


Research Article

# Evaluation of Common Bean (*Phaseolus vulgaris* L) Cultivars for Yield and Yield-Related Traits at Sekoru District, South Western Ethiopia

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## Abstract

The low productivity of common beans is attached to many yield constraints such as lack of improved varieties; poor management practices, biotic and abiotic factors. This study was conducted to evaluate the performance of improved common bean varieties for yield and yield related traits in the Sekoru district of the Jimma zone and identify high-yielding varieties for the study area. Eleven released and one local common bean variety were tested in two locations (Yero Sekoru and Inkure), using a randomized complete block design with three replications. Data were collected for 12 quantitative traits and subjected to analysis using SAS software. The interaction effect of genotype by location showed a highly significant variation for all traits except for plant height, dry biomass yield, and hundred seed weight. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits. Higher The phenotypic coefficient of variation was recorded for 100 seed weight (52.78), pod length (28.9), pods per plant (27.63), harvest index (25.94) and seed yield (24.6) and also a high genotypic coefficient of variance (GCV) was observed for 100 seed weight (20.24) and pods per plant (20.34). Low (20) and high (93.5) heritability in broad sense were recorded in days to 50% flowering and dry biomass yield, respectively. At the phenotypic level, all traits had a positive phenotypic significant correlation with seed yield per hectare except for primary branches per plant day to 95% physiological maturity and hundred seed weight, while a negative significant correlation with seed yield per hectare was observed for days to 50% flowering. Genotypic path coefficient analysis indicates that the traits studied showed a positive direct effect on seed yield per hectare, while plant height, primary branches and secondary branches per plant, days to 50% flowering, days to 95% physiological maturity and 100 seed weight exhibited a negative direct effect. However, a positive direct phenotypic effect was observed for traits such as dry biomass yield, pod length, primary branches per plant, seeds per pod, and days to 95% physiological maturity. Among the varieties tested in both locations, the highest yield was recorded for the Ser119 variety (2865.2 kg/ha) followed by the Ser125 variety (2699.2 kg/ha). Therefore, recommending these varieties to farmers in the study area is very important to increase production and income.

## Keywords

Common Bean, Heritability, Path Analysis, Genetic Advance

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## 1. Introduction

Increasing the yield of beans is important for millions of people in developing and developed countries around the world. Understanding the production physiology of this crop is one of the most important aspects to achieve this objective. Higher yields are only possible when various physiological processes or yield components are adequately balanced [1]. Yield improvement is an objective of most crop improvement programs. As in other crops, the grain yield of the common bean is a complex characteristic consisting of many morphological and physiological traits [2]. Their genetic resources exist as a complex array of major and minor gene pools, races, and intermediate types, with occasional introgression between wild and domesticated types. Thus, beans are a crop that is adapted to many niches, both in terms of agronomic and consumer preference. While its production is primarily based on small farms, beans are grown in monoculture bush beans to a complex association of indeterminate or climbing beans with maize, sugarcane, and other cereals or fruit crops.

The common bean (*Phaseolus vulgaris* L.) is one of the major legume crops grown in the world due to its high protein fiber and complex carbohydrate content. The common bean is an important grain legume for food and cash from small farmers around the world. However, the total potential benefits to be derived from the common bean as a source of food and income, its complementarities with non-leaf food, and its importance to the environment are underexploited [3]. In 2019, 28 million metric tons of common beans were produced worldwide. In Ethiopia, the area covered by common bean production in 2019/20 was 281,083.49 ha and with total production of approximately 4,855,470.93 Qt.

Common bean research in Ethiopia began in the late 1960s [4]. However, nationally coordinated research in Ethiopia began in the early 1970s by the Melkassa Agricultural Research Center (MARC). At the national level, so far, a large number of common bean germplasm were introduced and evaluated for adaptation and productivity by different institutes (research center and universities). Consequently, more than 68 common bean varieties have been released for some specific traits and for different altitude ranges until 2018. However, only a few genotypes would be suitable for all beans growing environments due to differences in consumer preferences and specificity in adaptation to climatic conditions and cropping systems.

Common bean production faces several constraints that limit its yield. Low soil fertility, diversity of plant pathologies, use of low-performance varieties, climate disturbance, and use of inappropriate farming practices are also the main constraints limiting common bean production among small-holder farmers. Common bean production is constrained by several biotic and abiotic environmental stresses. Biotic factors (field and post-harvest pests and plant diseases) and bio-

tic factors (drought, excessive rain/flooding, poor soil fertility, heat and cold stressors) are known to cause significant reductions in grain yields [5]. Bean anthracnose [*Colletotrichum lindemuthianum* (Sacc. & Magnus) Briosi & Cavarra] poses a major constraint on the production of dry beans in Ethiopia [6].

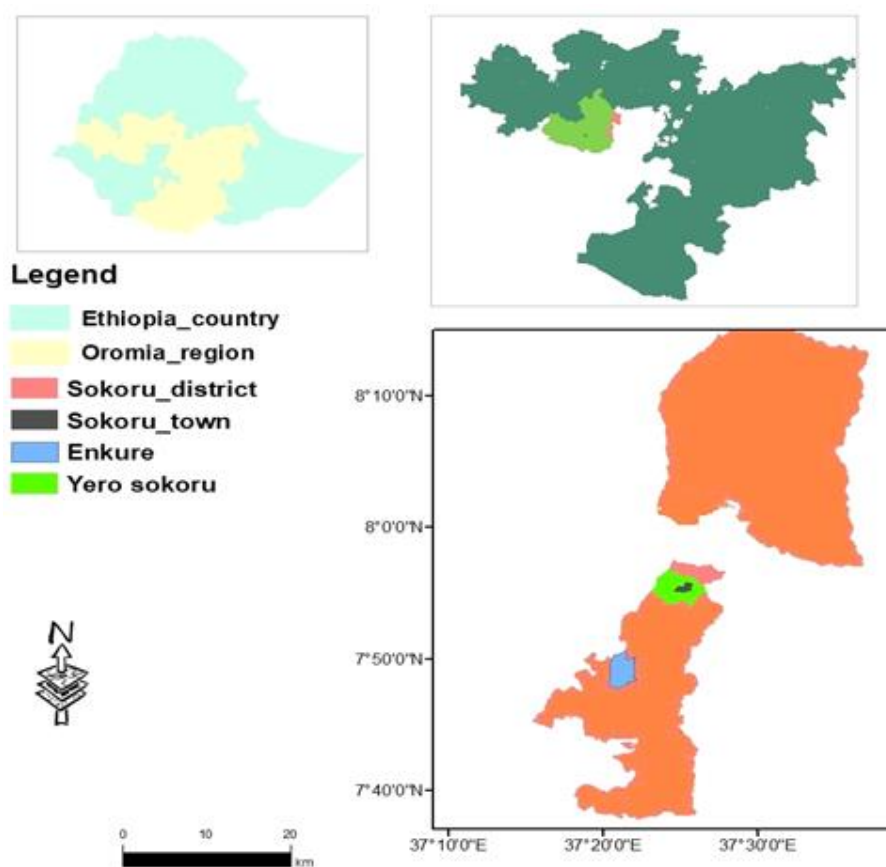
The common bean has been produced mainly in the Sekoru district, as all 39 farmers' villages have favorable agroecology and soil type for the production of common beans. Farmers produce common beans by intercropping with maize and most farmers use local varieties. However, the average productivity of common bean in the districts is very low (13qt/ha) compared to the productivity in the research center (19-35 qt/ha). At the national level, so far, a large number of common bean germplasm were introduced and evaluated for adaptation and productivity by different institutes (research center and universities). Consequently, more than 68 common bean varieties have been released for some specific traits and for different altitude ranges until 2018. However, only a few genotypes would be suitable for all beans growing environments due to differences in consumer preferences and specificity in adaptation to climatic conditions and cropping systems. Therefore, the objectives of this study were to evaluate the performance of some common bean cultivars for yield and yield related traits in the Sekoru district, Jimma zone, southwestern Ethiopia, and to identify the cultivar that performs the best for the district.

