MORPHOLOGICAL CHARACTERIZATION OF BALE AND WEST ARSI COFFEE (*Coffea arabica* L.*)* COLLECTIONS AT GERA, SOUTHWEST ETHIOPIA

MSc. Thesis

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ABAYNESH ASEGID

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Morphological Characterization of Bale and West Arsi Coffee (*Coffea arabica* L.*)* Collections at Gera, Southwest Ethiopia

By

Abaynesh Asegid

A thesis

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Major Advisor: Weyessa Garedew (PhD)

Co-Advisor: Fekadu Tefera (PhD)

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Prof. Sintayehu Alamerew Name of the Chairperson	..... Signature	01 NOV. 2019 Date
Dr. Wayessa Garedew Name of Major Advisor	..... Signature	1/11/19 Date
Dr. Wosene G/selassie Name of the Internal Examiner	..... Signature	1/11/19 Date
Dr. Bayeta Belachew Name of the External Examiner	..... Signature	1 NOV. 2019 Date

DEDICATION

I dedicate this thesis document to my lovely family and parents: father, mother, sisters and brothers

STATEMENT OF THE AUTHOR

I declare and confirm for this thesis, the work is done by me for MSc thesis, which is not done before for any diploma and certification programs. I had followed all ethical and technical principles of scholarship in the preparation, data collection, data analysis and compilation of this thesis.

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Place: Jimma University College of Agriculture and Veterinary Medicine

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LIST OF ACRONYMS AND ABBREVIATIONS

CSA	Central Statistical Agency
ECFF	Environment and Coffee Forest Forum
GCV	Genotypic Coefficient of Variation
ICO	International Coffee Organization
IPGRI	International Plant Genetic Resource Institute
JARC	Jimma Agricultural Research Center
M.a.s.l	Meter above sea level
PCV	Phenotypic Coefficient of Variation
SAS	Statistical Analysis System
USDA	United States Department of Agriculture

BIOGRAPHICAL SKETCH

Abaynesh Asegid was born in the Oromia region of Jimma zone Gomma Woreda. She attended her elementary education at Agaro Kuter Hulet from 1990-1996 and her secondary school from 1997-2003 at Agaro Senior Secondary School. After passing the Ethiopian School Leaving Certificate Examination (ESLCE), she joined Agarfa Technical Vocational Education and Training College in 2003 and graduated in 2005 with a diploma in Plant science. She was employed in September, 2006 at Goma woreda agricultural office. In September 2010 she got a regular Bachelor Degree education and graduated with Bachelor of Science in Horticulture in 2011. She again went back to Gumay Woreda Agricultural Office and served up to April, 2014. In May, 2014, she was employed by Ethiopian Institute of Agricultural Research (EIAR), at Jimma Agricultural Research Center as junior researcher in crop research. Then she joined the postgraduate program of Jimma University to pursue her MSc degree in plant breeding in September 2017.

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MORPHOLOGICAL CHARACTERIZATION OF BALE AND WEST ARSI COFFEE (*Coffea arabica* L.*)* COLLECTIONS AT GERA, SOUTHWEST ETHIOPIA

ABSTRACT

Morphological characterization of coffee accessions is a precondition for the improvement of coffee varieties for yield and disease resistance. A total of 133 coffee accessions collected from Bale and West Arsi zone were characterized using morphological traits to estimate the extent of variability among the collection at Gera Agricultural Research Sub Center along with four standard checks. The experimental treatment was laid using an augmented design with three blocks of single row with six trees per plot. The experiment was superimposed during 2018/19 cropping seasons on four years old coffee trees which was planted in July, 2015. Data on 25 quantitative and 12 qualitative traits was recorded from three representativ e trees per plot. The analysis of variance revealed a significant (P<0.05) difference among the collections for most of the quantitative traits considered. The highest (2886.33 kg/ha) and lowest (20.31 kg/ha) mean bean yield was recorded from accession B184/07and B77/07, respectively. Higher mean yield coupled with resistance to CBD were recorded from accessio n B184/07 and B29/07.Genotype variations were greater than environmental variation for all traits except plant height and number of secondary branches. Higher percent (%) and closer variation of GCV and PCV value were demonstrated by traits such as coffee leaf rust, coffee berry disease, bean yield and number of secondary branch and percent of bearing primary branch. High estimates of heritability and genetic advance as percent of mean were observed for coffee leaf rust, coffee berry disease, number of secondary branch, percent (%) of bearing primary branch, bean yield and height up to first primary branch. Coffee yield was positively and significantly correlated with percentage (%) of bearing primary branch (rg=0.64), coffee leaf rust (rg=0.39) and canopy diameter (rg=0.39). Fruit thickness, canopy diameter, height up to primary branch, percentage of bearing primary branch and coffee leaf rust exhibited positive direct effect with coffee yield. Cluster analysis based on quantitative characters grouped the accessions into six clusters of different size. The higher inter cluster distance were observed between clusters II and VI (142.82), followed by cluster I and VI (100.94). Principal component analysis with eigenvalue greater than one exhibited 70.55 % of the total variation, and the highest contribution of traits for total variation accounted by the first and second principal components with respective value of 25.88% and 20.86%. Accordingly, fruit length (0.75%), fruit thickness (0.87%), fruit width (0.86%), coffee berry disease (0.42%) and number of secondary branch (0.32%), % of bearing primary branch (0.39%) and canopy diameter (0.42%) had more contribution to the total variation. Shannon-waver diversity index (H') for different qualitative traits showed existence of diversity for stipule shape, fruit shape, leaf tip color, fruit color, growth habit, leaf shape, angle of insertion, leaf apex shape and branching habit. Generally, the result of the study showed existence of significant genetic vari ability among tested genotypes.

Keywords: Heritability; Correlation; Cluster Analysis; Path Analysis; Principal Component Analysis

1. INTRODUCTION

Coffee belongs to the genus *Coffea of* the Rubiaceae family, mostly grown in the tropical and subtropical regions (Berthaud and Charrier, 1988).It is an important commodity crop in Ethiopia (WeldeMichael *el al*., 2016). The genus *Coffea* L. comprises 124 species (Davis *et al*., 2011). However, only *C.arabica* (Arabica coffee), *C. Canephora* (Robusta coffee); and *C. liberica* (Liberian or Liberica coffee, or excels coffee) are the economically important species of the genus (Davis *et al*., 2006). *Coffea arabica* the only allopolyploid (2n = 4x = 44) coffee species and self-fertile (Lashremes *et al*., 2000; Silvarolla *et al*., 2004). Arabica coffee has its primary center of origin and genetic diversity in the high lands of Southwestern, Ethiopia (Sylvain, 1955). Over the past 50 years, both production and consumption of coffee have risen considerably. Approximately 60 percent of the world's coffee production comes from Arabica, while the remaining 40 percent is contributed by Robusta; the former considered a superior quality and fetches a higher price (Moat *et al.,* 2017). Globally, the total coffee production is estimated to be 169**.** 06 million of 60-kg bags, of which Arabica coffee production is about 103.60 million of 60-kg bags, while Robusta coffee production was estimated to be 65.46 million 60-kg bags (ICO, 2019). Economically, coffee is the second most exported commodity after oil, and employs over 100 million people worldwide (Gray *et al*., 2013). Coffee is not only one of the highly preferred international beverages, but also one of the important agricultural commodities in the world.

Ethiopia is the largest producer of arabica coffee in Africa contributing about 4.1% of total world coffee production (USAD, 2018). According to, ICO (2017) Ethiopia is Africa's largest coffee producer and the world's fifth largest exporter of Arabica coffee. The total cultivated coffee area in Ethiopia is estimated around 725, 961.24 ha. The annual estimate of national production of coffee is about 7.49 million of 60-kg bags and national average yield is low (619 kg/ha) (CSA, 2018). Twenty-five percent of the population in one-way or on other derives their livelihood from its production or trading and it represents the major agricultural export crop, providing 25% of the foreign exchange earnings (USDA, 2019).

World arabica coffee production is largely based on using a very small number of cultivars: *C. arabica* var. typica Cramer, *C. arabica* var. bourbon (Krug and Carvalho, 1951). The low

genetic diversity observed within those cultivars makes this crop, particularly vulnerable to biotic and climatic hazards. However, Ethiopia holds a unique position in the world as *Coffeaarabica* the primary center of origin and primary center of diversity. The reason for diversity in most of coffee is growing in areas of humid (moist) evergreen forest area **(**Moat *et al.,* 2017). However, the major coffee growing area are found in Oromia Region, of South West Ethiopia (Wollega, Illubabor, Jimma-Limu, Tepi, Kaffa and Bench-Maji) (Lelisa, 2018; Moat *et al., 2017*). Southern Nations Nationalities Peoples Region is the second coffee producing region in Ethiopia. Whereas modest coffee production in Amhara region and minor output in Benishangul-Gumuz region (Moat *et al.,* 2017; Gole, 2013). In Ethiopia, Coffee grows at various altitudes, ranging from 1500 to 1800 meters above sea level (Paulos, 1994). However, Arabica best thrives and produced between altitudes of 1300 and 1800 meters above sea level with the annual rainfall amount ranging from 1500 to 2500 mm. In some cases, it also grows in the area as low as up to 550 meters above sea level (like Gambela) where the annual rainfall ranges from 1000 to 2000 mm (Bayetta, 2001).Coffee growing at a minimum temperature ranging from12–14˚C, the ideal average and maximum temperatures is 18–22˚C and 25–27˚C, respectively (Moat *et al.,* 2017). The ideal soil for cultivation is nearly at 7.0 P^H (Paulos, 1994).

Different research findings illustrate the importance of the Ethiopian coffee genetic materials in breeding programs for high productivity and disease resistance (Adugna, 2005; Labouisse *et al*., 2008). Bellachew (1997), explained the existence of wide genetic variability in natural Arabica coffee populations. Coffee variability assessment for yield and its component characters becomes essential before planning a breeding strategy for genetic improvement. From 1966-2016about 6923 coffee accessions have been collected from different coffee producing areas of the country and conserved at Jimma Agricultural Research Center (JARC) and its' Sub-centers (Desalegn, 2017). Although the demand and supply of coffee seeds are incompatible, up to date the JARC has released about 42 improved varieties (35 pure lines and seven were hybrids) for different localities. Previous coffee research program focuses on development of high yielding, disease resistance and wider adaptable coffee variety. However, it lacks stable yield and resistance across coffee growing regions. Because, different localities have different agro ecology and unique inherent quality coffee types, consequently, the national coffee research program (Jima Agricultural Research Center) initiated local

Landrace Arabica Coffee Variety Development Strategy. To establish develop coffee improvement programs for each coffee growing region that possesses specific coffee quality and fetch premium price in the world market (Mesfin *et al.,* 2009).The strategy is useful for location specific coffee technology generation and promotion under diverse coffee growing agro-ecologies which is the main breeding strategy of the center.

Jimma Agricultural Research Center having the mandate to coordinate coffee research in Ethi opia has collected about 133 coffee germplasm from Bale and West Arsi Zones of Oromia Regional State. However, these materials have not been characterized and their genetic potential for disease resistance and yielding potential is not well known. Hence, it is relevant to characterize and conserve these coffee accessions to reduce the loss of coffee genetic resources and use in a breeding program to improve the productivity of the crop by developing high yielding and disease resistant coffee varieties for Bale and Arsi areas. Therefore, characterization of these Bale and west Arsi coffee collections is crucial with the following general and specific objective.

General objective

- To characterize the existing Bale and Arsi collections and document for use in breeding program intended to develop improved varieties for the areas

Specific objective

- To characterize and estimate the genetic variability in coffee germplasm accessions collected from Bale and West Arsi coffee growing areas using morphological traits

2. LITERATURE REVIEW

2.1. Taxonomy, Morphology and Reproductive Biology of *Coffea arabica*

Coffee is a tropical woody plant of the Rubiaceae family which is classified into two genera (Leory, 1980; Berthaud and Charrier 1988; Bridson and Verdcourt 1988). These are the genus *Coffea* and *Psilanthus*. The genus *Coffea* subdivided in to two subgenera: *Coffea* (*Eucoffea*) and *Mascarocoffea* (Charrier and Berthaud 1985). The genus *Coffea* is economically the most important (Wellman, 1961), and comprises more than 124 species (Davis *et al*., 2011). The genus *Coffea* is differing greatly in phenotypic features like size, adaptation habits etc. and thus its taxonomic history was very debating (Lashremes *et al.*, 1997). The basic chromosome number for the genus *Coffea* is n = 11. Arabica coffee is the only polyploidy and self-fertile (over 95 %) species of the genus *Coffea,* with chromosome number 2n = 4x = 44, while others are diploid (2n = 2x = 22) and self-infertile (Lashermes *et al*., 1999; Coulibaly *et al*., 2002; Silvarolla *et al*., 2004).

Coffea arabica is a shrub or small tree, and it may reach a size of 4 to 5 meters. The plant has a dimorphic habit of branching in which vertical (orthotropic) branches form horizontal (plagiotropic) branches, which bear the flowers and the fruits in clusters. Flowers of *C. arabica* with short corolla, long style and exerted stamen are typical of the genus *Coffea*. Such floral morphology would permit natural cross-pollination, but nevertheless, C. arabica is largely autogamous, and fruit set after self-pollination is 60% or higher (Carvalho *et al*., 1969). Most studies on the degree of natural cross-pollination carried out on cultivars of C. arabica, which underwent many cycles of selection. Using the recessive marker genes Cera (Yellow endosperm) and Purpurascens (purple leaves) Vander Vossen (1974) in Kenya found that 7 to 15 percent of natural cross-pollination in *C. arabica*. Most diploid species have proved to be highly self-incompatible, and are allogamous (out crossing). Inflorescences develop from serial buds mainly on horizontal branches. Each inflorescence normally carries one to five flowers. The flowers have a short pedicel and a rudimentary calyx. The petals are fused and form corolla with five lobes.

The pistil of the coffee flower consists of an inferior ovary and a long style with two stigmatic lobes. The ovary is bilocular each with one anatropous ovule and flower initiation occurs after

sufficient rainfall following a dry period (Van der Vossen, 1974). The total period of flowering is normally not more than three days with the majority of flowers opening on the first and the second day. Pollen shedding starts very soon after opening of the flowers early in the morning and the stigma is then receptive. Flowers wither in one or two days after pollination. It takes six to eight months from flowering to fruit ripening. The coffee fruit usually contains two seeds. Ripe fruits have a thick fleshy mesocarp (pulp) and a hard endocarp (parchment). In addition, each seed is enveloped in a silver skin (testa), which is a remnant of the integument (perisperm). The tough endocarp is to protect the seed from digesting enzyme activities in the gut of frugivores such as birds and mammals. The fleshy, sugar containing mesocarp and the vivid coloration due to anthocyanins of the exocarp act as a reward and attract the dispersing animals, respectively (Urbaneja *et al.*, 1996).

2.2. History, Origin and Distribution of *Coffea arabica*

All *Coffea* species are native to the tropical forests of Africa, Madagascar and islands of the Indian Ocean, while species of *Psilanthus* occur in Asia and tropical Africa (Bridson and Verdcourt 1988). It is confined to the plateau of southwestern Ethiopia and on the Boma plateau of Sudan (Wellman, 1961). The equatorial lowland forests of West and Central Africa that stretches from Guinea to Uganda are the home of diverse forms of *C.canephora*, while the natural populations of C. *arabica* are restricted to the montane rain forests of South Western Ethiopia (Berthaud and charier, 1988).

Arabica coffee was introduced to Yemen by Arab traders from Ethiopia across the Red Sea around the 6^{th} century in the form of beans (Gole *et al.*, 2002). The Arabic origin of coffee was obtained from the fact that the knowledge of beverage and tree was described from the materials from southern Arabia (Yemen) to which Linnaeus gave a scientific name and Yemen was the only source of coffee germplasm over most of the recorded history of *C. arabica* (Sylvia; 1958).Coffee was first thought to be originated from Yemen on the Arabian Peninsula when Europeans saw it grown there at much later date.

However, on the basis of botanical evidence, *C. arabica* confirmed to have originated on the plateaus of Southwestern Ethiopia from where it spreads to Yemen and then around the world. *Coffea arabica* is endemic to the afromontane rain forest of Ethiopia where wild coffee

populations still grow in southwest highlands. Distribution of wild coffee Arabica also extended to the opposite sides of the Great Rift Valley, which is south west of the Rift Valley (Wollega, Illubabor, Jimma-Limu, Tepi Kaffa and Bench-Maji) and east and south east of the Rift Valley (Sidama including Yirgacheffe), Bale, Arsi, Central Eastern Highlands and Hararge) (Anthony *et al*., 2001; Moat *et al.,* 2017). According, to Streinge (1956), Anthony *et al*. (2002), Sylvian (1958) and Dench *et al*., (2006), this was confirmed by the fact that within small area, the wild coffee plants of Ethiopia have relatively high genetic variability as compared to the cultivated coffee populations from Yemen that showed a characteristically low genetic diversity. Gole (2003) reported that the presence of high genetic diversity of coffee in Ethiopia attributed to the presence of indigenous traditional production system of coffee in the country.

Then, coffee plant was taken from Yemen to Java and from there to the Botanical Garden of Amsterdam (Netherlands) in 1706, whose vigorous progenies (seedling from one mother tree) were sent to Paris in 1718 from which *C. arabica* var. typica was obtained and distributed to Asia, then to Europe and South America, parts of Africa, etc. In short, this plant traveled from the Arabian port of Mocha to Java across Holland to its final destination in Paris. The other *C. arabica L.* sources were introduced into Burboun Islands (now Reunion) by the French at about 1715 and 1718 where it was planted and produced small seed beans yielding a different variety of Arabica coffee of the world such as Burboun, which reached the New World nearly a century later and are the progenitor of Brazils and Mexico's coffee. In 1893, the coffee from Brazil was introduced into Kenya and Tanzania, not far from its place of origin of Ethiopia, ending its transcontinental journey. The spreads of coffee around the world was based on the limited number of trees. Originating from the limited number of plants along with its self-pollinating nature left the world coffee with narrow genetic diversity (Steiger *et al*., 2002; Gole *et al*., 2002).

2.3. Genetic Diversity of Coffee

Genetic diversity is a heritable variation present within and among biological entities such as plants, animals and microorganisms (Lowe *et al*., 2004). Ethiopia is the main store house of genetic diversity for Arabica coffee (Moat *et al.,* 2017). According to Lowe *et al*., (2005),

genetic diversity is a commonly used expression to refer to heritable variation present within and among biological entities such as plants, animals and microorganisms. The phenotypic variations as well as cultivation under diverse environmental conditions indicate the presence of Arabica coffee genetic diversity in Ethiopia (Bayetta, 2001; Yigzaw, 2005).These genetic variations enumerated at three levels: species, populations and individual levels. Since, Ethiopia is the only centers of origin and diversifications of *Coffea arabica*, there are a high genetic diversity, which mainly attributed to its diverse ecological features such as suitable altitude, ample rainfall, optimum temperature, fertile soils etc. and the presence of indigenous methods of coffee production system in the country (Gole *et al*., 2001; Yeshitila *et al.*, 2004).

The differential response of coffee genotypes for different biotic and abiotic factor by itself is an indication for the genetic diversity present in the country. Tesfaye *et al*., (2008) reported that coffee accession showed variability in level of sensitivity to water stress. Moreover, research findings (Taye, 2006; Beining, 2008) also reveal the presence of significant diversity in drought adaptation and avoidance mechanisms among the wild coffee populations in Ethiopia. They also vary in frequency of occurrence along rainfall gradients and soil profile depths (Taye *et al*., 2004), indicating the existing variability among the cultivated coffee landraces and their adaptation strategies under specific environments.

The existence of coffee genetic diversity based on morphological characters confirmed by many investigators at different time. Montagnon and Bouharmont (1996) reported diversity among Ethiopian coffee genotypes for different agro-morphological characteristics. Mesfin (2008) also reported the presence of wide genetic diversity among 141 coffee germplasm accessions collected from South and Southeast Ethiopia. Similarly, Olika *et al*., (2011) reported high genetic diversity among 49 Limu coffee accessions for morphological and organoleptic characteristics. In addition, the presence of high-level 0f hetrosis among elite indigenous coffee cultivars (Mesfin and Bayetta, 1989; Bayetta, 20018) and the development of thirty-five CBD resistant pure lines and seven high yielding coffee hybrid varieties are in one way or another confirming the genetic diversity of coffee in the country. The gene pools of wild *Coffeaarabica* populations are severely endangered because of unsustainable utilization coupled with rapid population growth, which is the root cause of deforestation due to demand for agricultural and settlement areas that have aggravated the erosions of genetic

diversity (Denich *et al*., 2006). The current situation of deforestation and land use change in Southwest and South East part of Ethiopia affects the *Coffea* genetic resources (Gole, 2003).

2.4. Coffee in the Ethiopian Economy

Coffee plays an important role in the world economy. It is the second most valuable exported commodity on earth after oil (Pendergrast 1999). Coffee provides one of the most widely drunk beverages in the world, and is a very important source of foreign exchange earnings for many countries. More than 50 developing countries are earning 25 % of their foreign exchange from coffee (ITC, 2002). Coffee production is important to the world economy and about more than 125 million people in the world, derive their income directly or indirectly from its products in cultivation, processing, trading, transportation and marketing (Lashermes *et al.*, 2011; Gray *et al*., 2013).

Ethiopia contributes about 4.1 percent of world's Coffee production (USDA, 2018) and 40.7 percent of the total production of coffee in Sub-Saharan Africa (ICO, 2017). Accordingly, in Ethiopia, ninety five percent of coffee is produced by Smallholder farmers who own less than two hectares of land, while the remaining five percent grown on modern commercial farms (USDA, 2018). Ethiopia produces and exports one of the best highland coffees in the world. In addition, about 25% of Ethiopia's populations also depend on coffee for their livelihood (USDA, 2019). During the 2017/18 marketing year alone, Ethiopia registered a record of almost 917 million U.S. dollars from coffee exports (USDA, 2019).

