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Association of Yield and Yield Related Traits of Some Coffee (*Coffee Arabica L.*) Genotypes: Implication for High Yielding Selection, Ethiopia

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Abstract

Variability among genotypes and the association of yield and yield related traits are among the prominent criteria for crop improvement. The current study carried out with the intention to determine association between clean coffee yield and yield related traits and to study the association among yield related traits. A total of 26 coffee genotype were involved in the study. The experiment was conducted at Haru and Mugi sub-centres and set up in RCBD with three replications. Around 23 quantitative traits were recoded and analysed using R-software. From the combined analysis, significant difference among genotypes was observed in Number of Node per Primary Branch (NNPB) in all fruit traits and resistance to coffee leaf rust. Due to high GxE effects, non-significant difference was observed among genotypes in many traits. Including in yield, the GxE was significantly different in all bean traits, growth traits except NNPB, leaf traits except leaf length and from fruit traits except fruit width. Because of discrepancy performance, it is difficult to recommend common genotypes for two locations; thus, it is better to divide ecologies some similar to Mugi and other similar to Haru in edaphic and climate condition and focus generating technology separately for individual location. Number of Bearing Primary Branch (NPB) (gr=0.99**) Average Length of Primary Branch (ALPB) (gr=0.99**), NNPB (gr=0.99**) exhibited strong positive genotypic correlation with yield at Haru. Plant height, NPB, total node number and diameter of main stem had shown positive genotypic correlation with yield at both locations. Also, most of these traits showed positive association with each other. Bean thickness (0.99**) showed strong positive correlation with yield at Haru, but most fruit and bean traits were negatively correlated with yield at Mugi. Generally, one has to be cognizant to select genotypes with thick girth and tall in height possessing high node number from which high number primary branch emanate and wider canopy diameter having high number of bearing primary branch during yield improvement *via* selection.

Keywords: Arabica coffee; Association; Bean traits; Fruit traits; Genotypic correlation and Growth traits

Introduction

Coffee is a perennial crop which belongs rubacieas family and genus *coffe* [1]. Among 141 coffee species both *Coffee arabica L.* and *Coffee canephora P.* are the principal species in the world coffee production and market [2,3]. Arabica coffee is tetrapliod and predominantly autogamous but Canephora is diploid and allogamous species [4,5]. In addition to corolla the nature of pistil and stamen position of coffee Arabica flower contribute great role in its autogamous. Also *Coffea arabica* is shade lover species and has high biennial characteristic in bearing yield relative to *Coffea canephora species*.

Coffee is a cash crop and the second dominant trade commodity in the world. From all coffee species *Coffea arabica* contributes more than 60% in the world coffee production [3]. It is highly preferred by consumers around the world due to its superiority in flavour and low caffeine constituent. Coffee is a main source of income for coffee producing countries and it serve as income source for 25 million livelihoods in the world. Ethiopia which is the home land for Arabica coffee, earns up to 31% foreign exchange income from Arabica coffee alone [6]. Hence around 15 million livelihood in Ethiopia depend directly and indirectly on Arabica coffee production [7,8].

Arabica coffee production increment is prominent to increase the income of coffee producers and realize food security especially in developing countries. Also in order to response exponentially increasing demands of consumers boosting yield with required quality is priority issue. Thus to solve yield disease insect pest and quality problems for the last five and half decades different breeding methods have been followed and powerful technologies were developed. In Ethiopia 35 pure lines and 7 hybrids totally 42 high yielding disease resistance and acceptable quality coffee varieties had been released for low, mid and high land coffee producing ecologies [9]. To realize food security and response the current world demand on Arabica coffee, yield potential improvement is still remain alarming issue.

Yield is quantitative traits contributed by huge yield component and agronomic traits. These traits have direct and/or indirect positive associated with yield [10]. This enables breeders and other experts who work on coffee genetic improvement to use as indices for yield improvement via selection and/or hybridization. For instance, *Coffea arabica* has open mid-open compact and mid-compact growth habit

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which are among the indicative traits in hetirosis achievement during hybridization depending upon the combining ability of the parents [11]. Also yield related traits such as plant height number of primary branch number of secondary branch node number per main stem girth canopy diameter leaf traits, bean traits and fruit traits are traits that used as indices during coffee yield potential improvement. Different scholars indicated that the association of some of these traits with clean coffee yield and each other [12,13,10]. However there is less information on association of leaf, fruit and bean traits with yield with other growth traits and each other which may affect selecting high yielding coffee genotype. Thus the present study implemented with the intention to estimate the association between yields related traits and coffee clean bean yield and to study the existing association among yield related traits at genotypic level.

Materials and Methods

The experiment was conducted at Haru and Mugi agricultural research sub centres (Table 1). Both Haru and Mugi agricultural research sub centres are under Jimma Agricultural Research Center (JARC).