## 2. Materials and Methods

### 2.1. Description of Experimental Sites

The Sekoru district is located 105 km from the city of Jimma, the total land of the district is 92744 ha from this amount the land used for crop production is 52481 ha, the forest land 3970 ha, the grazing land 8440 ha, the arable land 6003 ha and others 21850 ha. The climate of the district is high land 10%, medium land 60%, and low land 30%. Measure crops grown in the area of Maize, Teff, Sorghum, Wheat, and common bean, the soil type is Nitosol 75% and verity soil 25%. The experiment was carried out in two locations Yero Sekoru and Inkure, located 65 km from each other (Figure 1). Both sites are found in the Sekoru district of two kebeles and represent different locations. The coordinate Yero sekoru (7 to 37) is located at altitude 1787, with an average annual rainfall of 1458 with a minimum and maximum temperatures of 12 and 28.3 respectively. Location Inkure, (7 50 1 " to 37 21'45") is located at an altitude of 1520 m with an average annual rainfall of 1430 with minimum and maximum temperatures of 17.3 and 28.0 respectively. The research was carried out at the nursery site of the Sekoru Agricultural Office for Yeroskoru and For Inkure on the

farmers' field.



**Figure 1.** Map of the study sites.

## 2.2. Experimental Materials

The research was carried out on a total of twelve varieties of common beans, eleven genotypes of common beans re-

leased obtained from Jimma and Melkassa Agricultural Research Center, and one local variety (Table 1). The major selection criteria were based on yield, diseases resistance, and early maturity.

**Table 1.** Common bean varieties used in the study.

Varieties	Altitude	Color	Yield per hectare		Year of release
			Research	Farmers field	
SER125	1450-2000	Red	35	22	2014
SER119	1450-2000	Red	33	25	2014
SUG131 (Deme)	1450-2000	Red Speckled	19-24	18-22	2008
Awash2	1450-2000	White	28-31	18-22	2013
ISC-15541Gobe rasha-1	1450-2000	Red	21	18	1998
Nasir	1450-2000	Dark red	30	23-27	2003
SAB736 (Ado)	1450-2000	Large White	20-25	18-22	2014
SAB632 (Tafach)	1450-2000	Speckled	22-26	19-24	2014

Varieties	Altitude	Color	Yield per hectare		Year of release
			Research	Farmers field	
Awash01	1450-2000	White	24	20	1990
KATB1 (Ada)	1300-1650	Yellow	19-33	17-25	2013
KATB9 (Dandesu)	1300-1650	Red	22-30	19-23	2013
Local variety (Toma)	1400-2000	Red	-	13	-

### 2.3. Experimental Design and Trial Management

The experiment was carried out in the Randomized Complete Block Design (RCBD) with three replications. Six rows, each with 30 plants, were used on a 2.4 m by 3 m plot. A distance of 1m was left between the plots and the blocks. Spacings of 40 cm and 10 cm were used between rows and plants, respectively. The land was flat (0-1% slope) and ploughed three times and was very well prepared free of weeds and debris and the layout of the plot was held using the Pythagoras theorem technique. NPSB fertilizer was applied in the form of a base dressing before sowing, at a rate of 100 kg per ha (72 g per plot), while UREA was applied at a rate of 50 kg per ha (36 g per plot) in the form of a top dressing three weeks after sowing or after the first weeding time. Seed sowing was held in the second week of August 2020 in both locations; each variety was sown in each plot randomly; hand weeding was done twice.

### 2.4. Data Collection

#### 2.4.1. Quantitative Traits Data

Based on the standard evaluation system of the International Board for Plant Genetic Resources [7], morphological traits are collected from the four middle rows of each plot. The following quantitative morphological and agronomic traits were collected.

#### 2.4.2. Plant Base Data

**Plant height:** The height of the plants was measured from five randomly taken plants in the maturity stage from the ground level to the tip of the main stem using the four middle rows and averaged with the number of measured plants. **Number of pods per plant:** The number of pods per plant from five randomly selected plants was counted and averaged. **Number of seeds per pod:** The number of seeds per pod was counted from the pods harvested from five randomly selected plants. **Number of branches per plant:** The number of primary and secondary branches from the sample plant from each plot was counted and averaged to the number of

sample plants. **Pod length:** The pod length of five pods from each sample was measured in cm and averaged to five pods.

#### 2.4.3. Plot Base Data

**Days to flowering (DF):** Days to 50% flowering were recorded as the number of days from sowing to 50% of plants that produced flowers. **Days to physiological maturity (DM):** Days to 95% physiological maturity: was recorded by counting the number of days from the date of emergence to the date when 95% of the stems, leaves, and pods in a plot change to a light yellow color. **Dry biomass yield (kg):** The dry biomass yield was determined by taking the total weight of the harvest that included the seeds from each net plot area at physiological maturity. **Hundred seed weight (g):** The weight of the hundred seeds was determined by taking 100 seeds from randomly taken plants that have grown in the net plot area with a moisture content of 10%. **Harvest index:** The harvest index was expressed as the ratio of seed yield per total dry biomass of sampled plants multiplied by 100. **Grain Yield (GY):** The grain yield per hectare was taken by weighing the grain yield in kg obtained from each plot and converting it to kilograms per hectare at 10% moisture content.

### 2.5. Statistical Data Analysis

#### Analysis of Variance (ANOVA)

The model for RCBD of individual location is;

$$Y_{ij} = \mu + G_i + B_j + ij$$

Where:  $Y_{ij}$  = Observed value of genotype  $i$  in block  $j$ ,  $\mu$  = Grand mean of the experiment,

$G_i$  = Effect of genotype  $i$ ,  $B_j$  = Effect of block  $j$ ,  $ij$  = Error effect of genotype  $i$  in block  $j$

The following statistical model was used for the combined analysis of variance over locations:

$$Y_{ijk} = \mu + G_i + E_j + GE_{(ij)} + B_{k(j)} + ijk$$

Where:  $Y_{ijk}$  = Observed value of genotype  $i$  in block  $k$  of the environment (location)  $j$ ,

$\mu$  = Grand mean,  $G_i$  = Effect of genotype  $i$ ,  $E_j$  = Effect of

environment or location effect,  $GE_{(ij)}$  = Effect of interaction of genotype  $i$  with environment  $j$ ,  $B_{(j)}$  = Effect of block  $k$  in location (environment)  $j$ ,  $ijk$  = Error (residual) effect of genotype  $i$ , in block  $k$  of environment  $j$

After the data were checked for normality, the data were subjected to Analysis of Variance for individual location using SAS software. Since there was a homogeneous variance of error between the locations, a combined data analysis was employed. When ANOVA showed significant difference, mean separations were performed using the least significant difference (LSD) test at 5% probability level.

