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Variability and Association among Yield and Yield Components in Coffee (*Coffea arabica* L.) Collected from Gewata Area, South Western Ethiopia

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Abstract

Understanding genetic variability among Gewata coffee accessions is essential for improving yield and guiding effective breeding programs. With the objective of determining the level of genetic variability and association among yield and yield related traits. A total of fifty five coffee accessions collected from Kafa zone Gewata district were characterized using morphological traits at Melko main center & Gera sub -center along with five standard checks. The experiment was conducted using an augmented design with four blocks of single row with six trees per plot during 2023/24 cropping season by superimposing on four years age of coffee trees planted since July 10, 2020. Data on 19 quantitative traits was recorded from three representative trees per plot. The combined analysis of variance revealed significant differences between locations and genotypes at probability levels of $p<0.05$ and $p<0.01$. High PCV and GCV values were recorded for traits such as yield, coffee berry disease, number of secondary branches, number of primary branches, canopy diameter, and leaf area. High heritability value were recorded for traits BL (89%), BW(78%), CD(73%), NPB(73%), FL(70%), LA(66%), LW(64%) and NMSN (64%). Higher estimates of heritability coupld with a substantial genetic advance as a percentage of the mean, were observed for bean length, bean width, canopy diameter, number of primary branches, leaf area, leaf width, and the number of main stem nodes. The highest (941.38 kg/ha) and lowest (108.23 kg/ha) mean bean yield was recorded from accession GW-42/19 and GW-23/19, respectively. Coffee yield had significant positive correlations with canopy diameter (rg = 0.41), number of primary branches (rg = 0.46), number of secondary branches (rg = 0.67), stem girth (rg = 0.47), length of the first primary branch (rg = 0.72), number of main stem nodes (rg = 0.63), and plant height (rg = 0.38). In general the present study revealed significant variability in most of the traits of interest in Coffea arabica, offering potential for exploitation. However, it is recommended that a characterization approach utilizing advanced molecular techniques be employed.

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Keywords

Coffea Arabica L, Gewata coffee accessions, Genetic variability, Morphological traits, Yield traits

Introduction

Coffee (*Coffea arabica* L.) belongs to the genus *Coffea*, which is part of the *Rubiaceae* family, one of the largest families of flowering plants, consisting 500 genera and 6, 000 species (Ferreira *et al.,* 2019). Currently, around 139 species are classified under the *Coffea* genus (Guyot *et al.,* 2020). However, only two species dominate coffee

production worldwide: *Coffea arabica* L. and *Coffea canephora* P. *Coffea arabica* L. accounts for over 60% of global coffee production, while *Coffee canephora* contributes less than 40%(Farah and Dos Santos, 2015). Notably, *Coffea arabica* L. is the only tetraploid species (2n = 4x = 44) within the genus and is self-fertile, whereas the other species are diploid (2n = 2x = 22) and exhibit genetic self-incompatibility (Clarindo and Carvalho, 2008). Arabica coffee has its primary center of origin and genetic diversity in the high lands of Southwestern, Ethiopia (Lashermes *et al.,* 1996 ; Tesfaye *et al.,* 2014). In Ethiopia coffee is cultivated across a wide altitudinal range from 550 to 2750 meters above sea level. However, Arabica coffee performs best at elevations between 1300 and 1800 meters above sea level. Optimal production requires annual rainfall between 1500 and 2500 mm and air temperatures ranging from a minimum of 15 °C to a maximum of 30 °C.

Global coffee production is estimated to reach 178. 8 million bags for the 2025/26 period, with around 95. 5 million bags attributed to Arabica coffee and 83. 3 million bags to Robusta coffee (USDA, 2025/26). Ethiopia stands as the largest coffee producer in Africa and ranks fifth globally for Arabica coffee exports. In Ethiopia about 790, 000 hectares of land are occupied by coffee, with an estimated annual production of 11. 56 million bags, or 694, 000 tons, in the 2025/26 cropping season (USDA, 2025/26). The crop is crucial to the livelihoods of over 15 million smallholder farmers and other actors in the coffee sector and contributing 30% of the nation's total export revenue (ECTA 2025). Coffee is not only a vital export crop for Ethiopia but also holds significant cultural and socio-economic importance (Leroy *et al.,* 2006). *Coffea arabica* L. is characterized by its lower bitterness, lower caffeine, better flavour and sweet taste with an aromatic fragrance than Robusta (Canephora). It is more appreciated by consumers and is sold at distinctly higher price than Robusta (Leroy *et al.,* 2006; Romano *et al.,* 2014). Ethiopian coffees are often categorized by their distinct associated coffee tastes and regions as follows: “mocha” (chocolate) for Harar coffee, spicy for Sidamo coffee, floral for Yirgacheffe coffee, winy for Jimma and Limmu coffees, and fruity for Wellega (Lekemt) coffee Kufa (2012).

Jimma Agricultural Research Center has developed and released 44 new coffee varieties, including 35 pure lines and 9 hybrids, for different regions of Ethiopia. These varieties are noted for their high yields, disease resistance, and acceptable quality (Merga and Wubshet, 2021). Despite the importance of coffee in Ethiopia’s economy and the presence of huge genetic resources, a favorable climate, and soil types for coffee production and productivity, the crop yield is by far very low 0. 83 ton ha (USDA, 2024). Researchers have repeatedly cited several key factors behind this low production and productivity: including lack of high-yielding improved varieties with consistent performance in wide ranges of environments, biotic, abiotic (low soil fertility, poor agronomic management), and failure to use appropriate technology (improved variety, fertilizer) and insufficient access to well-characterized breeding material (Tadesse *et al.,* 2020; Ayele *et al.,* 2021).

Coffee grown across diverse environments shows substantial genetic variation in traits such as yield, quality, disease resistance, and other agronomic features, both within and between regional populations (Bayetta *et al.,* 1993). Information on crop plant species genetic diversity in their center of origin and of the relationships among elite breeding material has a significant impact on the improvement of crop plants (Hallauer *et al.,* 1988). Previous research has explored genetic variability in various coffee accessions: for instance, (Olika *et al.,* 2011) analyzed 49 coffee accessions from Limmu; Ermias *et al.,* (2011) focused on 81 accessions from western Wollega and (Weldemichael *et al.,* 2013) examined 16 accessions from northwest and southwest Ethiopia. The presence of genetic variability in coffee is essential for its further improvement by providing options for the breeders to develop new varieties and hybrids of coffee (Merga and Wubshet, 2021). Limited attention has been given to assess the diversity and conservation of Gewata coffee genetic resources.