Location	Alt.(m) a.s.l	Temperature (°C)		Rainfall (mm)	Latitude	Longitude	Soil type	Distance from JARC
		Min.	Max.					
Mugi	1570	17	29	1655	8°4'00''	34°4'00''	Nitosol	610 km
Haru	1752	16	27	1727	8°59'21''	35°47'56''	Sandy clay loam	360 km
Source: Dubale [14]; Alemseged and Taye [15].								

Table 1: Description of the study areas.

Materials, agronomic practices and experimental design

The experiment was implemented on 22 coffee accessions which consolidated from three baths of collections (1998, 1999 and 2001 years of collection) with four checks; totally, 26 coffee genotypes involved in this study (Table 2). The accession were collected from different coffee growing agro-ecologies of Wollega western Ethiopia. The experiment was set up in RCBD with three replications; six coffee trees were planted per plot with the spacing of 2 m × 2 m between plant and row and 3 m between replications. All agronomic practices such as temporal shade and permanent, fertilizer application and weed control had been applied as per recommendation [16].

No.	Accessions	Woreda	Peasants Association	Specific location	Collection altitude (m. a.s.l)
1	W02/98	Haru	Wora Baro	Kori	1740
2	W34/98	Haru	Wora Baro	Kori	1790
3	W98/98	Haru	Chageli	Gincho Gamo	1800
4	W141/98	Gimbi	H. Giorgis	Kiti Negede	1620
5	W163/98	Gimbi	Homa Arsama	Homa Arsama	1600-1670
6	W167/98	Gimbi	Homa Arsama	Homa Arsama	1600-1670
7	W175/98	Gimbi	Homa Arsama	Homa Arsama	1600-1670
8	W188/98	Gimbi	Homa Biribir	Homa Biribir	1550-1600
9	W191/98	Gimbi	Homa Biribir	Homa Biribir	1500-1570
10	W203/98	Gimbi	Siba Yesus	Nayesoo Kiti	1560
11	W212/98	Gimbi	Sibo Charo	Abaku qaba	1560
12	W01/99	Haru	Guracha Holata	Jilcha Nacha	1660
13	W40/99	Haru	Dogi Adere	Tilli Kalo	1720
14	W109/99	Ayira Gliso	-	Meso	1600
15	W03/00	Ayira Guliso	Waro Seyo	Meso	1500
16	W09/00	Ayira Guliso	Boke Keda	Roge	1600
17	W50/00	Ayira Guliso	Kurfessa birbir	Layo	1580
18	W52/00	Ayira Guliso	Kurfessa birbir	Kurfe	1520

19	W06/01	Ayira Guliso	Lalo Asella	Warrago Arsema	1600
20	W08/01	Ayira Guliso	Tosiyo mole	Abetu Gole	1620
21	W15/01	Ayira Guliso	Buro Hasabar	Abetu Gole	1700
22	W38/01	Ayira Guliso	Nebo Daleti	Basha Amench	1600
Checks					
1	Mana sibu (W78/98)				1550
2	Sinde (W92/98)			Weyesa Hirpha	1590
3	Chala (W76/98)			Adan Tarara	1740
4	Haru-I (66/98)			Bmura Kuso	1800

Table 2: Background description of the coffee accessions.

Methods and data recorded

The data of growth parameters were recorded following the IPGRI descriptor [17]. For yield and disease data all plants per plot were used to record the necessary data.

- **Plan Height (PH) (cm):** Height from the ground level to the tip of the main stem, Height Up to First Primary Branch (HFPB) (cm): Measurement of height above the ground up to the first primary branch, Total Node Number of main stem (TNN): Counts of number of nodes on the main stem, Internodes Length of the main stem (IL) (cm): Obtained by computing per tree as (PH–HFPB)/ TNN-1, diameter of the Main Stem (DM) (mm): Measured the diameter of the main stem at five cm above the ground, Number of Primary Branches (NPB): Counted number of primary branches per main stem, Number of Secondary Branches (NSB): Counted number of secondary branches per tree, Average Length of Primary Branches (ALPB) (cm): It was measured from the point of attachment to the main stem to the apex, Number of Nodes Per Primary Branch (NNPB): average value of the four longest branches at the middle of the stem per plant, Number of Bearing Primary Branches (NBPB): Number of bearing primary branch counted per tree, Percentage of Bearing Primary Branches (PBPB) (%): It was computed per tree as (NBPB/NPB) 100, Canopy Diameter (CD) (cm): Average length of coffee tree canopy measured twice (East-West and North-South).
- **Leaf length (LL), Leaf With (LW):** Average length and width of five matured leaves and Leaf area (LA) (cm): Calculated as: LA=K × LL × LW, K is constant specific to cultivars and canopy classes (0.67) [18].
- **Bean Length (BL) (mm), Bean Width (BW) and Bean Thickness (BT):** Average length of ten normal matured seeds measured at the longest widest and thickness part respectively;
- **Fruit Length (FL) Fruit Width (FW) and Fruit Thickness (FT) (mm):** Average of five normal matured green fruits measured at the longest widest and thickness part respectively
- weight of fresh cherries per plot was recorded in gm and converted in to kg/ha
- Estimated by using following method developed by Zadoks and Schein [19].