### 2.5.1. Estimation of Phenotypic and Genotypic Variance

The phenotypic and genotypic variance for the analysis of the pooled data in the two locations was calculated using the formula suggested by Hallauer and Miranda [8] as follows.

$$\sigma^2_p = \sigma^2_g + \frac{n\sigma^2_{ge}}{e} + \sigma^2_e / re$$

Where,  $\sigma^2_p$  = Phenotypic variance

$\sigma^2_g$  = Genotypic variance

$\sigma^2_e$  = environmental variance

$\sigma^2_{ge}$  = variance of genotype x environment interaction

$r$  = number of replication and  $e$  = number of environments

Genotype variance  $\sigma^2_g = (MS_g - MS_{ge}) / r$

Genotype x location interaction variance  $\sigma^2_{gl} = (MS_{ge} - MS_{error}) / r$

Then by using the methods suggested by Burton [9] and Johnson *et al.* [10] phenotypic and genotypic coefficient of variation was estimated as a percentage of the corresponding phenotypic ( $\sigma^2_p$ ) and genotypic ( $\sigma^2_g$ ) standard deviations of the mean of the trait. Hence,

Where:  $\sigma^2_{ph}$  = Phenotypic variation;  $\sigma^2_g$  = Genotypic variation and  $\bar{x}$  = Grand mean of the trait.

**Table 2.** Outline of analysis of variance for individual location.

Source of variation	DF	SS	MS	F ratio
Replications (r)	r-1	SS <sub>r</sub>	SS <sub>r</sub> /r-1	
Genotypes (g)	g-1	SS <sub>g</sub>	SS <sub>g</sub> /g-1	
Error	(r-1)(g-1)	SS <sub>e</sub>	SS <sub>e</sub> /(g-1)	MS <sub>g</sub> /MS <sub>e</sub>
Total	rt-1	TSS		

**Table 3.** Outline of analysis of variance for combined location.

Source	d.f	SS	MS	F-Value
Environment (E)	e-1	MSE	s <sub>2e</sub> + gs <sub>2r</sub> (e) + rg s <sub>2e</sub>	
Replication within E	(r-1)	MSE/ME	s <sub>2e</sub> + g s <sub>2r</sub> (e)	MS <sub>r</sub> /e/Me
Genotypes (g)	g-1	MS <sub>r</sub> /E	s <sub>2e</sub> + gs <sub>2ge</sub> + ers <sub>2g</sub>	MS <sub>3</sub> /MS <sub>e</sub>
GEI	(e-1)(g-1)	MS <sub>g</sub>	s <sub>2e</sub> + gs <sub>2g</sub>	MS <sub>4</sub> /MS <sub>e</sub>
Error	e(g-1)(r-1)	MS <sub>gei</sub>		
Total	Erg-1			

Note that: DF = degree of freedom, MS = mean squares, r = replication, g = genotypes e = environments, MSE = mean squares due to environments, MS<sub>r</sub>/E = mean squares due to replication (environments), MS<sub>g</sub> = mean squares due to genotypes, MS<sub>GEI</sub> = mean squares due to GEI and MS<sub>e</sub> = mean squares due to residual

### 2.5.2. Estimation of Heritability and Genetic Advance

#### Heritability

The broad-sense heritability values for all parameters ( $H^2$ ) were estimated based on the formula provided by Allard (1999) as follows:

$$H^2 = \sigma^2_g / \sigma^2_p \times 100$$

Where,  $h^2$  = heritability in broad sense,  $\sigma^2_g$  = Genotypic variance and,  $\sigma^2_p$  = Phenotypic variance. Genetic Advance Under Selection (GA)

Genetic advance (GA) and genetic advance as a percent-



age of the mean (GAM), the predicted response to selection was estimated using the method suggested by Allard [16] and Johnson et al. [10] assuming selection intensity at 5% (2.06). And hence, and  $GAM = (GA/x) \times 100$ .

### 2.5.3. Phenotypic and Genotypic Correlation Coefficient Analysis

The correlation analysis was performed using SAS software version 9.3. To estimate the phenotypic and genotypic correlation coefficients, the covariance estimates between all pairs of the traits need to be calculated using the formula:

$$\text{Genotypic covariance } (\sigma g_{xy}) = \frac{MSPg - MSPe}{r}$$

$$\text{Phenotypic covariance } (\sigma p_{xy}) = \sigma g_{xy} + \frac{\sigma e_{xy}}{r}$$

Where,  $MSPe$  = mean sum of the cross product for error,  $MSPg$  = mean sum of the cross products for genotypes and  $r$  = number of replications. Phenotypic correlation ( $r_p$ ), the observable correlation between two variables, which includes both genotypes and environmental components of the two variables, will be estimated using the formula suggested by Johnson *et al.* [10] and Singh and Chaudhury [11].

$$R_{pxy} = (pcovx.y) / (\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}})$$

$$R_{gxy} = (gcovx.y) / (\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}})$$

Where:  $R_{pxy}$  and  $r_{gxy}$  are phenotypic and genotypic correlation coefficients, respectively;  $pcovx.y$  and  $gcovx.y$  are phenotypic and genotypic covariance between variables  $x$  and  $y$ , respectively;  $\sigma^2_{px}$  and  $\sigma^2_{gx}$  are phenotypic and genotypic variances for variable  $x$ ; and  $\sigma^2_{py}$  and  $\sigma^2_{gy}$  are phenotypic and genotypic variances for variable  $y$ , respectively.

### 2.5.4. Path-Coefficient Analysis

The direct and indirect effects of yield-related traits on yield per plot will be worked out through path coefficient analysis. The analysis will be performed following the method suggested by Dewey and Lu [12]. The formula will be described as follows Where:  $r_{ij}$  = Mutual association between the independent traits ( $i$ ) and the dependent trait ( $j$ ), as measured by the correlation coefficient.

$P_{ij}$  = Component of direct effects of the independent trait ( $i$ ) on the dependent variable ( $j$ ) as measured by the path coefficient and,  $\Sigma r_{ik}p_{kj}$  = Summation of the components of the indirect effect of a given independent trait ( $i$ ) on the given dependent trait ( $j$ ) via all other independent traits ( $k$ ).