To make the most of the available genetic heritage, Jimma Agricultural Research Center, responsible for coordinating coffee research in Ethiopia, collected about 55 coffee germplasm samples from the Gewata district in the Keffa region, Southwest Ethiopia to capture diversity for broader coffee genetic resource and supporting the future of coffee improvement programs. However, these materials have not been fully characterized for phenotypic and genotypic variability study, and their genetic potential for traits such as disease resistance and yield remains largely unknown. Therefore, it is crucial to characterize and conserve these coffee accessions to prevent genetic erosion and use them in breeding programs aimed at enhancing productivity through the development of high-yielding, disease-resistant coffee varieties suited for the Gewata area and similar agro-ecologies. Therefore, this study was conducted to

determine the level of genetic variability among Gewata coffee collection using morphological traits and the association among yield and yield related traits.

Materials and Methods

Description of the Study Area

The study was carried out at Jimma Agricultural Research Center (JARC) and Gera Agricultural Research Sub-center (GARSC). Jimma Agricultural Research Center (JARC) is situated 352 kilometers Southwest of Addis Ababa at latitude of 7°40'00" N and a longitude of 36°47'00" E, with an elevation of 1, 753 meters above sea level. The area experiences an average annual rainfall of 1, 572 mm, with a mean minimum temperature of 11. 6°C and a mean maximum temperature of 26. 3°C. The soil at the center is classified as reddish-brown Nitosol, characterized by a pH of 5. 2 and medium to high levels of exchangeable cation.

Gera Agricultural Research Sub-Center (GARSC) is located 421 kilometers Southwest of Addis Ababa and 74 kilometers from JARC, positioned at latitude of 7°07'00" N and a longitude of 36°00'00" E, at an altitude of 1, 940 meters above sea level. This region has an average annual rainfall of 1, 878. 9 mm, with minimum and maximum air temperatures averaging 10. 4°C and 24. 4°C, respectively. The soil in this area consists of Acrisols and Nitosols, with a pH range of 5 to 6 and medium to high levels of exchangeable cations (Paulos, 1994; Paulos and Tesfaye, 2000).

Experimental Materials

In 2019, a total of 55 *Coffea arabica* accessions were collected from the Gewata district in the Kaffa Zone, Southwestern Ethiopia. This collection was conducted as part of a broader coffee genetic resource initiative aimed at supporting the future of coffee improvement programs. In total, 60 coffee accessions, including five standard checks varieties (74110, 75227, 74140, Yachi, and Dessu/Merda Cheriko), were used in the study. Geographical origin of the studied coffee (*Coffea ararbca* L.) germplasm accessions were detailed in (Table 1).

Experimental Design and Trial Management

The study was superimposed on four-year-old coffee trees during the 2023/24 cropping season. The experiment was initiated on July 10, 2020, following an augmented design. Each experimental plot consisted of a single row containing six coffee trees. The spacing between rows and individual plants was 2 meters by 2 meters, while the spacing between blocks was 3 meters. These accessions were cultivated under uniform conditions, utilizing *Sesbania sesban* as temporary shade trees. Additionally, all management practices followed standard coffee agronomic protocols to ensure consistency across the trial IAR (1996).

Methods and Data Recorded

Quantitative data for each coffee accession were gathered using standardized descriptors as outlined by the International Plant Genetic Resources Institute (IPGRI, 1996). Data on 19 distinct agro-morphological traits were collected from three trees per accession, with the average values used for subsequent analysis. Data taken during the study were LL= leaf length (cm), LW=leaf width (cm), LA= leaf area (cm^2), PH= Plant height (cm), NMSN=number of main stem node(no), HUFPB= height up to first of primary branch (cm), NSB= number of secondary branch (no), NPB= number primary branch (no), SG=stem girth (mm) LFPB= length of first primary branch (cm), CD=canopy diameter(cm), FL= fruit length (mm), FW = fruit width (mm), FT= fruit thickness (mm), BL= bean length (mm), BW=bean width (mm), BT= bean thickness (mm), CBD= coffee berry disease(%) and YLD=yield (kg/ha).

Data Analysis

The data were analyzed using analysis of variance (ANOVA) with the SPAD (Statistical Package for Augmented Design), employing a randomized complete block augmented design by using R Software version 4. 4. Analyses of variance for combined data over locations were carried out to see variability between genotypes, locations and genotype x environmental interaction using Statistical tool for agricultural research R Software version 4. 4. Thus, performance of genotype over location was estimated to identify the genotype performance across locations and showed genotype x environmental interaction (Table 2). Random model which included genotype and location as random factor and genotype × location interaction was used.

The variance components of combined analysis of variance over location were estimated according to the following statistical model: $Yijk = \mu + Gi + Lj + Bk (Lj) + GLij + Ɛijk$. Where, Yijk was the observation for genotype ‘i’ at location ‘j’ in replication ‘k’. In the model

'μ' was the overall mean 'Gi' the effect of the genotype 'i', 'Lj' was the effect of environment 'j', 'Bk' block effect, 'GLij' the interaction between genotype and location or environment and 'Ɛijk' was the random error associated with the' kth observation on genotype 'i' in environment.

For combined analysis of variance over locations, the homogeneity of error variance was tested using F-max method of Hartley (1950). This was based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error given by the following formula. F-max $= \frac{\textbf{Largest MSE}}{\textbf{Smallest MSE}}$ Traits that showed heterogeneous error variances were square root transformed before combining.

The phenotypic and genotypic variance and coefficient of variation were estimated according to (Johnson *et al.,* 1955) as:

$(\sigma^2 g) = \frac{MSg - MSe}{r}$ for individual location, σ2p = σ 2g + σ2e/r (Mse/r) for individual location Variance components for the data combined over locations were computed as the following. $(\sigma^2 g) = \frac{MSg - MSgl}{rl}$ for over location, $(\sigma^2 gl) = \frac{MSgl - MSe}{r}$, $\sigma^2 p = \sigma 2g + \frac{\sigma 2e}{rl} + \frac{\sigma 2gl}{l}$ for over location.

Where, σ2p = phenotypic variance, σ2 g = genotypic variance, σ 2gl= variance of genotype x environmental interaction, σ2e = environmental variance (Error mean square), MSg = mean square of genotypes, MSe = mean square of error and r = Number of replications

Phenotpic coefficent of variation $(PCV) = \frac{\sqrt{\sigma P}}{\bar{x}} x100$

Genotypic coefficent of variation $(GCV) = \frac{\sqrt{\sigma g}}{\bar{x}} x100$

Environmental variance $(ECV) = \frac{\sqrt{\sigma 2e}}{\bar{x}} x100$

Where x̄ = Sample mean

PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Deshmukh *et al.,* (1986).