Data analysis

Analysis of Variance (ANOVA) was computed for quantitative characters analysis random model had been used in order to test the variability among genotypes for combined over locations (Table 4). This was performed using R-software version 4.1 software package and significant difference tested at 5% ($p<0.05$) level. The statistical model followed: $Y_{ijk}=\mu+G_i+ L_j+B_k$ (L_j)+$GL_{ij}+\varepsilon_{ijk}$. Where, Y_{ijk} was the observation for genotype 'i' at location 'j' in replication 'k'. In the model 'μ' was the overall mean 'G_i' the effect of the genotype 'i', 'L_j' was the effect of environment 'j', 'B_k' block effect, 'GL_{ij}' the interaction between genotype and location or environment and 'ε_{ijk}' was the random error associated with the' kth observation on genotype 'i' in environment

Analysis of association: Phenotypic (rp) and genotypic (rg) correlations between two traits were estimated using the following formula [20]; Gcov (x,y)=(MSPg-MSPe)/r, Pcov (x,y)=gcov (x,y) +Cov (exy), Where r and g are numbers of replications and genotypes respectively, Gcov (x, y)=genotypic covariance between traits x and y, Pcov (x, y)=Phenotypic covariance between character x and y, Cov (exy)=environmental covariance between character x and y; The correlation was estimated using the following formula:

$$rp = \frac{PCOV(x,y)}{\sqrt{\sigma^2_{Px} \times \sigma^2_{Py}}}$$

Where, σ^2px=phenotypic variance for character x, σ^2py=phenotypic variance for character y, rg=(Where, σ^2gx=genotypic variance for character x, σ^2gy=genotypic variance for character y;

Note: In this paper only genotypic correlation was included and discussed.

Results and Discussion

Most bean, fruit, leaf and growth traits had showed highly significant to significant difference in genotype by environmental interaction (GxE) including yield (Table 3). However, GxE was non-

significant in Coffee Leaf Rust (CLR), Number of Node per Primary Branch (NNPB), Leaf Length (LL) and Fruit Width (FW). There was non-significant difference among coffee genotypes for all agronomic traits except in NNPB in which genotype contribution is 51.8%; conversely, high significant difference observed between locations in these traits. Variability was observed among Arabica coffee accessions using these quantitative traits [21-23]. The contribution of genotype for yield was 43.2%; whereas, 19.1% and 37.4% were contributed by location/environment and GxE respectively. Additionally, except in fruit traits, all leaf and bean traits indicated non-significant among genotypes form pooled analysis. This is due to high GxE mean square (MSGxE) against which Mean Square of Genotypes (MSG) had tested. Highest genotype contribution 83.2% recorded for CLR flowed by 70.1, 69 and 61.5 which were recorded for Fruit Length (FL), Fruit Thickness (FT) and Bean Width (BW) respectively. The GxE contribution range from 22.4 to 45.6% for growth traits except Plant Height (PH) and Number of Bearing Primary Branch (NBPB) which showed 17.9 and 11.7% respectively. For most of these traits, environmental (Econt.) contribution was higher than both genotype and GxE. Significant difference observed between location in all growth traits; however, non-significant difference had recorded in leaf, fruit and bean traits except in Fruit Width (FW) and Bean Thickness (BT). High GxE and high contribution of environment resulted the discrepancy performance of coffee genotypes across locations.