The residual effect ( $U$ ) will be calculated using the formula:

$$U = \sqrt{1 - R^2}$$

$$\text{Where } R^2 = \Sigma P_{ij}r_{ij}$$

## 3. Results and Discussion

### 3.1. Analysis of Variance

Mean squares from the analysis of variance (ANOVA) of twelve common bean varieties for twelve traits are presented for Yero sekoru, Inkure and combined analysis of the two locations, respectively (Tables 4, 5 and 6). The result of the variance analysis shows that the effect of location and common bean varieties interaction exhibited a significant ( $p < 0.01$ ) difference ( $p < 0.01$ ) for all traits except plant height, dry biomass yield and 100 seed weight (Table 7). The significant effect of the interaction of the location of the characteristics of the variety revealed that the performance of the varieties was influenced by environmental variables in the two locations, resulting in an inconsistency of the performance of common bean varieties in the two locations for such plant traits. This demonstrated the importance of testing varieties in various places and seasons to ensure their stability for use as viable genetic materials for crop improvement and production in a particular region [13]. The result of the variance analysis of variance shows that the genotypes were highly significant for all traits of the combined data. Regarding the present experiment, the existence of genotypic variation in grain yield and yield components has been reported for common bean [14]. Data for number of pods per plant, seeds per pod, branches per plant, plant height, seed yield, and 100 seed weight showed highly significant ( $p < 0.01$ ) differences ( $p < 0.01$ ) between varieties. The current variations in the yield components between varieties are consistent with previous reports [15]. According to the findings, significant variability was observed for plant height, days to 50% flowering, days to 90% physiological maturity, pods per plant, seed yield per pod, hundred seed weight and yield characters [16]. Arya and Ajai [17] reported the highest variances for the yield of the green pods per plant followed by the number of pods per plant, the weight of 100 seeds, and the height of the plant. Similarly, Kamaluddin and Shahid [18] reported significant variation in plant height, number of pods per plant, 100 seed weight and seed yield per plant.

**Table 4.** Mean squares from the analysis of variance for different sources of variation of 12 common bean varieties tested at the Yerosekuru location in 2020/2021.

Traits	Rep df=2	Mean square			
		Treatment df=11	Error MS DF=22	R <sup>2</sup>	CV%
Plant height	0.89	5.3 <sup>**</sup>	0.49	0.97	1.72
Primary branches	0.1	0.72 <sup>**</sup>	0.05	0.88	6.41
Secondary branches	0.02	5.1 <sup>**</sup>	0.05	0.98	3.94
Days to flowering	0.36	35.91 <sup>**</sup>	2.85	0.82	4.42
Days to maturity	0.19	19.08 <sup>**</sup>	2.01	0.83	1.58
Pods per plant	0.81	32.16 <sup>**</sup>	0.74	0.96	7.52
Pod length	0.76	7.89 <sup>**</sup>	0.29	0.93	9.02
Seeds per pod	0.07	3.34 <sup>**</sup>	0.09	0.95	6.02
Dry biomass yield	50550.86	1150024.24 <sup>**</sup>	19976.86	0.97	3.69
Hundred seed weight	0.3	194.2 <sup>**</sup>	1.15	0.99	3.67
Seed yield	2271	947161.18 <sup>**</sup>	40365	0.92	8.41
Harvest index	0.002	0.08 <sup>**</sup>	0.003	0.93	8.9

where; \*\* highly significant at 0.01. \* Significant at 0.05, cv= coefficient of variation, df = degree of freedom, rep= replication

**Table 5.** Mean squares from analysis of variance for different sources of variation of 12 common bean varieties tested at the Inkure location in 2020/2021.

Traits	Rep df=2	Mean square			
		Treatment df=11	Error MS df=22	R <sup>2</sup>	CV%
Plant height	0.3	2.78 <sup>NS</sup>	1.03	0.73	2.55
Primary branches	0.3	0.63 <sup>**</sup>	0.05	0.88	8.71
Secondary branches	0.4	5.1 <sup>**</sup>	0.05	0.98	4.23
Days to flowering	1.04	2.22 <sup>NS</sup>	1.41	0.62	3.12
Days to maturity	0.38	21.95 <sup>**</sup>	1.47	0.94	1.42
Pods per plant	0.03	5.95 <sup>*</sup>	0.85	0.89	8.61
Pod length	0.06	2.37 <sup>*</sup>	0.49	0.83	13.14
Seeds per pod	0.89	0.71 <sup>NS</sup>	0.33	0.69	12.43
Dry biomass yield	31465.04	797996.95 <sup>**</sup>	18808.7	0.98	3.54
Hundred seed weight	0.004	133.97 <sup>**</sup>	0.8	0.99	3.03
Seed yield	693.38	420323.3 <sup>**</sup>	51228.47	0.89	10.19
Harvest index	0.001	0.03 <sup>*</sup>	0.005	0.86	11.84

where; \*\* highly significant at 0.01. \* Significant at 0.05, cv= coefficient of variation, df = degree of freedom; rep= replication

**Table 6.** Mean squares from the combined analysis of variance for different sources of variation of 12 common bean varieties tested at both locations in 2020/2021.

Traits	Loc df=1	Mean square				CV%
		Rep(Loc)df=4	Treatment df=11	Loc x (Trt) df=11	Error df=44	
Plant height	5.14*	3.25	8.09**	0.71 <sup>NS</sup>	0.99	2.43
Primary branches	0.88 <sup>NS</sup>	0.2 <sup>NS</sup>	0.61**	0.44**	0.99	12.13
Secondary bra	3.15 <sup>NS</sup>	0.7 <sup>NS</sup>	6.39**	2.24**	0.41	11.3
Days to flowering	3.56 <sup>NS</sup>	1.69 <sup>NS</sup>	15.44**	22.25**	2.15	3.87
Days to maturity	329.4**	0.5 <sup>NS</sup>	28.84**	22.66**	1.45	1.39
Pod per plant	34.83**	1.02 <sup>NS</sup>	29.95**	9.91**	1.13	9.88
Pod length	2.48 *	1.53*	7.16**	3.84**	0.59	13.44
Seed per pod	5.02**	0.06 <sup>NS</sup>	3.57**	0.67**	0.19	8.91
Dry B/ yield	147.35 <sup>NS</sup>	61523 <sup>NS</sup>	2200276.6**	13560 <sup>NS</sup>	31016.9	4.59
Hundred S/ we	2.84 <sup>NS</sup>	0.41 <sup>NS</sup>	399.84**	0.36 <sup>NS</sup>	0.89	3.19
Seed yield	157922 <sup>NS</sup>	100655 <sup>NS</sup>	1064672.4**	368050.45**	64289.9	10.82
Harvest index	0.01 <sup>NS</sup>	0.01 <sup>NS</sup>	0.09**	0.03**	0.01	12.79

where; \*\* highly significant at 0.01. \* Significant at 0.05, cv= coefficient of variation, df=degree of freedom, Loc=location, Rep= replication

### 3.2. Mean Performance of Traits of Common Bean Varieties

#### *Plant Height and branches*

The average value for plant height ranged from (38.65cm) to (42.32cm). The tallest mean plant height was recorded for the varieties ser119 (42.32cm), Awash2 (41.55) and KATB1 (41.38cm) while the lowest height is recorded for the varieties Goberasha (38.65cm), Dame (39.55cm) and local (38.7cm) (Table 7). The height of the plant was also reported to vary considerably between bean varieties from 33 to 70 cm and 35.63 to 53.04 cm [19]. According to Su *et al.* [20] short plant height attributes to drought tolerance capacity that will lower the transpiration rate and ultimately reduce moisture stress during drought. But, in nonmoisture-stressed environments, tall plant height is important to produce better numbers of branches and more pods per plant. In terms of the present study, the varieties with high plant height produced more branches per plant and a large number of pods per plant, which contributes to a better amount of seed per plant. This result is supported by Al-Ballat and Al-Araby [21] who reported that the height of the plant is positively and significantly correlated with the number of pods per plant and the seed yield per plant. The number of pods / plant

showed significant differences between treatments. The average value for the primary and secondary branch ranged from (2.28cm) to (3.09cm) and (2.75cm) to (6.39 cm), respectively. The longest mean primary branch length was recorded for the variety Ser 119 (3.09cm) and the lowest length was recorded for the varieties Awash o1 (2.28cm), and Goberasha (2.28cm) and the local variety (2.07) In terms of the secondary branch, the longest secondary branch was measured for the varieties Ser119 (6.95cm), Ser125 (6.39cm) and Awash 2 (6.34cm) while the lowest was measured for the local variety (2.75cm) (Table 7) As the number of branches increases, it may have both positive and negative impacts on the crop productivity.