Heritability in broad sense was computed for each character as suggested by Allard (1960) and, Holland *et al.,* (2003) as:-

For individual location,

$H^2b = \frac{\sigma^2 g}{\sigma^2 P}$ for individual location, $H^2b = \frac{\sigma^2 g}{\sigma^2 P}$ Where $\sigma^2 p = \sigma 2g + \frac{\sigma 2e}{rl} + \frac{\sigma 2gl}{l}$ for over location

Heritability was classified as suggested by Robinson *et al.,* (1949) into low (0-30%), moderate (30-60%) and high (>60%).

Estimation of expected genetic advance:- calculated as suggested by Allard (1960) as: GA=K*σp*h^2b, Where, GA = expected genetic advance, σp = the phenotypic standard deviation, H^2b = heritability in broad sense, K = Selection differential (K = 2. 06 at 5% selection intensity).

Genetic advance over mean =GAM %= $\frac{GA}{X} * 100$, Where, GA and X represent genetic advance and sample mean. It was categorized as low, moderate and high as given by Johnson *et al.,* (1955). The value found 0-10% was Low; 10-20%: Moderate, 20% and above was High.

Phenotypic (rp) and genotypic (rg) correlations between two traits were estimated using the formula suggested by Miller *et al.,* (1958).

Results and Discussion

Analysis of Variance (ANOVA)

Analysis of Variance for Individual locations

The results from the analysis of variance (ANOVA) conducted at two different locations indicated significant differences between genotypes both at 0. 05 and 0. 01 probability levels (Table 3).

At Melko, morphological traits such as leaf width (LW), height up to the first primary branch (HUFPB), stem girth (SG), fruit length (FL), and fruit thickness (FT) exhibited highly significant differences among genotypes (p<0. 01)(Table 3). In contrast, traits like leaf area (LA), plant height (PH), number of secondary branches (NSB), fruit width (FW), bean length (BL), and bean width (BW) showed significant differences at the probability

level (p<0. 05). However, no significant differences were observed in leaf length (LL), number of main stem nodes (NMSN), length of the first primary branch (LFPB), number of primary branches (NPB), canopy diameter (CD), bean thickness (BT), yield (YLD), and hundred bean weight (HBW).

At Gera, significant differences were observed for traits such as plant height (PH), height up to the first primary branch (HUFPB), stem girth (SG), canopy diameter (CD), yield (YLD), and coffee berry disease (CBD) at a highly significant level (p<0. 01) (Table 3). Traits like the length of the first primary branch (LFPB), number of primary branches (NPB), and bean width (BW) showed significant differences at the 0. 05 probability level (p<0. 05). In contrast, no significant differences were found for leaf length (LL), leaf width (LW), leaf area (LA), number of main stem nodes (NMSN), number of secondary branches (NSB), fruit length (FL), fruit width (FW), fruit thickness (FT), bean length (BL), and bean thickness (BT).

These findings are consistent with the work of (Olika Kitila *et al.,* 2011), who reported significant variation among 49 accessions for 22 traits. Similarly, studies by Atinafu (2015), (Abdulfeta Tariku and Ashenafi Ayano, 2018) and (Alemayehu *et al.,* 2022) also identified substantial variability in different traits among tested Arabica coffee genotypes, highlighting the potential for genetic improvement through selection.

Combined Analysis of Variance

The combined analysis of variance (ANOVA) revealed highly significant differences (p < 0. 001) between locations for several traits, including leaf length (LL), leaf width (LW), leaf area (LA), length of the first primary branch (LFPB), number of primary branches (NPB), number of secondary branches (NSB), canopy diameter (CD), fruit length (FL), bean length (BL), bean width (BW), yield (YLD), and coffee berry disease (CBD) in (Table 4). Traits such as the number of main stem nodes (NMSN), height up to the first primary branch (HUFPB), and fruit thickness (FT) showed highly significant differences (p < 0. 01) between locations. However, traits like stem girth (SG), fruit width (FW), and bean thickness (BT) exhibited no significant differences. These results are consistent with the findings of (Abdulfeta Tariku and Ashenafi Ayano, 2018, Yirga *et al.,* 2021b), who reported variability among Arabica coffee germplasm collected from Southwestern Ethiopia using similar agronomic traits.

Their analysis of variance also revealed highly significant differences (p < 0. 001) between genotypes for plant height (PH), height up to the first primary branch (HUFPB), stem girth (SG), canopy diameter (CD), fruit length (FL), bean length (BL), yield (YLD), and coffee berry disease (CBD) between genotypes. These findings are consistent with Alemayehu (2018), who reported highly significant differences among *Coffea arabica* genotypes. Traits such as leaf width (LW), number of main stem nodes (NMSN), length of the first primary branch (LFPB), and bean width (BW) showed highly significant differences (p < 0. 01) between genotypes, while leaf area (LA), number of primary branches (NPB), and fruit thickness (FT) displayed significant differences (p < 0. 05) between genotypes. Similar findings were reported by Yigzaw (2005) and Olika *et al.,* (2011), who observed significant variation among Ethiopian *Coffea arabica* accessions for vegetative growth, fruit, and bean characteristics. Traits like leaf length (LL), number of secondary branches (NSB), fruit width (FW), and bean thickness (BT) showed no significant differences.

The analysis of variance also revealed highly significant differences (p < 0. 001) between locatiom by genotypes for coffee berry disease (CBD). Traits such as plant height (PH), stem girth (SG) and bean width (BW) showed highly significant differences (p < 0. 01) among location by genotypes. Canopy diameter (CD) and yield (YLD) showed significant differences (p < 0. 05). Comparable results were reported by Getachew *et al.,* (2022). The remaining 13 traits showed no significant differences between location by genotypes.