2.5. Molecular and Morphological Characterization in coffee

Germplasm characterization is the recording of distinctly identifiable characteristics, which are heritable. Through the discovery of development of molecular marker, it can now be identified at the molecular level based on changes in the DNA and their effect on the phenotype. Molecular changes can be identified by the many techniques that have been used to label and amplify DNA and to highlight the DNA variation among individuals. Application of molecular marker techniques to diversity questions must take into account, whether or not the data derived from a technique provide the right type of information for answering the question being addressed (Karp *et al.,* 1997).The choice of appropriate molecular markers depends on the accessibility and cost effectiveness of the marker techniques. Molecular markers have

been replacing or complementing traditional morphological and agronomic characterization, since they are virtually unlimited, cover the whole genome, are not influenced by the environment, and less time consuming. Limitation of Marker techniques are expensive and not simple to score. There are various PCR based DNA markers existing to see the diversity within a population of coffee such as random amplified polymorphic DNA (RAPD), inverse sequence-tagged repeat (ISTR), inter-simple sequence repeats (ISSR) and simple sequence repeat (SSR) or microsatellites (Powell *et al.,* 1996).

However, in conventional plant breeding, genetic variation is usually identified by visual selection. Morphological characteristics were among the earliest genetic markers used for assessment of variation and are still of great importance and; these characters are inexpensive and simple to score. The sharing of physical features often accepted as an indication of relatedness. There are several sets of physical character assessment for different crops at different developmental stages such as seed, juvenile, adult vegetative, flower and fruit. However, these sets of characters lack adequate coverage of the genome, strongly influenced by environmental factors, and apparently controlled by several genes (Wang &Tanksley, 1989). Besides, assessment of morphological characters in perennial plants such as coffee, often require a lengthy and expensive evaluation during complete vegetative growth.

In Ethiopia, the geographic location of coffee within its homeland is good indication for the existence of genetic variation within a population. Study on the morphological characters on *C. arabica* in Ethiopia has confirmed the presence of high phenotypic diversity among germplasm collected and maintained in the ex situ gene bank of Ethiopia (Mesfin and Bayetta, 2004). More genetically diverse strains of C. *arabica* exist in Ethiopia than anywhere else in the world, which has lead botanists and scientists to agree that Ethiopia is the centre for origin, diversification and dissemination of the coffee plant (Fernie, 1966; Bayetta, 2001). Different cultivars have been distinguished on the basis of morphological (plant height, branching habit, leaf colour, leaf shape internode length, bean size, stem girth etc) traits. Wide range of variability with respect to these characters has been observed for different accessions. Such traits of variability have been enabled Ethiopian coffee breeders in screening of selected coffee berry diseases resistant varieties and heterotic hybrid cultivars through crossing (Mesfin and Bayetta, 1983).

2.6. Variance Components

Phenotypic and Genotypic Variability

Variability is defined as the presence of differences among individuals of a population due to differences in their genetic composition and environment in which they are raised (Falconer and Mackay, 1996). Accordingly, phenotypic variability is the observable variation present in a character in a population. It includes both genotypic and environmental variation and, as a result its magnitude differs under different environmental conditions. Genotypic variation, on the other hand is the component of variation which is due to the genotypic differences among individuals within a population, and is the main concern of plant breeders (Singh, 2001).

Naturally occurring genetic variability is useful in any plant breeding program. It is the amount of the total genotypic and phenotypic variability that exists in a crop germplasm dictates the initiation of crop improvement programs and develops better varieties. Of the total variability present in a population the genetic component is most important to the breeder as it could be transmitted to the progeny. In addition, right management of this type of variability can produce stable gain in the performance servable traits of variation present in a population; and it is a combined effect of genotypic value and environmental deviation (Wels h, 1990). Genotypic variations, on the other hand, is the component of variation, which is due to the genetic differences among individuals within a population and is the main concern of pl ant breeding (Singh, 2003). Genotypic variance was separated from total phenotypic variance depend on additive and non-additive components. Additive genes are considered to control traits with high heritability and genetic advance the phenotypic selection thus would be effective.

Mesfin and Bayetta (2008) reported that the estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (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.

Olika *et al*., (2011) 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. Fekadu (2017) reported that highest GCV value were recorded by characters leaf area, number of secondary branches, primary branch, berry yield and CBD percent incidence as compare to other traits. Gizachew (2015) reported that much higher PCV value than GCV value for CBD and CLR indicating the higher influence of environment on these traits.

2.7. Heritability and Genetic Advance

Heritability is the measure of the correspondence between breeding values and phenotypic values Falconer and Mackay (1996). High heritability estimates indicate a character is controlled by those genes which are less influenced by the environment and vice versa and it also give a useful indication of the relative values of selection based on the phenotypic expression. Information on the nature and magnitude of variability and heritability in a population is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969). Since, it is Great importance for breeders to know the heritability of the agronomical characters to improve the yield effectively. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is the breeding value, which determines how much of the phenotype would be inherited in-to the next generation (Tazeen *et al.,* 2009). However, heritability per se is not enough in predicting the effectiveness and outcome of selection unless it is considered together with genetic advance (Allard, 1999).

Fekadu *et al*., (2017) report that heritability estimates of the seven growth characters were moderate to high (0.33 to 75), while the other six including berry yield, exhibited lower heritability (below 0.24).The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960), whereas, heritability in narrow sense expresses the extent to which phenotypes are determined the genes transmitted from parents.

Desalegn (2018) reported the high estimates of heritability (>50%) for stem diameter (83.3%), coffee berry disease reaction (80.2%), fruit length (78.7%), coffee leaf rust reaction (75.5%),

coffee bean yield (74.7%), bean width (69.2%), number of primary branches (66.1%), number of main stem nodes (65.7%), height up to first primary branch (65.2%), hundred bean weight (64.5%), fruit width (58.8%), length of longest primary branch (56.5%), plant height (55.8%) and canopy diameter (51.3%). Gizachew, (2015) had reported high heritability for hundred green bean weight, number of secondary branches and canopy diameter.). Getachew (2012) reported that moderately low heritability for fruit length, coffee berry disease severity, plant height, average inter node of main stem, leaf length, number of primary branches, average length of primary branches and clean coffee yield per tree. Ermias (2005) has observed low heritability for percent of bearing primary branches.

Highest (≥20%) genetic advance as percent of mean was observed for coffee berry disease severity (69.67%) followed by coffee leaf rust severity (52.42%) and number of secondary branches (33.01) (Masreshaw, 2018). High genetic advance with high heritability estimates offer the most effective condition for selection (Larik *et al.*, 2000). The utility of heritability therefore increases, and used to calculate genetic advance, which indicates the degree of gain in character obtained under a particular selection pressure. The knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009, Ullah *et al*., 2011).

Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). High heritability does not always indicate high genetic gain, heritability with genetic advance considered together predict the ultimate effect for selecting superior varieties (Ali *et al.*, 2002). However, higher estimates of heritability coupled with better genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics (Ajmal *et al.*, 2009). 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) (Masresha, 2018).The estimates of genetic advance as percent of mean (GAM) that could be expected from selecting the top 5% of the coffee genotypes were high for coffee berry disease, coffee leaf rust, average green bean yield, stem diameter, average inter node length of stem, number of primary branches, plant height and average length of primary branches (23.46%) (Gizachew *et al.,* 2017).

Similarly, Abdi (2005) reported that high GAM for green bean yield per plant, leaf area, number of secondary branches, leaf width, leaf length and 100 green bean weights. This author also reported moderate GAM for number of main stem nodes, number of secondary branches, hundred green bean weight, leaf length, angle of primary branches, percent of bearing primary branches, canopy diameter, leaf area and leaf width and low GAM for fruit length and bean width. In addition, Yigzaw (2005) observed relatively high values of genotypic coefficient of variation, broad sense heritability and genetic advance for various characters. Moderately high GAM were exhibited by Number of primary branch (11.9%), number of secondary branch (13.6%), hundred bean weight (10%) and leaf area (11.7%) (Abdulfeta, 2018). (Yigzaw, 2005) reported that importance of combined use of genetic coefficient of variation, heritability and genetic advance for effective improvement of a particular trait in a population.

2.8. Character Association

Hallauer and Miranda (1988) define correlation is the measure of linear association between two traits. Creative crop improvement scheme refers to the collection of superior alleles into single targeted genotype (Tripathi *et al.,* 2011). The nature and extent of genetic variation governing the inheritance of characters and association will facilitate effective genetic improvement. It is noticeable that information of morphological and physiological aspects of crop is also a key feature to plan a resourceful breeding program. Thus, the genetic reconstruction of plant architecture is required for developing high yielding crop varieties (Yadav *et al*., 2011).

It is imperative that breeders need to understand the magnitude of variation, correlation and inheritance of important agronomic traits. Yield in perennial crop is one of the most important and complex traits in plant breeding experiments. Continued improvement of yield remains the top priority in most of the breeding programs (Yan *et al.,* 2002). In coffee, the outcome of yield depends on various growth characters, and their combinations, such as stem girth, canopy width, number of primary branches and number of secondary branches (Dancer, 1964 and Srinivasan, 1982). Fekadu *et al*., (2016) reported the characters that combined high heritability value (0.55 to 0.75) and high genetic correlation (0.51 to 0.91) which includes

girth, canopy diameter and plant height followed by length of primary branches, internodes length of stem and internodes length of primary branches. In coffee, the outcome of yield depends on various growth characters, and their combinations, such as stem girth, canopy width, number of primary branches and number of secondary. In addition, a number of other agronomic characters; such as plant height, leaf area, number of nodes on primary branches, number of fruits , etc can directly or indirectly influence yield (Mesfin, 1982). Hence, it is crucial in the improvement of yield traits to have a clear understanding of the relationships between yield and other agronomic characters influencing productivity (Araus *et al.,* 2001).

Therefore, to estimate the magnitude of correlations among the yield and yield component parameters; Correlation coefficient quantifies the relationship between two variables. It simply measures mutual association without cause and effect relationship (Dewey and Lu, 1959). Correlation analysis is a handy technique, which provides information that selection for one-character results in progress for other positively correlated characters (Manggoel *et al.,* 2012). The importance of correlation studies in selection program is appreciable when highly heritable characters are associated with the important characters like yield. Correlation coefficients, although very useful in quantifying the size and direction of trait associations, can be ambiguous if the high correlation between two traits is a consequence of the indirect effect of other traits (Bizeti *et al*., 2004).

A positive value of correlation shows that the changes of two variables are in the same direction, specifically high value of one variable are associated with high values of other and vice versa. When correlation is negative the movements are in opposite directions, that is, high values of one variable are associated with low values of the other (Yadav *et al*., 2011). Depending on the sign of genetic correlations between two traits can either facilitate or impede selection progress. Correlation value (r = 1) implies perfect (100%) correlation, where both traits vary hand in hand, (r = -1) means there is 100 % correlation between two characters, but they vary in opposite direction, and (r = 0) carries the implication that there is no correlation at all between the two characters (Falconer and Mackay, 1996).

Correlation can be measured in different indices (coefficient) based on different statistical hypothesis and these are: Pearson correlation coefficient, Spearman rank correlation coefficie nt and Spearman semi quantitative correlation coefficient, Gamma correlation coefficient (Ro

sner ,1995). For example Karl Pearson (1857-1936) coined the Pearson product-moment correlation coefficient (r_{prs}= Pearson correlation coefficient) and a major contributor to the early development of statistics. Assumes both variable (variables x and y) are interval or ratio variables and are well approximated by a normal distribution, and their joint distribution is bivariate normal. Pearson correlation coefficient can take values from 1 to +1 and considering strong correlation if the correlation coefficient is greater than 0.8 and a weak correlation if the correlation coefficient is less than 0.5 (Spearman, 1987).

The presence significant difference between Arabica Coffee accessions for different character s had been reported by (Walyaro, 1983; Marandu *et al*., 2004; Mesfin and Bayetta 2005; Yigz aw, 2005; Olika *et al*., 2011; Getachew *et al*., 2013; Gizachew and Hussien, 2017). Coffee yield had positive genotypic and phenotypic correlations coefficients levels with all characters except the height up to first primary branch. Yigzaw, (2005) and Olika *et al*., (2011) reported positive and significant correlation of most of the quantitative characters with yield. Srinivasan (1980) reported high positive correlation of stem girth and length of primary branches with yield. Similarly, Walyaro and Van der Vossen (1979) also reported significant and positive genotypic correlations between yield and girth at the base of the main stem. Walyaro (1983) and Marandu *et al*., (2004) also reported that coffee yield is influenced by most important characters like number of primary branches, canopy diameter, plant height and main stem diameter.

Similarly, Ermias (2005) also reported weak and non-significant correlation of internode length with average yield. In this finding, bean yield significantly and negatively correlated with only height up to first primary branch for both genotypic and phenotypic levels. In addition, canopy diameter, plant height and main stem diameter showed significant positive correlation with most of the characters (Olika *et al*., 2011 and Lemi *et al.*, 2017). In studies of genetic divergence and the processes of evaluation and selection, it is important to maintain traits that correlated with the majority of traits (Ferrao *et al*., 2008).

2.9. Path Coefficient Analysis

Path coefficient analysis measures the direct influence of variable up on another and permits the separation of the correlation coefficient into components of direct and indirect effect

(Dewy and Lu, 1959). Also show the cause and effect of different yield component would provide better index for selection rather than mere correlation coefficients. Path coefficient analysis partitions the genetic correlation between yield and its component traits into direct and indirect effects and hence has effectively used in identifying useful traits as selection criteria to improve yield (Akinwal *et al*., 2011; Sadeghi, 2011). Yield in coffee is commerciall y an important trait, which considered in most, if not all, breeding goals of coffee improveme nt. Therefore, it is desirable to know the direct and indirect effect of yield related traits in coffee. These traits could be useful indicators in breeding programs to select coffee genotype for yield.

Positive direct effect of length of first primary branch and canopy diameter on coffee yield, so that they are effective for the improvement of coffee yield (Lemi *et al.,* 2017). Ermias (2005) also observed positive direct effect of plant height whereas, negative direct effects of canopy diameter and length of primary branch on yield. Moreover, Srinivasan (1980) reported that greater weight should be given for longer primaries and shorter inter nodes in selection for yield, as they had direct positive effects. Gizachew (2015) also reported the highest positive direct effect of plant height (10.80) followed by leaf length (6.02), leaf width (5.99), hundred green bean weight (3.46), coffee berry disease (2.93), percentage of bearing primary branches (2.40), stem diameter (2.21) and average length of primary branches (1.92). Abdulfeta (2018) reported highest positive correlation (0.38) and highs direct effect (0.45) of number of secondary branches on green bean yield

2.10. Cluster Analysis and Divergence Analysis (D^2)

Cluster analysis is a numerical classification technique that defines groups of clusters of individuals. The first is non-hierarchical classification, which assigns each item to a class. The second type is hierarchical classification, which groups the individuals into clusters and arranges these into a hierarchy for studying relationships in the data (Crossa, 1990). Moreover , cluster analysis is multivariate method that groups observations into clusters. The observatio ns or objects within each cluster are similar, between clusters are dissimilar to each other (John & Sons, 2002). Highly similar objects are close to each other while dissimilar objects lie a distance from each other; thus, larger distances correspond to smaller similarity. The

cluster analysis can be performed using a measure of similarity levels and Euclidean distance (Everitt, 1993).

Hierarchical cluster methods produce a hierarchy of clusters from small clusters of very similar items to large clusters that include dissimilar items. Hierarchical methods usually produce a graphical output known as a dendrogram or tree that demonstrates this hierarchical clustering structure. Some hierarchical methods are divisive; those progressively divide the one large cluster comprising all of the data into two smaller clusters and repeat this process until all clusters have divided. Other hierarchical methods are agglomerative (round mss colle ction) and work in the opposite direction by first finding the clusters of the most similar items and progressively adding less similar items until all items have been included into a single lar ge cluster. Multivariate analysis of morphological quantitative characters and qualitative char acters (using cluster analysis) has been used previously to measure genetic relationships within crop species Examples include *Coffee arabica* (Mesfin and Bayetta, 2008).

Divergence analysis used to estimate the genetic distance/divergence of the coffee germplasm populations or use to classify the divergent genotypes into different groups. Moreover, measures the forces of differentiation at intra (Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate characters are measured) and inter-cluster levels and determines the relative contribution of each component trait to the total divergent (Sharma *et al.,* 1990). Multivariate analysis by means of Mahalanobis D^2 statistics is a useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence at intra and inter-cluster levels (Das and Gupta, 1984).

The phenotypic similarity of 12 coffee genotypes was assessed using cluster analysis of 19 quantitative characters (Gizachew *et al.,* 2017). Cluster analysis based on coffee quantitative traits grouped 49 coffee genotypes in to four clusters, first, second, third and fourth groups consisted 26 (53%), 7 (14.29%), 15 (30.61%) and 1 (2.04%) accession, respectively indicatin g that coffee accessions of the same cluster group were at least morphologically similar Olika *et al*., (2011). The clustering pattern of the accessions revealed the existence of diversity in the coffee accessions for the characters studied. Cluster analysis confirmed the presence some variation among genotypes. Abdi (2009) also reported phenotypic diversity among 49 Harerg

e coffee accessions for 16 quantitative characters which were grouped in 6 clusters. Similarly, Olika *et al.* (2011) has made cluster analysis based on 22 quantitative traits which grouped 49 Limmu coffee genotypes in to IV clusters.

Gizachew *et al.* (2017) clustered 124 coffee accessions into 10 distinct groups based on seven qualitative traits. Divergence analysis used to estimate the genetic distance of the coffee germplasm populations or use to classify the divergent genotypes into different groups. Moreover, measures the forces of differentiation at intra (genotypes grouped in to the same cluster presumably diverge little from one another as the aggregate characters are measured) and inter-cluster levels and determines the relative contribution of each component trait to the total divergent (Sharma *et al.,* 1990). Olika., *et al*., (2011) report that smallest inter cluster distance (5.24) was observed between clusters I and III while the highest and highly significant inter cluster distance (93.74) was between cluster III and cluster IV suggesting the coffee materials among clusters were divergent from each other.

2.11. Principal Component Analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Its aim is to transform the data from one set of coordinate axes to another, which preserves, as much as possible, the original configuration of the set of points and concentrates most of the data structure in the first principal component axis. Various limitations have noted for this technique (Zobel *et al*., 1988). Crossa (1990) pointed out that the linear regression method uses only one statistic, the regression coefficient, to describe the pattern of response of a genotype across environments, and most of the information wasted in accounting for deviation. Principal component analysis (PCA) is a generalization of linear regression that overcomes this difficulty by giving more than one statistic, the scores on the principal component axes, to describe the response of a genotype.

Yigzaw, (2005) report that analysis of 18 quantitative characters for six principal components accounted 91.5 % of the total variation. Muvunyi *et al*., (2017) grouped 21 coffee genotypes into three main principal components (PC), which accounted for 78.3 % of the total variation. First three principal axes having greater than one Eigen value accounted for over 86.98 % of

the total variation among the 14 quantitative traits describing the coffee hybrid progenies (Fekadu, 2017). Masreshaw (2018) reported that traits such as:- average inter-node length of primary branches, average length of primary branches, canopy diameter, fruit width, fruit thickness, bean width, bean thickness and hundred bean weight contributed more to the total variation. Desalegn (2018) also report hundred bean weight, bean length, bean width, bean thickness, fruit length and plant height had more contribution to the total variation

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted at Gera Agricultural Research Sub Center. The center is located 425 km southwest of Addis Ababa, capital city of Ethiopia. Gera is located at $7^0$46 N latitude and 36^0 26' E longitudes, at an altitude of 1974 meters above sea level. The mean annual rainfall of the area is 1880 mm with average maximum and minimum air temperatures of 24.5^{o}C and 10.4^{o}C respectively. The center has contained Acrisols and Nitoso soil with P^H of 5-6 and medium to high exchangeable cation (Paulos, 1994; Paulos and Tesfaye, 2000).

