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Research Article

Genetic Gain Trend in Yield and Advanced Selection of Yayo Coffee (*Coffea arabica* L.) Land Race Collection

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Coffea arabica L., the dominant cash crop in the world market, is native to rain forest of Ethiopia where it is believed to exist with high genetic diversity. Estimating genetic parameters are momentous in deciding breeding method to be followed for crop genetic improvement including Arabica coffee. The study was conducted with the intention to gauge genetic gain trend in coffee yield and to select advanced promising lines of Yayo coffee landrace for the next breeding step. The study was laid down at Metu research subcenter in 2013, using 124 coffee accessions that were established in simple lattice design under two sets each comprising 62 accessions including two checks. The over six year's pooled analysis of variance indicated the handiness variability in yield performance among accessions. Moderate genotypic variance (15.46 to13.56%), heritability (56.16–81%), and expected genetic gain (15.52–20.8%) were observed. The genetic parameters and the superiority of check in yield over accessions elucidated that high yielder variety development by selection is difficult unless heterosis attaining breeding method followed, particularly for these Yayo coffee landrace origin. Common high genetic gain trend (49.19 and 100 $\text{kg}\cdot\text{ha}^{-1}$) and response to selection (196.76 and 400 $\text{kg}\cdot\text{ha}^{-1}$), selection differential 471.9 and 739.23 $\text{kg}\cdot\text{ha}^{-1}$ were revealed in over four harvesting seasons mean value for both sets. Thus, selection is more effective in earlier season than late. High yielding accessions, Y27 and Y93, gave 3013.1 and 125.8 $\text{kg}\cdot\text{ha}^{-1}$ yield gain over the high yielder check correspondingly. Despite the top 15 and 10 high yielders were selected from set-I and set-II, respectively, a total of 20 accessions with contrasting desirable traits were selected and established in crossing block for genetic improvement purposes via heterotic hybrid variety development program. These accessions were tolerant to major coffee disease and have desirable agronomic traits.

1. Introduction

Coffee is a herbaceous tree that belongs to family Rubiaceae and genus Coffea. It is a cash crop that can be propagated principally by seed. The dominant and noble in quality beverage from coffee species is *Coffea arabica* L. This coffee species is allotetrapliod and self-pollinated with some extent of outcross (10%) [1, 2]. It is native to south western Ethiopia where ample of diversity is authenticated by different scholars. Arabica coffee in its native ecology Ethiopia is growing under diverse environmental areas which range in altitude about 560–2600 m. a. s. l. that receives annual rainfall of 800–2000 mm [3–5]. This crop is mostly grown in tropical and subtropical regions [6, 7].

Arabica coffee is a predominant species which shares about 70% of the world coffee production [8–10]. Coffee contributes directly and indirectly for the livelihood of 125 million peoples in the world [5, 11]. Ethiopia is the only country that produces Arabica coffee only. Around 15 million (16% of population) of Ethiopian people lead their livelihood by the income generated from this commodity [11, 12]. Besides, Arabica coffee shares the largest percentage

(29%) among the exported materials that earn foreign exchange income in the country.

Despite its high economical values and immense efforts made to develop 42 improved varieties by Jimma Agricultural Research Center from the last five and half decades [13, 14], coffee production in Ethiopia still remained low. Coffee production is hindered by different factors such as diseases, insect pest, and climate change [5, 7, 15]. The current climate change became opportunistic for newly emerging diseases like thread blight and insect pests like trips which are currently devastating coffee production in south western Ethiopia. Other contributing factors to low coffee productivity/production could be low technology adoption by farmers and the use of local varieties and traditional practices, very weak and nonuniform extension work by regionals agricultural offices, feeble on continuing the research legacy through extension work by the local experts, and exploiting genetic potential to the maximum for each coffee producing areas is still less than expected. Thus, to overcome low yield via the use of improved varieties and maximum exploitation of the genetic potential in each of the specific coffee producing regions of the country focus needs to be given to local landrace variety development program of coffee breeding strategy.

The knowledge of prominent genetic parameters determines the success in genetic improvement of any crop whether via pure line selection or hybridization activities. Estimation of phenotypic and genetic variance is basic for heritability estimation from which genetic gain of any desirable traits is derived [16, 17]. Plant breeders anticipated genetic gain periodically to compare the efficiency of different breeding strategies in attaining the improvement of desirable traits [18, 19]. Hence, estimation of genetic gain in addition to other genetic parameter in any desirable traits indicates breeders' success in selection of promising line and developing outstanding varieties [20]. For *Coffea arabica* L., the genetic gain of 213.89 $\text{kg}\cdot\text{ha}^{-1}$ recorded in yield per cycle of selection and 7.41 cm, 5 in number, 3 in number, and 7.41% genetic gain were reported for primary branch length, number of secondary branch, number of bearing primary branch, and percent of bearing primary branch, respectively [21]. For selection at 5% superior genotypes of Arabusta (C. Arabica x C. Robusta hybrid), 699.3 $\text{kg}\cdot\text{ha}^{-1}$ genetic gain was reported in coffee yield per cycle of selection [22]. Similarly, Atinafu et al. [23] reported 201.8 $\text{kg}\cdot\text{ha}^{-1}$, and Lemi and Ashenafi [24] obtained 345.68 $\text{kg}\cdot\text{ha}^{-1}$ genetic gains in clean yield per cycle for the top 5% high yielders' selection from the population of Arabica coffee.