Range and Mean Performance of Accessions

The combined means and ranges for the 19 quantitative traits across 60 coffee accessions are presented in (Table 5). The performance of the accessions exhibited considerable variation for the following traits: leaf length (9. 80–16. 90 cm), leaf width (3. 92–7. 20 cm), leaf area (25. 74–79. 80 cm²), plant height (100. 8–300. 2 cm), number of main stem nodes (16. 67–40), height up to first primary branch (17. 83–44. 3 cm), stem girth (30. 5–58. 56 mm), length of the first primary branch (64. 3–136 cm), number of primary branches (30. 3–81. 3), number of secondary branches (12–165. 33), canopy diameter (93. 4–223. 33 cm), fruit length (12. 63–19. 37 mm), fruit width (11. 13–15. 17 mm), fruit thickness (9. 86–12. 49 mm), bean length (8. 68–15. 16 mm), bean width (6. 02–9. 45 mm), bean thickness (3. 56–9. 426 mm), yield (27. 8–1993. 26 kg/ha), and coffee berry disease

incidence (0. 71–5. 23%). Among these traits, the highest ranges were observed for coffee yield, plant height, number of secondary branches, canopy diameter, and length of the first primary branch, which contributed significantly to the overall variability of the coffee accessions.

The results revealed that characters exhibiting a broader range of values also displayed higher mean values. This substantial variation offers a valuable opportunity for yield improvement. The significant variability observed across the different traits suggests a wide genetic diversity among the accessions for all studied characters. The high range and mean values for each trait of interest indicate significant potential for improving various desirable traits through selection as a short-term strategy and hybridization as a long-term strategy.

These findings align with those reported by Yigzaw (2005) and (Olika Kitila *et al.,* 2011), and are consistent with the observations of (Alemayehu *et al.,* 2022; Masreshaw, 2018), and (Abdulfeta Tariku and Ashenafi Ayano, 2018), all of whom documented the presence of considerable variation in the majority of quantitative traits measured among the coffee materials in their respective studies. Similarly, (Weldemichael *et al.,* 2017) reported the presence of the highest range among tested materials for critical agronomic traits, such as average coffee yield per tree and the number of secondary branches.

Estimation of Variance Components

Genotypic and phenotypic variance

The combined variability analysis results for 19 coffee quantitatives traits genotypic and phenotypic variance are presented in (Table 6). High PCV and GCV values were observed for yield, coffee berry disease, number of secondary branches, number of primary branches, canopy diameter, and leaf area. Medium PCV and GCV values were recorded for leaf width, number of main stem nodes, height up to the first primary branch, bean length, and bean width. Low GCV values were observed for leaf length, plant height, length of the first primary branch, fruit length, and fruit thickness, while low PCV values were noted for fruit length, stem girth, fruit width, and fruit thickness.

The high and medium PCV and GCV values suggest that selection for these traits could be crucial for improving the Gewata coffee population through selection and hybridization. For most traits, the genotypic coefficients of variation were nearly identical to their corresponding phenotypic coefficients of variation, indicating a significant influence of both genotypic and phenotypic factors in the expression of these traits.

The current findings are consistent with Olika Kitila *et al.,* (2011), who reported high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values for traits such as yield and number of secondary branches, and moderate values for height up to the first primary branch and hundred-bean weight. Similarly, Atinafu *et al.,* (2017) reported significant genotypic variation among coffee collections, with PCV ranging from 4. 52% to 60. 89% and GCV ranging from 3. 92% to 56. 52%. These findings align with the results of (Alemayehu *et al.,* 2022), who also observed high PCV and GCV values for coffee bean yield, coffee berry disease and coffee leaf rust resistance.

The present study further reveals that the combined result, PCV values were higher than GCV values for all the quantitative traits studied, indicating that the observed variation in the coffee accessions is due to both genetic and environmental factors. The magnitude of the differences between the genotypic and phenotypic coefficients of variation reflects the extent of environmental influence on each trait. Large differences suggest a strong environmental effect, while smaller differences indicate a greater genetic contribution (Akinwale *et al.,* 2011).

Broad sense heritability (h^2_b%)

In the present study, high heritability estimates (>60%) were observed for several traits, such as bean length (89%), bean width (78%), canopy diameter (73%), number of primary branches (73%), fruit length (70%), leaf area (66%), leaf width (64%), and number of main stem nodes (64%). Moderate heritability estimates were recorded for yield (57%), leaf length (38%), height up to the first primary branch (46%), length of the first primary branch (42%), number of secondary branches (49%), and coffee berry disease (38%). Low heritability estimates were recorded for plant height (24%), stem girth (22%), fruit width (21%), fruit thickness (23%) and bean thickness (26%).

The findings of this study are consistent with those of (Alemayehu *et al.,* 2022), who reported high heritability estimates (>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 to the first primary branch (65. 2%), hundred-bean weight (64. 5%), fruit width (58. 8%), length of the longest primary branch (56. 5%), plant height (55. 8%), and canopy diameter (51. 3%).

According to Singh and Kumar (2005), traits with very high heritability are relatively easier to select for, as the genotype closely corresponds to the phenotype, with minimal environmental influence. In contrast, selection for traits with low heritability is often more challenging or even impractical due to the significant influence of environmental factors. High value of heritability showed relatively great influence of genetic factor on those traits indicating the selection of traits for the next breeding program and the possibility of improving genotypes for desired traits (Yigzaw, 2005; Wagner *et al.,* 2014).

Estimates of expected genetic advance (GAM %)

Based on the genetic advance expressed as a percentage of the mean, high GAM values were observed for yield (84. 57%), coffee berry disease (69. 33%), number of secondary branches (52. 08%), number of primary branches (36. 56%), canopy diameter (45. 11%), leaf area (35. 5%), number of main stem nodes (22. 1%), leaf width (20. 81%), bean length (31. 27%), and bean width (22. 58%). These findings are consistent with those of (Beksisa and Ayano, 2016), who reported high genetic advance for yield, total plant height, and canopy diameter. The estimate of genetic advance is considered a more effective selection tool when used in conjunction with heritability estimates (Johnson *et al.,* 1955). This study aligns with the results of (Weldemichael *et al.,* 2017), who observed high GAM for coffee berry disease reaction (88. 86%), clean coffee yield per tree (24. 03%), number of secondary branches per tree (22. 34%), height to the first primary branch (20%), and hundred-bean weight (20%). The results also corroborate findings by (Olika *et al.,* 2011), who noted high expected genetic advance as a percentage of the mean for traits such as height to the first primary branch and coffee yield when selecting the top 5% of genotypes.

In this study, high heritability associated with high genetic advance was observed for traits such as bean length, bean width, canopy diameter, number of primary branches, leaf area, leaf width, and number of main stem nodes. Medium heritability and genetic advance were recorded for leaf length, length of the first primary branch, and height to the first primary branch. High GAM and medium heritability were recorded for the number of secondary branches, yield, and coffee berry disease. High heritability with medium genetic advance was observed for fruit length.