As leaves compete for light and the resources required to produce biomass, a large number of branches can result in a poor photosynthetic rate, reduced leaf area, and short stem length of the branches. On the contrary, the research findings on pigeon pea carried out by Ram *et al.* [22]. Furthermore, Kandarkar *et al.* [23] also presented that the number of branches per plant showed the highest direct positive effect on grain yield, indicating that genotypes with a better number of branches will result in more yield. The present study partially supports the above findings in that the varieties with more branches (Ser 125 and Ser 119) produced a better amount of grain yield.



**Table 7.** Mean of different traits of Common bean varieties tested at two locations in Sekoru district in Jimma zone in 2020/2021.

Varieties	PH (cm)	PB (cm)	SBPP (cm)	DF	DTM	PPP	PL	SPP	DBY (kg/ha)	HSW	SY (kg/ha)	HI
SER125	41.14 <sup>b</sup>	2.88 <sup>cd</sup>	6.39 <sup>ab</sup>	37.5 <sup>fed</sup>	87.83 <sup>c</sup>	11.99 <sup>b</sup>	6.76 <sup>b</sup>	5.41 <sup>b</sup>	4091.0 <sup>c</sup>	19.73 <sup>g</sup>	2699.2 <sup>ba</sup>	0.67 <sup>bc</sup>
SER119	42.32 <sup>a</sup>	3.09 <sup>a</sup>	6.95 <sup>a</sup>	38.17 <sup>bed</sup>	87.66 <sup>c</sup>	15.45 <sup>a</sup>	7.67 <sup>a</sup>	6.08 <sup>a</sup>	5218.33 <sup>a</sup>	24.63 <sup>d</sup>	2865.2 <sup>a</sup>	0.55 <sup>cd</sup>
Deme	39.55 <sup>de</sup>	2.5 <sup>e</sup>	5.61 <sup>de</sup>	39.5 <sup>bac</sup>	92.17 <sup>a</sup>	10.63 <sup>cd</sup>	5.36 <sup>d</sup>	4.7 <sup>c</sup>	4524.00 <sup>b</sup>	36.08 <sup>b</sup>	2308.0 <sup>dc</sup>	0.51 <sup>e</sup>
Awash2	41.25 <sup>ba</sup>	2.5 <sup>e</sup>	6.24 <sup>ac</sup>	38.1 <sup>edc</sup>	84.17 <sup>d</sup>	11.37 <sup>cb</sup>	6.32 <sup>cb</sup>	5.63 <sup>ba</sup>	3625.5 <sup>d</sup>	20.87 <sup>fe</sup>	2581.8 <sup>bac</sup>	0.72 <sup>ba</sup>
Gobe rash	38.65 <sup>e</sup>	2.29 <sup>e</sup>	4.99 <sup>df</sup>	38 <sup>fedc</sup>	87.7 <sup>c</sup>	9.49 <sup>d</sup>	5.07 <sup>d</sup>	4.35 <sup>c</sup>	3486.8 <sup>edf</sup>	38.31 <sup>a</sup>	2011.7 <sup>e</sup>	0.57 <sup>ed</sup>
Nasir	41.01 <sup>b</sup>	2.5 <sup>e</sup>	5.99 <sup>cd</sup>	36.33 <sup>fg</sup>	86.5 <sup>c</sup>	11.18 <sup>cb</sup>	6.28 <sup>cb</sup>	5.21 <sup>b</sup>	3594.8 <sup>ed</sup>	24.43 <sup>d</sup>	2537.7 <sup>bdc</sup>	0.71 <sup>ba</sup>
SAB736	39.5 <sup>d</sup>	2.52 <sup>de</sup>	5.66 <sup>cde</sup>	38.37 <sup>bdc</sup>	87.83 <sup>c</sup>	10.42 <sup>cd</sup>	5.51 <sup>cd</sup>	4.35 <sup>c</sup>	3056.8 <sup>g</sup>	36.47 <sup>b</sup>	2346.2 <sup>dc</sup>	0.77 <sup>a</sup>
SAB632	41.05 <sup>b</sup>	2.99 <sup>b</sup>	6 <sup>cd</sup>	36.83 <sup>feg</sup>	87.87 <sup>c</sup>	10.83 <sup>cb</sup>	5.8 <sup>cd</sup>	4.56 <sup>c</sup>	3293 <sup>f</sup>	38.47 <sup>a</sup>	2420.5 <sup>bdc</sup>	0.74 <sup>ba</sup>
Awash01	39.79 <sup>dc</sup>	2.28 <sup>eg</sup>	5.66 <sup>cde</sup>	39.83 <sup>ba</sup>	87 <sup>c</sup>	10.39 <sup>cd</sup>	5.11 <sup>d</sup>	4.54 <sup>c</sup>	4176.3 <sup>c</sup>	19.83 <sup>fg</sup>	2278.0 <sup>ed</sup>	0.55 <sup>ed</sup>
KATB1	41.38 <sup>ba</sup>	2.96 <sup>c</sup>	5.85 <sup>cd</sup>	36.33 <sup>fg</sup>	87.5 <sup>c</sup>	11.31 <sup>cb</sup>	5.94 <sup>cb</sup>	5.29 <sup>b</sup>	4045.3 <sup>c</sup>	34.92 <sup>c</sup>	2433.7 <sup>bdc</sup>	0.62 <sup>dc</sup>
KATB9	40.9 <sup>bc</sup>	2.53 <sup>de</sup>	5.72 <sup>cde</sup>	35.16 <sup>g</sup>	87.67 <sup>c</sup>	10.85 <sup>cb</sup>	5.93 <sup>cbd</sup>	5.24 <sup>b</sup>	3503.7 <sup>ed</sup>	38.21 <sup>a</sup>	2439.5 <sup>bdc</sup>	0.70 <sup>ba</sup>
Loc /var	38.7 <sup>de</sup>	2.7 <sup>d</sup>	2.75 <sup>g</sup>	40.67 <sup>a</sup>	90.17 <sup>a</sup>	5.4 <sup>e</sup>	3.19 <sup>e</sup>	3.14 <sup>d</sup>	3402.17 <sup>ef</sup>	21.43 <sup>f</sup>	1194.7 <sup>f</sup>	0.35 <sup>f</sup>
LSD	1.16	0.37	0.74	1.71	1.40	1.24	0.89	0.51	204.92	4.24	295.03	0.09
CV	2.46	12.12	11.3	3.87	1.38	9.88	13.26	8.91	4.59	11.94	10.82	12.79