Most genetic gain that authors reported in clean coffee yield and yield-related traits is per cycle of selection or genetic gain of a year, which gives less information about genetic gain progress with respect to desirable trait/s over multiple harvesting seasons. The estimation of realized changes in genotypic values for coffee yield over multiple cycles is referred to as realized genetic trend [19] which is very important in the selection of advanced lines for the next breeding program. However, such kinds of information which can be used to predict the multiple seasons' genetic gain in clean coffee yield concurrent advanced line selection in improvement program has been lacking. Using local landrace variety development program of coffee breeding strategy, huge number of accession from Yayo coffee landrace were evaluated for many years. However, from the results of this study, there has been a gap to identify the genetic gain trend in yield and its fate needs to be determined. Hence, the current field experiment is designed to determine the genetic gain trend in clean coffee yield and to identify advanced selection of high yielding Yayo coffee accessions for the next breeding program.

2. Materials and Methodology

2.1. Description of the Study Area. The current experiment was conducted at Metu agricultural research subcenter of Jimma agricultural research center. The subcenter is at a distance of 272 km from Jimma agricultural research center and located 8°19' 0″ to North and 35°35' 0″ to East. This area has an altitude of 1558 m a. s. l. and with rainfall annually rain fall of 1829 mm, and minimum and maximum annual temperature 12.7°C and 28.9°C, respectively.

3. Materials and Experimental Design

The experimental materials used for the present study consist a total of 124 accessions of Yayo coffee land race that were collected from different coffee growing ecologies Yayo district, south western Ethiopia. The study was laid down in two sets (set-I and set-II) using simple lattice design in August 2013. In each set, 62 coffee accessions with two checks were comprised to conduct the study (Table 1). The coffee seedling was planted using spacing of 2°m × 2°m between row and plant with a total of six coffee seedlings planted per plot. All agronomic management such as fertilizer, shade, weeding, sucker management, and mulching were applied uniformly in all the plots as per the recommendation [25].

3.1. Method Used and Data Recorded. The coffee yield data was recorded per plot using fresh red cherry in Gram per plot from the crop bearing trees over harvesting time in cropping seasons [26]. Data for the dried coffee fruit at the last period of harvesting was recorded as drying Gram per plot, and the dry yield data was multiplied by 2.6 to convert to red cherry in Gram before computing the mean yield of genotypes. The mean of red cherry data was computed by dividing the total amount of red cherry in Gram per plot for the total number of bearing coffee trees per plot. Then, the mean of red cherry per tree was converted to clean coffee yield in Qha^{-1}, by multiplying red cherry by 0.00417 (conversion factor). Finally, the yield data in Q ha^{-1} was converted to $\text{kg}\cdot\text{ha}^{-1}$ which is the SI unit for weight. Yield data of the studied coffee accession was undertaken over six consecutive harvest years.

3.2. Statistical Analysis. All yield data collected were subjected to R-software and SAS version of 9.4 [27] for statistical data analysis. Analysis of variance was performed for yield and availability of variability indicated which is a rudimentary for estimating genetic gain, genetic gain trend, and

Table 1: Description of Yayo coffee accessions studied at Metu research sub-center (set-I and set-II).

Set-I							Set-II						
Accessions code	Region	Zone	District	Specific location	Alt. (m a.s.l)	No. Accessions	Accessions code	Region	Zone	District	Specific location	Alt. (m a.s.l)	No. of accessions
Y01–Y07	Oromia	Illuababora	Yayo	Debisa	1200	7	Y63–Y67	Oromia	Illubabor	Yayu	Dogi	1400	5
Y08, Y10-Y11	Oromia	Illuababora	Yayo	Geba	1250	3	Y68–Y71	Oromia	Illubabor	Yayu	Sembo	1350	4
Y09	Oromia	Illuababora	Yayo	Geba	1260	1	Y72–Y73	Oromia	Illubabor	Yayu	Sembo	1380	2
Y12–Y14	Oromia	Illuababora	Yayo	Geba	1200	3	Y74–Y80	Oromia	Illubabor	Yayu	Sembo	1400	7
Y15	Oromia	Illuababora	Yayo	Geba	1350	1	Y81–Y86	Oromia	Illubabor	Yayu	Geba	1350	6
Y16-Y17	Oromia	Illuababora	Yayo	Geba	1225	2	Y87–Y93	Oromia	Illubabor	Yayu	Achebo	1380	7
Y18	Oromia	Illuababora	Doreni	Geba	1350	1	Y94	Oromia	Illubabor	Yayu	Achebo	1480	1
Y19,Y21–Y22	Oromia	Illuababora	Doreni	HaroMenka	1350	3	Y95–Y102	Oromia	Illubabor	Yayu	Geri geba	1480	10
Y20	Oromia	Illuababora	Doreni	HaroMenka	1225	1	Y105–Y107	Oromia	Illubabor	Yayu	Gordeya	1480	3
Y23–Y25	Oromia	Illuababora	Yayo	Masongo	1250	3	Y108–Y109	Oromia	Illubabor	Yayu	Gordeya	1300	2
Y26–Y29	Oromia	Illuababora	Yayo	Masongo	1200	4	Y110–Y112	Oromia	Illubabor	Yayu	Gordeya	1650	3
Y30–Y35	Oromia	Illuababora	Yayo	Masongo	1250	6	Y113–Y124	Oromia	Illubabor	Yayu	Degitu	1650	12
Y36–Y49	Oromia	Illuababora	Yayo	Geba	1300	14	74110	Oromia	Illubabor	Metu	Bishari	1700	Check
Y50	Oromia	Illuababora	Yayo	Geba	1350	1	74112	Oromia	Illubabor	Metu	Bishari	1700	Check
Y51	Oromia	Illuababora	Yayo	Geba	1400	1	Total						64
Y52–Y62	Oromia	Illuababora	Yayo	Daggi	1400	11							
74110	Oromia	Illubabor	Metu	Bishari	1700	Check							
74112	Oromia	Illubabor	Metu	Bishari	1700	Check							
Total						64							

Note. both set-I and set-II are 124 accessions; totally, 126 coffee genotypes with checks.

Table 2: Analysis of variance skeleton for a year.