3.2. Experimental Materials

One hundred thirty three C. *arabica* accessions were collected from Bale and west Arsi Zone of three districts, in Oromia region (Table 1, Figure 1) to address these localities for coffee collection, and future coffee varieties development and genetic resource conservation program. The collected accessions together with four coffee berry disease resistant (CBD) and high yielding checks (74110, 74148, 74165, and 75227) were planted at Gera Agricultural Research Sub Center in July 2015.The aim was to test their reaction to coffee berry disease as well as their performance for yield and yield component. Gera Research Center is selected since it is hotspot area for coffee berry disease development. It is assumed that those materials which show resistant to CBD at Gera are also resistant in other coffee producing areas of the country. The present study was superimposing on these coffee collations grown under the *Sesbania sesban shade at Gera.*

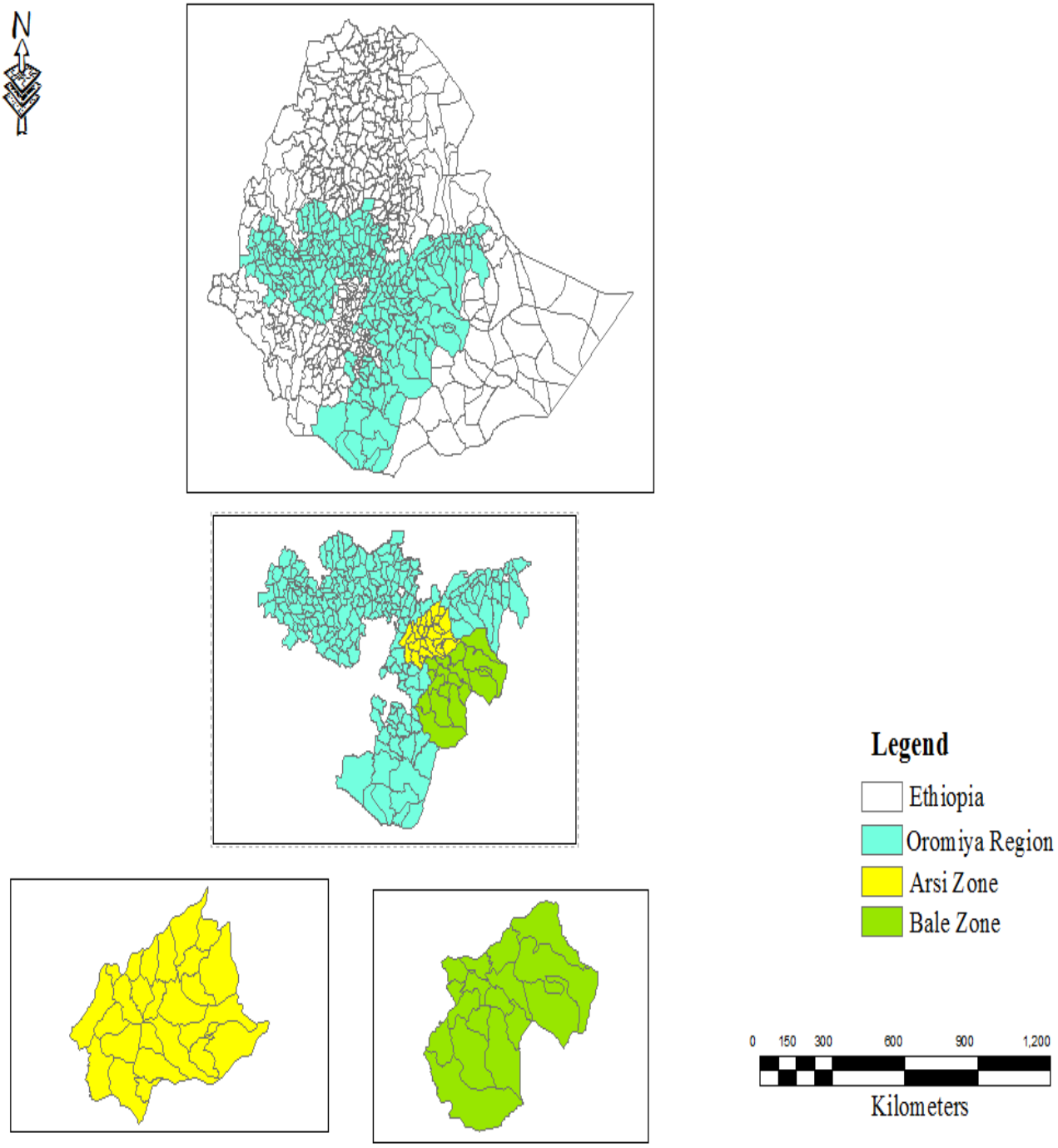

Figure 1 Geographical location of the origin of the collections and experimental site

Table.1 Geographical origin of coffee accessions used in this study

Acc. No.	Zone	Woreda	Peasant association	Specific location	Alt.m asl.	Acc. No.	Zone	Woreda	Peasant association	Specific location	Alt.m asl.
B204/07	Bale	Gololcha	Kura	Mekdala	1950	B300/07	W/Arsi	Nensebo	Workatown(0)	Gomata	1780
B77/07	Bale	Ginir	Tulicha	Kilkile	1240	B175/07	Bale	Gololcha	Dinsa	Gumero	1850
B68/07	Bale	Ginir	Harale	Manaya	1400	B262/07	W/Arsi	Nensebo	Kore	Tulu qala	1750
B69/07	Bale	Ginir	Harale	Medo	1380	B267/07	W/Arsi	Nensebo	Kore	Tulu qala	1780
B71/07	Bale	Ginir	Harale	Medo	1380	B309/07	W/Arsi	Nensebo	Rafisa	Uchuro	1870
B37/07	Bale	Ginir	E/buko	Harawa8	1880	B116/07	Bale	Ginir	Chancha	Guagura	1500
B144/07	Bale	Ginir	Odaroba	Dabale	1340	B273/07	W/Arsi	Nensebo	Kamap	Tulu qala	1780
B82/07	Bale	Ginir	Tulcha	Kilkile	1240	B13/07	Bale	Ginir	Suragafite	Abekera	1640
B89/07	Bale	Ginir	Chancho	Gara	1460	B29/07	Bale	Ginir	Harawa	Gorobube	1780
B93/07	Bale	Ginir	Chancho	Gara	1440	B91/07	Bale	Ginir	Chancho	Gara	1480
B181/07	Bale	Gololcha	Dinsa	Qaladi	1900	B311/07	W/Arsi	Nensebo	Rafisa	Uchuro	1870
B186/07	Bale	Gololcha	Dinsa	Borema	1950	B170/07	Bale	Gololcha	Dirregudo	Araremu	1660
B65/07	Bale	Ginir	Harale	Manaya	1400	B297/07	W/Arsi	Nensebo	Workatown(0)	Ketene-2	1780
B57/07	Bale	Ginir	Harale	Manaya	1380	B282/07	W/Arsi	Nensebo	Kore	Tuluqala	1740
B217/07	Bale	Gololcha	Qanjila	Yaya	1830	B293/07	W/Arsi	Nensebo	Workatown(01)	Ketene-2	1750
B224/07	Bale	Gololcha	Qanjila	Huro	1820	B110/07	Bale	Ginir	Ginir town	Ginir town	1860
B240/07	Bale	Gololcha	Kajawa	Kajawa	1930	B165/07	Bale	Gololcha	Diregudo	Dimina	1900
B231/07	Bale	Gololcha	Kajawa	Kajawa	1930	B287/07	W/Arsi	Nensebo	Workatown(01)	Ketene-2	1760
B251/07	Bale	Gololcha	Buriya	Kosi	1570	B67/07	Bale	Ginir	Harale	Manaya	1400
B265/07	W/Arsi	Nensebo	Kore	Tulu qala	1740	B302/07	W/Arsi	Nensebo	Workatown(01)	Ketene-2	1780
B268/07	W/Arsi	Nensebo	Kore	Tulu qala	1780	B172/07	Bale	Gololcha	Diregudo	Araremu	1960
B269/07	W/Arsi	Nensebo	Kore	Tulu qala	1780	B292/07	W/Arsi	Nensebo	Workatown(01)	Ketene-2	1750

Acc. No.	Zone	Woreda	Peasant association	Specific location	Alt. masl.	Acc. No.	Zone	Woreda	Peasant association	Specific location	Alt. (masl.
B274/07	W/Arsi	Nensebo	Kore	Tulu qala	1750	B39/07	Bale	Ginir	E/buko	Harawa8	1880
B275/07	W/Arsi	Nensebo	Kore	Kumburfa	1750	B317/07	W/Arsi	Nensebo	Solena	Burqitu	1800
B276/07	W/Arsi	Nensebo	Korema	Ketene-2	1750	B159/07	Bale	Ginir	Ardatan	Ardatan	1440
B281/07	W/Arsi	Nensebo	Korema	Ketene-2	1740	B318/07	W/Arsi	Nensebo	Tuluqala	Beledikicha	1880
B288/07	W/Arsi	Nensebo	Workatown(1)	Ketene-2	1760	B76/07	Bale	Ginir	Tulcha	Kilkile	1240
B270/07	W/Arsi	Nensebo	Korema	Ketene-2	1780	B112/07	Bale	Ginir	Ginir town	Ginir town	1860
B271/07	W/Arsi	Nensebo	Korema	Ketene-2	1780	B31/07	Bale	Ginir	Harawa	Gorobube	1800
B280/07	W/Arsi	Nensebo	Korema	Ketene-2	1750	B113/07	Bale	Ginir	Ginir town	Ginir town	1840
B308/07	W/Arsi	Nensebo	Rafisa	Uchuro	1920	B174/07	Bale	Gololcha	dinsa	Gemoro	1850
B73/07	Bale	Ginir	Harol	Lagawagaya	1370	B184/07	Bale	Gololcha	dinsa	Borema	1950
B306/07	W/Arsi	Nensebo	Workatown(1)	Ketema-2	1260	B223/07	Bale	Gololcha	Qanjila	Horo	1 820
B88/07	Bale	Ginir	Chancho	Gara	1460	B232/07	Bale	Gololcha	Kajawa	Kajawa	1930
B321/07	W/Arsi	Nensebo	Tuluqala	Beledikicha	1880	B108/07	Bale	Ginir	Ginir town	Ginir town	1860
B143/07	Bale	Ginir	Odaroba	Dabale	1340	B86/07	Bale	Ginir	Chancho	Gara	1460
B285/07	W/Arsi	Nensebo	Workatown(1)	Ketene-3	1780	B145/07	Bale	Ginir	Odaroba	Debale	1340
B95/07	Bale	Ginir	Chancho	Chancho	1490	B109/07	Bale	Ginir	Ginir town	Ginir town	1860
B126/07	Bale	Ginir	Chancha	Guagura	1480	B167/07	Bale	Gololcha	Diregudo	Dimina	1920
B261/07	W/Arsi	Nensebo	Kore	Tulu qala	1750	B313/07	W/Arsi	Nensebo	Refisa	Ochoro	1920
B187/07	Bale	Gololcha	Dinsa	Borema	1940	B55/07	Bale	Ginir	Harale	Manaya	1380
B81/07	Bale	Ginir	Tulcha	Kilkile	1240	B157/07	Bale	Ginir	Ardatan	Ardatan	1440
B290/07	W/Arsi	Nensebo	Workatown(1)	Ketene-2	1750	B107/07	Bale	Ginir	Chancha	Ginir town	1860
B266/07	W/ Arsi	Nensebo	Kore	Kamap	1780	B117/07	Bale	Ginir	Chancha	Guagura	1500
B244/07	Bale	Gololcha	Kajawa	Mechafera	1900	B218/07	Bale	Gololcha	Qanjila	Raya	1 830

Acc. No.	Zone	Woreda	Peasant asso.	Specif. loca.	Alt.	Acc. No.	Zone	Woreda	Peasant asso.	Specific loc.	Alt. .
B326/07	W/ Arsi	Nensebo	Tuluqala	Alando	1860	B327/07	W/Arsi	Nensebo	Tuluqala	Alando	1860
B277/07	W/ Arsi	Nensebo	Korema	Kamap	1780	B41/07	Bale	Ginir	Waltae	Dimile	1860
B310/07	W/ Arsi	Nensebo	Rafisa	Uchuro	1920	B124/07	Bale	Ginir	Chancha	Guagura	1480
B56/07	Bale	Ginir	Harale	Manaya	1380	B79/07	Bale	Ginir	Tulicha	Kilkil	1240
B278/07	W/ Arsi	Nensebo	Korema	Ketene-2	1250	B191/07	Bale	Gololcha	dinsa	Aredahoro	1940
B299/07	W/ Arsi	Nensebo	Gomata	Ketene-2	1780	B225/07	Bale	Gololcha	Qanjila	Horo	1 820
B279/07	W/ Arsi	Nensebo	Korema	Ketene-2	1750	B173/07	Bale	Gololcha	dinsa	Gemoro	1850
B238/07	Bale	Gololcha	Kajawa	Kajawa	1880	B28/07	Bale	Ginir	Harawa	Gorobube	1780
B289/07	W/Arsi	Nensebo	Workatown(1)	Ketene-2	1760	B20/07	Bale	Ginir	Suragafite	Najo	1760
B304/07	W/Arsi	Nensebo	Workatown(0)	Gomata	1780	B21/07	Bale	Ginir	Suragafite	Najo	1760
B235/07	Bale	Gololcha	Kajawa	Kajawa	1930	B192/07	Bale	Gololcha	dinsa	Aredahoro	1940
B286/07	W/Arsi	Nensebo	Korema	Ketene-3	1760	B202/07	Bale	Gololcha	Kura	Meqdela	1950
B272/07	W/ Arsi	Nensebo	Kore	Tulu qala	1780	B166/07	Bale	Gololcha	Diregudo	Dimina	1900
B258/07	Bale	Gololcha	Buriya	Kosi	1570	B11/07	Bale	Ginir	Suragafite	Abekera	1640
B307/07	W/ Arsi	Nensebo	Rafisa	Uchuro	1920	B155/07	Bale	Ginir	Ardatan	Ardatan	1440
B125/07	Bale	Ginir	Chancha	Guagura	1480	B160/07	Bale	Gololcha	Diregudo	Dimina	1900
B236/07	Bale	Gololcha	Kajawa	Kajawa	1920	B284/07	W/Arsi	Nensebo	Kore	Ketene-3	1780
B237/07	Bale	Gololcha	Kajawa	Kajawa	1910	B291/07	W/Arsi	Nensebo	Workatown(01)	Ketene-2	1750
B239/07	Bale	Gololcha	Kajawa	Kajawa	1880	B129/07	Bale	Ginir	Chancha	Gibiseter	1440
B264/07	W/ Arsi	Nensebo	Kore	Tulu qala	1740	B05/07	Bale	Ginir	Suragafite	Abekera	1640
B298/07	W/Arsi	Nensebo	Workatown(0)	Ketene-2	1780	74148	Elubabor	Metu			
B305/07	W/Arsi	Nensebo	Workatown(0)	Ketene-4	1800	74165	Elubabor				
B315/07	W/Arsi	Nensebo	Solena	Sefera jiru	1850	74110	Elubabor	Metu			
B303/07	W/Arsi	Nensebo	Workatown(1)	Ketene-2	1800	75227	Kefa	Wishwish			

3.3. Experimental Design, Trail Management and Season

The study was superimposed on four years old coffee trees in 2018/19 cropping season. The experiment was established in July 2015 in an augmented design with three replications using 133 accessions and four standard checks. Each plot consisted a single row of six trees. Spacing between rows and plants were 2m x 2m. Spacing between block was 4 meter (Gizach ew, 2015)**.** Mulching was done immediately after planting. The seedlings were protected from direct sunlight by constructing grass hut over individual seedling. The huts were removed when the dry months ends. Temporary *Sesbania* shade trees were planted using spacing between trees of 4m by 4 m. Other management practices such as: - slashing and pruning were also uniformly applied as per recommendation throughout cropping season.

3.4. Data Collected

Both quantitative and qualitative morphological data were collected from each coffee accessio n using coffee descriptors adopted from International Plant Genetic Research Institute (IPGRI , 1996). The accessions were evaluated for 25 quantitative and 12 qualitative traits as describe d below. Qualitative traits were collected, using the standard coffee descriptor of IGPRI (1996) as described below. Coffee berry disease severity and Coffee leaf rust disease severity in percentage were also recorded through visual assessment.

3.4.1. Quantitative traits

Leaf length (cm): average of five normal (node 3 from the terminal bud) leaves, were measured from petiole end to apex.

Leaf width (cm): average of five normal (node 3 from the terminal bud) leaves, were measured at the widest part.

Leaf area (cm^2) was calculated by multiplying leaf length and width by constant 0.67.

Fruit length (mm): average of five normal and mature green fruits of each tree were measured at the longest part using digital caliper.

Fruit width (mm): average of five normal and mature green fruits of each tree were measured at the widest part using digital caliper.

Fruit thickness (mm): average of five normal and mature green fruits of each tree were measured at the thickest part using digital caliper.

Bean length (mm): averages of five normal beans of each tree were measured at the longest part.

Bean width (mm): average of five normal beans of each tree was measured at the widest part.

Bean thickness (mm): average of five normal beans of each tree was measured at the thickest part.

Petiole length (cm): average of five normal leafs of each tree was measured from the base to the insertion with the blade using tap meter.

Coffee bean yield (kg/ha): weight of fresh cherries in gram per plot was recorded and mean of six trees was converted into yield of clean coffee kg/ha**.** Clean coffee bean (quintal/ha) = fresh cherries in gram per tree x 0.00417. Clean coffee bean (kg/ha) was calculated as (clean coffee bean (quintal/ha) x 100) (Desalegn, 2018).

Height up to first primary branch (cm): height from the ground up to first primary branch was measured using tape meter.

Total tree height (cm): the length from the ground level to the tip of the tree was measured using tape meter**.**

Number of main stem node (no): the number of nodes from bottom to the top of the tree was counted.

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 (IGPRI, 1996).

Main stem diameter (mm): was measured as a diameter of the main stem at five cm above the ground using caliper.

Number of primary branches (no): total number of primary branches was counted per tree

Number of secondary branch (no): number of secondary branch on primary branch was counted per tree.

Length of primary branch (cm): The average lengths of six selected primary branches (from bottom, middle and top of the tree) were measured using tape meter.

Number nodes on primary branches (no): number of nodes per six selected primary branches from bottom, middle and top of the tree was counted and recorded.

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.

Canopy diameter (cm): Average length of tree canopy was measured twice, east-west and north- south direction by using tape meter.

100 Bean weight (g): Oven was used to drying coffee bean to reduced to 0 % moisture content and the weight was measured using sensitive balance (calculated as bean weight at 0 % moisture content x 100/ (bean No x 0.89) (IPGRI, 1996).

Coffee berry disease (CBD): severity percentage was visually estimated as the percentage of diseased berries (damaged coffee berries over all barriers of bearing branch) by observing areas of infected parts of coffee berry from whole coffee branch of six trees per plot.

Coffee leaf rust (CLR): Severity was directly estimated as the percentage of leaves per tree (damaged leaves over all the top, middle and bottom part of the tree) by observing areas of infected parts of coffee leaf from whole coffee branch of three trees per plot.

3.4.2. Qualitative traits

Data for 12 qualitative characters was collected according to the International Plant Genetic. Resources Institute (IPGRI, 1996) coffee descriptor on a plot basis.

Growth habit: 1 (Open), 2 (Intermediate), 3 (Compact).

Stem habit: 1 (stiff), 2 (flexible).

Branching habit: 1(Very few branches (primary), 2 (many branches (primary) with few secondary branches), 3 (many branches (primary) with many secondary branches), 4 (many branches (primary) with many secondary and tertiary branches)

Angle of insertion on main stem: 1 (Drooping), 2 (Horizontal spreading, 3 (Semi- erect).

Young leaf tip color: 1 (Greenish), 2 (Green), 3 (Brownish), 4 (Reddish brown), 5 (Bronzy).

Leaf shape: 1 (obovate), 2 (Ovate), 3 (Elliptic), 4 (lanceolate), 5 other

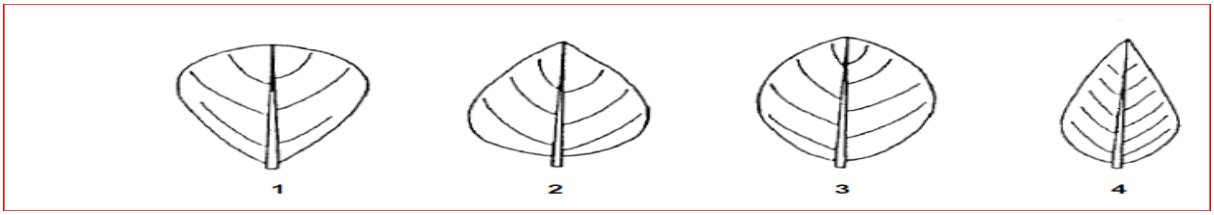

Figure 2 Picture description of leaf shape (Source: IPGRI, 1996)

Leaf apex shape: 1(Round), 2(Obtuse), 3(Acute), 4(Acuminate), 5(Apiculate), 6(Spatulate)

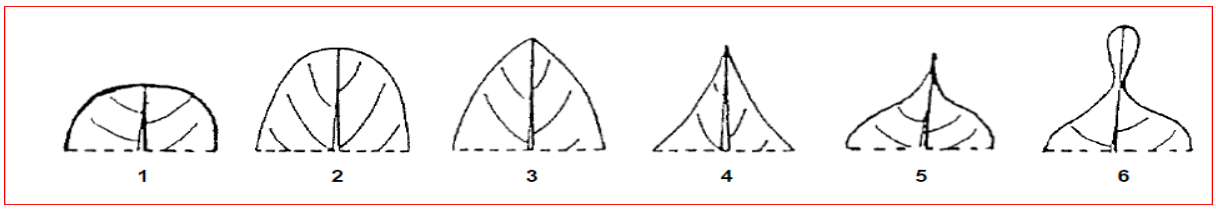

Figure 3 Picture description of Leaf apex shape (Source: IPGRI, 1996)

Stipule shape: 1 (Round), 2 (Ovate), 3(Triangular), 4 (Deltate), 5 (Trapezium)

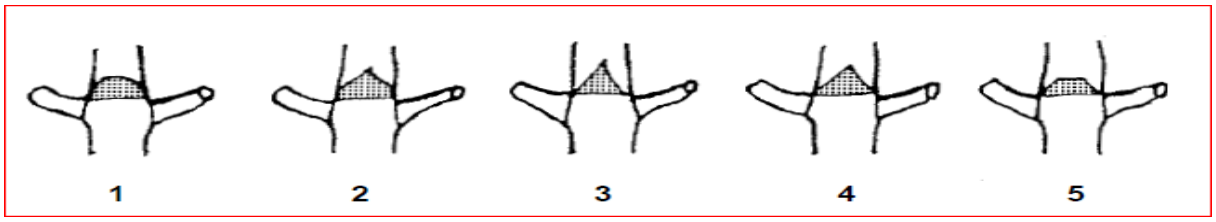

Figure 4 Picture description of Stipule shape (Source: IPGRI, 1996)

Fruit shape: 1(Round), 2 (Obovate), 3 (Ovate), 4 (Elliptic), 5 (Obolong)

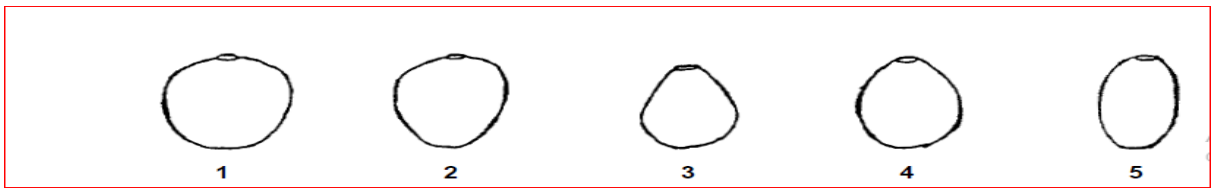

Figure 5 Picture description of Stipule shape (Source: IPGRI, 1996)

Fruit color: data was collected by Observed on mature fruits 1 Yellow 2 Yellow-orange 3 (Orange) 4 (Orange-red) 5 (Red) 6 (red purple) 7 (Purple) 8 (Purple-violet) 9 (Violet) 10 (Black) 11 (Other): characterized based on the Color Chart of the Royal Horticultural Society of London (RHS 1966 5th ed.).

