**g** =genotypic variance, σ^2p =phenotypic variance, GCV =genotypic coefficient of variation, PCV =phenotypic coefficient of variation, $H^{2=}$broad Sense Heritability, GA =expected genetic advance , GAM =expected genetic advance as percentage of mean, TPH= total plant height, AILMS= average inter node length of main stem, SD= stem diameter, CD= canopy diameter, NPB= number of primary branches, NSB=number of secondary 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, FW= fruit width, FT= fruit thickness, BL= bean length, BW= bean width, BT = bean thickness ,HWT= hundred bean weight, CBD =coffee berry disease, CLR =coffee leaf rust ,YLD= yield per tree

The genetic advance as present of the mean at 5% selection intensity (GAM) was presented in Table 4. Estimates of GAM ranged from 2.91 for bean thickness to 69.67 for coffee berry disease severity. As stated by Johnson *et al*. (1955), GAM was categorized as low (0-10%), medium (10-20%) and high (≥20%). As per this suggestion, the highest (≥20%) GAM was observed for coffee berry disease severity (69.67%) followed by coffee leaf rust severity (52.42%) and number of secondary branches (33.01). This indicated that these traits are controlled more of by additive genes (Panse, 1957). Moderate GAM (10-20%) were obtained for average inter-node length of primary branches (17.56%), yield per tree (12.47 %), hundred bean weight (12.03%), number of nodes of primary branches (11.99%) and stem diameter (10.13%).

In contrast, average inter-node length of main stem, total plant height, number of primary branches, canopy

diameter, bean length, average length of primary branches, leaf length, bean width, fruit width, fruit thickness and bean thickness showed low estimates of GAM (<10 %).The low GCV and low GAM observed for these traits indicated that the characters were under high environmental influence; hence selection based on these traits would be less effective.

High heritability estimate accompanied by the high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone (Johnson *et al*., 1955). Accordingly, High heritability coupled with high genetic advance as percent of mean was obtained for number of secondary branches, while High heritability with moderate GAM was attained for average inter-node length of primary branches, number of nodes of primary branches, stem diameter, and hundred beans weight, suggesting that these trait were more of under the influence of additive gene action, which means relatively fixable and heritable in to the next generation. Therefore, these traits can be improved through direct selection more easily than other traits considered in the study. Subsequently, combined high GCV, moderate heritability and high GAM were recorded for CBD reaction (60.34, 31.32, and 69.67%) and CLR reaction (40.18, 39.99, and 52.42%) in the order of magnitude; whereas moderate GCV (12.09%), moderate heritability (25.00%) and moderate GAM (12.47%) were recorded from yield per tree, suggesting that yield is complex in nature mainly because of its quantitative inheritance.

Similarly, bean length, bean width, and canopy diameter had high heritability with low genetic advance, while the remaining traits showed moderate heritability along with low genetic advance. Moderate to high heritability with low genetic advances suggest that the traits are influenced by environmental effects and are most likely governed by both additive and non-additive (dominant, epistemic) types of gene action (Abate *et al*., 2018). This would make complicated to improve these traits through simple selection, as far as cross breeding is the best alternative options for improvement of such kinds of traits. Saravanan *et al*., (2003) also suggested that if a trait is controlled by non-additive types of genes then selection for traits should be postponed and performed safely in advanced /succeeding generations.

The current finding is partly in agreement with Olika *et al*. (2011) who studied on Lemu 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. Getachew *et al*.(2017) found high Heritability (H) coupled 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, Lemi and Ashenafi (2016) found high heritability with high GAM for number of main stem nodes, stem diameter and internodes length, whereas, yield per tree recorded moderate heritability and high GAM on Lemu coffee collections.

CONCLUSIONS

The results of this study has confirmed the existence of enormous genetic variability among the 64 *Coffeaarabica* germplasm for most of the traits considered that could be exploited in future breeding programs. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all studied quantitative traits, suggesting the observed variation in the coffee accessions were both the combination of genotypic and environment effect. High heritability coupled with moderate to high genetic advance as percent of mean was obtained for average inter-node length of primary branches, number of nodes of primary branches, stem diameter, hundred beans weight and secondary branches, suggesting that these traits were under the influence of additive gene action. Therefore, these traits can be improved through direct selection more easily than other traits considered in the study. The remaining traits showed moderate to high heritability along with low genetic advance, suggesting that the traits are influenced by environmental effects and are most likely governed by both additive and non-additive type of gene action, this would make complicated to improve these traits through simple selection, as far as cross breeding is the best alternative method for improvement of such a kind of traits.

To sum up, the existence of genetic variability in the base population is a key resource to exploit through selection and cross breeding in crop improvement program. The present study confirmed the existence of enormous genetic variability among coffee germplasm for various important morphological traits. Hence there is an opportunity to exploit these traits in order to develop genotypes that perform better than the existing varieties for the future coffee improvement program.

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