Traits	MSB (df=4)	MSG (df=25)	Gcont. %	MSL (df=1)	Econt. %	MSG*L (df=25 GXEcont.	GXEcont. %	MSE (df=100)	CV %
Growth traits									
PH	4.15**	0.95 ns		147.36**		1.48***	0.46	5.12	
	(4887.75**)	(700.46 ns)	11.7	(105798.44**)	70.5	(1072.39***)	17.9	-326.76	-10.23
HFPB	2.11 ns	39.95 ns	40.2	730.64***	29.4	30.26***	30.4	9.5	11.95
TNN	0.26**	0.11 ns		13.19***		0.18***		0.05	4.38
	(35.84**)	(11.55 ns)	13.6	(1357.89***)	64	(19.04***)	22.4	-5.22	-8.91
DM	0.35*	0.16 ns		19.25**		0.33***		0.11	5.61
	(47.59*)	(24.21 ns)	13	(2853.14**)	61.2	(48.25***)	25.9	-18.05	-11.69
IL	2.03*	0.75 ns	36.8	9.04**	17.6	0.93***	45.6	0.33	9.36
CD	798.47**	460.09 ns	25	22637.13**	49	473.22**	25.7	224.84	17.17
NPB	64.66**	49.39 ns	28.9	2045.8**	47.9	39.68***	23.2	15.7	11.08
NSB	41.41 ns	187.28 ns	28	7770.10***	46.5	170.68**	25.5	74.77	20.58
NBPB	9.00 ns	17.68 ns	17.1	1841.92**	71.2	12.12**	11.7	7.4	15.88
PBPB	4.05 ns	75.90 ns	22.2	4150.60**	48.5	100.71**	29.4	50.39	14.9
ALPB	0.59**	0.30 ns		4.59*		0.26**		0.13	3.92
	(198.08**)	(105.23 ns)	39.8	(1640.02*)	24.8	(93.80**)	35.4	-44.63	-7.8
NNPB	4.46 ns	7.21*	51.8	84.10**	24.2	3.33 ns	23.9	2.33	7.96
Leaf traits									
LL	2.81**	0.91 ns	51.1	8.76 ns	19.7	0.52 ns	29.2	0.44	4.41
LW	0.27*	0.24 ns	51.2	0.03 ns	0.3	0.22**	48.5	0.11	5.24
LA	112**	53.93 ns	51.6	120.58 ns	4.6	45.83*	43.8	27.94	8.02
Fruit traits									
FL	1.57*	1.95*	70.1	0.07 ns	0.1	0.83*	29.8	0.56	5.5
FW	0.34 ns	0.74**	25.6	47.83***	65.9	0.25 ns	8.6	0.19	4.13
FT	0.36*	0.83*	69	1.13 ns	3.8	0.33***	27.2	0.14	4.02
Bean traits									
BL	1.71***	0.46 ns	51.8	2.57 ns	11.6	0.33***	36.6	0.05	3.11
BW	0.34***	0.14 ns	61.5	0.06 ns	1.1	0.08***	37.4	0.02	3.26
BT	0.02 ns	0.10 ns	43	1.67**	27.9	0.07***	29.1	0.02	5.79
YLD	129557.52**	69243.67 ns	43.2	766228.09 ns	19.2	59593.41*	37.4	34089.2	44.38
CLR	2.33 ns	7.66***		0.08 ns		1.83 ns		1.67	53.66
	(117.7 5 ns)	(387.34***)	83.2	(1.73 ns)	0	(78.17 ns)	16.8	-96.13	-116.03

Gcont: Genotype contribution; Econt: Environmental contribution and GXEcont: GXE contribution. PH: Plant Height (cm); HFPB: Height up to the First Primary Branch (cm); TNN: Total Node nNmber of main stem, DM: Diameter of main stem (mm); IL: Internodes' length of main stem (cm); CD: Canopy Diameter (cm); NPB: Number of Primary Branch; NSB: Number of Secondary Branch; NBPB: Number of Bearing Primary Branch; PBPB: Percent of Bearing Primary Branch; ALPB: Average Length of Primary Branch (cm); NNPB: Number of Nodes per Primary Branch; LL: Leaf Length (cm); LW: Leaf Width (cm); LA: Leaf Area (cm^2); FL: Fruit Length (mm); FW: Fruit Width (mm); FT: Fruit Thickness (mm); BL: Bean Length (mm); BW: Bean Width (mm); BT: Bean Thickness (mm); YLD: Yield kg/ha, CLR-Coffee Leaf Rust (%),*, **, ***and ns: Represent significant different at probability level of 0.05, 0.01, 0.001 and non-significant different respectively.

Table 3: Combined analysis of variance for quantitative traits.

This indicates that it is very difficult to obtain genetic progress in selecting genotypes with high performance at both locations, *i.e.,* the identification of genotypes with high performance over a wide coffee producing area is very difficult. Thus, it seems better to divide coffee growing areas into similar ecologies, some similar to Haru and others similar to Mugi and focus on developing coffee varieties with specific adaptation to these ecologies. This confirmed by who found the inconsistence performance of Arabica coffee genotypes across locations [24,25].

If we select five genotypes with highest bean yield where the correlation between the two locations was almost zero no common genotype was selected at both locations (Table 4). Also, for girth/ diameter of main stem (DM) at each location (about 5% selection intensity), no genotype was common for both locations (Table 5). The five genotypes with highest DM over both locations give lower DM at both Haru and Mugi, (reduction of 4.5 and 5.1%, respectively). It is obvious that if more stringent selection intensity is used, this discrepancy (reduction) will be higher; selection based on mean performance is inferior to selection at specific locations. The correlation between DM at the two locations was negative; Hence, two of the five genotypes having wider fruit were selected at both locations (Table 6). Also, For CLR where the correlation between the two locations was positive (r=0.67***), three of the five genotypes with lowest CLR infection were selected at both locations (Table 7). This may be due to high contribution of genotype than GxE contribution for the traits. For CLR genotypic contribution was 83.2% and 25.6% for Fruit Width (FW), whereas the GxE contribution was 8.6 and 16.8% for FW and CLR respectively.

	Haru	Mugi	Reduction	Combined	Reduction
	W203/98	W09/00		W09/00	
	W167/98	W02/98		W212/98	
	Haru-I	W08/01		W167/98	
	W03/00	Sinde		W02/98	
	W212/98	W188/98		W203/98	
Mean Haru	467.4	329	29.6	437.64	6.4
Mean at Mugi	500.4	745.3	32.9	581.25	22.01
Mean combined	483.9	537.2		509.45	

Table 4: The five highest yielding genotypes at Haru, at Mugi and over locations.