Yigzaw (2005) observed relatively high values of the genotypic coefficient of variation, broad-sense heritability, and genetic advance for certain traits. Moreover, the combined use of genetic coefficient of variation, heritability, and genetic advance is crucial for the effective improvement of specific traits in a population. Genetic advance provides a more precise understanding of the potential for selection in segregating generations. Higher heritability estimates, coupled with favorable genetic advance, confirm the potential for developing new genotypes with desirable traits through selection (Bayetta, 2001; Olika *et al.,* 2011**).**

Phenotypic and genotypic correlations of coffee yield with other traits

Phenotypic correlations

The phenotypic correlation analysis of coffee bean yield revealed statistically significant and positive correlations with several traits: canopy diameter (rp = 0. 84), number of primary branches (rp = 0. 75), number of secondary branches (rp = 0. 88), stem girth (rp = 0. 62), length of the first primary branch (rp = 0. 79), number of main stem nodes (rp = 0. 73), leaf area (rp = 0. 70), leaf width (rp = 0. 36), and leaf length (rp = 0. 31). Coffee berry disease (rp=-0. 50) showed a significant negative correlation. These findings are consistent with those reported by Alemayehu Taye *et al.,* (2023) and Mesfin Kassa *et al.,* (2024), who demonstrated that vigorous canopy development and enhanced branching architecture are positively associated with higher productivity, whereas increased disease incidence adversely affects bean yield.

Genotypic correlations

The present study showed that clean coffee bean yield was positively and significantly associated with canopy diameter (rg = 0. 41), number of primary branches (rg = 0. 46), number of secondary branches (rg = 0. 67), stem girth (rg = 0. 47), length of the first primary branch (rg = 0. 72), number of main stem nodes (rg = 0. 63) and plant height (rg = 0. 38) while coffee berry disease (rg= -0. 46) showed negatively correlated with coffee bean yield.

Table.1 Geographical origin of the studied coffee (*Coffea ararbca* L.) germplasm accessions at JARC main center & Gera sub center.

Acc.No	District	P.association	Alt (m)	Acc.No	District	P.association	Alt (m)
GW-01	Gewata	Wadio	1700	GW-29	Gewata	Senterio	1742
GW-02	,,	,,	1700	GW-30	,,	,,	1743
GW-03	,,	,,	1700	GW-31	,,	,,	1740
GW-04	,,	,,	1700	GW-32	,,	,,	1740
GW-05	,,	,,	1700	GW-33	,,	,,	1736
GW-06	,,	,,	1700	GW-34	,,	,,	1721
GW-07	,,	,,	1760	GW-35	,,	,,	1760
GW-08	,,	,,	1760	GW-36	,,	,,	1782
GW-09	,,	Medapo	1580	GW-37	,,	,,	1748
GW-10	,,	,,	1580	GW-38	,,	,,	1782
GW-11	,,	,,	1580	GW-39	,,	,,	1879
GW-12	,,	,,	1630	GW-40	,,	,,	1850
GW-13	,,	,,	1630	GW-41	,,	,,	1806
GW-14	,,	Bera	1930	GW-42	,,	,,	1738
GW-15	,,	,,	1928	GW-43	,,	Konda Geter	1644
GW-16	,,	,,	1928	GW-44	,,	,,	1644
GW-17	,,	,,	1928	GW-45	,,	,,	1645
GW-18	,,	,,	1905	GW-46	,,	,,	1648
GW-19	,,	,,	1905	GW-47	,,	Chebero	1635
GW-20	,,	,,	1905	GW-48	,,	Medabo	1608
GW-21	,,	,,	1923	GW-49	,,	,,	1608
GW-22	,,	,,	2058	GW-50	,,	Emicho	1881
GW-23	,,	Minigdo	1690	GW-51	,,	,,	1835
GW-24	,,	,,	1690	GW-52	,,	Wodio	1881
GW-25	,,	,,	1706	GW-53	,,	,,	1678
GW-26	,,	,,	1687	GW-54	,,	,,	1680
GW-27	,,	,,	1687	GW-55	,,	,,	1680
GW-28	,,	Senterio	1739				
Checks	at Jimma					at Gera	
1.74110					1.74110		
2.75227					2.75227		
3.Dessu					3.M/cheriko		
4.74140					4.74140		
5.Yachi					5.Yachi		

Table.2 ANOVA table skeleton for combined analysis.

SV	DF	MS	EMS
R (location)	l (r-1)	MSr	$\sigma^2e + gl\ \sigma^2r$
Location	l-1	MSl	$\sigma^2e + r\sigma^2gl + gr\sigma^2l\ \sigma$
Genotype	g_{-1}	MSg	$\sigma^2e + r\sigma^2gl + rl\sigma^2g$
GxE	(g-1) (l-1)	MSgxl	$\sigma^2e + r\sigma^2gl$
Error	(r-1) (c-1)l	MSerror	σ^2e

Where, SV-Source of variance, DF- Degree of freedom, MS- Mean square, EMS-Expected mean square, GXL-Genotype by Location interaction, l-location, r-replication and g- genotype, σ2p= phenotypic variance, σ2 g = genotypic variance, σ2gl= variance of genotype x environmental interaction, σ2e = environmental variance (Error mean square), MSg = mean square of genotypes and MSe = mean square of error.

Table.3 Analysis of variance for individual locations quantitative traits.