Source of variation	Df	SS	MS	F-value F-tab (0.05)
Replication	r–1	SSr	MSr	MSr/MSb
Genotype (unadj)	g^2–1	SSg	MSg	MSg/MSe
Genotype (adj.)	g^2–1	SSg	MSg	MSg/MSe
Block with in replication (adj.)	r (g–1)	SSb	MSb	MSb/MSe
Intra block error	(g–1) (rg–g–1)	SSe	MSe	
Total	(r) (g^2)–1			

Table 3: Combined analysis of variance for over years.

Source of variation	Df	SS	MS	F-value F-tab (0.05)
Replication	r–1	SSr	MSr	MSr/MSb
Genotype (adj.)	g^2–1	SSg	MSg	MSg/ MSgy
Genotype (unadj.)	g^2–1	SSg	MSg	MSg/ MSgy
Block with in replication	r (g–1)	SSb	MSb	MSb/MSe
Year	y–1	SSy	MSy	MSy/ MSgy
G xY	(y–1) (g^2–1)	SSgxy	MSgxy	MSgxy/ MSe
Intra block error	(K–1) (rk–k–1)	SSe	MSe	

heritability. The significant difference among accessions for yield was tested at 5% ($p < 0.05$) probability level. Statistical random model was used for data analysis, and both genotypes and seasons were random factors. The following statistical model was followed, $Yij = \mu + Gi + Xk\ (j) + \beta j + \varepsilon ijk$ for single year data (Table 2) and $Yijkr = \mu + Gi + Cr + \beta j\ (Yr) + Xk\ (j) + (\mathrm{GC})\ ir + \varepsilon ijkr$ for over years data (Table 3). Where $Yijk$ = response of Y trait from the i^{th} Genotype under j^{th} replication and Cr = effects of r^{th} level of years, μ = overall mean effects, gi = effects of i^{th} level of Genotypes, βj = effects of j^{th} level of replication within year, $Xk\ (j)$ = effects of K^{th} level of incomplete blocks within replications, and εijk = the residual or random error component. PROC mixed procedure was used for statistical analysis. Homogeneity of variance was tested using Bartlett test [28] before pooled analysis of over years yield data. Mean separation test between Coffee genotypes was carried out using least significance difference (LSD). Advanced selection for the next breeding program was done at 24 % (the comprising the top 15 high yielders) and 16% (comprising the top 10 high yielders) for set-I and Set-II, respectively; the top fifteen and ten high yielders coffee accessions were selected according to their yield performance over six harvesting years.

3.2.1. Response to Selection. The genetic gain value of traits reponses to selection per cycle of selection; calculated as $R = ih\sigma p$, where i is the selection intensity, h is the standard deviation of heritability, and σp is the phenotypic standard deviation.

3.2.2. Selection Differential. SD = $i\sigma p$, where SD is the selection differential, σp is the phenotypic standard deviation, and i is the selection intensity.

3.2.3. Estimation of the Rate of Genetic Gain. The expected gain per unit of time is referred to as the rate of genetic gain which can be computed by a method developed by Falconer [29]which is as follows: ($\Delta GA = R/L$); where ΔGA is the rate of genetic gain, R is the response to selection, and L is the time required for selection. In general, the mean predicted yield gain across years (Y) can be estimated as [30, 31]: where i = standardized selection differential, h^2 = estimated broad sense heritability on a genotype mean basis, and sp = square root of the estimated phenotypic variance across years. $h^2 = \sigma^2{}_g/(\sigma^2{}_g + \sigma^2{}_{gy}/Y + \sigma^2{}_e/\mathrm{YR})$ for over years; where $\sigma^2{}_g$ is the genotype, $\sigma^2{}_{gy}$ is the GY interaction and $\sigma^2{}_e$ is the experimental error components of variances (all estimated from ANOVA for the combined data), and R and Y are, respectively, the number of replicates and harvesting years (cycles) assumed/hypothesized for selection.

3.2.4. Components of Variance. Error ($\sigma^2 e$), genotypic (σ^2g), and phenotypic ($\sigma^2 p$) variance was computed following the formula suggested by Hallauer et al. [32], and Singh and Chaudhary [33]. $\sigma^2 e = \mathrm{Mse}/r$; Mse–mean square of error, $\sigma^2\mathrm{g} = (\mathrm{Msg\text{-}Mse})/r$; Msg-mean square of genotypes, r-replication, and $\sigma^2 P = \sigma^2 e + \sigma^2\mathrm{g}$.

3.2.5. Broad Sense Heritability. Broad sense heritability is calculated as follows: $H^2 = \sigma^2\mathrm{g}/\sigma^2 p$ for single year, where σ^2g is the genotypic variance and $\sigma^2 p$ is the phenotypic variance, and $H^2 = \sigma^2{}_g/(\sigma^2{}_g + \sigma^2{}_{gy}/Y + \sigma^2{}_e/\mathrm{YR})$ for over years; where $\sigma^2{}_g$ is the genotype variance, $\sigma^2{}_{gy}$ GY is the interaction variance and $\sigma^2{}_e$ is the experimental error of variance (all estimated from combined data), and R and Y are the number of replicates and harvesting years (cycles) assumed/hypothesized for selection, respectively.

3.2.6. Phenotypic and Genotypic Coefficient of Variation. Phenotypic and genotypic coefficient of variation is computed as follows: $\mathrm{GCV} = (\sqrt{\sigma^2\mathrm{g}})/x$ and $\mathrm{PCV} = (\sqrt{\sigma^2 p})/x$ where GCV is the genotypic coefficient of variance, PCV is the phenotypic coefficient of variance and x-general mean.