	Haru	Mugi	Reduction	Combined	Reduction
	Mena Sibu	W08/01		W08/01	
	W06/01	W188/98		W15/01	
	W203/98	W15/01		W06/01	
	Chala	W167/98		W212/98	
	Haru-I	W175/98		Sinde	
Mean Haru	35.5	29.4	17.2	33.9	4.5
Mean at Mugi	38.2	46.9	18.6	44.5	5.1
Mean combined	36.8	38.1		39.2	

Table 5: The five genotypes with highest DM at Haru, at Mugi and over locations.

	Haru	Mugi	Reduction	Combined	Reduction
	W141/98	W50/00		W141/98	
	W08/01	W141/98		W08/01	
	Sinde	W163/98		W50/00	

	W06/01	W188/98		W109/99	
	W109/99	W08/01		Sinde	
Mean Haru	10.6	10.3	2.8	10.5	0.9
Mean at Mugi	11.2	11.5	2.6	11.4	0.9
Mean combined	10.9	10.9		10.9	

Table 6: The genotypes with highest FW at Haru, at Mugi and over locations.

	Haru	**Mugi**	**Reduction**	**Combined**	**Reduction**
	W52/00	W191/98		W109/99	
	Chala	W38/01		W175/98	
	W09/00	Chala		Chala	
	W175/98	W02/98		W52/00	
	W191/98	W52/00		W191/98	
Mean Haru	0.88	1.44	-63.6	0.94	-6.8
Mean at Mugi	1.33	1.12	-18.8	1.27	-13.4
Mean combined	1.11	1.28		1.11	

Table 7: The five most tolerant genotypes for CLR at Haru, at Mugi and over locations.

Association among traits

Genotypic correlation at Haru: Traits with positive correlation with bean yield merge first with it to form the cluster of bean yield; first merges NNPB, then PBPB, NBPB and cluster consisting of PH, TNN, NPB, and DM joins the cluster of bean yield until finally BT and BW merge with the cluster of Bean yield (Figure 1). The finding of confirmed the positive association of PH, NPB and CD with clean coffee yield [13]. Number of secondary branches which had the strongest negative genotypic correlation (rg=-0.990**) lies on the opposite side of bean yield. In contrary, from previous experimental result positive correlation between yield and NSB was reported [26]. All traits with negative genotypic correlation with bean yield such as HFPB, IL, LW, LA, BL, and CLR first merge with the cluster of NSB and finally merge with cluster of bean yield. Of the traits that had positive genotypic correlation with bean yield, FL (rg=0.61) and LL (rg=0.46) are in the cluster of NSB because FL had strong positive correlation with BL (rg=0.68) while LL had strong correlation with HFPB (rg=0.66). Additionally, almost all these traits are positively correlated with each other at genotypic level at this location. Plant height (PH) had strong and significant positive genotypic correlation with TNN (0.904**), DM (0.830**) and NPB (0.771*); also, it showed positive correlation with CD, HFPB, with some leaf, fruit and bean traits. TNN had positive correlation with NBPB (0.766*), NNPB (0.764*) and NPB (0.852**). Internode Length (IL) positively correlated with Fruit Width (FW) (0.816*) and FT (0.633); CD had positive correlation with ALPB (0.990**); NPB showed positive correlation with NBPB (0.897**).Genotypes with high bean yield are expected to have stronger (vigour) plants with wider stem diameter (DM rg=0.40), and possess more number of nodes on the main stem (TNN) (rg=0.990**) and hence, more number of primary branches (NPB) (rg=0.78).

Such genotypes also are expected to have taller plants (PH) (rg=0.79). Primary branches are expected to possess many nodes and longer (NNPB and ALPB) (rg=0.990** for both). Many of the primary branches should bear berries (NBPB and PBPB with rg=0.990** for both). Such genotypes logically have wider canopy (CD) (rg=0.3). They are expected to have longer leaves (LL)(rg=0.46) and longer fruits (FL) (rg=0.61). In line with this result, reported that PH, DM and TNN had positive genotypic correlation with yield [27]. Similar results reported by on association among these quantitative traits [28].

In contrary, the highest yielding genotypes are expected to have low placement of the first primary branch (HFPB), shorter internodes, narrower leaves and smaller Leaf Area (LA), shorter beans (BL) and non or lower infestation by Coffee Leaf Rust (CLR) due to negative correlation of these traits with bean yield (Table 8). This may be due to pleiotropic gene effect that resulted from previous selection [29].

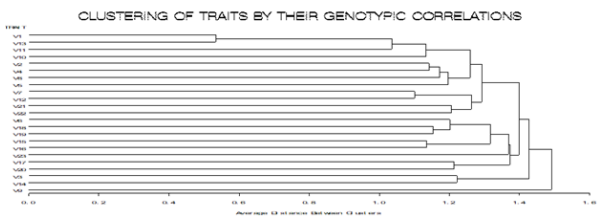

Figure 1: Clustering of traits by their genotypic correlation at Haru.