Melko					Gera				
Plant Traits	Blocks (df=3)	Genotypes (df=59)	Error (df=)12	CV%	Plant Traits	Blocks (df=4)	Genotypes (df=59)	Error (df=)16	CV%
LL	2.54*	1.22^{ns}	0.72	5.91	LL	0.70^{ns}	0.78^{ns}	1.05	7.97
LW	0.20^{ns}	0.43**	0.09	4.99	LW	0.28^{ns}	0.30^{ns}	0.28	10.57
LA	115.07*	98.46*	32.36	9.95	LA	34.70^{ns}	31.46^{ns}	34.68	13.51
PH	195.61^{ns}	1006.77*	349.47	9.25	PH	1818.06**	346.87**	66.80	4.12
NMSN	4.64^{ns}	12.10^{ns}	8.09	9.94	NMSN	12.21^{ns}	9.13^{ns}	6.63	10.49
HUFPB	1.90^{ns}	29.94**	4.44	6.76	HUFPB	19.45^{ns}	31.59**	7.39	9.97
SG	20.03^{ns}	33.94**	6.23	5.50	SG	15.50^{ns}	14.33**	5.77	5.28
LFPB	21.05^{ns}	37.12^{ns}	20.19	4.64	LFPB	273.40*	184.72*	72.47	7.92
NPB	80.41^{ns}	87.93^{ns}	65.30	13.68	NPB	29.00^{ns}	31.01*	13.60	8.00
NSB	840.46*	559.79*	191.39	24.19	NSB	1217.76^{ns}	680.19^{ns}	697.28	29.59
CD	1541.18^{ns}	1360.23^{ns}	764.78	20.74	CD	92.91*	319.87**	25.70	2.70
FL	0.04^{ns}	1.20**	0.18	2.49	FL	1.15^{ns}	1.14^{ns}	0.85	5.96
FW	0.42*	0.28*	0.11	2.49	FW	0.27^{ns}	0.43^{ns}	0.39	4.75
FT	0.28**	0.29**	0.03	1.63	FT	0.38^{ns}	0.25^{ns}	0.24	4.35
BL	0.21^{ns}	0.83*	0.32	5.50	BL	0.18^{ns}	0.89^{ns}	0.48	5.53
BW	0.04^{ns}	0.27*	0.10	4.63	BW	0.50*	0.29*	0.12	4.27
BT	0.02^{ns}	0.07^{ns}	0.04	4.92	BT	0.12^{ns}	0.08^{ns}	0.09	5.93
YLD	26348.97^{ns}	25699.59^{ns}	21674.74	43.68	YLD	109884.55^{ns}	160519.07**	36707.49	30.00
HBW	0.64^{ns}	4.04^{ns}	2.17	10.55	CBD	0.82^{ns}	44.82**	1.96	37.95

*, **, ***and ns- represent significant different at probability level of 0.05, 0.01, 0.001 and non-significant different respectively. df = degree of freedom, CV= coefficient of variation, LL= leaf length(cm), LW=leaf width (cm), LA= leaf area (cm^2), PH= Plant height (cm), NMSN=number of main stem node (no), HUFPB= height up to first primary branch (cm), SG=stem girth (mm) LFPB= length of first primary branch (cm), NPB= number of primary branch (no), NSB= number of secondary branch (no), CD= canopy diameter (cm),), FL= fruit length (mm), FW = fruit width (mm), FT= fruit thickness(mm), BL= bean length (mm), BW=bean width (mm), BT= bean thickness (mm), HBW=hundred bean weight (gm), YLD= yield (kg/ha) and CBD= coffee berry disease (%).

Table.4 Over location combined analysis of variance for 19 quantitative traits.

Mean Square						
Traits	Loc (df=14)	Geno (df=59)	Loc:Block (df=14)	Loc:Geno (df=59)	Error (df=56)	CV (%)
LL	81.19***	1.50^{ns}	2.76^{ns}	0.84^{ns}	1.23	8.19
LW	28.94***	0.50**	0.50*	0.26^{ns}	0.20	8.18
LA	6866.7***	97.3*	158.4**	50.2^{ns}	44.20	13.36
PH	809.24*	1003.47***	1846.88***	473.65**	184.52	6.86
NMSN	760.72**	17.47**	21.34*	5.27^{ns}	7.42	10.15
HUFPB	612.80**	57.97***	35.38***	10.15^{ns}	5.82	8.48
SG	2.38^{ns}	40.21***	46.64***	14.04**	5.84	5.38
LFPB	3280.8***	155.8**	262.8**	70.7^{ns}	57.29	7.52
NPB	7199.4***	82.1*	101.9*	41.0^{ns}	36.70	11.44
NSB	42080***	835^{ns}	2447***	637^{ns}	476.24	29.83
CD	99120***	1053***	1265**	661*	343.26	11.60
FL	78.41***	2.04***	1.28^{ns}	0.48^{ns}	0.56	4.64
FW	0.00^{ns}	0.40^{ns}	0.41^{ns}	0.40^{ns}	0.33	4.35
FT	1.52**	0.30*	0.29^{ns}	0.27^{ns}	0.15	3.49
BL	197.72***	1.34****	0.38^{ns}	0.45ns	0.41	5.61
BW	50.00***	0.31**	0.50**	0.27**	0.11	4.45
BT	9.67^{ns}	15.12^{ns}	70.05^{ns}	29.80^{ns}	173.82	5.91
YLD	5553043***	120227***	70613^{ns}	78244*	37022.44	35.81
CBD	20.61***	0.88***	0.77***	0.78***	0.09	27.10

*, **, ***and ns- represent significant different at probability level of 0.05, 0.01, 0.001 and non-significant different respectively.

Table.6 Estimates of variance, coefficients of variations, broad sense heritability and genetic advance for combined mean over two locations of 60 coffee accessions

Traits	EV	GV	PV	ECV	GCV	PCV	H	GA	GAM
LL	1.10	1.30	2.40	7.73	8.42	11.43	54	1.73	12.78
LW	0.26	0.47	0.72	9.35	12.58	15.67	64	1.13	20.81
LA	56.47	110.91	167.38	15.11	21.17	26.01	66	17.66	35.50
PH	489.79	2.98	492.79	11.17	1.87	11.21	24	0.28	0.14
NMSN	7.11	12.86	19.97	9.94	13.37	16.65	64	5.93	22.10
HUFPB	10.74	9.27	20.01	11.51	10.69	15.71	46	4.27	14.99
SG	14.02	3.15	13.88	8.33	4.12	8.29	22	0.08	0.18
LFPB	81.04	57.67	138.71	8.95	7.55	11.70	42	10.09	10.02
NPB	44.27	120.64	164.91	12.57	20.75	24.26	73	19.35	36.56
NSB	724.16	697.30	1421.46	36.79	36.10	51.54	49	38.10	52.08
CD	611.50	1671.07	2282.57	15.48	25.59	29.91	73	72.05	45.11
FL	0.56	1.28	1.84	4.65	7.03	8.43	70	1.95	12.09
FW	0.38	0.08	0.37	4.69	5.16	4.65	21	0.04	0.16
FT	0.24	0.06	0.26	4.33	1.32	4.53	23	0.09	0.79
BL	0.43	3.36	3.79	5.78	16.13	17.13	89	3.55	31.27
BW	0.24	0.84	1.08	6.57	12.40	14.04	78	1.67	22.58
BT	75.70	19.57	74.67	167.57	9.17	166.42	26	0.25	4.74
YLD	65396.87	85773.82	151170.68	47.59	54.50	72.35	57	454.45	84.57
CBD	0.57	0.35	0.93	69.96	54.66	88.78	38	0.75	69.33