Calyx limb persistence: 1(not persistent), 2 (persistent)

Fruit ribs: absence or presence of fruit ribs was recorded from three trees per plot

3.5. Statistical Analysis

3.5.1. Analysis of variance (ANOVA)

Data were subjected to analysis of variance (ANOVA) using SAS version 9.2 (SAS, 2010) based on augmented design (Table 4). The normality of collected data for each trait was tested

using SAS software 9.2. All traits are computed for Shapiro Wilk and Kolmogorov-Smirnov, no significant difference (Appendix Tabe.2) showed that the normal assumption for all collected traits. Least Significant Difference (LSD at P <0.05) was employed to identify accessions that are significantly different from each other. The analysis was done according to the following model (Federer, 1956).

$$\mathbf{Yij = \mu + gi + cj + \beta j + \varepsilon ij}$$

Where: yij is the observation of treatment i in j^{th} block μ is the general mean, g is the effect of test treatment, cj is the effect of control treatments in j^{th} block, βj is the block effects, (ε) is the error.

Table 1. Analysis of variance for augmented design

Source of variation	Df	SS	MS	F-value
Block (adj)	(b-1)	SSB	MSB	MSB/MSE
Trt (adj) dxs	(c+g)-1	SSt	MSTrt	MSt/MSE
Among- checks	(c-1)	SSC	MSc	MSC/MSE
Among-test	(g-1)	SSG	MSG	MSG/MSE
Test vs checks	1	SS TvsC	SSE/(c-1)(b-1)	
Error	(b-1)(c-1)			

Where: b = number of block, C =check varieties, g = genotype, Df=degree of freedom, SS=sum square, MS=mean square, SSB and MSB are sum square and mean square of blocks respectively; SSG and MS_G are sums of squares and mean of genotypes, respectively, SSC and MSC are sum square and mean square of check variety, respectively; SSt and MSt are sum square and mean square of treatment, respectively.

3.5.2. Estimation of genotypic and phenotypic coefficient of variability

The variability among accession for each quantitative trait was estimated by simple measures such as mean, range, standard deviation, phenotypic and genotypic variances, and coefficients of variation. The phenotypic and genotypic coefficients of variation were computed using the formula suggested by Burton and de Vane (1953) as follows.

Phenotypic variance ($\boldsymbol{\sigma^2 P}$) $= \boldsymbol{\sigma^2 g + \sigma^2 e}$

Genotypic variance $\left(\boldsymbol{\sigma^2 g}\right) = \frac{\mathbf{(MSt - Mse)}}{\mathbf{r}}$

$\sigma^2 e$ = Environmental variance

Where, σ^2p = Phenotypic variance, σ^2g = Genotypic variance, MSt = mean square of treatmen t, Mse = mean square of error, r = number of replicated/blocks

Phenotypic Coefficient of Variation$(\mathbf{PCV}) = \frac{\sqrt{\boldsymbol{\sigma^2 P}}}{(\bar{\mathbf{x}})}\mathbf{x\ 100)}$

Genotypic Coefficient of Variation $(\mathbf{GCV}) = \frac{\sqrt{\boldsymbol{\sigma^2 g}}}{(\bar{\mathbf{x}})}\mathbf{x\ 100)}$

Where$\bar{x}$ = Grand Mean of the Population

3.5.3. Estimation of heritability (in broad sense)

Heritability (H): Broad sense heritability for all characters was estimated as the ratio of genot ypic variance to the phenotypic variance and expressed in percentage according to the method s suggested by Falconer (1989)

Heritability in broad sense $(\mathbf{h^2 b}) = \frac{(\boldsymbol{\sigma^2 g})}{(\boldsymbol{\sigma^2 P})}\ \mathbf{x\ 100}$

Expected Genetic Advance (GA)

The expected genetic advance expressed under selection in broad sense, assuming selection intensity of 5% of the superior progeny was estimated in accordance with the methodology described by Johnson *et al*., (1955) as:

Expected Genetic Advance $(\mathbf{GA}) = \mathbf{K} * \boldsymbol{\sigma ph} * \mathbf{h^2 b}$

Where, GA = the expected genetic advance under selection;

σph = the phenotypic standard deviation; square root of phenotypic variance.

h^2b = heritability in broad sense and k is selection Intensity (K = 2.063)

The genetic advance as percent of population mean was estimated following the Procedure of Johnson *et al*., (1955).

Genetic advance as percent of population mean $(\mathbf{GAM}) = \frac{\mathbf{GA}}{(\bar{\mathbf{x}})} * \mathbf{\ 100}$

Where, GAM= Genetic advance as percent of population mean, GA=Genetic advance under selection and $\bar{x}$=Grand Mean of the population. Genetic advance as percent mean will be low, moderate and high as given by Falconer and Mackay (1996) where 0-10%: Low, 10-20%: Moderate and 20% and above are high.

3.5.4. Correlation analysis

The correlation coefficients were worked out to determine the degree of association of a chara cter with yield and also among the yield components. Phenotypic and genotypic correlation co efficients were computed using SAS software 9.2 from the components of variance and covariance based on the method described by Singh and Chaudhary (1997). As cited by Gizac hew (2015) phenotypic correlation (r_p), the observable correlation between two variables, whi ch includes both genotypes and environmental components between two variables, was estima ted using the following formula:

$$\boldsymbol{rp} = \frac{\boldsymbol{a^2 p_{xy}}}{\sqrt{\boldsymbol{\sigma^2 p_{\sigma^2 p_y}}}}$$

Where, rp=phenotypic correlation coefficient, σ^2pxy=Phenotypic
Covariance between character x and y, σ^2px=Phenotypic variance for
Character x and σ^2py=Phenotypic variance for character y

$$\boldsymbol{rg} = \frac{\boldsymbol{a^2 g_{xy}}}{\sqrt{\boldsymbol{\sigma^2 g_{x_{\sigma^2 g_y}}}}}$$

Where, rg=Genotypic correlation coefficient, σ^2gxy=Genotypic
Covariance between character x and y, σ^2gx=Genotypic variance for
Character x and σ^2gy=Genotypic variance for character y.

The coefficient of correlation at phenotypic level was tested for its significance with Table for simple correlation coefficient using n-2 df as suggested by Gomez and Gomez (1984) orusing " table, with observed t expressed as

$$\boldsymbol{t} = \frac{\mathbf{r_{pxy}}\sqrt{\mathbf{n-2}}}{\mathbf{1-r^2 pxy}}$$

The coefficient of correlation at genotypic level was tested using the formula:

$t = r_{gxy}/SE_{rgxy}$

Where r_{gxy}= genotypic correlation coefficient, SErgxy=standard error

$$\mathbf{SE_{rgxy}}\sqrt{\sqrt{\frac{\mathbf{1-r^2gxy}}{\mathbf{2h1^2h^2}}}}$$

Where h_1^2 and h_2^2 are broad sense heritability for the character 1 and 2

3.5.5. Path coefficient analysis

Path coefficient analysis was carried out at genotypic level to evaluate a number of direct and indirect effects of independent variables on dependent variable which is not obtained by correl ation study. A measure of direct and indirect effects of each character on bean yield was estim ated using a standardized partial regression coefficient known as path coefficient analysis, as suggested by Dewey and Lu (1959).

$$\mathbf{rij = Pij + \Sigma rikpkj}$$

Where: - rij = Mutual association between the independent character (i) and dependent Character (j) as measured by the correlation coefficient.

Pij = Component of direct effects of the independent character (i) on dependent character (j) as measured by the path coefficient and,

$\sum$ rikpkj = Summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k).

Residual effect (U) was estimated by the formula:

$U = \sqrt{1 - R^2}$ Where: - =Where: $\mathbf{- R^2 = \Sigma pijrij}$

pij = Component of direct effects of the independent character (i) and dependent character (j) as measured by the path coefficient. rij = Mutual association between the independent charact er (i) and dependent character (j) as Measured by the correlation coefficient.

3.5.6. Cluster analysis

Cluster analysis is a process of identification and categorization of subsets of objects and a multivariate technique whose primary purpose is to group individuals or objects based on the characteristics they possess. However, in this study sets of quantitative morphological data were subjected to cluster analysis to determine the variability among the accessions. For clust er analysis and the data matrix consisting of variables that are not in the same unit, the values

for each quantitative trait was standardized to variance of unity and mean zero before computi ng distances. Hierarchical clustering was employed using the similarity coefficients among the 137 **c**offee accessions. Clustering was performed using the proc cluster procedure of SAS version 9.2 (SAS institute, 2010). The dendrogram constructed based on the average linkage and Euclidean distance was used as a measure of dissimilarity. The number of cluster was determined by following the approach suggested by Copper and Miligan (1988) by looking in to statistics namely Pseudo F and Pseudo t^2.

3.5.7. Genetic divergence

Genetic divergence measure a group distances based on multiple traits of genotypes into different groups. Twelve quantitative traits were analyzed using the procedure Proc discrim of SAS version 9.2 software (SAS, 2010). The generalized distance between any two set of genotypes was defined as: Genetic divergence between and within clusters were calculated using the generalized Mahalanobis's D^2 statistics (Mahalanobis, 1936) using the equation:

$$\mathbf{D^2p} = (\mathbf{Xi} - \mathbf{Xj})\ \mathbf{S^{-1}}\ (\mathbf{Xi} - \mathbf{Xj})$$

Where, D^2 P= the distance between any two groups i and j, Xi and X_j = the p mean vectors of accessions $_i$ and $_j$, respectively. S^{-1} = the inverse of the pooled covariance matrix. The D^2 values obtained for pairs of clusters were tested for significance at 0.05 level of significance against the tabulated values of $x^{2,}$ for 'P' degrees of freedom, where p is the number of variables considered (Singh and Chaudhary, 1987).

3.5.8. Principal component analysis (PCA)

The principal component analysis was use to minimize the character into a new set of linearly combined measurements and to identify those traits contributing large part of the total variation among the accessions. Principal component with Eigen values greater than one were considered to explain observable variability. The analysis was done using Statistical Analysis System Version 9.2 (SAS, 2010).

3.5.9. Shannon weaver diversity indices (H')

Shannon waver diversity index are used to compare phenotypic diversity among qualitati ve characters. A higher H` value indicates presence of diversity for the trait (Hennink and Zewan, 1991). Accordingly, Shannon-Weaver Diversity Index (H) can range from 0 to 1. A value near zero indicates that every individual belong to one and the same class. Where as, value one indicates existence of diversity. Shannon Index (H') was calculated using the formula,

$$\mathbf{H = -\sum_{i=0}^{n} pilnpi} \quad , \qquad E_H = H/H_{max} = H/\ln S, \qquad H_{max} = \ln S$$

i=1

Where S is the number of traits category in a qualitative trait of Bale and West Arsi coffee accessions, E_H is Shannon's equitability, H is Shannon diversity index and pi is the relative proportion of the total number of entries (N) in the i^{th} class (Spellerberg and Fedor, 2003).

4. RESULTS AND DISCUSSION

4.1. Morphological Traits Evaluation using Quantitative Traits

4.1.1. Analysis of variance

The mean square showed that there was significant difference differences among the accessions ($P<0.05$) for bean yield, fruit thickness, canopy diameter, fruit length, fruit width, coffee berry disease (CBD), Coffee leaf rust (CLR), number of secondary branches, percent (%) of bearing primary branch and height up to first primary branch (Table 3).Those traits are a good chance to improve the accessions through selection and breeding. This study result agrees with the findings of Olika *et al*., (2011) who found that significant variations among 49 accession for 22 characters. Atinafu (2015), Abdulfeta (2018) and Desalegn (2018) also found a substantial amount of variability for different traits among tested genotypes of arabica coffee, which shows the possibility to bring improvement through selection. Bayetta (1997) also reported high genetic variability within the Arabica coffee population for yield, growth characters and coffee berry disease resistance. Moreover, Mesfin and Bayyeta (2008) reported the mean square of treatment showing that significant difference among 100 Hararge coffee accession for 14 quantitative characters.

In the studied traits checks Versus accessions that compared 133-tested accession to the 4-standard checks were significant for all characters except stem diameter, number of primary branches, number of nodes on main stem, bean length, bean thickness, number of nodes on a primary branch (Table 3). This also showed that existence of variation between collected accessions and control check varieties.

Table 2 Analysis of variance for 25 quantitative traits

Traits	Mean square						
	Blocks	All entries	Test within Accessions	Checks within	Checks vs Accessions	Error	CV
	(d.f=2)	(d.f=136)	d.f=132)	(d.f=3)	(d.f=1)	(d.f=6)	(%)
TH	396.89^{ns}	417.32^{ns}	395.32^{ns}	258.48^{ns}	3707.46**	244.57	9.36
SD	82.65^{ns}	2531.33^{ns}	2452.45^{ns}	1475.61^{ns}	16091.78^{ns}	916.82	7.35
NPB	2.69^{ns}	42.79^{ns}	37.35^{ns}	148.53^{ns}	174.92^{ns}	40.00	15.15
NNOMS	58.54**	18.24^{ns}	17.91^{ns}	34.14**	15.25^{ns}	5.51	8.26
CD	608.23**	371.41**	345.29**	501.45**	3431.70**	47.26	4.19
AINL	2.05*	0.48^{ns}	0.46^{ns}	0.57^{ns}	3.09**	0.30	14.25
FL	0.02^{ns}	1.76**	1.52**	0.47**	37.54**	0.02	0.93
FT	0.45^{ns}	0.50*	0.46^{ns}	0.27^{ns}	6.64**	0.14	3.11
FW	0.32*	0.52**	0.50**	0.52**	3.47**	0.05	1.64
BL	0.05^{ns}	0.10^{ns}	0.10^{ns}	0.04^{ns}	1.43^{ns}	0.05	3.12
BT	0.09^{ns}	0.08^{ns}	0.05^{ns}	0.01^{ns}	0.01^{ns}	0.05	5.81
BW	0.45^{ns}	0.10^{ns}	4.83^{ns}	1.78^{ns}	58.73**	5.23	13.69
LL	1.50^{ns}	1.60^{ns}	1.53^{ns}	2.22*	9.07**	0.50	5.99
LW	0.15^{ns}	0.53^{ns}	0.43^{ns}	1.52**	10.87**	0.20	7.44
LS	33.95^{ns}	95.46^{ns}	84.38^{ns}	194.55*	1262.16**	29.72	12.88
PL	0.02^{ns}	0.01^{ns}	0.01^{ns}	0.01^{ns}	0.15**	0.01	11.37
LFPB	24.77^{ns}	58.39^{ns}	50.46^{ns}	184.65*	735.47**	30.08	7.81
HBW	7.22^{ns}	5.16^{ns}	5.35^{ns}	1.78^{ns}	32.01*	4.15	13.73
CBD	446.10^{ns}	971.64**	919.73**	161.78^{ns}	10272.56**	166.24	34.52
RUST	178.78**	69.39**	69.77**	25.83^{ns}	144.18**	8.22	32.40
YLD	10898.27^{ns}	395375.66*	400139.36*	217765.67^{ns}	305504.01*	114453.28	35.61
NSB	223.63	1642.99**	1644.49**	793.15	3994.35**	220.37	23.01
NNOPB	5.70**	21.35^{ns}	5.86^{ns}	0.11^{ns}	0.84^{ns}	2.12	8.34
HUFPB	3.00^{ns}	46.84**	41.51**	19.48*	703.78**	3.72	6.05
PO BPB	53.36^{ns}	300.77**	298.85^{ns}	16.85**	1423.53**	23.39	6.05

*, ** Significance at 0.05 and 0.01 level of probabilities, ns= non significance difference, df = degree of freedom, CV= coefficient of variation, PH= Plant height, SD= stem diameter (cm), NPB= number of primary branch (no), NNOMS= number of node on main stem (no), CD= canopy diameter, AINL= average inter node length of main stem (cm), FL= fruit length (mm), FT= fruit thickness(mm), FW = fruit width (mm), BL= bean length (mm), BT= bean thickness (mm), BW=bean width (mm), LL= leaf length(cm), LW=leaf width (cm), LS= leaf size (mm), PL=petiole length (cm), LFPB= length of first primary branch (cm), HBW=hundred bean weight (gr), CBD= coffee berry disease, RUST= coffee leaf rust, YLD= yield (kg/ha), NSB= number of secondary branch, NNOPB= number of node on primary branch (no), HUFPB= height up to first primary branch (cm),POBPB=percentage of bearing primary branch.

4.1.2. Mean performance of accessions

Mean and range of 133 accessions for 25 quantitative traits is presented in Table 4. A wide range of variation was recorded for a total height (110-223.0), canopy diameter (98.0-226.4), number of primary branches (26.3-64.5), number of nodes on a primary branch (18.3-39.7), stem diameter (294.0-529.5), length of first primary branch (53.2-89.9), hundred bean weight

(11.6-23.7) and height up to first primary branch (20.546.0).The maximum mean value of these characters were almost double the minimum mean values. The maximum value was three times higher than the minimum values for the average internode length of main stem (1.8-5.5) and leaf size (22.1-71.8).

Additionally, bean yield (0.0-2851.7kg/ha), coffee berry disease (0.0-100%), coffee leaf rust (0.0-46.7%), number of secondary branches (8.5-181.5), number of primary branches (26.3-64.5), percent (%) of bearing primary branch (1.7-87.5) showed a higher range of variation. The maximum mean values of those measured quantitative traits of accessions demonstrated almost three times higher in minimum mean value. This indicating existence of a wider range of variation among tested coffee genotypes used in this study and help that for easy identificat ion of desirable character of interest for future coffee breeding programs.

These results were agreed with findings of Desalegn (2018), Atinafu (2015), Masreshaw (2018), and Abdulfeta (2018) who reported the existence of wider variation for most of measu red quantitative traits between coffee materials employed in their respective studies. Getache w *et al.,* (2017) had reported that presence of the highest range between the tested materials for important agronomic traits, such as average coffee yield per tree, CBD resistance level and number of secondary branches.

The mean yield of accessions showed the highest range of variation for characters, bean yield (950.1 kg/ha), coffee berry disease (37.2%), coffee leaf rust (8.9 %) percent (%) of bearing primary branch (57.0), numbers of node on primary branch (62.8) and the number of secondar y branches (57.0). Likewise, main stem diameter (411.8 cm), canopy diameter (164.0 cm), leaf size (423.), number of primary branches (44.2), height up to first primary branch (31.8), leaf size (42.3) and average internode length (3.82 cm) showed a wider range of variations. The lower and higher mean yield among measured quantitative traits was recorded by accessi on B77/07 and B184/07 with respective mean values of 20.3 and 2886.33 (Appendix 1). Similarly, 27 (20%), 43(34%), 57(43%) and 72 (54%) coffee accessions recorded higher mean yield than the standard check varieties 74110, 75227, 74148 and 74165, respectively. Accordingly, for more than nine accessions higher mean yield was recorded from Bale by B184/07, B29/07, B270/07, B286/07, B186/07, B181/07, B88/07, B28/07 and B13/07 with

respective mean value of 2886.33, 1939.74, 1839.93,1778.45, 1719.58, 1711.91, 1628.93, 1562.94 and 1546.59 in kg/ha. Three moderately high yielder coffee accessions also recorded from West Arsi by accessions: B321/07, B289/07 and B285/07 with respective mean values of 1679.90, 1676.36, and 1533.43 in kg/ha (Appendix Table 1).The result shows the presence of considerable variation among tested Bale and West Arsi coffee accessions.

Visual field evaluation for coffee berry disease (CBD) and coffee leaf rust (CLR) severity reaction showed a significance difference (<0.05) among the accessions. More than 58 Coffee accessions scored above 50% CBD severity. However, nine accessions exhibited less than 5%. These accessions are B184/07, B291/07, B317/07, B108/07, B313/07, B297/07, B277/07, B109/07 and B289/07 with recorded mean value of 5.05%, 0.85%, and 0.05%, 2.95%, 2.95%, 4.34%, 4.54%, 4.95% and 2.2% respectively. The former three consecutive accessions had shown lower CBD reaction than 74148 standard checks (Appendix Table 1). About 63% of the accessions (84 accessions) exhibited low levels of CLR severity. Out of these, nine accessions (B29/07, B13/07, B282/07, B272/07, B267/07, B287/07, B298/07, B236/07, and B277/07) exhibited a lower level of CLR with respective severity value of 2.72 %, 2.72 %, 2.72 %, 5.39 %, 0.61 %, 0.61 %, 2.28%, 1.05 % and 3.9 % (Appendix Table 1).

Generally, accessions B184/07 and B29/07 from Bale collections, and B321and B289/07 from West Arsi exhibited higher to moderate mean yield coupled with resistance to CBD. This result indicated the existence of genetic variation among tested genotypes; which are advantages to select high yielding and CBD resistance coffee accession for future uses in coffee breeding programs. These findings are in line with Abdulfeta (2018), Masreshaw, (2018), Desalegn (2018) who reported the existence of variability among tested coffee accessions.

Table 3 Mean values and range of 137 Bale and West Arsi coffee accessions for quantitative traits

Traits	Maximum	Minimum	Range unit	Mean
Plant height (cm)	223.0	110	113	167.1
Stem diameter (cm)	529.5	294.0	235.5	411.8
Number of primary branch(no)	64.5	26.3	38.3	44.17
Number of node on main stem (no)	39.7	18.3	21.4	28.43
Canopy diameter (cm)	226.4	98.0	128.4	164.0
Average inter node length(cm)	5.5	1.8	3.7	3.8
Fruit length(mm)	20.3	13.7	6.6	16.
Fruit thickness (mm)	13.5	10.2	3.3	11.9
Fruit width (mm)	15.6	11.7	3.9	13.6
Bean length (mm)	12.0	8.3	37	3.8
Bean thickness (mm)	4.8	3.3	1.5	3.8
Bean width (mm)	7.7	6.0	1.7	6.7
Leaf length (cm)	15.1	8.5	6.6	11.9
Leaf width(cm)	7.1	3.5	3.6	5.3
Leaf size (cm)	71.8	22.1	48.7	42.3
Petiole length (cm)	1.2	0.6	0.6	0.9
Length of first primary branch (cm)	89.9	53.2	36.7	70.3
Hundred bean weight (gr)	23.7	11.6	12.1	16.7
Coffee berry disease (%)	100	0.0	100	37.2
Coffee leaf rust (%)	46.7	0.0	46.7	8.9
Yield (kg/ha)	2851.7	0.0	2191.5	950.1
Percent % of bearing primary branch	87.4	1.7	85.7	57.0
Number of secondary branch (no)	181.5	8.5	173.0	25.5
Number of node on primary branch (no)	24.7	12.5	12.2	62.8
Height up to first primary branch (cm)	46.0	20.5	25.5	31.8

4.1.3. Phenotypic and genotypic coefficient of variation

The estimates of genotypic, environmental and phenotypic variance, genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance expressed as percent of the mean (GAM) were presented in Table 5. The results revealed that the genotype variations are greater than that of environmental variation for all traits measured except plant height and number of nodes on primary branch. This result indicates greater influence of genetic variation in controlling the experiment of yield and yield contributing traits under Gera environment.