PH: Plant height; PB: primary branch; SBPP: secondary branch per plant; DF: days to 50% flowering; DTM: days to 80% physiological maturity; PPP: pods per plant; PL: pod length; SPP: seeds per pod; DBY: dry biomass yield; HSW: hundred seed weight; SY: seed yield; HI: harvest index; CV: coefficient of variation; LSD: Least significant difference; Means with same factor and column followed by the same letter are not significantly different at a level of significance of 5%

#### *Days to flowering and Days to physiological maturity*

The mean value of days to 50% flowering and 80% physiological maturity ranged from (35.16 days) to (40.67) and (84.17 days) to (92.17 days), respectively. The result of the analysis of variance shows that the varieties for days for 50% flowering exhibited highly significant variations ( $p < 0.01$ ) results of previous research have also shown significant differences for days to flowering [28, 33]. The varieties that took fewer mean days to 50% flower were KATB9 (35.16), KAT B1 (36.33), Nasir (36.33) and SAB632 (36.83) while those that took a long day were Local variety (40.67), Awash 01 (39.83), Deme (39.5) (Table 7). The highest and medium seed-producing varieties (Ser125, Awash 2, Nasir, SAB 632, KAT B1 and KAT B9) had a statistically similar number of days to flower. Under rain-fed conditions, reported a shorter period from sowing to first flowering for adapted cultivars of common bean. Thus, the present finding matched this report and this phenological plasticity has contributed to the high seed yield performance of these varieties. The mean short day (84.17day) to 80% maturity period was recorded for the variety Awash2 and the longest day 80% maturity period (92.17day) and (90.17) was recorded for the variety SUG131 (Deme) and the local variety, respectively, these are also the least yielding varieties (Table 7). Therefore, as they are the latest maturing varieties for the study areas and are

good for production in areas where rain falls for at least three months.

#### *Number of pods per plant, Pod length, and seed per pod*

The mean value of pods per plant ranged from (5.40) to (15.45). The highest pod number (15.45) was recorded for the variety (Ser119) and the lowest pod number (5.40) was recorded for the local variety. Prakash and Ram, [24] reported the variation in the number of pods per plant which ranged from 10.46 to 30.22 in the French bean. The result reveals that the mean value of the pod length ranged from (3.19cm) to (7.67cm). The Ser119 variety has a longer pod length (7.67 cm), while the Local (Toma) variety has the shortest pod length (3.19cm), and also the average value of seed per pod ranged from (3.14) to (6.08). The highest number of seeds per pod was recorded for the Ser119 (6.08) and Awash2 (5.63) variety, while the lowest average number of seeds per pod (3.14) was recorded for the local variety (Table 7). In line with these findings, several authors reported significant variation between common bean varieties for days to maturity, plant height, number of seeds per pod, number of pods per plant, hundred seed weight, grain yield [14, 25].

#### *100 seed weight*

The average value of hundred seed weight ranged from (19.83) to (38.47). The highest average hundred seed weights were recorded for the varieties SAB632 (38.47), Goberasha

(38.31) and KAT B1 (38.21), while the lowest was recorded for the varieties Awash 01 (19.83), Awash2 (20.87) and local variety (21.43). The weight of the hundred seed is also one of the most important yield components that reflect the magnitude of seed development that ultimately reflects the final yield of the crop (Table 7).

#### *Seed yield*

The mean value of the seed yield ranged from (1194.7kg/ha) to (2865.2 kg / ha); interestingly, the maximum average seed yield /ha was obtained from the variety Ser119 (2865.2kg/ha) and Ser 125 (2699.2) while the lowest average seed yield/ha (1194.7kg/ha) was recorded for the local variety (Table 7). Today, the development of the superior varieties in terms of yield and other many different traits is very critical to address the required challenges of human population growth and climate change. Overcoming these difficult challenges will be harder in the absence of plant genetic improvement to increase agricultural productivity through addressing the problem of yield reduction and its links with pest management and climate change. Most varieties performed above the overall mean, except Goberasha and the local variety. Reported seed yield performance of the common bean genotypes studied in the range of 1300 to 3500 kg /ha. The rankings of the varieties were different for the seed yield performance in the locations. The highest-yielding variety, Ser119 and Ser125 showed higher seed yield performance in two of the test locations. Yeroskoru Ser119 (2870.7 kg/ha), Ser 125 (2696.7 kg / ha) and Inkure Ser119 (2859.7kg/ha), Ser125 (2701.7kg/ha). This result is consistent with the findings stated by Daniel *et al.* [14] who discovered significant differences in grain production between common bean varieties. Similarly, Gebre-Egziabher *et al.* [25] and Dembele and Ashenafi [26] found similar results on the same crop and found significant variation between varieties.

### **3.3. Variance Components**

#### *Genotypic and phenotypic coefficients of variation*

The present study indicated that the phenotypic variance and the phenotypic coefficient of variance were higher than their corresponding genotypic variance and the genotypic coefficient of variance respectively for the traits studied (Table 8). This indicated that the influence of the environment on the expression of these traits was high. The phenotypic coefficient of variance (PCV) ranged from 3.72% for plant height to 40.46% for primary branches per plant, while the genotypic coefficient of variance (GCV) ranged from 2.69% for plant height to 27.69% for hundred seed weight (Table 8).

According to Subramanian and Menon [27] phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) values greater than 20% less than 10% and between 10% and 20% are regarded as high, low, and medium, respectively. Based on this, a high phenotypic coefficient of variance (PCV) was observed for the primary branches

per plant (40.46) pod length (28.9), 100 seed weight (27.91), pods per plant (27.63), harvest index (25.94), secondary branch per plant (25.14) and seed yield (24.6), and also a high genotypic coefficient of variance (GCV) was observed for 100 seed weight (27.69), pods per plant (20.34) and primary branches per plant (20.25). Moderate PCV was observed for primary branches per plant, seeds per pod, and dry biomass yield. Moderate GCV was observed for primary branches per plant, pod length, seeds per pod, dry biomass yield, seed yield, and harvest index, while low PCV and GCV were observed for day to flowering, day to maturity, plant height, and secondary branch per plant (Table 8). This reflected the pronounced influence of environmental factors on the expression of these characters. In all variance analysis, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. However, the relatively larger magnitude of difference between the two was observed in seed yield ha<sup>-1</sup>, primary branch per plant, secondary branch per plant, harvest index and pod length. This indicates the greater influence of environmental factors than genetic factors on the expression of these traits. In these traits, selection based on phenotype performance may not be appropriate. Wani *et al.* [28] suggested that a larger difference between GCV and PCV is due to a larger influence of the environment on that trait. In common beans, Wani *et al.* [28] reported a wide range of GCV and PCV values were reported by Wani *et al.* [28]; Ahmed and Kamaluddin [15].