EV-Environment variance, GENV-Genotype variance, PHV-Phenotype variance, ECV-Environment coefficient of variance, GCV%-Genotype coefficient of variance, PCV%-Phenotype coefficient of variance, H^2b-Broad sense heritability, GA-Genetic advance, GAM%-Genetic mean advance, LL-Leaf length (cm), LW-Leaf width (cm), LA-Leaf area (cm2), PH-Plant height (cm), NMSN- Number of main stem node(no), HFPB-Height up to first primary branch (cm), SG-Stem girth (mm), LFPB- Length of first primary branch (cm), NPB-Number of primary branch(no), NSB-Number of secondary branch(no), CD-Canopy diameter (cm), FL-Fruit length (mm), FW-Fruit width (mm), FT-Fruit thickness (mm), BL-Bean length(mm), BW-Bean width (mm), BT-Bean thickness(mm), YLD-Yield(kg/ha) and CBD-Coffee berry disease (%).

Table.7 Genotypic (above diagonal) and phenotype (below diagonal) correlation coefficient among 19 important characters

Variable	LL	LW	LA	PH	NMSN	HUFPB	SG	LFPB	NPB	NSB	CD	FL	FW	FT	BL	BW	BT	CBD	YLD
LL	1	0.52**	0.75**	0.15	-0.16	-0.07	0.07	0.08	0.06	0.01	0.07	0.29*	0.03	-0.08	0.25*	0.03	-0.06	0.13	-0.11
LW	0.38**	1	0.84	0.26*	-0.25	0.04	0.09	0.19	-0.05	-0.04	0.18	0.24	0.19	0.08	0.27*	0.04	0.08	0.15	0.03
LA	0.58**	0.69**	1	0.38**	-0.10	0.01	0.25*	0.34*	0.10	0.09	0.24	0.36*	0.21	0.06	0.32*	0.03	0.00	0.03	0.14
PH	0.02	0.04	0.24*	1	0.35*	0.02	0.33*	0.50**	0.43**	0.39**	0.52**	0.21	0.11	0.11	0.12	0.00	-0.03	-0.21	0.38**
NMSN	0.04	0.09	0.38**	0.07	1	-0.32*	0.41**	0.52**	0.83**	0.62**	0.37**	-0.02	0.04	-0.03	-0.05	-0.18	-0.04	-0.35*	0.63**
HUFPB	-0.04	0.09	0.11	0.03	-0.19	1	0.18	-0.02	-0.27*	-0.15	0.02	-0.28*	-0.20	0.27*	-0.16	0.38**	-0.01	-0.07	-0.21
SG	0.08	0.23*	0.55**	0.23*	0.61**	-0.07	1	0.64**	0.35*	0.62**	0.64**	0.04	-0.01	0.11	0.06	0.08	-0.03	-0.36*	0.47**
LFPB	0.27*	0.36**	0.64**	0.17	0.58**	0.02	0.64**	1	0.46**	0.69**	0.62**	0.18	0.02	0.03	0.19	0.07	0.07	-0.48**	0.72**
NPB	0.06	0.06	0.36**	0.11	0.87**	-0.31*	0.66**	0.57**	1	0.57**	0.38**	-0.06	0.11	-0.02	-0.05	-0.12	-0.07	-0.29*	0.46**
NSB	0.21	0.23*	0.54**	0.17	0.74**	-0.19	0.63**	0.84**	0.76**	1	0.66**	0.04	-0.02	0.04	0.01	0.02	0.00	-0.60**	0.67**
CD	0.20	0.35**	0.69**	0.22*	0.67**	-0.05	0.82**	0.83**	0.69**	0.81**	1	0.00	-0.08	0.02	0.03	0.11	0.07	-0.44**	0.41**
FL	0.13	0.08	0.21	0.07	0.03	-0.06	0.07	0.21	-0.02	0.19	0.18	1	0.45**	0.09	0.65**	-0.04	-0.10	-0.01	0.14
FW	0.02	0.06	0.16	-0.19	0.06	-0.16	0.10	0.05	0.13	0.15	0.11	0.56**	1	0.54**	0.32*	0.09	0.03	0.02	0.10
FT	-0.04	0.04	0.14	0.08	-0.00	0.18	0.08	0.03	0.02	0.07	0.04	0.39**	0.65**	1	0.09	0.42**	-0.06	-0.07	0.04
BL	0.03	0.14	0.18	0.18	-0.24*	-0.02	0.16	0.08	-0.18	-0.05	0.16	0.46**	0.18	0.13	1	0.39**	-0.01	-0.03	0.07
BW	0.03	0.08	0.20	0.31*	-0.13	0.27	0.08	0.07	-0.15	0.00	0.04	-0.04	-0.04	0.13	0.25	1	0.02	-0.11	-0.04
BT	0.16	0.25*	0.28*	0.16	0.04	0.03	0.16	0.22	0.10	0.23*	0.23*	0.06	0.07	-0.02	0.29*	0.44**	1	-0.08	0.11
CBD	0.02	0.15	-0.08	-0.08	-0.44**	0.04	-0.25*	0.42**	-0.50**	-0.55**	-0.42**	-0.06	-0.04	0.04	0.05	0.01	-0.26*	1	-0.46**
YLD	0.31 **	0.36**	0.70**	0.20	0.73**	-0.14	0.62**	0.79**	0.75**	0.88**	0.84**	0.14	0.12	0.05	-0.02	0.05	0.28*	-0.50**	1

*, ** = Significant at 5% and 1%, respectively.

Where: LL= leaf length(cm), LW=leaf width (cm), LA= leaf area (cm^2), PH= plant height(cm), NMSN=number of main stem node(no), HUFPB= height up to first primary branch (cm), SG=stem girth(mm) LFPB= length of first primary branch (cm), NPB= number of primary branch (no), NSB= number of secondary branch (no), CD= canopy diameter(cm), FL= fruit length (mm), FW = fruit width (mm), FT= fruit thickness(mm), BL= bean length (mm), BW=bean width (mm), BT= bean thickness (mm), CBD= coffee berry disease (%) and YLD=yield(kg/ha).