According to Deshmukh *et al*., (1986), phenotypic and genotypic coefficients of variation val ues 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. In this study genotypic and phenotypic coefficients of variation were ranges from (1.2 to 51.0) and (2.7 to 54.3), respectiv ely. The higher estimated percent(%) value for both genotypic (GCV) and phenotypic coeffici ent of variation (PCV) were recorded by coffee leaf rust (51.0, and 54.3), coffee berry disease (43.9 and 48.2), bean yield (32.2 and 38.2), number of secondary branch (33.8 and36.3) and percent (%) of bearing primary branch (30.15 and 31.4), respectively. For most of the traits ge notypic coefficients of variation were very close to their corresponding estimates of phenotypi c coefficient of variation, suggesting the greater role of both in the expression of these traits.

These findings agree with Olika *et al*., (2011) who found higher PCV and GCV value for a number of secondary branches and green bean yield. Desalegn (2018) also reported the highest PCV and GCV for coffee bean yield, coffee berry disease and coffee leaf rust. Both moderate GCV and PCV value were recorded for height up to first primary branch (11.9 and 12.4) and leaf size (11.1 and 13.3). Whereas, high and moderate PCV value alone was observed for number of nodes on a primary branch (20.6), average internode length (11.1%) and hundred bean weights (10.3), respectively. These findings partially agree with Getachew *et al.,* (2017) who reported moderate PCV and GCV for height up to first primary branch and hundred bean weights with PCV values of 14.57 and 12.07% and with GCV values of 11.9 and 10.8 %, respectively.

Low values (<10 %) GCV and PCV value were recorded for plant height, stem diameter, number of primary branches, number of nodes on main stem, canopy diameter, internode length of the main stem (cm), fruit length, fruit thickness, fruit width, bean length, bean thickness, bean width, leaf length, leaf width, petiole length, length of first primary branch, hundred bean weight, number of secondary branches, number of nodes on primary branches. Suggested that the traits are rendering to high environmental influences and hence lower oppo rtunity exists for improvement of these traits through simple selection in the tested genotypes.

This result for estimates of the phenotypic coefficient of variation (PCV) were showed closer related value with a corresponding genotypic coefficient of variation (GCV) indicating the greater role of both in the expression of characters (Bhagasaral *et al*., 2017). Accordingly, the present study result of GCV and PCV value was demonstrated that higher and somewhat closer values for PCV and GCV for coffee leaf rust (51.02, and 54.34), coffee berry disease

(43.9 and 48.2), bean yield (32.21 and 38.21), number of secondary branch (33.75 and 36.27) and percent of bearing primary branches (30.15 and 31.40). The narrow gap for both GCV and PCV value indicate less influence of environment on them. In contrast, Getachew *et al.,* (2017) reported that the wider gap between PCV and GCV for bean yield, coffee berry disease severity, number of primary branches, number of secondary branches and number of main stem node. Masreshaw (2018) also reported the high value and wider gap for PCV and GCV value for CBD and CLR because of environmental influence on tested traits. Desalegn (2018) also report higher PCV and GCV value together with larger differences in CBD, CLR and coffee yield, suggesting the variation exerted due to environment.

Table 4 Estimates of components of Variance, PCV, GCV, Heritability and Genetic Advance

Characters	GV	EV	PV	GCV	PCV	H^2 (%)	GA	GAM (%)
TH	57.6	81.5	139.1	4.5	7.1	41.4	6.5	3.9
SD	538.2	305.6	843.8	5.6	7.1	63.8	30.5	7.4
NPB	0.3	13.3	13.6	1.2	8.4	1.9	0.0	0.1
NNOMS	4.2	1.8	6.1	7.3	8.7	69.8	3.0	10.4
CD	108.1	15.8	123.8	6.3	6.8	87.3	18.7	11.4
AINL	0.1	0.1	0.2	6.5	10.5	38.3	0.2	5.1
FL	0.6	0.0	0.6	4.6	4.7	98.6	1.6	9.4
FT	0.1	0.0	0.2	2.9	3.4	72.0	0.5	4.3
FW	0.2	0.0	0.2	2.9	3.1	90.4	0.7	5.4
BL	0.4	0.2	0.6	5.9	7.6	59.4	0.7	7.2
BT	0.01	0.02	0.0	2.4	4.1	33.3	0.1	1.6
BW	0.02	0.02	0.0	1.9	2.7	49.0	0.1	1.9
LL	0.4	0.2	0.5	5.1	6.2	68.8	0.9	7.3
LW	0.1	0.1	0.2	6.3	8.0	62.8	0.4	8.2
LS	21.9	9.9	31.8	11.1	13.3	68.9	6.7	15.7
PL	0.0	0.0	0.0	6.3	9.0	50.0	0.1	6.5
LFPB	9.4	10.0	19.5	4.4	6.3	48.5	3.1	4.4
100BW	1.6	1.4	3.0	7.5	10.3	53.2	1.4	8.2
CBD	268.5	55.4	323.9	43.9	48.2	82.9	28.0	75.0
RUST	20.4	2.7	23.1	51.0	54.3	88.2	8.2	92.8
YLD	93640.8	38151.1	131791.9	32.2	38.2	71.1	448.6	47.2
POBPB	92.5	7.8	100.3	30.2	31.4	92.2	18.7	58.5
NSB	474.2	73.5	547.7	33.8	36.3	86.6	38.9	60.3
NNOPB	4.8	22.7	27.5	8.6	20.6	17.5	0.8	3.1
HUFPB	14.4	1.2	15.6	11.9	12.4	92.1	7.4	23.1

CV = coefficient of variation, TH = total height, SD = stem diameter (cm), NPB = number of primary branch (no), NNOMS = number of node on main stem (no), CD = canopy diameter (mm), AINL = average inter node length of main stem (cm), FL = fruit length(mm), FT = fruit thickness (mm), FW = fruit width (mm), BL= bean length (mm), BT = bean thickness (mm), BW = bean width (mm), LL = leaf length (cm), LW = leaf width (cm), LS= leaf size (cm), PL = petiole length (cm), LFPB = length of first primary branch (cm), 100BW = hundred bean weight (gr), CBD = coffee berry disease, RUST = coffee leaf rust, HUFPB = height up to first primary branch, YLD = yield (kg/ ha), POBPB = percent (%) of bearing primary branch (no), NSB = number of secondary branch, NNOPB = number of node on primary branch, HUFPB = height up to first primary branch

4.1.4. Broad sense heritability and genetic advance

Broad sense heritability estimates for 25 quantitative traits ranged from the lowest (1.94%) to highest (98.6 %) for a number of primary branches and fruit length, respectively (Table5). According, to Vernan and Agarwal (1982) heritability estimate is classified as low (<20%), medium (20-50%) and high (>50%) Verma and Agarwal (1982). High heritability estimate (>50%) were recorded for fruit length (98.6), coffee berry disease (82.9 %), percent (%) of bearing primary branches (92.2), height up to first primary branch (92.1%), number of secondary branches (91.3%), fruit width (90.4), coffee leaf rust (88.2%), canopy diameter (87.3%), fruit thickness (72.0%), bean yield (71.1%), number of node on main stem (69.8%), leaf size (68.9%), leaf length (68.8%), main stem diameter (63.8%), leaf width (62.8), bean length (59.4%) and hundred bean weight (53.2%). Hence, higher heritability value for most of the studied accessions based on measured characters shows less influence of environment in their expression. However, this suggested the greater usefulness of selection and improvement to be expected for future breeding programs.

The present finding partially agreed with Getachew *et al*., (2017) who found that (> 50%) of heritability for hundred bean weight (80.21%), number of nodes of primary branches (67.89%), stem diameter (67.16%), height up to first primary branch (66.6%), bean length (62.79%), bean width (61.43%) and average internode length of primary branches (58.33%), angle of primary branches (53.32%), leaf width (52.94%) and canopy diameter (51.95%).Thes e findings partially coincided with Dawit (2018), who found that heritability were higher for fruit length (58%), fruit width (67%), fruit thickness (61%), and number of node on primary branch (54%). Masreshaw (2018) reported that the high estimated heritability for the studied traits also indicated the greater effectiveness of selection and improvement in the future breedi ng programs; the genetic variance is mostly due to additive gene action.

Medium heritability was recorded for petiole length (50%), bean width (49%), and length of first primary branch (48.48), total height (41.4%), and average internode length (38.33). These results were also agreed with findings of Atinafu (2015). Abdulfeta (2018) reported that the estimate of high heritability suggested that the effective selection of accessions based on measured characters for future breeding programs.

Genetic gain as presence of mean at 5% percent selection intensity (GAM) was indicated in Table 5. Estimates of GAM for measured quantitative characters rang (0.05) for number of primary branch to (92.8) for coffee leaf rust. As Johnson *et al*. (1955) stated that genetic advance as the percent of mean was categorized as low (0-10%), medium (10-20%) and high (≥20 %). Based on this suggestion high genetic advance as percent of mean (GAM) were obtained by coffee leaf rust (92.8%), coffee berry disease (75.0%), number of secondary branch (60.28%), percent of bearing primary branch (58.28%), yield (47.21%) and height up to first primary branch (23.08%), respectively. Whereas, medium GAM (10-20%) were observed for canopy diameter and leaf size while the remaining all traits showed low genetic advance as percent of mean (<10%).

GAM value (>20%) coupled with higher heritability was recorded for coffee leaf rust (92.8%), coffee berry disease (75.0%), number of secondary branch (60.28%), percent of bearing primary branch (58.28%), yield (47.21%) and height up to first primary branch (23.08%). High heritability and genetic advance in arabica coffee was the indication for easy selection (Olika *et al.*, 2011). Moderate value of GAM reordered for leaf size (15.72%), canopy diameter (11.41%), and numbers of node on main stem (10.43%). The lower quantitati ve character of GAM also recorded for hundred bean weight, leaf width, main stem diameter, leaf length, bean length, petiole length, fruit width average internode length, length of first primary branch, fruit thickness, total height, numbers of node on primary branch, bean width, bean thickness, numbers of primary branch.

The magnitudes of heritability for most of the quantitative characters were moderate to high, which may be attributed due to their genetic difference of the genotypes in the study. Genetic progress expected from selection increases with an increase in genotypic variance. High heritability coupled with high genotypic coefficient of variation of the traits indicated that the traits respond effectively to phenotypic selection, hence traits which had moderately high heritability coupled with medium genotypic coefficient of variation in present study can be improved by conventional breeding through selection breeding.

4.1. 5. Phenotypic and genotypic association of coffee yield with other traits

Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient of compu ted quantitative traits were presented in Table 6. The result of coefficient of genotypic correlat ion showed that almost closely related to coefficient of phenotypic correlation. This indicated that equal contribution of both environment and genetic for trait expression.

Phenotypic correlation: the correlation analysis of coffee bean yield (kg/ ha) demonstrated statistically significant and positive association with percentage (%) of bearing primary branc hes (rp 0.64), coffee leaf rust (rp=0.39) and canopy diameter (rp=0.25) (Table 6). This indicat es, increasing those traits simultaneously increase green bean yield. Olika *et al.,* (2011) and Atinafu and Mohammed (2017) report that average green bean yield was positive and signific antly correlated with percentage of bearing primary branch and canopy diameter.

Unlike Olika *et al*., (2011), Atinafu (2015), Muvunyi *et al.,* (2017) and Abdulfeta (2018) coffee leaf rust severity was positively correlated with coffee yield at both phenotypic and genotypic correlations. The result was indicated when the green coffee yield increase, CLR severity was increased simultaneously. This might be because of the plant's resistance ability, decreased due to extensively utilize of stored food for yield increment. Accordingly, Plant arranges himself in order to develop leaf bud in the coming season rather than producing yield. While, coffee berry disease (CBD) negatively correlated with coffee bean yield, this is because of different genes or a single gene that controls more than one trait (pleiotropic gene), that has dominated on the trait may control them in different directions (Kearsey and Pooni, 1996). These findings were agreed with Masreshaw (2018), Atinafu (2015), and Abdulfeta (2018) who reported that negative correlation between coffee berry disease and coffee bean yield.

Genotypic correlation: coffee bean yield (kg/ha) positively and significantly correlated with percent (%) of bearing primary branch (r= 0.64), coffee leaf rust (CLR) (r= 0.44) and canopy diameter (r= 0.25) at genotypic level. These positive and significance associations among traits were due to the result of linkage between their genes or the result of pleiotropic genes or both (Kearsey and Pooni, 1996). This is grater important in coffee variety development program in order to improve simultaneous yield and yield contributing traits. Whereas, CBD

severity reaction had significant and negative correlation with, coffee bean yields. Suggested, selection for any one of these characters is not likely to result in improvement of the others. However, independent selection may have to be carried for improvement this traits. These findings partially agree with Olika *et al.,* (2011) who found that positive and significant genotypic correlation of yield per tree with plant height, stem diameter, canopy diameter, fruit length, bean length, leaf length, bean width, bean thickness, bean width, hundred bean weights, percentage of bearing primary branches and height up to first primary branch.

4.1.6. Phenotypic and genotypic correlation among morphological traits

Phenotypic and genotypic correlation showed that there was positive and significant (<0.01) correlation between traits such as: canopy diameter, fruit thickness, fruit width, number of secondary branch, height up to first primary branch and percent (%) of bearing primary branch indicated presence of close association with each other. Whereas, coffee leaf rust negatively correlated with fruit thickness (r = -0.19) and coffee berry disease (r = -0.31) this is confirmed improvement for negatively correlated trait antagonistically affect the other.

Fruit thickness were positively and significantly correlated with fruit length (rg=0.60), fruit width (rg=0.81), CBD (0.25), number of secondary branch (0.19), height up to first primary branch (0.16) and canopy diameter (0.21). This indicated existence of true relationship among accessions based on measured quantitative traits. However, it had negatively correlated with coffee leaf rust (0.19) and percent (%) of bearing primary branch (0.15). CLR (0.44) was positively and significantly correlated with percent of bearing primary branch (r = 0.39). Other traits such as: fruit thickness (r = 0.61), fruit width (r = 0.72), height up to first primary branch (r = 0.32) and canopy diameter (r = 0.20) were positively and significantly correlated with fruit length at genotypic level.

Generally, in this study some traits were positively and significantly correlated, as well as other significant and negatively correlated with yield and among each other. For positively associated traits simultaneously improvement of one trait will improve the other. Whereas, those traits, which were negatively correlated the improvement for one trait antagonistically affect the other. Such association might be raise because of additive or non-additive gen action and the other factors such as pleiotropic that could control the traits within the same

direction (Welsh, 2008). Also negative correlation of traits might be because of different genes or pleiotropic gene that has dominance on the trait may control them in different direction (Kearsey and Pooni, 1996).

Table 5 Genotypic (above diagonal) and phenotype (below diagonal) correlation coefficient among 10 important characters

Variable	YLD	FL	FT	FW	CBD	RUST	NSB	HUFPB	CANOP	POBPB
YLD		0.01	-0.02	-0.01	-0.62**	0.44**	0.03	0.14	0.25**	0.64**
FL	0.01		0.61**	0.72**	0.11	-0.05	0.08	0.32**	0.20**	-0.01
FT	-0.02	0.60**		0.81**	0.25**	-0.19*	0.19*	0.16*	0.21**	-0.15
FW	-0.01	0.71**	0.80**		0.13	-0.05	0.14	0.23**	0.22**	-0.08
CBD	-0.62**	0.11	0.26**	0.13		-0.31**	0.34**	0.12	-0.04	-0.64**
RUST	0.43**	-0.04	-0.19**	-0.04	-0.31**		0.00	0.03	0.11	0.39**
NSB	0.03	0.08	0.19*	0.14	0.33**	0.00		0.22**	0.20*	-0.10
HUFPB	0.14	0.32**	0.15	0.23**	0.12	0.04	0.22**		0.34**	-0.04
CANOP	0.25**	0.20**	0.19*	0.20**	-0.05	0.11	0.20**	0.34**		0.20**
POBPB	0.64**	-0.01	-0.15	-0.08	-0.64**	0.39**	-0.10	-0.04	0.20**	

*, ** = Significant at 5% and 1%, probability level respectively, ns = no significant difference, YLD=yield (kg/ha), FL= fruit length (mm), FT= fruit thickness (mm), FW = fruit width (mm), CBD= coffee berry disease RUST= coffee leaf rust, NSB= number of secondary branch, HUFPB= height up to first primary branch, CD= canopy diameter, POBPB=percent (%) of bearing primary branch

4.1.7. Path coefficient analysis

The highest and positive direct effect of path coefficient analysis recorded for fruit thickness (0.33) followed by percentage of bearing primary branch (0.29) and coffee leaf rust (0.22) (Table 7). However, the former trait showed higher and direct effect on coffee yield. But exhibited negative phenotypic correlation (-0.02) with coffee yield. The negative correlation it showed with coffee yield was mainly due to negative indirect effects via other traits: fruit length and CBD. Moderate magnitude of positive direct effect was recorded for height up to first primary branch (0.16) and number of secondary branches (0.15). This result also partially agrees with Getachew *et al*., (2013) who reported that fruit length, fruit thickness and height up to first primary branches showed a positive direct effect on yield. Lowest grade and

positive direct effect were exhibited for canopy diameter alone (0.05). These showed that using of above positive traits may directly contribute to coffee yield increment.

The negative direct effect and positive correlation were recorded via fruit length (-0.018). The result of fruit width (-0.25) showed, positive direct effect and negative association with coffee yield. Whereas, CBD **(**-0.48) exhibited both negative association and direct effect on coffee yield. The negative indirect effect of above traits needs to be managed during selection because the selection of traits might have reduced effect on yield of coffee. Likewise, Masres haw (2018) also report coffee berry diseases severity was a negative direct effect and negative correlation with yield per tree. The positive direct selections have highly effective for improve ment of coffee yield than negative direct effect because its influence the coffee yield directly.

Canopy diameter, height up to primary branch, percentage of bearing primary branch and coffee leaf rust exhibited significant at both genotypic and phenotypic correlation and positive direct effect with coffee yield indicate that improvement of these traits directly improves coffee yield. Desalegn (2018) reported positive direct effect of canopy diameter (0.41), height up to first primary branch (0.30), number of bearing primary branches (0.30) on coffee yield. The result was agreed with Lemi *et al*., (2017) who reported that canopy diameter and height up to primary branch showed significant at both phenotypic and genotypic correlation and positive direct effects recorded by canopy diameter on coffee yield.

The residual effect permits precise explanation about the pattern of interaction of other possibl e components of yield. In other words, residual effect measures the role of other independent variables which were not included in the study on the dependent variable. In this study, the estimated residual effect was 0.66% indicating that about 0.34% of the variability in yield was contributed by the characters studied in path analysis. This residual effect towards yield in this study might be mainly due to the other characters which were not included in the investigation and environmental factor. Therefore, the aspect of intensive germplasm exploration in the Bal e and West Arsi coffee considering additional characters was suggested in order to confirm the results. In general, the path analysis carried out in the present study revealed that the main components of bean yield, which had positive direct effect of bean yield, should be given high priority for making selection.

Table 6 Direct and indirect effect of bean yield and yield contributing characters

Variable	FL	FT	FW	CBD	RUST	NSB	HUFPB	CANOP	PBPB	rG
FL	**-0.018**	0.202	-0.176	-0.056	-0.010	0.012	0.053	0.010	-0.004	0.013
FT	-0.011	**0.333**	-0.200	-0.123	-0.042	0.028	0.027	0.010	-0.044	-0.022
FW	-0.013	0.271	**-0.246**	-0.061	-0.011	0.022	0.038	0.011	-0.024	-0.013
CBD	-0.002	0.085	-0.031	**-0.484**	-0.068	0.051	0.020	-0.002	-0.184	-0.616
RUST	0.001	-0.065	0.012	0.151	**0.216**	0.000	0.006	0.005	0.113	0.440
NSB	-0.001	0.062	-0.035	-0.163	0.000	**0.150**	0.037	0.010	-0.030	0.028
HUFPB	-0.006	0.055	-0.057	-0.059	0.007	0.033	**0.164**	0.017	-0.011	0.145
CANOP	-0.004	0.068	-0.053	0.019	0.023	0.030	0.056	**0.050**	0.057	0.247
PBPB	0.000	-0.051	0.020	0.311	0.085	-0.016	-0.006	0.010	**0.287**	0.640

Residual=0.64, FL= fruit length (mm), FT= fruit thickness (mm), FW = fruit width (mm), CBD= coffee berry disease RUST= coffee leaf rust, NSB= number of secondary branch, HUFPB= height up to first primary branch, CD canopy diameter, POBPB=percent (%) of bearing primary branch

4.1.8. Principal component analysis

Principal component analysis showed 4 PC (PC1, PC2, PC3, and PC4) exhibited greater than one Eigenvalue (2.59, 2.09, 1.31 and 1.07) and accounted 70.55 % of the total variation (Table 8). Accordingly, the first PCA accounted 25.88% of total variation, followed by the second (20.86%), the third (13.12%) and the fourth (10.7%). However, the first two principal components (PC1 and PC2) were contributed more to the total variation. The first PC contribu tes higher to the total variation (25.88%) due to greater contribution of positive discriminatory traits of fruit length (0.75%), fruit thickness (0.87%), fruit width (0.86%), coffee berry disease (0.42%) and number of secondary branch (0.32%). Variation in the second PC (20.86 %) was mainly influenced by fruit length (0.75%), fruit width (0.86%), and coffee berry disease (0.60), percent (%) of bearing primary branches (0.39%) and canopy diameter (0.42%). The third PC (13.12%) variation was exhibited also due to greater contributory traits of clean coffee yield (0.3), number of secondary branch (0.75%), canopy diameter (0.46%) and

percent (%) of bearing primary branch (-0.53%). Likewise, the fourth PC variation revealed by coffee leaf rust (-0.30%) and height up to first primary branch (0.90%).