Note: YLD=V1, PH=V2, PFPB=V3, TNN=V4, DM=V5, IL=V6, CD=V7, NPB=V8, NSB=V9, NBPB=V10, PBPB=V11, ALPB=V12, NNPB=V13, LL=V14, LW=V15, LA=V16, FL=V17, FW=V18, FT=V19, BL=V20, BW=V21, BT=V22, and CLR=V23.

No.	Traits	Haru Gr	Mugi Gr
1	PH	0.787	0.651
2	HFPB	-0.154	0.277
3	TNN	0.990**	0.481
4	DM	0.417	0.127
5	IL	-0.76	0.251
6	CD	0.262	0.034
7	NPB	0.778	0.43
8	NSB	-0.990**	-0.001
9	NBPB	0.990**	0.554
10	PBPB	0.990**	0.179
11	ALPB	0.990**	-0.167
12	NNPB	0.990**	-0.205
13	LL	0.46	-0.458
14	LW	-0.322	-0.39
15	LA	-0.161	-0.504
16	FL	0.612	-0.218
17	FW	0.017	-0.418
18	FT	0.052	-1.047*
19	BL	-0.435	-0.31
20	BW	0.371	-0.025
21	BT	0.990**	-0.452
22	CLR	-0.107	0.358

PH-Plant Height (cm), gr: genotypic correlation coefficient, HFPB: Height up to the First Primary Branch (cm); TNN: Total Node Number of main stem; DM: Diameter of Main stem (mm); IL: Internodes' length of main stem (cm); CD: Canopy Diameter (cm); NPB: Number of Primary Branch; NSB: Number of Secondary Branch; NBPB: Number of Bearing Primary Branch; PBPB: Percent of Bearing Primary Branch; ALPB: Average Length of Primary Branch (cm), NNPB: Number of Nodes per Primary Branch; LL: Leaf Length (cm); LW: Leaf Width (cm); LA: Leaf Area (cm^2); FL: Fruit Length (mm); FW: Fruit Width (mm); FT: Fruit Thickness (mm); BL: Bean Length (mm); BW: Bean Width (mm); BT: Bean Thickness (mm); YLD: Yield $Kgha^{-1}$ and CLR: Coffee Leaf Rust (%) and Inc.: Increment, *significant and **highly significantcorrelation.

Table 8: List of genotypic correlation coefficient at both locations.

	YLD	PH	HFPB	TNN	DM	IL	CD	NPB	NSB	NBPB	PBPB	ALPB	NNPB	LL	LW	LA	FL	FW	FT	BL	BW	BT	CLR
High	383.7	156.8	24	23.9	32.4	5.8	155.3	33.8	30.7	14.6	43.1	81.1	18.6	15.7	6.3	66.5	13.6	10	9.1	7.5	4.8	2.1	3.5
Low	307.6	139.5	22.2	21.2	30.4	5.8	150.5	29.9	41.8	12.2	41	76.9	17	15.6	6.2	65.1	13.4	9.9	9	7.7	4.7	2	3
Incr.	76.1	17.3	1.8	2.7	2	0	4.8	3.9	-11.1	2.4	2.1	4.2	1.6	0.1	0.1	1.4	0.2	0.1	0.1	-0.2	0.1	0.1	0.5
%	24.7	12.4	8.1	12.7	6.6	0	3.2	13	-26.6	19.7	5.1	5.5	9.4	0.6	1.6	2.2	1.5	1	1.1	-2.6	2.1	5	16.7

PH: Plant Height (cm); HFPB: Height up to the First Primary Branch (cm); TNN: Total Node Number of main stem; DM: Diameter of main stem (mm); IL: Internodes' length of main stem (cm); CD: Canopy Diameter (cm); NPB: Number of Primary Branch; NSB: Number of Secondary branch; NBPB: Number of Bearing Primary branch; PBPB: Percent of Bearing Primary Branch; ALPB: Average Length of Primary Branch (cm); NNPB : Number of Nodes per Primary Branch; LL: Leaf Length (cm); LW: Leaf width (cm); LA: Leaf Area (cm^2), FL: Fruit Length (mm); FW: Fruit Width (mm); FT: Fruit Thickness (mm); BL: Bean Length (mm); BW: Bean Width (mm); BT: Bean Thickness (mm); YLD: Yield ($Kgha^{-1}$), and CLR: Coffee Leaf Rust (%) and Inc.: Increment.

Table 9: The five highest and lowest yielding genotypes based on genotypes correlations at Haru.