4. Results and Discussion

4.1. Analysis of Variance. There was a highly significant difference ($p < 0.001$) among accessions of set-I in 2015 and 2016 harvesting seasons; while, there was also a significantly difference ($p < 0.05$) observed among accessions of this set in 2018 and 2019 harvesting seasons (Table 4). However, there was statistically nonvariable performance in clean coffee yield among the accession of set-I in 2017 and 2020

Table 4: Variance components and heritability of coffee yield for six harvesting seasons.

GVC	Harvesting years (set-I)							Harvesting years (set-II)						
	2015	2016	2017	2018	2019	2020	Mean	2015	2016	2017	2018	2019	2020	Mean
σ^2g	57912	34153	20742	149168	104326	78494	49622	9845	9939	31963	237569	−93912	344586	49622
GCV (%)	24.78	27.09	9.17	24.07	16.82	15.87	15.70	20.68	18.33	14.84	26.05	—	29.11	14.79
σ^2e	37486	32952	82263	208595	176374	627352	31107	27669	21165	74983	201293	315450	162701	23177
σ^2p	95399	67105	103005	357764	280701	705847	80729	37514	31104	106947	438863	221538	507287	56359
PCV (%)	31.81	37.97	20.43	37.28	27.60	47.59	20.02	40.37	32.43	27.14	35.40	36.90	35.32	19.27
H^2	60.71	50.90	20.14	41.69	37.17	11.12	61.47	26.24	31.95	29.89	54.13	-42.39	67.93	58.88
Ft	**	**	Ns	*	*	Ns	**	Ns	Ns	Ns	**	Ns	**	**

GVC-genetic variance component, σ^2g -genotypic variance, σ^2e -environmental variance, σ^2p -phenotypic variance, GCV-genotypic coefficient of variance, PCV-phenotypic coefficient of variance, H^2-broad sense heritability, Ft-*F*-test, **- highly significant, *- significant, and ns-non-significant.

harvesting seasons. From set-II, a highly significant difference yield was revealed among accessions in 2018 and 2020 yield harvesting years; this expected in Arabica coffee [34, 35]. But, accessions of set-II showed nonsignificant difference in yield performance in 2015, 2016, 2018, and 2019 harvesting years. Accessions of both sets (set-I and II) showed highly significant difference in mean of clean bean yield over six years. This pooled mean points out the handiness of variability among the examined accessions. The present results confirmed the finding of Dawit et al. [21] and Kitila et al. [36] who reported significant difference in yield among coffee genotypes for clean coffee yield.

4.2. Genotypic, Phenotypic Variance, and Heritability in Coffee Yield.

4.2. Genotypic, Phenotypic Variance, and Heritability in Coffee Yield. The genotypic and phenotypic coefficient of variance including broad sense heritability of clean coffee yield is elucidated in Table 4. The whole performance or phenotype of crops wasconditioned by environment and the inherent part by genetic factors of the genotype; especially perennial crops such as coffee are highly affected by cumulative environmental factors as it persists for 15 years and above years. The current results indicated high genotypic coefficient variance ($GCV > 20\%$) for yield in 2015 ($GCV = 24.78\%$), 2016 ($GCV = 27.09\%$), and 2018 ($GCV = 24.07\%$), and moderate GCV (10–20%) was recorded in 2019 ($GCV = 16.82\%$) and 2020 ($GCV = 15.87\%$) harvesting seasons for set-I. In contrast, the lowest GCV (<10%) was revealed in 2017 ($GCV = 9.17\%$) year in set-I. In line with this, Akpertey et al. [37] reported a high to moderate range of GCV (59.26 to17.58%) value in four harvesting seasons.

Besides in set I, high phenotypic coefficient of variance ($PCV > 20\%$) had been observed in all harvesting seasons which ranged from 47.59% to 20.43% in 2020 and 2017 harvesting years, respectively. In set I, moderate heritability (H^2 30–60%) 60.7, 50.9, 41.69, and 37.17% was recorded in 2015, 2016, 2018, and 2019 harvesting seasons; however, the lowest H^2 (<30%) was observed in 2017 (20.14%) and 2020 (11.12%) years which might be indicating genotypic variability as highly influenced by nonheritable factor. Such oscillation happens for H^2 across years as described by Mistro et al. [38] for coffee.

From yield trait in Set-II, the highest GCV value observed in 2020 and 2018 years was 29.11% and 26.05, respectively (Table 4). Whereas, moderate GCV (10–20%) was manifested in 2016 and 2017 harvesting years. The PCV of set-II is high ($PCV > 20\%$) across all seasons; but the highest was recorded in 2015 ($PCV = 40.37\%$) and in 2019 ($PCV = 36.90\%$) harvesting seasons. Concurring, moderate GCV and high PCV were obtained per year in yield for coffee as shown from past findings [21, 39]. This illustrates the highest percentage of variation attributed from nonhereditary parts for phenotypic expression in these seasons. The highest H^2 (>60%) was recorded in 2020 ($H^2 = 67.93\%$); moderate heritability was revealed in 2018 and 2016 seasons which were 54.13% and 31.95%, respectively. Negative H^2 (−42.39%) was revealed in 2019 season from set-II due to negative genotypic variance that resulted from high environmental variance effect. From the combined yield data over six years mean analysis, the estimated GCV, PCV, and H^2 values of 15.07%, 20.02%, and 61.47% for set-I and 14.79%, 19.37%, and 58.88% for set-II, respectively, were recorded which clearly indicated the existence of moderate variability and heritability in both sets. These imply that it is very difficult to release high yielder via direct selection especially considering accessions of Yayo coffee landrace comprised in this study.