However, Chahal and Goal (2002) revealed that characters with the largest absolute values closer to unit within the first principal component influence the clustering more than those with lower absolute values closer to zero. Accordingly, fruit length (0.75%), fruit thickness (0.87%), fruit width (0.86%), coffee berry disease (0.42%) and number of secondary branch (0.32%), percent (%) of bearing primary branches (0.39%) and canopy diameter (0.42%) had more contribution to the total variation and were the one that most differentiated the clusters and should be considered in selection diverse of parent for future crossing and breeding program. However, in PC2 and PC4 coffee berry disease (-0.72) and coffee leaf rust (-0.3) were negatively contributed for total variation respectively.

This finding partially agrees with Masreshaw (2018) who had reported that first principal component that accounted the highest total variation (21.99%) was due to the chief contribution of positive discriminatory traits like average length of primary branches, fruit width, fruit thickness and hundred bean weights. The result partially coincided with Tounekti *et al.*, (2017) who report that PC1 accounted for 51.01% of the total variation, which were due to greater contribution of fruit length (0.29), fruit width (0.30), fruit thickness (0.30), bean length (0.30), bean width (0.26) and bean thickness (0.22). Likewise Yigzaw (2005) also reported characters contributing for variation for coffee genotypes includes inter-node lengths, tree height, canopy diameter, number of branches, bean and fruit character.

Table 7 Eigen values and Eigenvectors of the first four principal components (PCA) for some important traits

Variables	PCA1	PCA2	PCA3	PCA4
Bean yield (kg/ha)	-0.20	0.79	**0.30**	0.17
Fruit length (mm)	**0.75**	**0.33**	-0.23	0.00
Fruit thickness (mm)	**0.87**	0.17	-0.09	-0.07
Fruit width (mm)	**0.86**	**0.31**	-0.15	-0.14
Coffee berry disease (%)	**0.42**	**-0.72**	0.17	-0.11
Coffee leaf rust (%)	-0.29	**0.60**	0.22	**-0.30**
Number of secondary branch(no)	**0.32**	-0.13	**0.75**	-0.21
Height up to first primary branch (cm)	0.18	-0.05	0.00	**0.90**
Canopy diameter	0.22	**0.42**	**0.46**	0.22
% of bearing Primary branch	-0.17	**0.39**	**-0.53**	-0.12
Eigenvalue	**2.59**	**2.09**	**1.31**	**1.07**
Difference	0.50	0.77	0.24	0.23
Percent of variation (%)	**25.88**	**20.86**	**13.12**	**10.7**
Cumulative variance (%)	**25.88**	**46.74**	**59.85**	**70.55**

4.1.9. Cluster analysis based on quantitative characters

Cluster analysis using 137 coffee accessions was grouped in to 6 clusters (Table 9). The largest numbers of accessions were grouped in a cluster I, II, III and IV. Whereas, small numbers of accession were grouped in cluster V and VI. Accordingly, cluster-II was the largest and consisted of 41 accessions (30%) followed by a cluster-I 37 accessions (27%), cluster- IV 29 accessions (21%), cluster-III 25 accessions (18%), cluster-V 4 accessions (3%) and cluster-VI 1 accessions (1%). A perennial self-pollinated standard check varieties (74165 and 74148) were grouped in cluster I, whereas 74110 and 75227 were grouped in cluster III and cluster IV, respectively.

Coffee collections were made in Bale and West Arsi zones, from three districts: Nensebo, Gololcha and Ginir, which was grouped into different clusters. In this study coffee accessions collected from the West Arsi zone: Rafisa kebele was grouped in a cluster I, III and IV. Whereas, accessions from the same district, Kore kebele grouped in cluster I, II, III and IV. This revealed that existence of higher genetic diversity in accession collected within same

districts. Variation of accessions revealed that due to admixture of different coffee genotypes through moving by human or other wild animals' from place to place.

These findings agree with Getachew *et al*., (2013*)* who reported that accessions collected from different kebeles clustered together, while accessions collected from same kebeles were clustered into different clusters. Bayeta (2001) and Seyoum (2003) also reported that, rather than geographical region morphological variation is more important because it shows variatio n in coffee.Generally, accessions collected from the same place clustered in to different group , whereas accession collected from different places grouped into the same clustered. Abdi (20 09) reported phenotypic diversity among 49 Hararge coffee accessions for 16 quantitative cha racters and found out that the accessions were grouped into 6 clusters.

Table 8 Distribution of Bale and West Arsi coffee accessions clustered based on D2 analysis

Clus No.	No. ace	Percent (%)	Name of accessions						
I	37	27	B275/07	B317/07	B69/07	B67/07	B265/07	B306/07	74165
			B82/07	74148	B110/07	B311/07	B239/07	B326/07	B76/07
			B315/07	B303/07	B125/07	B143/07	B155/07	B235/07	B258/07
			B157/07	B95/07	B262/07	B113/07	B224/07	B269/07	B264/07
			B305/07	B21/07	B293/07	B278/07	B160/07	B240/07	B217/07
			B37/07	B281/07					
II	41	30	B68/07	B71/07	B79/07	B11/07	B237/07	B165/07	B261/07
			B124/07	B57/07	B279/07	B81/07	B225/07	B192/07	B41/07
			B191/07	B292/07	B327/07	B117/07	B218/07	B89/07	B231/07
			B284/07	B129/07	B204/07	B159/07	B126/07	B107/07	B300/07
			B170/07	B202/07	B166/07	B288/07	B172/07	B223/07	B77/07
			B144/07	B232/07	B05/07	B274/07	B116/07	B31/07	
III	25	18	B285/07	B13/07	B266/07	B287/07	B93/07	B286/07	B313/07
			B55/07	B280/07	B307/07	B290/07	B39/07	74110	B309/07
			B321/07	B289/07	B56/07	B28/07	B88/07	B282/07	B186/07
			B112/07	B270/07	B181/07	B86/07			
IV	29	21	B65/07	B298/07	B308/07	B108/07	B271/07	B310/07	B174/07
			B291/07	B73/07	B244/07	B251/07	B277/07	B304/07	B318/07
			B236/07	75227	B297/07	B276/07	B299/07	B272/07	B267/07
			B91/07	B268/07	B109/07	B238/07	B173/07	B20/07	B167/07
			B187/07						
V	4	3	B175/07	B29/07	B273/07	B145/07			
VI	1	1	B184/07						

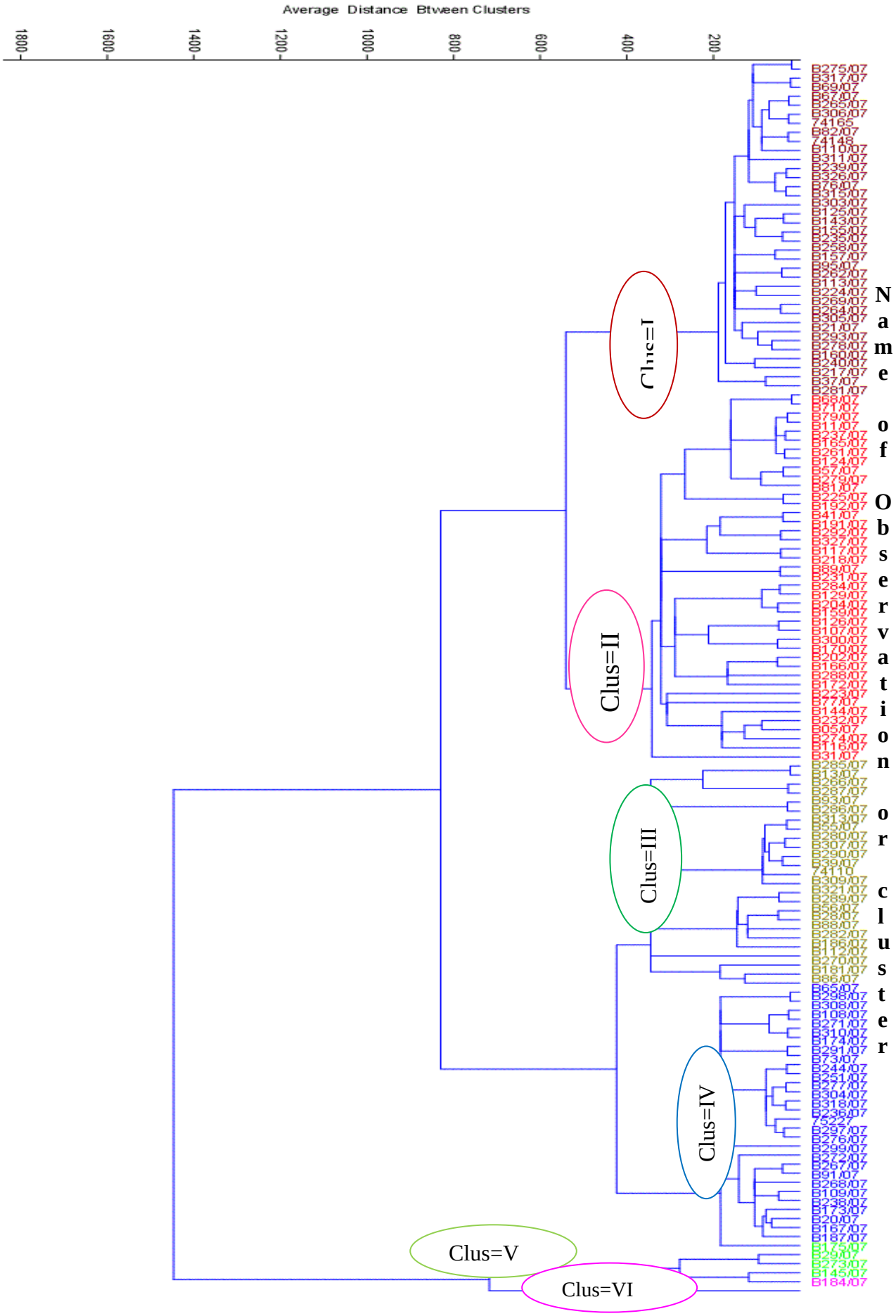

Figure 6. Tree diagram of 137 accessions using 10 quantitative traits

4.1.10. Cluster analysis of 12 qualitative traits

Cluster analysis of coffee accession for 137 qualitative traits grouped into five clusters with different numbers of accessions in each cluster (Table 10). The accessions distributed in such a way that 40 accessions grouped in to cluster-II (29 %) followed by a cluster-III consisted 34 accessions (25%), 31 % of accessions grouped in each cluster-II and IV and 1 accession (1%) grouped in cluster-V. Cluster-I contained predominantly stiff stem habit, spreading angle of insertion, green leaf tip color, round fruit shape, with absence of fruit ribs, without calyx limb persistent and many primary branches with few secondary branches. Cluster-II characterized by elliptic and oblong fruit shape, absence of both calyx limb persistent and fruit ribs. Mainly stiff stem habit, round fruit shape and absence of fruit ribs were grouped in to cluster III.

Only one accession alone grouped in cluster V and characterized by open growth habit, stiff stem habit, many primary branches with few secondary branches, and erect angle of insertion, Deltate stipule shape and green leaf tip color. Desalegn (2018) who reported that clustered of 64 accessions into six groups based on qualitative traits. Atinafu *et al.*, (2017) also reported cluster of 124 Sidama coffee accessions into 10 distinct groups based on seven qualitative traits.

4.1.11. Cluster mean of quantitative traits

The mean values of 137 coffee accessions from Bale and West Arsi zone base on 10 quantitati ve characters were clusters into six groups is presented in (Table 10). The diverse mean values of clusters revealed different characters of coffee accessions. Only one accession was presented at Cluster VI distinguish by characters wider canopy diameter (174.13), longer fruit length (16.83), narrow fruit thickness (11.77) and intermediately wider fruit width (13.55). Furthermore, this accession had characterized by high yield (2851.70 kg/ha), longer height up to first primary branch (42cm) and lower coffee berry disease severity (5.05%) which reveale d that greater opportunity to be used in crossing program to be selecting high yielding disease resistance coffee accessions for future breeding programs.

Cluster V contained four accessions know for it character of intermediate bean yield (2136.65 kg/ha), canopy diameter (168.85 cm), fruit length (16.67mm), fruit width (13.71mm), and height up to first primary branches (34.04 cm). Moreover, the higher mean values was showed

for wider fruit thickness (12.02 mm), a large number of secondary branch (117.44), percentag e of bearing primary branches (63.24) and coffee leaf rust (14.67). In cluster I both fruit length and number of secondary branch exhibited low cluster mean value whereas, for the rest traits signified medium cluster mean value.

Cluster II contained forty accessions which characterized by intermediate mean value for all traits except lower mean value is exhibited by canopy diameter (158.07 cm) and bean yield (246.12kg/ha). Furthermore, CBD severities exhibited high (70.35%) mean value. Accordingl y, the lower mean values of coffee yield coupled with higher CBD severity mean value will be not effective to be use in breeding program to get heterotic segregates. Accessions in cluster IV characterized by the longer and narrow for the fruit width (13.73 mm) and shorter height up to first primary branch (30.16) respectively, while the other was exhibited intermedi ate mean values.

Table 9 Mean values of 137 accessions for 10 coffee quantitative traits measured at Gera southwest Ethiopia during 2018/2019

Traits	I	II	III	IV	V	VI
CD	163.92	158.07*	173.41	167.56	168.85	174.13**
FL	16.32*	16.66	16.67	16.64	16.67	16.83**
FT	11.86	11.95	11.86	11.95	12.02**	11.77*
FW	13.56	13.66	13.52*	13.73**	13.71	13.55
CBD	36.62	70.35**	13.74	21.01	11.67	6.67*
RUST	8.14	3.27*	14.67**	10.79	14.67**	11.67
NSB	57.89*	71.29	59.34	63.81	117.44**	110.25
HUFPB	32.42	32.18	32.33	30.16*	34.04	42.00**
PBPB	62.20	54.06	58.33	61.30	63.24**	16.98*
YLD	778.19	246.12*	1547.09	1129.68	2136.65	2851.70**

**,* represents maximum and minimum values respectively, CD=Canopy diameter, FL=Fruit length (mm), FT=Fruit thickness (mm), FW=Fruit width (mm), CBD=Coffee berry disease (%), CLR=Coffee leaf rust (%), NSB=Number of secondary branch (no), HUFPB=Height up to first primary branch (cm), PBPB= percentage (%) of Bearing primary branch YLD=Bean yield (kg/ha)

4.1.12. Inter cluster distance (D^2) analysis based on quantitative traits

The chi-square test for the 6 clusters revealed that there were highly significant differences ($P<0.01$ $X^2 =21.67$) between the cluster except cluster I and II, I and III, I and IV, IV and II, IV and III (Table 12) indicating little genetic diversity between these clusters. This suggests that, crossing of genotypes from these clusters might not give higher heterotic value in F1 and narrow range of variability in the segregating F2 population. None significant and smallest inter- cluster distance were exhibited between cluster I and IV (2.337) whereas, the highest inter- cluster distance were exhibited between clusters II and VI (142.82), followed by cluster I and VI (100.94), VI and IV (76.06), II and V (73.89), III and VI (53.76), I and V (43.76), IV and V (27.71) II and III (26.24) indicating the presence of genetic variability between groups of tested genotypes.

Different genotypes with distant clusters could be used in the hybridization program to obtain a higher heterotic response in the hybrids and wide range of variation among the segregate. Since, the maximum inter cluster distance was observed between clusters II and VI (142.82), followed by cluster I and VI (100.94), which help to get a superior hybrid or recombinant by crossing between desirable lines of these clusters. However, the selection of parents should consider special advantages of each cluster and each genotype within a cluster depending on the specific objective of hybridization program. Crosses involving genotypes belonging to most divergent cluster distances could be used for hybridization program to obtain good manifestations of heterosis and wide variability (Singh and Chaudhary, 1987).

Table 10 Inter cluster distance for 10 quantitative traits of Bale and Wet Arsi zone coffee collection in Gera southwest Ethiopia

	I	II	III	IV	V	VI
I	0	5.528 ^{ns}	8.718^{ns}	2.377 ^{ns}	43.831**	100.935**
II		0	26.242**	13.993 ^{ns}	73.890**	142.817**
III			0	2.553 ^{ns}	15.906 ^{ns}	53.762**
IV				0	27.713**	76.058**
V					0	19.723*
VI						0

***,** **=Highly significant, ($p<0.01$) $x^2=21.67$, ($p<0.05$) $x^2=16$

4.2. Morphological Traits Evaluation using Qualitative Traits

4.2.1. Cluster analysis of 12 qualitative traits

Cluster analysis of coffee accession for 137 qualitative traits grouped into five clusters with different numbers of accessions in each cluster (Table 10). The accessions distributed in such a way that 40 accessions grouped in to cluster-II (29 %) followed by cluster-III consisted 34 accessions (25%), 31 % of accessions grouped in each cluster-II and IV and 1 accession (1%) grouped in cluster-V. Cluster-I contained predominantly stiff stem habit, spreading angle of insertion, green leaf tip color, round fruit shape, and many primary branches with few secondary branches. Cluster-II characterized by elliptic and oblong fruit shape, absence of both calyx limb persistent and fruit ribs. Mainly stiff stem habit, round fruit shape and absence of fruit ribs were grouped in to cluster III.

Only one accession alone grouped in cluster V and characterized by open growth habit, stiff stem habit, many primary branches with few secondary branches, and erect angle of insertion, Deltate stipule shape and green leaf tip color. Desalegn (2018) who reported that clustered of 64 accessions in to six groups based on qualitative traits. Atinafu *et al.,* (2017) also reported cluster of 124 Sidama coffee accessions into 10 distinct groups based on seven qualitative traits. Abdi (2009) reported phenotypic diversity among 49 Hararge coffee accessions for 16 quantitative characters and found out that the accessions were grouped into 6 clusters.

Table 11 Clustering patterns of 137 coffee accessions based on 12 qualitative characters

Clus	No.	No. acce	(%)	Name of accessions						
I		31	23	B275/07	B165/07	B112/07	B223/07	B86/07	B71/07	B89/07
				B268/07	B88/07	B299/07	B175/07	B76/07	B181/07	B232/07
				B281/07	B313/07	B108/07	B186/07	B231/07	B144/07	B308/07
				B306/07	B126/07	B270/07	B236/07	B318/07	B184/07	B297/07
				B191/07	B20/07	B91/07	B309/07			
II		40	29	B275/07	B165/07	B112/07	B223/07	B86/07	B71/07	B89/07
				B268/07	B88/07	B299/07	B175/07	B76/07	B181/07	B232/07
				B281/07	B313/07	B108/07	B186/07	B231/07	B144/07	B308/07
				B306/07	B126/07	B270/07	B236/07	B318/07	B184/07	B297/07
				B191/07	B20/07	B91/07	B309/07	B276/07	B310/07	B307/07
				B109/07	B192/07	B107/07	B269/07	B239/07		
III		34	25	B272/07	B174/07	B143/07	B93/07	B267/07	B300/07	B13/07
				B286/07	B311/07	B240/07	B67/07	B31/07	B167/07	B251/07
				B326/07	B95/07	B235/07	B305/07	B129/07	B170/07	B55/07
				B280/07	B125/07	B237/07	B117/07	B79/07	B225/07	B218/07
				B291/07	B69/07	B37/07	B321/07	B290/07	B56/07	B125/07
				B237/07	B117/07	B79/07	B225/07	B218/07	B291/07	B69/07
				B37/07	B321/07	B290/07	B56/07			
IV		31	23	B217/07	B81/07	B261/07	B258/07	B292/07	B39/07	B187/07
				B145/07	B264/07	B41/07	B173/07	B202/07	B293/07	B155/07
				B327/07	B160/07	B159/07	B284/07	B262/07	B273/07	B57/07
				B157/07	B113/07	B166/07	B116/07	B124/07	B298/07	B172/07
				B204/07	B287/07	B288/07				
V		1	1	B303/07						

4.2.2. Inter cluster distance (d^2) analysis on qualitative traits

The average inter cluster distance (D^2) analysis are presented in Table 12. The x^2-test for the five clusters result of qualitative traits indicates there was statistically significant ($P<0.01$) difference for all qualitative inter-clustered distance. This is agree with Desalegn (2018) who, reported that existence of highly significant ($P<0.01$) difference between all groups of cluster. The higher average inter-cluster distance value was recorded between I and V (1000.00) followed by II and V (798.08), IV and V (797.56), III and V (762.36) showed existence of wider genetic variability among tested groups of genotypes.

The crossing of clusters with narrow inter-cluster distance groups gives lower heterotic F1 offspring's. According to Singh *et al.,* (1987) maximum genetic recombination is expected

from the hybridization of the parents selected from divergent cluster groups. However, maximum genetic recombination and variation in the subsequent generation expected from crosses involving parents selected from cluster I and V followed by II and V, IV and V, III and. However the selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on specific objectives of hybridization (Singh, 2001; Chahal and Gosal, 2002). The result of above morphological characters showed the existence of distinct clustered groups and apparently divergent inter-cluster distances, these showed existence of genetic diversity to be used in selection and hybridization programs.

Table 12 Inter cluster distance for 12 qualitative traits of Bale and Wet Arsi coffee collection at Gera southwest Ethiopia

	I	II	III	IV	V
I	0	79.05**	93.05**	133.98**	1000.00**
II		0	33.67**	128.67**	798.08**
III			0	82.21**	762.36**
IV				0	797.56**
V					0

***,** **=Highly significant, ($p<0.01$) $x^2=24.72$, ($p<0.05$) $x^2=19.67$

4.2.3. Shannon weaver diversity index (H')

Estimation of (%) of frequency distribution, Chi-square, Shannon diversity index, Shannon's equitability and maximum Shannon's weaver diversity index for 12 qualitative traits presented Table.12. The overall mean of Shannon-waver diversity index (H') value was 0.79. The value of different qualitative traits ranges from a minimum value (0.24) to a maximum value (1.22), which revealed the existence of considerable diversity among 137 tested coffee accessions collected from Bale and West Arsi zone. Qualitative traits such as stipule shape, fruit shape, leaf tip color, fruit color, growth habit, leaf shape, angle of insertion, leaf apex shape and branching habit showed that the value of 1.22, 1.06, 1.02, 0.99, 0.96, 0.87, 0.83, 0.82, and 0.7 diversity index, respectively, which illustrate higher percent of contributions of generic diversity than the other traits.