#### *Heritability and Genetic Advance*

The general sense heritability ranged from 20% to 93.5% for the traits studied (Table 8). According to Jonson *et al.* [10] heritability values more than 60% considered high, whereas values less than 30% considered low and values between 30% and 60% are moderate. Based on this, high heritability was recorded for dry biomass yield (93.5), hundred seed weight (88.4) and seed per pod (61.7) indicating that the environment has little influence on the expression of the characters, suggesting direct selection using these characters as major contributors to yield components to improve yield of common bean genotypes. This high heritability may be due to additive gene effects; hence these traits are likely to respond to direct selection in order to improve common bean grain yield through direct selection for grain yield related traits. Similarly, Wondwosen and Abebe [29] obtained a high heritability (>60%) for the grain yield traits, hundred grain weight, days to maturity, days to flowering, number of seeds per pod, number of pods per plant to support our result. Similarly, Raffi and Nath [30] also reported high heritability (>60%) for days to flowering, days to maturity, yield, seed weight, pod length, plant height, which supports our findings. Esho, [31] reported high heritability for plant height, pod length, number of seeds per pod, hundred seed weight and seed yield. Alghamdi, [32] observed that the highest heritability estimates were recorded for the number of pods and the number of seeds per plant. Moderate heritability was observed for plant height, pods per plant, harvest index, seed yield, pod length, secondary branches per plant, and days to 80% physiological maturity, which may

occur due to influence of the environment on the polygenic nature of these traits. Low heritability was estimated for days to 50 % flowering and primary branches per plant, which limits the possibility of including the traits to select desirable genotypes. This may be due to the higher influence of the environment on the expression of phenotypic variation than genotypic variation.

The genetic advance as a percent mean ranged from 2.97% for day to 80% physiological maturity to 56.59% for 100 seed weight (Table 8). This result indicated that selecting the top 5% of the genotypes could result in an advance of 2.97-56.59% over the mean of the respective population. As suggested by Sivasubramanian and Madhavamenon [27] the genetic advance as a percentage of the mean was classified as low (<10%), moderate (10–20%) and high (>20%). Based on this result, a high genetic advance as percentage of the mean was observed for 100 seed weight, dry biomass yield, pods per plant, harvest index, seed yield, seeds per pod, pod length, primary branches and secondary branches per plant. A low percentage of genetic advance was also estimated for day to 50% flowering day to 80% physiological maturity and

plant height. If the value of genetic advance is high, the character is governed by additive genes, and selection will be beneficial for such traits. If genetic advance is low, the character is governed by nonadditive genes and heterosis breeding may be useful.

For the success of estimation of selection accompanying heritability with genetic advance, is useful. High heritability was observed along with high genetic advance for hundred seed weight, seeds per pod, and dry biomass yield. The traits that showed moderate heritability with a high genetic advance were secondary branches per plant, pods per plant, pod length, and seed yield. Hence, these traits should be given top priority during selection in common bean breeding because they are the main portion of genetic variation attributable to additive gene action, and selection may be effective in early generations for these traits. Low genetic advance along with low heritability was observed for days to 50% flowering, days to 80% physiological maturity, and plant height. This indicates that these traits were highly influenced by the environment and the direct selection of the traits is not promising.

**Table 8.** Heritability, genetic advance, and coefficient of variation.

Traits	Mean range	$\sigma^2_g$	$\sigma^2_p$	PCV %	GCV %	$H^2$ %	GA	GAM %
PH	38.65-42.32	1.18	2.27	3.72	2.69	52	3.99	9.86
PB	2.28-3.09	0.28	1.08	40.46	20.25	25	0.55	21.03
SBPP	2.75-6.95	0.99	2.01	25.14	8.37	50	1.45	25.68
DTF	35.17-40.67	2.22	11.06	8.77	3.93	20	1.37	3.62
DTM	84.17-92.17	4.56	13.09	4.13	2.44	34.9	2.6	2.97
PPP	5.40-15.45	4.8	8.86	27.63	20.34	54.2	3.32	30.85
PL	3.19-7.89	1.09	2.77	28.9	18.15	39.4	1.32	23.48
SPP	3.46-6.08	0.56	0.91	19.6	15.39	61.7	1.21	24.91
DBY	3056-5218.3	361543.3	386741.2	16.22	15.68	93.5	1197.6	31.23
HSW	19.73-38.47	66.49	67.56	27.91	27.69	88.4	16.67	56.59
SY	1194.7-2865.2	166730	332273.9	24.6	17.42	50.18	595.85	25.43
HI	0.35-0.88	0.01	0.03	25.94	18.7	51.9	0.17	27.76

Where  $\sigma^2_g$ =genotypic variance,  $\sigma^2_p$ =phenotypic variance, GCV= genotypic coefficient of variation, PCV=phenotypic, coefficient of variation,  $H^2$ =heritability in broad sense, GA=genetic advance, GAM=genetic advance as percent of mean PH=plant height PB=primary branches per plant, SBPP=secondary branches per plant, DTF= days to flowering, DTM=days to maturity, PPP= pods per plant, PL=pod length, SPP=seeds per pod, DBY=dry biomass yield, HSW = hundreds of seed weight, SY=seed yield, HI= harvest index.

### 3.4. Association of Traits

#### 3.4.1. Phenotypic Association

The phenotypic correlation coefficients among the yield-related traits are presented in Table 9, The seed yield per

hectare has a significant and positive phenotypic correlation with plant height, secondary branches per plant, pods per plant, pod length, seeds per pod, and dry biomass yield. This indicates that the correlation of these traits with seed yield could be utilized fruitfully to improve the potential of haricot bean yield. Gonçalves *et al.* [33] stated that the traits which have moderate to strong correlations with the desired traits

are important for successful indirect selection in the initial stages of plant breeding. This result is consistent with the findings of many researchers who found positive correlations between seed yield and plant height [34, 35]. In this study a non-significant association of seed yield per hectare with primary branches per plant and a negative significant correlation with days to physiological maturity of 80% and also a negative non-significant correlation of seed yield with days to maturity at the phenotypic level was observed.

In several traits, environmental correlations presented differences in value and sign, in relation to phenotypic and genotypic correlations, indicating that different physiological processes affect the genetic and environmental variations of these traits, and the environment may restrict direct selection [36]. Gonçalves *et al.* [33] Plant height was significantly and positively associated with secondary branches per plant, pods per plant, pod length, seeds per pod, dry biomass yield, and seed yield. A positive nonsignificant association was observed for primary branches per plant with plant height, secondary branches per plant, days to 80% physiological maturity, pods per plant, pod length, seeds per pod, dry bio mass yield, and seed yield.

### 3.4.2. Genotypic Correlation

Genotypic correlation coefficients among yield-related traits are presented in Table 10. The seed yield showed a positive and significant genotypic association with plant

height, secondary branches per plant, pods per plant, pod length and seeds per pod. Plant breeders can use genetic correlations because they are heritable. As suggested by Lopes *et al.* [37], indirect selection of traits can be performed when their correlation coefficient values with the desired trait are higher than 0.50. Consequently, in the present study, the correlation coefficient is considered weak when it is less than 0.50, moderate when it varies from  $\pm 0.50$  to  $\pm 0.69$  and strong when it varies from  $\pm 0.70$  to  $\pm 0.89$  and very strong when it is greater than  $\pm 0.90$ . The height of the plant showed a positive and significant association with secondary branches per plant, pods per plant, pod length, seeds per pod, and seed yield. A negative and significant association was found for days to 50% flowering with plant height, pod length, seeds per pod, and seed yield. Plant length and number of pods/plant have been observed to be correlated with seed yield/plant. These outcomes find the true association with seed weight and are considered as seed mass/plant predictors, according to which we can select plants with more height directly and with more number of pods/plant that can perform better and enhance seed yield/plant. Gonçalves *et al.* [33] also observed that these desired traits with a strong correlation are crucial for selection in plant breeding. In agreement with this result, Alghamdi [32] and Ballat and Araby [21] reported a positive and significant association of seed yield with plant height, pods/plant, and branches/plant and with other characters.