4.3. Annual Expected Genetic Gain and Response to Selection in Coffee Yield. The genetic gain percentage of mean (GAM (%)) together with heritability and GCV determines the supremacy of useable by breeder (additive) or dominance gene in desirable traits; they are vital in deciding breeding method to be followed. Moderate GAMs (10–20%), 12.26%, and 11.64% were recorded in 2018 and 2019 harvesting seasons, respectively; but in the other harvesting seasons, lower GAM (<10%) was observed, which ranged from 2.78 to 8.96% in set-I (Table 5). In set-II, high GAM (>20%), 21,39%, and 32.94% had been revealed in 2018 and 2020 years, respectively. Similarly, high per cycle GAM was estimated as reported by Atinafu et al. [23] and Kitila et al. [40] in coffee yield; moreover, it was reported that GAM fluctuation across seasons is an expected phenomenon Arabica coffee in yield [36]. In contrast, low GAM was recorded in other seasons. The annual GAM (%), GCV, and H^2 indicated that there is no harvesting season in which these three components' high value recorded simultaneously for both sets (Tables 4 and 5). The mean yield of over six harvesting

Table 5: Annual genetic gain and response to selection in yield.

GA&R	Harvesting seasons of set-I							Harvesting seasons of set-II						
	2015	2016	2017	2018	2019	2020	Mean	2015	2016	2017	2018	2019	2020	Mean
R	87.03	34.07	43.69	196.76	223.40	86.49	233.37	−7.63	34.27	49.51	400.17	−38.49	664.19	209.30
GAM (%)	8.96	4.99	2.78	12.26	11.64	4.90	16.45	−1.59	6.30	4.11	21.39	−3.02	32.94	14.75
SD (kgha^{-1})	143.36	66.94	216.97	471.90	601.08	777.77	379.67	−29.07	107.23	165.65	739.23	90.80	977.79	340.51
ΔGA	87.03	17.03	14.56	49.19	44.68	14.42	38.90	−7.63	17.13	16.50	100.04	−7.70	110.70	34.88

R-response to selection, SD- selection differential, R-response to selection, ΔGA- rate change of genetic gain, GA-genetic advance, GAM (%)-genetic mean advance.

seasons of both sets clearly manifested moderate GAM (16.45% and 14.755 for set-I and set-II, respectively), H^2 (61.4% and 58.88%), and GCV (15.70% and 14.79% in set-I and set-II correspondingly) (Tables 4 and 5). Thus, this calls heterosis achieving breeding method to develop heterotic genotype in yield over already released commercial local variety. The annual GAM in 2017 (2.78%) (Set-I) and (4.11%) (set-II) were very low due to low phenotypic variance and heritability value which were resulted from low annual genotypic variance (Tables 4 and 5).

From annual response to selection (R) and selection differential (SD), high values were recorded in 2018 (196.76 and 471.90) and 2019 (223.40 and 601.08, respectively) harvesting seasons in set-I (Table 5). Also, high rate of genetic gain 49.19 and 44.68 had been shown, respectively, in the same harvesting seasons. In set-II, high annual R and SD were observed in 2018 (400.17 and 739.23, respectively) and 2020 (664.19 and 977.79), respectively. The highest annual SD 777.77 and 977.79 were recorded in set-I and set-II, respectively. This pointed out high performance of the top 15 and 10 high yielder relative to the whole population in 2020 harvesting years. Under set-II, during early harvesting season rate of genetic gain and response to selection showed negative; this elucidated that the high yielders selected at 16% (top 10) show less performance at earlier season when compared with the original population. In both set-I and set-II, the R, GAM%, SD, and rate of genetic gain were inconsistent across harvesting seasons which might be accounted to be the genotypic expression being highly conditioned by environmental factors.

From the results of R and SD, it is possible to decide the fate of the experiment in 2018 or 2019 for set-I and in 2018 harvesting season for set-II; the top 15 and 10 had expressed clearly their yield potential from set- I and set-II correspondingly (Tables 5 and 6). The most top 15 high yielders found between 1 and 15 rank in 4YRS and 5YRS except four accession (Y14, Y45, Y61, and Y4 which ranked 21th, 20th, 18th, and 16th, respectively) and one accession Y14 (which ranked 24th) correspondingly (Table 6). Under set-II in 4YRS, except Y91, Y73, and Y96 (ranked 31th, 21th, and 15th) and in 5YRS except Y91, Y89, Y81, and Y105 (ranked 20th, 19th, 17th, and 12th, respectively) could perform top 10 like 6YRS. Thus, the average yield performance of over five years (5YRS) for set-I and over four years for Set-II was ideal harvesting seasons to decide the next breeding program. Such earlier decision is prominent for perennial crops such as coffee to save budget and time to proceed to the next research program.

Table 6: Rank of the top 15 and 10 selected accession using over four, five and six years yield performance from original population.

Set-I (15%)				Set-II (10%)			
Acc.	4YRS	5YRS	6YRS	Acc.	4YRS	5YRS	6YRS
Y27	1	1	1	Y93	1	10	1
Y61	18	13	2	Y81	9	17	2
Y14	21	24	3	Y80	2	5	3
Y36	3	7	4	y112	4	4	4
Y49	11	6	5	Y83	6	2	5
Y45	20	5	6	Y105	3	12	6
Y44	8	3	7	Y96	15	6	7
Y9	10	2	8	Y89	7	19	8
Y4	16	14	9	Y91	31	20	9
Y38	9	12	10	Y73	21	3	10
Y50	7	10	11				
Y1	6	8	12				
Y30	5	9	13				
Y48	2	4	14				
Y41	15	11	15				

Acc.-accessions, 4YRS:- average of over four years (2015 to 2018), 5YRS:- average of over five years (2015 to 2019) and 6YRS:- average of over six years (2015 to 20202).