Such view coincides, with the Masreshaw result (2018) who found that highest diversity for fruit color (1.22), followed by young leaf tip color (1.08), stipule shape (1.06), leaf shape (1.04), angle of insertion on primary branches (0.97), fruit shape (0.91), growth habit (0.90) and branching habit (0.73) which might be due to oligogenic nature of gene action and slight environmental interaction. Desalegn (2018) also report that those traits that contribution more for genetic variability are branching habit, fruit shape, and growth habit.

Low Shannon's equitability (E_H) indicates unbalanced frequency classes for an individual trait and indicates lack of diversity. The results of E_H between 0 and 1 range from least value 0.35 to highest value 0.93 reveals that the existence of variability among tested traits of Bale and West Arsi accession. Accordingly, leaf tip colors, fruit color, growth habit, fruit shape and stipule shape were more diverse as compare to calyx limb persistent and fruit ribs. The diversity index above 0.35 indicated that existence of diversity. The result was partially agreed with Yigzaw (2005) who found that traits such as leaf apex shape, plant habit, fruit shape and fruit color were more diverse compared to the overall appearance of the tree and young leaf color.

In addition, the higher percentage morphological of frequency distribution of coffee traits exhibited by absence of calyx leaf persistent (93.5%), followed by without fruit ribs (92.8%), and stiff morphological stem habit (80.4%) (Table.14).This result was in line with the work of Masreshaw (2018) who reported stiff stem, without fruit ribs, without calyx limb persistence gave higher percent of morphological frequency distribution than other traits. Other morphological traits such as branching habit of, many primary branches with few secondary branches (71%), angle of insertion for spreading character (65.9%), and lanceolate leaf shape (63.8%) also exhibited high morphological frequency. In this study trait such as intermediate growth habit (58.7 %), red purple fruit color (54.3%), elliptic leaf apex shape (52.9%), ovate stipule shape (50%), bronzy leaf tip color (48.6%), round fruit shape (46.4%) gave moderate percent of frequency distribution (Table 14).

Chi-square test value showed existences of dominant phenotypic variation among evaluated 12 qualitative traits were presented in (Table 14). The observe value was higher than the expected phenotypic value. However, all scored qualitative expressive traits showed a highly

significant difference. This indicates the recorded data showed dominant phenotypic classes for elliptic leaf apex shape (82.96) followed by a lanceolate leaf shape (83.00), many branches (primary) with few secondary branches for branching habit (58.78), spreading from the angle of insertion (44.02), obovate leaf shape (32.53) and leaf apex shaped (32.53), intermediate growth habit (26.6), round stipule shaped (20.2)), red-purple fruit color (18.3) and greenish Leaf tip color (10.5) showed dominant than other the same phenotypic classes

Table 13 Percent (%) contribution to variation, Chi-square, Shannon-weaver diversity index, maximum Shannon's weaver diversity index and Shannon's equitability for 12 morphological qualitative traits

Traits	Code	Phenotypic class	Proportion	% contribution.	Chi-square	H'	H_{max}	EH
Growth habit	1	Open	28	20.3	39.96**			
	2	Intermediate	81	58.7				
	3	Compact	29	21		0.96	1.1	0.88
Stem habit	1	Stiff	111	80.4	51.13**			
	2	Flexible	27	19.6		0.49	0.69	0.71
Branching habit	1	VFPB	4	2.9	99.3**			
	2	MPBWFSB	98	71				
	3	MPBWMSB	36	26.1		0.7	1.1	0.63
Angle of insertion	1	Drooping	11	8	72.83**			
	2	Spreading	91	65.9				
	3	Erect	36	26.1		0.83	1.1	0.75
Leaf tip color	1	Greenish	24	17.4	20.13**			
	2	Green	47	34.1				
	3	Bronzy	67	48.6		1.02	1.1	0.93
Leaf shape	1	Obovate	1	0.7	133.48**			
	2	Ovate	10	7.2				
	3	Elliptic	39	28.3				
	4	Lanceolate	88	63.8		0.87	1.39	0.63
Leaf Apex shape	1	Obovate	1	1.4	133.48**			
	2	Ovate	10	1.4				
	3	Elliptic	39	52.9				
	4	Lanceolate	88	44.2		0.82	1.39	0.59
Stipule shape	1	Round	4	2.9	107.43**			
	2	Ovate	69	50				
	3	Triangular	19	13.8				
	4	Deltate	40	29				
	5	Trapezium	6	4.3		1.22	1.61	0.76
Fruit shape	1	Round	64	46.4	67.04**			
	2	Obovate	1	0.7				
	3	Elliptic	49	35.5				
	4	Oblong	24	17.4		1.06	1.39	0.77
Fruit color	1	Orange red	39	28.3	28.80**			
	2	Red	24	17.4				
	3	Red-purple	75	54.3		0.99	1.1	0.9
Calyx limb p	0	Not	129	93.5	104.35**			
	1	Persistent	9	6.5		0.24	0.69	0.35
Fruit ribs	0	Absent	128	92.8	51.31**			
	1	Present	10	7.2		0.26	0.69	0.38

H'=Shannon-weaver diversity index, H_{max}=maximum Shannon's weaver diversity indexed, E_H =Shannon's equitability, VFPB= Very few branches (primary), MPBWFSB=many branches (primary) with few secondary branches, MPBWMSB=many branches (primary) with many secondary branches

5. SUMMARY AND CONCLUSION

Morphological characterization of Bale and Arsi coffee collections was done at Gera Researc h sub center to provide valuable information about the collections. The analysis of variance showed that significant differences among the coffee collections, including for bean yield, fruit thickness, canopy diameter, fruit length, fruit width, coffee berry disease (CBD), Coffee leaf rust (CLR), number of secondary branches, percent (%) of bearing primary branch and height up to first primary branch. This suggests the presence of high variability for yield and other related traits in the studied collections, there by indicating the possibility for furthergenetic analyses. There was high variation between the coffee accessions with traits measured. Higher mean yield coupled with resistance to CBD exhibited by accession, B184/0 7 and B29/07 with respective mean value of 2886.33 and 1939.74kg/ha from Bale areas. While, the accessions B32 and B289/07 gave moderately high yield from West Arsi with respective mean value of 1676.36, and 1533.43 kg/ha. These accessions can be promoted to next breeding programs.

For most traits genotypic coefficients of variation were very close to their corresponding estimates of phenotypic coefficient of variation. Closer phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for coffee leaf rust, coffee berry disease, bean yield, number of secondary branch and percent of bearing primary branch. The observed variation existed in coffee accessions indicated the combination of both genotype and environment in the expression of these characters. High (> 50 %) to moderate (20-50%) heritability was obtained for all traits except number of primary branch and number of node on primary branch. This indicates that less influence of environment in the expression of the characters and selection can be made through phenotypic performance. High genetic advance as percent of mean (GAM) were obtained for the trait coffee leaf rust (92.8%), coffee berry disease (75.0%), number of secondary branch (60.28%), percent of bearing primary branch (58.28%), yield (47.21%) and height up to first primary branch (23.08%), respectively. Whereas, medium GAM (10%-20%) were observed for canopy diameter and leaf size while the remaining all traits showed low genetic advance as percent of mean (<10%).

The high PCV, GCV, genetic advance as percent of mean value (>20%) coupled with higher to moderate heritability were recorded for coffee leaf rust, coffee berry disease, number of

secondary branch, percent (%) of bearing primary branch, yield and height up to first primary branch. This indicates that the traits are governed by additive effects of genes and improveme nt of the traits can be practiced through simple selection. Both phenotypic and genotypic correlation coefficient analyses showed positive and significant association of coffee yield with most traits like percent (%) of bearing primary branch, coffee leaf rust (CLR) and canopy diameter. CBD was negatively and significantly correlated with coffee yield. Canopy diameter, height up to primary branch, percentage of bearing primary branch and coffee leaf rust exerted positive direct effect on seed yield and can be considered as principal traits while working for coffee yield improvement.

Cluster analysis grouped 137coffee accessions in to six clusters based on their similarity. The highest inter-cluster distance occurred between clusters II and VI followed by I and VI. This is a good opportunity to be get heterotic offspring. Principal components analysis showed that about 70.55% of the total variation among genotypes through PC1 to PC4 and the total variation loaded largely by traits like canopy diameter, height up to first primary branch, percentage of bearing primary branch and coffee leaf rust. Shannon-waver diversity index (H’**)** in different qualitative traits, revealed that existence of genetic variation. Higher E_H for qualitative traits exhibited by leaf tip colors, fruit color, growth habit, fruit shape and stipule shape.

Generally, the present study showed existence of significant genetic variability among tested genotypes indicating the presence of a huge opportunity for further improvement through selection and other breeding approaches. Hence there is an opportunity to exploit these collection to develop varieties that perform better for Bale and West Arsi coffee germplasm for the future coffee improvement program. In order to confirm the present encouraging result, further research must be done with physiological, quality and biochemical analysis with the support of advanced molecular techniques which provides immense potential to ensure effective utilization, conservation and development of improved varieties.

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7. APPENDIXES

Appendix Table 1. Mean performance of clean coffee yield and yield related quantitative traits of Bale and West Arsi coffee accession at Gera, Southwest Ethiopia during 2018/19 cropping season

Accessions	CANOP	FL	FT	FW	POBPB
74148	141.13	14.43	10.89	12.68	69.18
74165	140.25	14.65	10.94	13.00	66.45
74110	142.67	14.67	11.30	12.97	69.70
75227	167.13	15.34	11.50	13.67	64.65
B204/07	160.67	18.50	12.78	14.53	39.43
B77/07	119.29	16.16	11.62	13.30	32.27
B68/07	146.29	14.68	11.57	13.22	57.82
B69/07	168.54	16.69	11.68	14.12	63.08
B71/07	143.29	18.01	12.03	14.56	54.87
B37/07	202.54	16.15	11.60	14.01	70.19
B144/07	172.29	17.07	11.89	12.76	57.97
B82/07	131.67	14.13	11.36	13.00	64.99
B89/07	146.54	17.22	12.25	14.54	61.19
B93/07	171.17	15.95	11.69	13.11	68.38
B181/07	216.17	17.46	12.62	14.82	64.68
B186/07	124.67	17.95	12.84	14.15	68.00
B65/07	147.29	17.57	12.04	14.10	63.44
B57/07	154.79	16.57	11.43	13.38	60.58
B217/07	171.67	18.92	11.98	14.34	59.00
B224/07	105.92	15.91	11.02	12.91	57.93
B240/07	182.67	14.72	11.31	13.15	63.86
B231/07	150.79	18.49	13.32	15.31	35.17
B251/07	155.29	16.38	12.35	13.50	66.56
B265/07	156.42	15.31	11.20	13.03	65.43
B268/07	161.79	18.10	12.12	14.98	63.30
B269/07	157.04	17.46	12.33	14.57	63.59
B274/07	124.04	15.44	11.66	13.80	46.17
B275/07	157.04	17.82	12.49	14.41	65.77
B276/07	169.92	18.30	11.75	14.47	70.26
B281/07	168.17	14.82	11.34	13.41	66.22
B288/07	166.29	20.31	13.15	15.17	36.71
B270/07	182.42	16.86	12.15	14.46	66.48
B271/07	176.42	15.71	11.55	13.03	69.33
B280/07	176.79	15.01	11.05	12.91	70.02
B308/07	149.67	17.02	12.19	14.27	54.85
B73/07	177.92	15.82	11.79	12.98	66.12
B306/07	165.46	16.51	11.85	13.53	71.57
B88/07	159.67	18.15	12.58	14.58	83.30

Accessions	CANOP	FL	FT	FW	POBPB
B321/07	154.04	16.21	11.75	13.66	70.00
B143/07	174.67	16.23	12.29	13.60	73.95
B285/07	159.92	15.84	10.85	12.77	61.65
B95/07	158.92	15.34	11.65	13.41	74.24
B126/07	153.88	16.86	11.31	12.76	87.96
B261/07	171.67	17.69	11.00	13.39	47.13
B187/07	193.17	15.94	11.10	13.16	69.29
B81/07	140.10	17.70	11.71	13.64	48.10
B290/07	178.04	14.28	11.07	12.67	79.75
B266/07	156.79	18.45	12.20	13.82	62.30
B244/07	156.92	15.56	12.25	14.14	66.46
B326/07	137.01	16.24	11.42	13.37	71.85
B277/07	145.51	15.32	11.27	13.11	66.09
B310/07	160.01	17.09	11.68	13.38	74.17
B56/07	156.39	15.34	11.55	13.67	74.31
B278/07	150.14	14.73	10.76	12.72	68.77
B299/07	154.51	16.10	11.33	13.15	67.88
B279/07	133.39	14.59	11.40	13.31	75.96
B238/07	169.01	14.64	12.03	13.64	61.54
B289/07	159.89	15.50	11.36	12.44	73.87
B304/07	178.89	15.87	12.00	13.33	63.29
B235/07	181.14	17.27	13.53	13.99	57.51
B286/07	173.26	16.02	13.35	13.75	62.76
B272/07	189.26	17.89	13.33	14.59	59.64
B258/07	164.26	16.89	13.01	13.65	68.77
B307/07	174.51	17.16	11.13	13.28	65.23
B125/07	170.51	14.52	11.14	12.53	62.76
B236/07	158.76	17.12	11.66	13.41	65.90
B237/07	183.39	17.17	13.02	13.93	42.72
B239/07	177.68	17.50	12.70	14.31	58.82
B264/07	153.18	17.64	13.16	14.63	46.59
B298/07	166.26	15.93	12.32	13.40	52.41
B305/07	152.76	13.81	11.95	13.03	46.71
B315/07	153.68	15.93	11.96	13.56	68.15
B303/07	170.51	17.54	12.53	13.92	56.73
B300/07	188.76	17.37	13.31	14.84	47.11
B175/07	152.14	17.13	11.91	14.25	67.67
B262/07	143.26	17.24	12.12	13.78	62.56
B267/07	192.39	17.64	13.54	15.05	63.85
B309/07	168.39	18.55	12.42	14.22	53.31
B116/07	188.51	15.97	12.78	13.93	65.66
B273/07	182.51	14.63	11.40	12.70	62.00
B13/07	177.76	17.37	12.57	14.13	61.28

Accessions	CANOP	FL	FT	FW	POBPB
B29/07	159.01	18.19	12.63	14.18	65.70
B91/07	134.89	17.47	13.22	15.45	51.99
B311/07	161.14	15.83	12.68	13.47	52.95
B170/07	174.51	18.79	12.81	14.45	67.23
B297/07	171.76	17.95	13.14	14.89	62.95
B282/07	216.51	17.58	12.62	14.39	63.60
B293/07	147.14	17.22	12.23	13.78	64.99
B110/07	145.01	18.45	12.01	14.07	59.19
B165/07	151.39	17.95	12.42	13.71	25.20
B287/07	151.39	18.84	12.19	12.92	60.38
B67/07	166.89	15.90	11.92	12.69	65.20
B172/07	178.70	16.35	10.79	13.23	7.22
B292/07	171.95	16.42	11.36	13.35	20.98
B39/07	195.45	16.76	11.63	13.72	75.25
B317/07	174.83	15.22	11.11	12.93	64.91
B159/07	166.33	17.22	11.24	13.46	20.31
B318/07	177.33	18.08	12.39	14.38	64.26
B76/07	156.45	17.23	13.08	14.19	58.43
B112/07	202.83	18.53	12.62	14.33	68.78
B31/07	181.20	15.62	11.68	13.96	26.37
B113/07	186.58	16.93	11.82	13.24	46.89
B174/07	171.45	15.07	11.08	12.42	64.68
B184/07	187.83	16.90	11.40	13.36	74.60
B223/07	144.20	17.78	11.85	13.77	19.49
B232/07	146.58	17.65	11.94	13.63	23.60
B108/07	173.08	17.26	11.95	13.30	79.63
B86/07	200.95	15.31	11.27	12.45	78.45
B145/07	184.95	16.62	11.99	13.11	72.86
B109/07	175.58	17.16	11.37	13.34	74.11
B167/07	181.20	17.03	12.21	13.69	61.66
B313/07	164.45	17.15	12.33	13.93	68.14
B55/07	155.58	15.29	11.09	12.60	65.62
B157/07	170.20	17.30	12.19	14.00	43.10
B107/07	182.58	17.42	10.90	13.08	59.64
B117/07	205.58	16.23	12.83	14.22	5.05
B218/07	169.20	15.94	11.62	13.16	5.83
B327/07	151.20	15.91	11.23	13.20	49.26
B41/07	137.58	17.79	12.44	14.16	25.74
B124/07	192.08	16.26	11.42	14.37	30.78
B79/07	171.53	15.84	11.61	13.10	31.90
B191/07	111.70	16.00	11.15	12.90	55.71
B225/07	178.20	17.47	12.51	14.51	40.20
B173/07	154.20	17.19	11.48	13.62	66.72

Accessions	CANOP	FL	FT	FW	POBPB
B28/07	167.83	16.37	11.70	13.17	65.63
B20/07	175.45	17.44	11.18	13.16	76.73
B21/07	158.58	17.03	11.43	13.70	35.82
B192/07	165.83	17.18	12.25	14.09	76.47
B202/07	169.03	15.11	11.00	12.69	5.75
B166/07	155.95	13.80	9.82	11.60	8.17
B11/07	169.45	16.28	12.57	13.70	17.08
B155/07	191.20	17.26	12.57	14.50	42.60
B160/07	181.45	16.41	11.80	13.22	54.49
B284/07	165.20	14.09	9.89	11.54	5.93
B291/07	153.58	14.49	11.20	12.44	66.79
B129/07	171.70	15.32	12.22	12.79	8.63
B05/07	172.83	15.89	12.38	14.07	5.02
CV	7.69	6.52	3.20	8.11	6.05
Mean	164	164	11.9	13.6	57
P value	0.0072	<.0001	0.0389	0.0028	0.0008
LSD(1)	11.84	0.33	0.42	0.36	3.95
LSD(2)	20.51	0.58	0.72	0.62	6.84
LSD(3)	14.50	0.41	0.51	0.44	4.84
LSD(4)	13.24	0.37	0.47	0.40	4.42

* LSD(1), between two control treatments; LSD(2), between two test treatments in the same block; LSD(3), between two test treatments not in the same block; LSD(4), between a test treatment and a control treatment.

Appendix Table 1 (Continued)

Accession	RUST	CBD	YLD	NSB	HUFPB
74148	12.33(7.0)	0.95(0.5)	921.45	46.3(6.8)	24.42
74165	11.66(6.7)	6.06(3.5)	818.32	31.5(5.6)	21.08
74110	9.00(5.1)	12.16(6.9)	1357.54	69.75(8.2)	27.00
75227	16.11(9.2)	17.87(9.9)	1097.47	41.08(6.4)	25.75
B204/07	5.94(3.4)	102.71(50.9)	125.64	61.2(7.8)	34.50
B77/07	6.27(3.6)	107.71(52.5)	20.31	85.3(9.3)	38.83
B68/07	5.94(3.4)	27.71(15.7)	303.95	18.4(4.0)	28.25
B69/07	7.61(4.3)	36.71(20.7)	698.43	42.4(6.4)	33.75
B71/07	10.61(6.1)	39.38(22.1)	289.66	22.7(4.5)	32.00
B37/07	12.27(7.0)	35.71(20.1)	636.05	37.5(6.0)	34.25
B144/07	12.27(7.0)	69.71(37.6)	380.84	37.5(6.0)	29.25
B82/07	6.27(3.6)	13.11(7.4)	777.83	24.5(4.7)	23.50
B89/07	10.61(6.1)	23.7(13.4)	468.25	23.5(4.6)	31.50
B93/07	12.27(7.0)	32.71(18.5)	1765.70	80.2(9.0)	36.50
B181/07	32.27(18.3)	17.91(10.1)	1711.91	33.5(5.7)	40.00
B186/07	27.27(15.5)	17.71(10.0)	1719.58	58.5(7.6)	32.50

Accession	RUST	CBD	YLD	NSB	HUFPB
B65/07	12.27(7.0)	8.71(4.9)	1213.68	22.7(4.5)	26.75
B57/07	5.94(3.4)	22.71(12.9)	340.40	62.5(7.9)	27.75
B217/07	13.94(8.0)	81.71(42.9)	898.34	117(11.0)	34.75
B224/07	13.94(8.0)	8.11(4.5)	761.15	14.2(3.3)	25.50
B240/07	7.94(4.5)	35.91(20.2)	912.94	25.2(4.8)	33.50
B231/07	7.94(4.5)	30.46(17.2)	435.26	31.7(5.5)	32.50
B251/07	8.94(5.1)	9.71(5.4)	996.75	46(6.8)	29.00
B265/07	12.61(7.2)	10.11(5.7)	837.71	61.5(7.9)	35.50
B268/07	13.94(8.0)	35.71(20.1)	1163.00	42.7(6.5)	39.50
B269/07	15.61(8.9)	26.71(15.1)	842.55	36.2(5.9)	41.25
B274/07	4.44(2.5)	7.71(4.3)	156.92	19.2(4.1)	23.50
B275/07	22.27(12.7)	31.71(17.9)	794.65	61(7.9)	33.00
B276/07	7.94(4.5)	10.31(5.8)	1210.17	57.2(7.6)	25.75
B281/07	10.94(6.2)	8.91(5.0)	573.92	37.2(6.0)	23.75
B288/07	6.27(3.6)	51.71(28.7)	184.02	80(9.1)	35.25
B270/07	10.61(6.1)	0.00(4.3)	1839.93	36(6.0)	34.50
B271/07	30.61(17.3)	14.71(8.3)	1000.37	78.5(8.9)	36.50
B280/07	35.61(20.1)	12.91(7.3)	1371.89	84.4(9.3)	25.50
B308/07	20.61(11.7)	15.71(8.9)	1071.54	68.7(8.3)	35.75
B73/07	7.94(4.5)	11.71(6.6	1095.44	46.2(6.7)	30.25
B306/07	5.61(3.2)	7.96(4.4)	846.88	55.4(7.4)	29.50
B88/07	25.61(14.6)	10.00(5.7)	1628.93	58.2(7.6)	42.50
B321/07	13.94(8.0)	0.50(0.28)	1679.90	34.7(5.8)	35.25
B143/07	33.94(19.2)	94.71(48.1)	585.38	76(8.8)	37.50
B285/07	12.27(7.0)	7.71(4.3)	1533.43	67(8.2)	25.75
B95/07	9.27(5.3)	40.71(22.9)	820.50	63.2(8.0)	29.00
B126/07	6.27(3.6)	44.2(44.2)	427.55	75.9(8.8)	34.00
B261/07	9.27(5.3)	96.71(48.8)	138.15	53(7.3)	34.75
B187/07	7.61(4.3)	12.71(7.2)	1004.05	110.7(10.6)	32.50
B81/07	13.94(8.0)	71.04(38.2)	282.43	26.5(4.9)	24.69
B290/07	17.27(9.8)	25.21(14.3)	1445.03	68.2(8.3)	34.00
B266/07	10.61(6.1)	17.71(10.0)	1319.37	61.4(7.8)	30.17
B244/07	18.94(10.8)	23.71(13.4)	1086.83	36.5(5.9)	29.50
B326/07	1.04(-0.5)	24.34(13.8)	861.24	56(7.5)	25.00
B277/07	3.95(2.3)	4.54(2.5)	1021.79	19.5(4.7)	23.00
B310/07	12.28(7.0)	14.34(8.1)	1014.75	56.8(7.5)	30.00
B56/07	35.61(8.6)	19.54(11.1)	1508.98	70.79(8.3)	26.00
B278/07	10.61(6.1)	16.74(9.5)	757.69	62.8(7.9)	20.25
B299/07	20.61(11.7)	12.34(7.0)	1040.00	42.5(6.6)	28.00
B279/07	0.61(0.4)	17.09(9.7)	354.31	37(6.2)	27.75
B238/07	-0.22(-0.1)	76.84(40.4)	1161.62	90(9.4)	31.00
B289/07	10.61(6.1)	2.20(1.2)	1676.36	66.3(8.1)	38.75