Association of traits and expected mean performance of genotypes at Haru: The means of various traits of the five highest yielding and the five lowest yielding genotypes were compared at Haru (Table 9). The two groups had average bean yields of 383.7 and 307.6 kg ha^{-1}, respectively; an advantage of 76.1 kg ha^{-1} or an increase of 24.7% in the highest yielding group. Direction of change was as expected from the genotypic correlations except in HFPB, IL, LW, LA and CLR, where means of the highest yielding genotypes increased by 8.1, 0.0, 1.6, 2.2 and 16.7% instead of decreasing as expected from the negative genotypic correlation between bean yield and these traits. This may be due to weak negative correlation (weak negative effect on yield) with bean yield and strong correlation with other traits which had strong positive correlation with yield. The higher infestation by CLR of the highest yielding genotypes is due to genotypes moderate resistance and resistant to infection of CLR and weak correlation of CLR with yield (rg=-0.1) at Haru. For NSB and BL these means were lower by 26.6 and 2.6%, respectively, as expected from negative correlation with bean yield.

For traits having positive genotypic correlation with bean yield, means of the five highest yielding genotypes was increased by more than 10% in PH (12.4%), TNN (12.7%), NPB (13.0%) and NBPB (19.7%). Also, highest yielder genotypes increased in NNPB by 9.4%. At Haru, high yielding genotypes had taller plants with many nodes on the main stem and bearing many primary branches with many nodes. Many of these nodes produced berries (fruits), *i.e.* such plants had more number of bearing nodes on each primary branch.

Genotypic correlations at Mugi: Agronomic traits such as PH, HFPB, TNN, DM, IL, CD, NPB, NBPB and PBPB had positive correlation with clean coffee bean yield at genotypic level; CLR showed positive correlation with yield which is expected due to high cherry bearer coffee genotypes exposed to CLR infection. However, bean yield had negative correlation with NSB (near zero), with all leaf, fruit and bean traits. However, Abdulfeta, et al. [30] reported the positive correlation between NSB and clean coffee yield. The correlation of bean yields with FT -1.0 which was strong correlation.

Therefore, PH, IL, DM, NBPB, TNN, NPB, and CLR were the first to form cluster with bean yield (Figure 2). These traits had genotypic positive association with each other; PH was positively correlated with IL (0.783*), DM (0.501), NBPB (0.512), TNN (0.389) and NPB (0.418). Also, IL had positive genotypic correlation with coffee tree girth (0.775) and NBPB (0.217); additionally, coffee main stem girth (CD) showed positive correlation with NBPB (0.825*), TNN (0.216) and NPB (0.462). Likewise, the past finding confirmed the positive association between clean bean yield and PH, IL, DM, NBPB, TNN and NPB and positive association among yield related traits themselves [13,30,28]. Although NSB had negative genotypic correlation near zero with bean yield, its association with PH, TNN, DM and NPB was relatively strong and it combined with cluster of bean yield. HFPB was relatively closely correlated with percentage bearing primary branch which later joined the cluster of clean bean yield. Also, CD was relatively closely correlated with ALPB, LL, NNPB and these four traits form cluster which later joined with yield cluster. Fruit thickness which showed strong genotypic correlation (-1.0) with yield was found at the last opposite side of clean yield cluster. Traits like LW, BW, LA, FL, BT, BL and FW which showed negative genotypic correlation to bean yield first merge or form cluster with fruit thickness which later joined with the cluster of bean yield. This result agreed with the finding of Fikadu, et al. [31] and Gizachew and Hussien [12] who reported that the positive genotypic correlation of bean yield with PH, NPB and CD and positive association among each other.

Correlation and expected mean performance at Mugi: On the genotypic level yield of the highest yielding genotypes was increased by 99.2%, PH by 15.2%, TNN by 9.4%, DM by 13.2%, NPB by 10.4%, NBPB by 19.6% and PBPB by 9.7% which was expected from their positive correlation with yield (Table 10). Although NSB had small negative genotypic correlation with bean yield it was increased by 13.1% in the elite selections. ALPB and NNPB were also increased by 5.4 and 2.1% although they were expected to decrease. This may be due to their weak correlation effect on bean yield. The reductions in leaf, fruit and bean traits were all lower than 5.0%; the highest being that of BT (8.3%) which is expected from their negative effect on bean yield at this location. The highest yielding lines had 38.4% more infestation by coffee leaf rust as compared to the five lowest yielding lines. Hence, the high yielding genotypes should possess much number of primary branches, many bearing number of primary branch, many number of nodes per main stem, wider (vigour) main stem, distant internodes length, taller plant (height), few number of secondary branch, small leaf length, narrow leaf area, small fruit and bean size at this location. At Mugi location, CLR showed negative correlation with IL, LL, and BT. Thus, during selection for CLR resistance, genotype having distant internodes length suggested to be selected at this location.