4.4. Genetic Gain Trend and Response to Selection. The annual genetic gain and response to selection were directly proportional to selection differential (Figure 1). Also, the rate of genetic gain had been positively correlated with response to selection. Genetic gain and response to selection showed discrepancy across years in both sets (set-I and set-II) mainly due to the selection at 24% (top 15) and 16% done using over six years yield performance. However, the discrepancy in set-I was negligible; except in 2nd harvesting seasons, both R and GA were showed increasing trend to the end (5th season). Also, the bienniality nature of the selected high yielders coffee genotypes might have affected the repeatability of genetic gain trend and response to selection. In agreement to this finding, inconsistent genetic gain had been reported by Mistro et al. [38] across eight harvesting seasons in Arabica coffee. The exponential increment of response to selection and rate of genetic gain recorded from 3rd to 5th and from 3rd to 4th coffee yield harvesting seasons in set-I and set-II, respectively could be considered as decisive parts for determining the fate of this experiment. The trends of genetic gain and response to selection start declined after 5th season in set-I; in set-II, abating after 4th and start inclining after 5th which may be accounted to biennial problem and top 10% incongruity in yield performance across seasons. Thus, it was economical and momentous if promising line

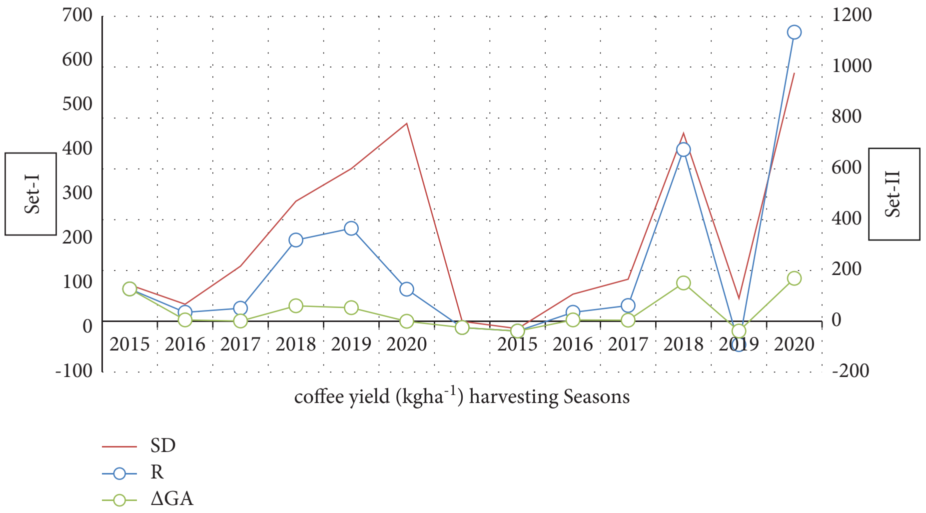

Figure 1: Repeatability of genetic gain trend and response to selection across coffee yield harvesting seasons for set-I and set-II.

selection was planned at 4th harvesting season for both sets with special care for those having high biennial nature. In agreement, Mistro et al. [38] reported that selection for yield is more effective at the earlier (before five years) than the late crop bearing stage.

4.5. Combined Analysis of Variance Over Years. Highly significant variation in yield performance was observed among coffee accessions and years in both sets (Table 7). Coffee genotypes in set-I sowed consistent performance across years; but inconsistent yield performance were observed in set-II coffee genotypes (Table 7). Similarly, from the pooled mean of eight years clean coffee highly significant differences among coffee genotypes and significant G ∗ Y variation has been reported [38]. The GCV and PCV of pooled analysis authenticated the existence of moderate variability (10–20%) among genotypes. High H^2 (81.91%) and moderate (56.16%) were recorded in set-I and set-II, respectively. Likewise, moderate GAM (19.05%), H^2 (38.22%), and GCV (14.56%) were estimated in Arabica coffee from the mean of over six years yield [24]. In contrast to the current result, Akpertey et al. [37] reported low H^2 using pooled mean of over five years' coffee yield. High H^2 in set-I was not due to high genotypic variability but low contribution of genotypes by year interaction (−26.40%). Also, 20.82% and 15.52% of GAM were recorded in set-I and set-II, respectively. Moderate genetic gain was reported from the combined over five years' mean of coffee yield at 10% of selection level [37] and at 5% selection level [38, 41]. Additionally, high contribution of nonheritable part detected in set-I and set-II (106% and 69.98%, respectively). The pooled analysis of H^2, GCV, and GAM from both sets confirmed that it is difficult to develop best performing line/s in yield via direct selection unless heterotic development via hybridization program is followed. The top 15% high yielders from set-I recorded better response to selection (R), rate of genetic gain (ΔGA), and selection differential (SD) than the top 10% from set-II.

Table 7: Over year variance component, heritability, genetic gain and response to selection.

Set-I				Set-II		
GVC&R	YLD	Cont. (%)	Ft	YLD	Cont. (%)	Ft
σ^2g	53339.08	20.16		27906.79	11.44	
GCV	15.46			13.56		
σ^2gy	−69841.2	−26.40		45338	18.58	
σ^2 e	281064.8	106.24		170715.80	69.98	
σ^2p	65120.94			49689.44		
PCV	17.08			18.09		
H^2	81.91			56.16		
R	310.98			191.24		
ΔGA	51.83			31.87		
GAM (%)	20.82			15.52		
SD	379.67			340.51		
Genotypes			**			**
G ∗ Y			Ns			*
Years			**			**

GVC-genetic variance component, YLD-yield, cont. – contribution, Ft-ftest, σ^2g -genotype variance, σ^2e -environment variance, σ^2p -phenotype variance, GCV-genotype coefficient of variance, PCV-phenotype coefficient of variance, H^2-broad sense heritability, σ^2gy-genotype by year interaction variance, R-response to selection, ΔG-rate of genetic gain, GAM (%)-genetic gain of percentage of mean, SD-selection differential, G ∗ Y- genotypes by year interaction.