Accession	RUST	CBD	YLD	NSB	HUFPB
B304/07	3.95(2.3)	14.74(8.3)	1036.80	60.8(7.8)	37.00
B235/07	-1.05(-0.5)	69.34(37.1)	666.78	87(9.2)	26.25
B286/07	3.95(2.3)	10.00 (5.1)	1778.45	62.8(7.9)	23.50
B272/07	-5.39(-3.0)	38.34(21.5)	1178.30	99.5(9.8)	37.00
B258/07	-7.05(-4.0)	56.34(30.9)	687.24	71.3(8.4)	33.50
B307/07	38.95(10.6)	33.34(18.8)	1375.40	52.3(7.2)	31.25
B125/07	-2.72(-1.5)	10.34(5.8)	728.19	33.8(5.9)	31.75
B236/07	5.61(3.2)	20.34(11.5)	1121.59	30.5(5.7)	31.25
B237/07	-2.39(-1.3)	92.34(46.6)	185.15	96(9.7)	27.25
B239/07	7.28(4.2)	27.67(15.6)	700.14	35.5(6.1)	42.50
B264/07	-3.72(-2.1)	61.84(33.6)	698.75	17.5(4.5)	34.17
B298/07	2.28(1.4)	11.34(6.4)	1217.00	19.5(4.7)	28.75
B305/07	-4.05(-2.3)	49.34(27.3)	665.39	22.3(5.0)	26.25
B315/07	5.61(3.2)	41.84(23.4)	836.78	87.5(9.2)	28.17
B303/07	-5.72(-3.2)	65.34(35.2)	853.04	76(8.6)	31.00
B300/07	-7.39(-4.2)	85.34(43.9)	281.75	173(12.9)	14.75
B175/07	13.95(8.0)	32.34(18.2)	2031.48	94.3(9.6)	43.00
B262/07	-5.72(-3.2)	89.34(45.4)	632.86	60.3(7.7)	29.75
B267/07	0.61(0.4)	66.34(35.7)	1157.45	112.5(10.4)	30.00
B309/07	8.95(5.1)	12.54(7.1)	1461.03	78.3(8.7)	26.25
B116/07	-7.72(-4.4)	97.34(48.3)	348.47	124(10.9)	43.00
B273/07	9.28(5.3)	23.34(13.2)	2312.21	142(11.7)	38.25
B13/07	-2.72(-1.5)	4.00(2.7)	1546.59	52.8(7.3)	38.75
B29/07	-2.72(-1.5)	8.00(4.2)	1939.74	97.3(9.7)	40.00
B91/07	5.95(3.4)	8.34(4.7)	1086.14	26(5.3)	23.75
B311/07	-4.05(-2.3)	6.54(3.7)	812.01	39.5(6.4)	31.75
B170/07	-2.39(-1.3)	63.34(34.3)	260.90	152.3(12.1)	42.25
B297/07	-2.39(-1.3)	4.34(2.4)	1068.55	22.2(5.0)	28.75
B282/07	-2.72(-1.5)	15.84(9.0)	1528.58	28.3(5.5)	32.50
B293/07	25.61(14.4)	88.34(45.1)	695.41	87.5(9.2)	26.75
B110/07	-3.72(-2.1)	13.34(7.5)	885.57	41.8(6.5)	44.50
B165/07	-6.72(-3.8)	91.34(46.2)	185.84	87.8(9.2)	25.75
B287/07	0.61(0.4)	36.01(20.2)	1316.74	28.3(5.5)	30.50
B67/07	-1.05(-0.5)	48.5426.9)	696.25	34.3(6.0)	31.50
B172/07	10.45(6.0)	87.95(41.5)	36.72	38.2(6.1)	45.75
B292/07	6.11(3.5)	74.62(37.0)	342.48	61.7(7.9)	26.50
B39/07	17.11(9.7)	9.85(-5.4)	1474.36	64.7(8.1)	36.50
B317/07	9.11(5.2)	0.05(0.2)	857.86	55.2(7.4)	31.50
B159/07	27.11(15.4)	64.20(32.9)	184.06	75.2(8.7)	43.00
B318/07	17.11(9.7)	18.95(10.8)	1102.90	84(9.3)	33.75
B76/07	12.11(6.90	7.95(4.7)	894.07	45.7(6.7)	29.25
B112/07	12.11(6.9)	27.95(15.6)	1390.82	77.2(8.8)	41.00

Accession	RUST	CBD	YLD	NSB	HUFPB
B31/07	8.78(5.0)	70.95(35.6)	271.28	121.7(11.1)	42.75
B113/07	7.11(4.0)	49.95(26.6)	665.55	94.5(9.8)	34.50
B174/07	17.11(9.7)	9.05(-5.0)	1294.05	42.2(6.5)	30.50
B184/07	15.45(8.8)	5.05(-2.7)	2886.33	112(10.7)	48.75
B223/07	4.11(2.3)	50.45(26..8)	450.59	62.4(7.9)	17.33
B232/07	3.78(2.1)	42.95(23.2)	275.45	42.2(6.5)	27.00
B108/07	4.45(2.5)	2.95(1.9)	1121.44	79.7(9.0)	30.00
B86/07	9.11(5.2)	24.95(14.0)	1675.46	87.2(9.4)	28.00
B145/07	18.78(10.7)	28.95(16.1)	2254.82	113.5(10.7)	28.25
B109/07	5.78(3.3)	4.95(3.0)	1242.68	78.7(8.9)	41.00
B167/07	18.78(10.7)	61.95(31.9)	1152.61	98.2(10.0)	44.75
B313/07	9.11(5.2)	2.95(1.9)	1462.23	34.7(5.8)	25.00
B55/07	10.45(6.0)	13.15(7.6)	1436.17	42.2(6.5)	36.00
B157/07	4.11(2.3)	6.06(32.8)	887.05	92(9.7)	33.75
B107/07	3.78(2.1)	65.95(33.6)	521.48	75(8.7)	43.75
B117/07	4.28(2.4)	87.95(41.5)	58.40	63.2(8.0)	40.25
B218/07	3.78(2.1)	87.95(41.5)	64.34	46.2(6.8)	29.00
B327/07	5.78(3.3)	54.62(28.7)	359.37	29.7(5.4)	29.00
B41/07	3.78(2.1)	62.95(32.4)	177.45	22.2(4.6)	45.00
B124/07	5.78(3.3)	69.20(34.9)	218.63	66.5(8.2)	36.00
B79/07	4.11(2.3)	80.45(39.1)	208.21	60.4(7.8)	31.00
B191/07	4.11(2.3)	77.95(38.2)	170.16	23.7(4.8)	33.00
B225/07	5.78(3.3)	56.95(29.8)	526.11	87.7(9.4)	27.50
B173/07	22.11(12.6)	53.95(28.4)	1242.47	141.5(12.0)	28.00
B28/07	9.11(5.2)	5.4(3.1)	1562.94	90.7(9.6)	42.50
B20/07	7.11(4.0)	65.45(33.4)	1192.33	121(11.1)	40.75
B21/07	7.45(4.2)	44.95(24.2)	899.38	118(11.0)	42.75
B192/07	5.45(3.1)	71.95(36.0)	546.12	75(8.7)	21.50
B202/07	3.78(2.1)	87.95(41.5)	94.05	168.7(13.1)	27.67
B166/07	12.45(7.1)	87.95(41.5)	117.34	127.5(11.4)	31.00
B11/07	7.45(4.2)	82.95(39.9)	217.42	63.2(8.0)	37.50
B155/07	10.45(6.0)	75.95(37.5)	628.51	94.2(9.8)	39.25
B160/07	7.45(4.2)	67.95(34.4)	820.68	61.5(7.8)	30.75
B284/07	3.78(2.1)	87.95(41.5)	118.55	47.5(6.9)	32.25
B291/07	9.11(5.2)	0.85(-0.3)	1305.56	51(7.2)	31.75
B129/07	3.78(2.1)	79.20(38.6)	96.66	61.5(7.8)	25.75
B05/07	4.11(2.3)	87.95(41.5)	318.61	66.2(8.2)	29.25
CV	32.40	34.52	35.61	23.64	6.07
Mean	8.9	37.2	950.1	25.5	57
P value	0.0059	0.0159	0.0547	0.0294	0.0024
LSD(1)	1.44	7.87	0.14	1.67	1.28
LSD(2)	2.49	13.63	0.24	1.06	2.22

LSD(3)	1.76	9.64	0.17	1.83	1.57
LSD(4)	1.61	8.80	0.16	1.29	1.43

Values in the brackets indicate transformed mean

Appendix Table 2. Visual data recorded for 137 coffee accessions based on 12 qualitative traits at Gera southwest Ethiopia during 2018/2019

Accession	Growth habit	Stem habit	Branching habit	Angle of insertion	Leaf tip color	Leaf shape	Leaf apex shape	Stipule shape	Fruit shape	Fruit color	Calyx limb p	Fruit ribs
74148	3	2	3	2	2	4	4	2	1	6	1	0
74165	3	2	3	2	2	4	4	2	1	6	1	0
B277/07	3	2	2	2	2	4	4	2	1	6	1	0
B238/07	2	1	2	2	2	4	5	4	1	4	0	0
B289/07	2	1	2	1	2	4	5	4	1	4	0	0
B65/07	2	2	2	2	2	4	4	2	1	5	0	0
B317/07	2	2	2	2	2	4	4	3	1	5	0	0
B73/07	2	1	2	2	2	4	4	3	1	6	0	0
B11/07	2	1	2	2	2	4	4	2	1	6	0	0
74110	3	1	3	2	2	4	4	4	1	6	1	0
B278/07	3	1	3	2	2	4	4	4	1	5	1	1
B285/07	2	1	3	2	2	4	4	4	1	4	1	0
B29/07	2	1	3	2	2	3	4	4	1	4	0	0
B224/07	2	1	2	2	1	3	4	2	1	4	1	0
B110/07	2	1	2	2	2	3	4	2	1	4	0	0
B28/07	3	1	2	2	2	4	4	2	1	4	0	0
B21/07	3	1	3	2	1	4	4	2	1	4	0	0
B05/07	2	1	2	2	1	3	5	2	1	4	0	0
B265/07	2	2	2	2	1	4	5	3	1	5	0	0
B266/07	2	1	3	2	2	4	5	3	1	6	0	0
B271/07	2	2	2	1	2	4	5	4	1	5	0	0
B82/07	3	1	1	3	1	4	4	4	1	6	0	1
B279/07	3	1	2	3	2	4	4	4	1	6	0	0
B244/07	3	2	2	2	3	4	4	3	1	6	0	0
75227	3	1	2	3	2	4	4	1	1	6	0	0
B315/07	2	2	2	3	2	3	4	2	1	6	0	0
B68/07	1	1	3	3	1	2	5	2	1	6	0	0
B282/07	1	1	2	3	2	3	5	1	1	6	0	0
B274/07	3	1	2	2	1	4	3	3	1	6	1	0
B304/07	1	1	2	3	1	4	4	2	1	5	0	0
B77/07	2	1	2	1	1	3	5	3	1	6	0	0
B275/07	2	1	2	2	1	4	4	2	5	6	0	0
B165/07	2	1	2	2	1	4	4	2	5	6	0	0
B112/07	2	1	2	2	2	4	4	2	5	6	0	0
B223/07	3	1	2	2	2	4	5	2	4	6	0	0
B86/07	3	1	3	2	2	4	5	2	4	6	0	0

Appendix Table 2. (continued)

Accession	Growth habit	Stem habit	Branching habit	Angle of insertion	Leaf tip color	Leaf shape	Leaf apex shape	Stipule shape	Fruit shape	Fruit color	Calyx limb p	Fruit ribs
B71/07	1	1	1	3	1	4	5	1	5	6	0	0
B89/07	1	1	1	3	1	4	5	2	5	5	0	0
B268/07	2	1	2	2	2	4	5	2	4	6	0	1
B88/07	1	1	2	2	2	4	5	2	5	6	0	1
B299/07	3	1	2	2	2	4	4	2	4	4	0	0
B175/07	2	1	3	2	2	4	4	2	4	4	0	0
B76/07	2	1	2	2	2	4	5	2	4	4	0	0
B181/07	2	1	2	2	2	3	5	5	5	6	0	0
B232/07	2	1	2	2	1	3	5	4	5	6	0	0
B281/07	2	1	2	3	2	4	5	4	5	4	0	0
B313/07	2	1	2	3	2	4	4	4	4	4	0	0
B108/07	3	1	3	2	2	4	4	2	4	5	0	0
B186/07	2	2	3	2	2	4	5	5	5	4	0	1
B231/07	2	2	3	2	1	3	5	5	5	5	0	1
B144/07	2	1	2	3	2	3	5	2	5	6	0	1
B308/07	2	1	2	2	2	4	4	4	5	4	0	1
B306/07	2	1	2	3	1	4	5	4	5	6	0	0
B126/07	2	1	2	2	2	4	4	4	5	6	0	0
B270/07	1	1	2	3	2	4	4	3	4	6	0	1
B236/07	1	1	3	3	2	4	4	2	4	6	0	0
B318/07	2	2	2	3	2	3	5	2	4	5	0	0
B184/07	2	1	3	3	2	4	5	2	4	5	0	0
B297/07	2	1	2	3	1	3	5	2	5	4	0	0
B191/07	2	2	2	3	1	4	5	2	4	4	0	0
B20/07	2	1	2	2	1	4	4	2	5	4	0	0
B91/07	1	1	2	3	2	4	4	2	4	5	1	0
B309/07	2	1	2	3	2	3	4	1	4	4	0	0
B276/07	1	1	2	2	2	3	5	4	4	4	0	0
B310/07	2	1	3	2	2	4	4	4	4	5	0	1
B307/07	1	1	3	3	1	4	4	1	4	5	0	0
B109/07	3	2	2	2	1	4	4	4	4	4	0	0
B192/07	3	2	2	3	1	4	4	4	4	6	0	0
B107/07	2	1	2	2	1	2	5	5	4	6	0	0
B269/07	1	2	2	2	1	4	5	3	4	5	0	1
B239/07	1	1	2	3	2	2	5	2	4	6	0	0

Accession	Growth habit	Stem habit	Branching habit	Angle of insertion	Leaf tip color	Leaf shape	Leaf apex shape	Stipule shape	Fruit shape	Fruit color	Calyx limb p	Fruit ribs
B272/07	2	1	2	2	5	4	4	4	1	4	0	0
B174/07	2	1	2	2	5	4	4	4	1	4	0	0
B143/07	2	1	2	2	5	4	4	3	1	4	0	0
B93/07	1	1	3	2	5	4	4	2	1	5	0	0
B267/07	2	1	3	2	5	4	4	2	1	5	0	0
B300/07	2	1	2	2	5	4	4	2	1	6	0	0
B13/07	2	1	2	1	5	4	4	2	1	6	0	0
B286/07	1	1	2	2	5	3	5	2	1	4	0	0
B311/07	1	1	2	2	5	3	4	2	1	4	0	0
B240/07	2	1	2	2	5	3	4	2	1	5	0	0
B67/07	2	1	2	2	5	3	4	2	1	6	0	0
B31/07	3	1	3	2	5	4	4	2	1	6	0	0
B167/07	3	1	2	2	5	4	4	2	1	6	0	0
B251/07	2	2	2	2	5	4	5	2	1	5	0	0
B326/07	3	2	2	2	5	4	5	2	1	4	0	0
B95/07	1	1	2	1	5	3	4	4	1	5	0	0
B235/07	1	1	2	2	5	3	4	4	1	6	0	0
B305/07	2	1	2	3	5	2	5	4	1	6	0	0
B129/07	2	1	2	2	5	3	5	4	1	6	0	0
B170/07	3	1	3	2	5	4	4	4	1	4	0	0
B55/07	2	1	2	2	5	4	4	2	1	4	0	0
B280/07	3	1	3	2	5	4	5	2	1	5	0	0
B125/07	1	2	2	2	5	2	4	4	1	6	0	0
B237/07	2	2	3	3	5	3	5	2	1	4	0	0
B117/07	2	1	2	3	5	2	5	2	1	4	0	0
B79/07	2	1	2	1	5	2	5	4	1	6	0	0
B225/07	1	1	3	2	5	3	5	4	1	6	0	0
B218/07	2	1	2	3	5	3	5	4	1	4	0	0
B291/07	2	2	2	1	5	4	4	3	1	6	0	0
B69/07	1	1	1	2	5	3	5	2	1	6	0	0
B37/07	2	1	2	1	5	2	5	2	1	6	0	0
B321/07	2	2	2	1	5	4	5	3	1	4	0	0
B290/07	2	2	2	3	5	3	5	2	1	6	0	0
B56/07	2	1	3	1	5	4	5	5	1	5	0	0
B217/07	2	1	2	3	5	4	5	3	5	4	0	0
B81/07	2	1	2	3	5	4	5	3	4	4	0	0
B261/07	1	1	2	2	5	3	5	2	4	6	0	0

Accession	Growth habit	Stem habit	Branching habit	Angle of insertion	Leaf tip color	Leaf shape	Leaf apex shape	Stipule shape	Fruit shape	Fruit color	Calyx limb p	Fruit ribs
B258/07	1	1	2	2	5	2	5	2	4	6	0	0
B292/07	2	2	2	2	5	4	4	2	4	6	0	0
B39/07	2	1	2	2	5	4	4	2	4	6	0	0
B187/07	2	1	2	2	5	3	5	3	4	6	0	0
B145/07	2	1	2	2	5	3	5	2	4	6	0	0
B264/07	1	1	2	2	5	3	5	4	5	6	0	0
B41/07	2	1	2	2	5	3	5	4	5	6	0	0
B173/07	3	1	3	2	5	4	4	3	4	6	0	0
B202/07	3	1	3	2	5	4	4	2	4	6	0	0
B293/07	2	1	3	2	5	3	4	2	4	6	0	0
B155/07	2	1	3	2	5	4	4	2	4	6	0	0
B327/07	2	1	2	3	5	4	4	4	4	6	0	0
B160/07	1	1	2	3	5	4	4	4	4	6	0	0
B159/07	2	1	2	2	5	3	4	4	5	6	0	0
B284/07	2	1	2	2	5	4	4	3	4	6	0	0
B262/07	2	1	2	2	5	4	4	2	4	4	0	0
B273/07	3	1	3	2	5	4	4	2	4	4	0	0
B57/07	2	2	3	2	5	3	5	2	4	6	0	0
B157/07	3	1	3	2	5	3	5	2	4	6	0	0
B113/07	3	1	3	3	5	4	5	4	4	6	0	0
B166/07	3	1	3	2	5	4	4	4	4	6	0	0
B116/07	2	1	3	1	5	4	4	3	4	6	0	0
B124/07	2	1	2	2	5	2	5	4	4	6	0	0
B298/07	1	2	2	2	5	3	5	2	4	5	0	0
B172/07	2	1	2	2	5	3	4	2	5	6	0	0
B204/07	1	1	2	3	5	4	3	2	5	6	0	0
B287/07	1	1	2	2	5	4	4	2	4	5	0	0
B288/07	2	2	3	2	5	1	5	3	5	4	0	0
B303/07	2	1	2	3	2	3	1	4	4	6	0	0

Appendix Table 3. Test for Normality of residuals in each of the separate ANOVA model using the Shapiro-Wilk (W) and Kolmogorov-Smirnov test

Shapiro-Wilk (W)						**Kolmogorov-Smirnov**		
Traits	**Value of W**	**P-value=Pr<W**	**Traits**	**Value of W**	**P-value=Pr<W**	**Traits**	**Value of D**	**P-value=Pr>D**
TH	0.987213	0.2023	BL	0.990335	0.260	Yield	0.064106	0.1491
GIRTH	0.990683	0.4535	BT	0.98627	0.1634			
NPB	0.992252	0.6181	BW	0.991327	0.5233			
NNOMS	0.987104	0.1969	LL	0.985597	0.1351			
CANOPY	0.991229	0.5079	LW	0.990598	0.4453			
AINL	0.985469	0.1337	PL	0.983319	0.0756			
FL	0.981921	0.0529	LFPB	0.990512	0.4371			
FT	0.986066	0.1520	HBW	0.983366	0.0786			
FW	0.993776	0.7870	LS	0.982186	0.0566			