Table.5 The combined means and ranges for the 19 quantitative traits

Traits	MIN.	MAX.	Mean
LL	9.8	16.9	13.55
LW	3.92	7.2	5.43
LA	25.74	79.8	49.75
PH	100.8	300.2	198.1
NMSN	16.67	40	26.83
HUFPB	17.83	44.3	28.47
SG	30.5	58.56	44.95
LFPB	64.3	136	100.63
NPB	30.3	81.3	52.94
NSB	12	165.33	73.15
CD	93.4	223.33	159.72
FL	12.63	19.37	16.1
FW	11.13	15.17	13.15
FT	9.86	12.49	11.23
BL	8.68	15.16	11.36
BW	6.02	9.45	7.4
BT	3.56	9.26	5.19
YLD	27.8	1993.26	537.38
CBD	0.71	5.23	1.08

These correlations suggest that increasing these traits will likely result in higher coffee yields. This underscores the importance and reliability of these traits in improving coffee yield. Consequently, selection for one of these traits may concurrently enhance other related traits. Similar results have been reported by Arega Tesfaye *et al.,* (2021), who found that branching characteristics and stem vigor were positively correlated with coffee yield, and by Mesfin Kebede *et al.,* (2023), who reported that coffee berry disease negatively affects bean yield.

In the context of genetic divergence, evaluation, and selection processes, it is crucial to maintain traits that are highly correlated with multiple other traits (Ferrão *et al.,* 2008). The strong relationship between yield and yield-related traits offers an opportunity to leverage these correlations in selection programs aimed at developing high-yielding genotypes. Therefore, breeders should prioritize these traits in selection and crop improvement programs. These findings are consistent with those of (Yigzaw 2005; Olika *et al.,* 2011), and (Beksisa *et al.,* 2017), who reported positive and significant correlations between most quantitative traits and yield. Additionally, coffee berry disease severity showed a significant negative correlation with coffee bean yield, suggesting that selection for any one of these traits may not directly result in improvements in other traits. Therefore, independent selection may be necessary to enhance these traits individually.

Phenotypic and genotypic correlations among morphological traits

Phenotypic correlations

The estimated phenotypic correlations among the morphological traits are presented in (Table 7). Leaf length exhibited a positive and significant phenotypic correlation with leaf width, leaf area, and the length of the first primary branch. Similarly, leaf width showed a positive and significant phenotypic correlation with leaf area, stem girth, length of the first primary branch, number of secondary branches, canopy diameter, and bean thickness. Leaf area demonstrated a positive and significant correlation with plant height, number of main stem nodes, stem girth, length of the first primary branch, number of primary branches, number of secondary branches, canopy diameter, and bean thickness. The number of main stem nodes was positively and significantly correlated with stem girth, length of the first primary branch, number of primary branches, number of secondary branches, and canopy diameter, while it showed a negative correlation with

coffee berry disease. Stem girth exhibited a positive and significant correlation with the length of the first primary branch, number of primary branches, number of secondary branches, and canopy diameter, while it negatively correlated with coffee berry disease. The length of the first primary branch was positively and significantly correlated with the number of primary branches, number of secondary branches, canopy diameter, and coffee berry disease.

Similar findings were reported by Merga (2019), who observed significant positive phenotypic correlations among leaf traits, canopy diameter, stem diameter, and branching characteristics in Ethiopian Arabica coffee genotypes. Likewise, Degefa *et al.,* (2021) reported that leaf area, leaf width, canopy diameter, and the number of primary branches were positively associated with other important morphological and yield-related traits, emphasizing the importance of these vegetative characters in coffee improvement programs.

Genotypic correlation

The genotypic correlations among the traits are presented in (Table 7). Plant height exhibited a positive and significant correlation with the number of main stem nodes, stem girth, length of the first primary branch, number of primary branches, number of secondary branches, and canopy diameter. The number of main stem nodes showed a positive and significant correlation with stem girth, length of the first primary branch, number of primary branches, number of secondary branches, canopy diameter, and height up to the first primary branch. Conversely, it was negatively correlated with coffee berry disease. Stem girth demonstrated a positive and significant correlation with the length of the first primary branch, number of primary branches, number of secondary branches, canopy diameter, and a negative correlation with coffee berry disease. The length of the first primary branch was positively and significantly correlated with the number of primary branches, number of secondary branches, canopy diameter, and negatively correlated with coffee berry disease. These findings are consistent with previous reports indicating that vigorous vegetative growth traits are positively associated with each other and can contribute to improved coffee productivity and reduced disease susceptibility (Bayetta Bellachew, 2001; Adugna Debela, 2017; Mesfin Kifle *et al.,* 2020).

In this study, some traits exhibited positive and significant correlations with yield, while others showed significant negative correlations, both with yield and among each other. Traits that were positively correlated indicate that the improvement of one trait would likely result in an improvement of the other. In contrast, traits with negative correlations suggest that enhancing one trait may have an antagonistic effect on the other. These associations may arise from additive or non-additive genetic effects, as well as other factors such as pleiotropy, where a single gene influences multiple traits in the same direction (Welsh *et al.,* 2008). The negative correlations between traits could also be attributed to the involvement of distinct genes or pleiotropic genes that exert dominance over the traits, potentially controlling them in opposing directions (Kearsey and Pooni, 1996).

In conclusion, Ethiopia is endowed with immense potential of diverse coffee materials and a wide range of contrasting ecological conditions conducive to coffee cultivation. This study presents a comprehensive analysis of the genetic variability within the Gewata coffee population, a significant coffee accession recognized for its potential to enhance yield and its components. The current study demonstrated significant genetic variability among the tested genotypes, highlighting substantial potential for further improvement through selection and other breeding strategies. This variability presents an opportunity to exploit genotypes like (GW-42/19, GW-41/19, GW-26/19, GW-10/19, GW-49/19, GW-39/19, GW-48/19, GW-07/19 and GW-19/19) with the highest mean yield value recorded. This identification of superior genotypes with high yield potential offers promising avenues for enhancing coffee production and sustainability in the region. This study result also revealed (GW-42/19, GW-41/19, GW-26/19 and GW-10) the presence of highest yield, best genotypes over the released standard checks, which could suggest the possibility of a direct selection and for hybridization program.

Generally, the existence of genetic variability and association among traits in the base population is a key for these top-yielding genotypes and for the development of superior varities of coffee germplasm which could contribute for Gewata areas and similar agro-ecologies and for further coffee breeding improvement programs. Furthermore, in order to confirm these promising results, comprehensive studies incorporating physiological, quality and biochemical analyses are required, supported by advanced molecular techniques. Such integrated approaches hold significant potential for the effective utilization, conservation, and development of improved varieties in Ethiopia.

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