4.6. Advanced Selection for the Next Breeding Program. The top 15 and 10 high yielder coffee genotypes were selected depending upon their yield performance over six years (Tables 8 and 9). The high yielders' yield potential ranged from 1614.9 to 2312 kg·ha^{-1} and 1493.8 to 1795 kg·ha^{-1} from set-I and set-II, respectively. Coffee genotype Y61 showed high yield next to Y27 from set-I (Table 8); despite statistically nonsignificant Y27 and Y61 recorded 313.1 kg·ha^{-1} and 102.6 kg·ha^{-}1, respectively, over high yielder check 74110. Also, Y93 gave 125.3 kg·ha^{-1} yield advantage over high yielder check 74112 (Table 9). These three genotypes were resistance to major coffee diseases like coffee berry disease (CBD) and coffee leaf rust (CLR) under field

Table 8: List of 15 top high yielder accessions of set-I.

Sr. no	Acc.	2015	2016	2017	2018	2019	2020	Mean
1	Y27	1949.9	789.2	1784.1	2312.3	3591	3447	2312.3
2	Y61	910.6	417	1914.3	1900.8	2688.3	4780	2101.8
3	Y14	1199.3	883.5	1535.3	1339.6	2133.7	4741	1972.1
4	Y36	1407.7	634.2	1305.5	3047.6	1850	3281	1921
5	Y49	698.1	643.2	1880.9	2385.6	2839.4	2865	1885.3
6	Y45	1110.3	352.7	1937.6	1565.1	3535.5	2038	1756.6
7	Y44	978.2	681.8	1713.4	2342.2	2809.5	1950	1745.8
8	Y9	868.5	493.5	1881.1	2376.9	3041.3	1587	1708.1
9	Y4	1271.9	826.2	1666.5	1624.9	2403.3	2313	1684.3
10	Y38	1346.4	711	2018.2	1610.7	2192.7	2226	1684.2
11	Y50	1361.6	590.7	1947.5	1848	2188.6	2030	1661
12	Y1	805.4	731.5	1854.3	2504.8	2148.9	1882	1654.5
13	Y30	1063.3	1508.1	1623.4	1858.4	1890.4	1981	1654.1
14	Y48	813.3	1068.6	1943.6	2651.4	2044.4	1228	1624.8
15	Y41	932.3	907	1817.6	1776.4	2456.1	1800	1614.9
	Checks							
	74112	468.7	1016.4	569.2	2835.6	1349	2286	1420.8
	74110	431.9	1092.2	1476.5	3398.6	2691.7	2904	1999.2
	Mean cor.	1114.45	749.21	1788.22	2076.31	2520.87	2543.3	1798.72
	Mean pop.	971.09	682.28	1571.25	1604.41	1919.80	1765.5	1419.05
	SD (%)	14.76	9.81	13.81	29.41	31.31	44.05	26.76
	LSD	550.25	515.89	Ns	1298	1193.5	Ns	501.24
	CV (%)	28.20	37.63	25.82	40.26	30.94	63.45	50.19

Mean (pon):- mean of the original population/accessions, mean (corn):- mean of core collection/15 top yielder accessions, DS (%):- differential selection in percent, LSD:- least significant differences, CV:-coefficient of variation, acc.-accessions.

Table 9: List of 10 top high yielder accessions of set-II.

Sr. no.	Acc.	2015	2016	32017	2018	2019	2020	Mean
1	Y93	347.5	421.2	1664.5	3482	550.5	4304.6	1795
2	Y81	432.6	609.9	1482.9	2694.5	808.2	3814.2	1640.4
3	Y80	688.1	1055	1458.9	2470	1251.4	2872.4	1632.6
4	y112	625.5	761	1505.2	2734.8	1343	2821	1631.8
5	Y83	293.3	815.2	1575.1	2807.8	1547.8	2736.8	1629.3
6	Y105	642.2	993	1686.8	2316.1	725.6	3087.5	1575.2
7	Y96	602	617.7	1891.5	1515.1	2255.2	2329.4	1535.1
8	Y89	296.1	545.6	1311.1	3176.2	586.9	3137.2	1508.8
9	Y91	204.3	530.3	987.6	2562	1500	3200.5	1497.5
10	Y73	375.3	396.2	1328.1	2435.3	2485.3	1942.5	1493.8
		Checks						
	74112	361.6	528.2	1100.5	2656.3	2507.9	2863.7	1669.7
	74110	924.4	539.5	453.1	2474.2	834	2823.1	1341.4
	Mean cor.	450.69	651.07	1370.44	2610.36	1366.32	2994.41	1579.22
	Mean pop.	479.76	543.84	1204.79	1871.13	1275.52	2016.62	1231.94
	SD (%)	−6.06	19.72	13.75	39.51	7.12	48.49	28.19
	LSD	472.74	413.46	778.22	1275.10	1596.20	1146.30	432.67
	CV (%)	49.03	37.83	32.14	33.91	62.27	28.29	47.43

Mean (pon):- mean of the original population/accessions, mean (corn):- mean of core collection/15 top yielder accessions, DS (%):- differential selection in percent, LSD: - least significant differences, CV:-coefficient of variation, acc. - accessions.

condition; Y27 and Y61 showed 0.03 and 5.08 in CBD and 10.42 and 7.67 in CLR correspondingly (Table 10). Also, Y93 was highly resistant to CBD and CLR under field. Additionally, they had shown high survival rate, uniform performance, and vigor in overall growth performance. Most top 15 and 10 high yielders showed resistance to CBD and CLR under field. The CBD reaction of these selected genotypes ranged from 0.03 to 12.22% and 0.00 to 14.17 in CLR which indicates that they are resistant to these major diseases.

Also, these coffee genotypes had been selected depending upon other desirable agronomic traits such as vigorous, growth habit (open, medium, and compact), stem habit (stiff and flexible), many number of primary branch and many primary branch with secondary branch, high leaf to crop ratio, different bean size, and very less to no necking

Table 10: The agronomic traits and disease reaction background of some selected coffee accessions.