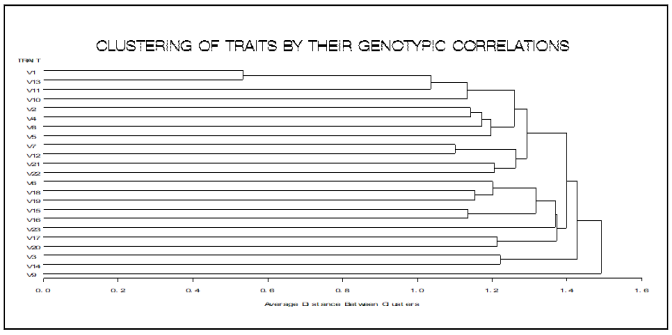

Figure 2: Clustering of traits by their genotypic correlation at Mugi.

Note: YLD=V1, PH=V2, PFPB=V3, TNN=V4, DM=V5, IL=V6, CD=V7, NPB=V8, NSB=V9, NBPB=V10, PBPB=V11, ALPB=V12, NNPB=V13, LL=V14, LW=V15, LA=V16, FL=V17, FW=V18, FT=V19, BL=V20, BW=V21, BT=V22, and CLR=V23.

	YLD	PH	HFPB	TNN	DM	IL	CD	NPB	NSB	NBPB	PBPB	ALPB	NNPB	LL	LW	LA	FL	FW	FT	BL	BW	BT	CLR
High	678.3	222	28.3	30.4	43	6.7	190.6	41.4	51.9	22	54.1	91.3	19.4	15.1	6.3	63.6	13.8	11	9.2	7.3	4.7	2.2	2.5
Low	340.5	194	28	27.8	38	6.2	175.4	37.5	45.9	18.4	49.3	86.6	19	15.3	6.4	65.5	13.6	11	9.3	7.5	4.7	2.4	1.8
Inc.	337.8	29.4	0.3	2.6	5	0.5	15.2	3.9	6	3.6	4.8	4.7	0.4	-0.2	-0.1	-1.9	0.2	0	-0.1	-0.2	0	-0.2	0.7
%	99.2	15.2	1.1	9.4	13.2	8.1	8.7	10.4	13.1	19.6	9.7	5.4	2.1	-1.3	-1.6	-2.9	1.5	0	-1.1	-2.7	0	-8.3	38.9

PH: Plant Height (cm); HFPB: Height up to the First Primary Branch (cm); TNN: Total Node Number of main stem; DM: Diameter of main stem (mm); IL: Internodes' length of main stem (cm); CD: Canopy Diameter (cm); NPB: Number of Primary Branch, NSB: Number of Secondary Branch; NBPB: Number of Bearing Primary Branch; PBPB: Percent of Bearing Primary Branch; ALPB: Average Length of Primary Branch (cm); NNPB: Number of Nodes per Primary Branch; LL: Leaf Length (cm); LW: Leaf Width (cm); LA: Leaf Area (cm^2); FL: Fruit length (mm); FW: Fruit Width (mm); FT: Fruit Thickness (mm); BL: Bean Length (mm); BW: Bean Width (mm); BT: Bean Thickness (mm); YLD: Yield $Kgha^{-1}$ and CLR: Coffee Leaf Rust (%) and Inc.: Increment.

Table 10: The five highest and lowest yieldinggenotypes based on genotypic cor relations at Mugi.

Conclusion

The present study combined analysis indicated non-significant difference among genotypes in all traits except in Number of Node Preprimary Branch (NNPB), fruit traits and reaction to coffee leaf rust. This is due to high GxE effect against which the mean square of genotypes of overall location tested. However, variability among genotypes revealed at individual location for most traits. Significant different was observed between locations in all growth traits, fruit width and bean thickness; also, there were significant difference in GxE in all bean traits and growth traits except in NNP and from leaf and fruit traits except in leaf length and fruit width respectively. As results of high GxE effects, high discrepancy performance was observed on coffee genotypes across location. Thus, it is ideal to group location as areas similar to Mugi in edaphic and climatic condition and Haru separately for further performance analysis and specific ecology adaptation.

Plant height, total node number, diameter main stem/girth, number of primary branch, number of bearing primary branch, Average Length of Primary Branch (ALPB), Number of Node per Primary Branch (NNPB) showed positive genotypic correlation with yield at both locations except ALPB and NNPB at Mugi. Most of these traits had strong positive genotypic correlation with each other. Thus, one has to be conscious to select genotypes with tall height, many number node on stem, possess huge long primary branch with many node and high berry bearing capacity and thick girth during high yielding coffee variety selection. The selection intensity at 5% of high yielding and low yielding genotypes indicated the superiority high yielder material over low yielding in these traits which was expected from their positive association with yield. All fruit traits and bean thickness showed positive genotypic correlation at Haru, but negative correlation at Mugi. Whereas, height up to the first primary branch and internode length had showed negative genotypic correlation at Haru, but vice versa at Mugi. In general, it is better to consider coffee genotype which emanate the first primary branch relatively close to ground and possessing very short length between consecutive branches on main stem at Mugi, but the opposite at Haru during yield improvement *via* selection.

Data Availability

The data of this finding study are available with the corresponding author at any time if reasonably requested by concerned body.

Conflicts of Interest

The authors affirmed that there is no conflict of interest among them.

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