Ser no.	Accessions	CBD	CLR	Selected from set-II Survival rate (%)	Vigor (1–5)	Stem charct.	Fruit	Remark
1	Y27	0.03	10.42	83.33	4	Stiff	MR	Compact, zigzag margin & medium leaf size, thin 1° primary branch & MD on one trees
2	Y9	0.17	3.00	100	4	Stiff	SR	High survival rate, low necking, resistance to CBD and CLR and vigor
3	Y44	3.14	4.5	85	5	Stiff	MR	Open, uniform, smooth margin & medium leaf, highly vigor and tall
4	Y48	5.19	5.83	100	5	Stiff	MR	Open, uniform and no necking, zigzag margin, narrow & small leaf, have many very interesting desirable traits and very high yield
5	Y45	1.87	14.17	66.7	4	Stiff	LR	Open, zigzag margin & medium leaf size, no necking, strong primary branch having many leaf to fruit ratio.
6	Y49	2.34	10.33	66.7	4	Stiff	MO	Open, uniform, low necking, highly resistant to CBD
7	Y36	7.86	1.83	83.33	4	Stiff	MO	Mid -compact, uniform and no necking at the middle and bottom canopy, zigzag margin, small and narrow leaf
8	Y1	4.40	11.67	83.33	4	Stiff	MR	Open, uniform smooth margin & medium leaf size, and vigor
9	Y30	8.36	3.33	100	4	Stiff	MO	Open, many no. of 2° branch, resistant to CLR
10	Y50	12.22	4.34	100	3	Stiff	MR	Zigzag margin& medium leaf, high survival rate and resistance to CLR
11	Y41	3.03	24.33	83.33	4	Stiff	SR	Mid-compact, uniform and no necking, zigzag margin small and narrow leaf
12	Y38	3.39	6.08	83.33	4	Stiff	MR	Resistance to CBD and CLR, vigor and uniform
13	Y61	5.08	7.67	100	4	Stiff	MO	Mid-open, uniform, medium necking and vigor, smooth margin and medium leaf size
14	Y4	7.71	16.00	100	4	Stiff	LR	Open, medium necking and very good in vigor, highly uniform, very long primary branch, zigzag margin and medium leaf size
Ser no.	Genotype	PCBD	PCLR	Selected from Set-II Survival rate (%)	Vigour (1–5)	Stem charct.	Fruit	Remark
15	Y83	0.64	1.33	83.33	3	Stiff		Highly resistance to CLR and CBD and vigor
16	Y73	0.07	3.33	100	4	Stiff	MR	Low necking, open growth habit with few primary and secondary branch and vigor
17	Y112	0.19	13.3	100	4	Flexible	LO	Mid-open, bending type above middle main stem, very low necking and uniform and large oblong fruit
18	Y96	1.72	8.00	80	4			Vigor, resistance to CBD and CLR
19	Y93	1.25	0.00	100	4	Flexible	SR	Compact, highly uniform, no necking, very high number of primary and leaf to fruit ratio, serrated, small and narrow leaf and small round fruit, highly resistant to CBD and CLR
20	Y105	0.75	0.83	83.33	3	Stiff		Stiff stem habit, uniform, relatively highly resistant to CBD and CLR

Note. vigour (1-poor, 2-fair, 3-good, 4-very good and 5-excellent), CLR-coffee leaf rust, CBD-coffee berry disease, fruit (MR-medium round, MO–medium oblong, LR-large round, LO- large oblong, SR-small round).

(Table 10). These traits are breeders' desirable traits which are very important in genetic improvement. Out of the top 15 and 10 genotypes, 20 genotypes which have contrast traits and divergent were selected and established in crossing block to utilize for further coffee genetic improvement purpose; the rests were included in Germplasm conservation.

5. Summary and Conclusion

Significantly variable performance in clean coffee yield was observed among 124 coffee accessions that were tested under two sets. In most harvesting seasons, accessions from set-I and set-II performed significantly different. Oscillation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), expected genetic gain (GAM), and heritability (H^2) was observed across harvesting seasons. Also, genetic gain trend and response to selection showed discrepancy from year to years which resulted from environmental effect and might be from the bienniality nature of Arabica coffee. The combined analysis revealed moderate GCV (15.46 and 13.56%), GAM (20.8 and 15.52%), and H^2 (81.9 and 56.16%) which implies the difficulty of variety development via direct selection unless heteirotic achieving breeding method was followed. High H^2 (81.91%) in set-I was not due to high GCV (>20%) but resulted from low contribution of genotypic by environmental interaction in coffee phenotype expression. High genetic gain trend was observed commonly in set-I (49.19 $\mathrm{kg{\cdot}ha^{-1}}$) and set-II (100.04 $\mathrm{kg{\cdot}ha^{-1}}$) from the mean of four harvesting seasons; this pointed out that the selection is more effective and economical in earlier season.

The top 15 high yielders were selected from set-I and 10 from set-II based on pooled mean of yield over six years. Despite nonsignificant difference, the high yielder accessions Y27 and Y93 gave 313.1 $\mathrm{kg{\cdot}ha^{-1}}$ and 125.8 $\mathrm{kg{\cdot}ha^{-1}}$ yield advantage over nationally released coffee varieties from set-I and set-II, respectively. In addition to high yielding, the top 15 and 10 high yielder genotypes were resistance to major coffee diseases: coffee berry disease (CBD) and coffee leaf rust (CLR). Out of these, 20 genotypes which are divergent in morphological characteristics were selected and established in crossing block to utilize for genetic improvement via hybridization, and the rest were included in Germplasm conservation.

Data Availability

The data of this finding study are available with the corresponding author upon reasonable request.

Conflicts of Interest

The authors declare that there are no conflicts of interest.

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