**Table 9.** Phenotypic (above diagonal) Genotypic (below diagonal) correlation coefficient for agronomic traits of Haricot bean varieties tested in Y / Sekoru and Inkure.

	PH	PB	SBPP	DTF	DTM	PPP	PL	SPP	DBY	HSW	SY
PH		0.16ns	0.47**	-0.30**	-0.09ns	0.56**	0.55**	0.64**	0.29*	-0.15ns	0.56**
PB	0.20ns		0.17ns	-0.01ns	0.08ns	0.23ns	0.14ns	0.03ns	0.16ns	0.28*	0.22ns
SBPP	0.61*	0.18ns		-0.24*	-0.16ns	0.50**	0.51**	0.46**	0.25*	-0.06ns	0.48**
DTF	-0.81**	0.08ns	-0.39ns		-0.06ns	-0.29*	-0.47**	-0.42**	0.08ns	-0.21ns	-0.45*
DTM	-0.19ns	-0.05ns	-0.29ns	0.65*		-0.19ns	-0.15ns	-0.17ns	0.20ns	-0.06ns	-0.12ns
PPP	0.91**	0.41ns	0.76**	-0.54ns	-0.23ns		0.87**	0.85**	0.49**	-0.03ns	0.87**
PL	1.00**	0.25ns	0.84**	-0.67*	-0.36ns	1.01**		0.84**	0.32**	-0.06ns	0.69**
SPP	0.96**	0.06ns	0.66*	-0.70*	-0.37ns	0.95**	1.00**		0.41**	-0.12ns	0.56**
DBY	0.50ns	0.18ns	0.27ns	0.21ns	0.35ns	0.68*	0.56ns	0.58ns		-0.30*	0.31**
HSW	-0.19ns	0.29ns	-0.05ns	-0.52ns	0.09ns	-0.03ns	-0.07ns	-0.13ns	-0.31ns		-0.01ns
SY	0.91**	0.30ns	-0.71*	-0.65*	-0.35ns	0.97**	0.98**	0.95**	0.48ns	-0.01ns	

When, PH= plant height, PB=primary branch, SBPP=secondary branch per plant, DTF=days to 50% flowering, DTM=days to maturity, PPP=pods per plant, PL=pod length, SPP=seeds per pod, DBY = dry biomass yield, HSW = hundreds of seed weight, SY=seed yield



### 3.4.3. Analysis of the Phenotypic Path Coefficients

The analysis of the phenotypic path coefficient showed that dry biomass production (0.839) had a high positive direct effect on seed production per hectare followed by pod length (0.098) and seeds per pod (0.028) (Table 10). The indirect effects of a large number of other characters through this trait were also positive. These traits also showed a positive and significant phenotypic correlation with seed yield per hectare. Many researchers found a positive direct effect on seed production for plant height [33, 35]; number of days to maturity [38]; number of pods per plant [39]; number of seeds per pod [39] and 100 or 1000 seed weight [33, 40]. In contrast, negative direct effects on seed yield have been reported for plant height [15]; number of leaves per plant and

number of days to flowering [41]; number of days to maturity [30]; number of pods per plant and number of seeds per pod [40]; pod length [35] and 100 or 1000 seed weight [41]. In this study, a negative direct effect on seed yield per hectare was observed for plant height (-0.007), hundred seed weight (-0.029), days to 50% flowering (-0.039), secondary branches per plant (-0.046) and pods per plant (-0.059) and similarly indirect effects of other different characters through these traits were negative. The negative direct effect of these characters on seed yield per hectare indicates that direct selection of these traits may be ineffective in improving seed yield per hectare. The positive correlation observed between these traits and seed yield at the phenotypic level is explained by the positive indirect effect they produce through pod length and dry bio mass yield.

**Table 10.** Phenotypic path coefficient of traits of common bean varieties evaluated in Yerosekoru and Inkure, Sekoru district of Jimma zone in the 2020/2021 cropping season.

	PH	PB	SBPP	DTF	DTM	PPP	PL	SPP	DBY	HSW	rp
PH	-0.007	0.007	-0.019	0.005	0.006	-0.029	0.048	0.015	0.462	-0.001	0.56**
PB	-0.002	0.027	-0.012	0.009	0.007	-0.029	0.047	0.009	0.353	-0.002	0.22 <sup>ns</sup>
SBPP	-0.003	0.007	-0.046	0.009	0.005	0.028	0.05	0.013	0.353	-0.002	0.48**
DTF	0.001	-0.006	0.011	-0.039	-0.002	0.017	-0.046	-0.12	-0.201	0.012	-0.45*
DTM	-0.002	0.009	-0.011	0.003	0.021	-0.015	0.024	0.004	0.229	-0.008	-0.12 <sup>ns</sup>
PPP	-0.004	0.013	-0.023	0.012	0.001	-0.059	0.085	0.02	4.605	-0.008	0.87**
PL	-0.004	0.013	-0.024	0.019	0.005	-0.051	0.098	0.02	4.571	-0.011	0.69**
SPP	-0.004	0.009	-0.021	0.017	0.003	-0.049	0.083	0.028	0.568	-0.007	0.56**
DBY	-0.004	0.016	-0.019	0.009	0.006	-0.042	0.067	0.019	0.839	-0.007	0.31**
HSW	-0.001	0.012	-0.003	0.016	0.005	-0.016	0.035	0.007	0.19	-0.029	-0.01 <sup>ns</sup>

R=0.0112

When, PH= plant height, PB=primary branch, SBPP=secondary branch per plant, DTF=days to 50% flowering, DTM=days to maturity, PPP=pods per plant, PL=pod length, SPP=seeds per pod, DBY = dry biomass yield, HSW = hundreds of seed weight

### 3.4.4. Genotypic Path Coefficient Analysis

In this study, the genotypic path coefficient analysis showed that dry biomass yield (0.646) showed the highest genotypic direct effect on seed yield per hectare followed by pod length (0.119) and pods per plant (0.077) (Table 11). In addition to dry biomass yield, other traits also showed a positive and significant genotypic correlation with seed yield per hectare. The direct positive direct effect of these traits implies that direct selection of these traits can be effective in improving seed yield per hectare of haricot bean. The indirect effects of other characters through these traits were also positive for a large number of traits. The genotypic direct effect of days to 50% flowering (-0.001), primary branches

per plant (-0.005), days to 80% physiological maturity (-0.024), secondary branches per plant (-0.031), hundred seed weight (-0.038) and plant height (-0.045) on seed yield per hectare was negative. This indicates that using this trait as selection criteria in improving seed yield per hectare may not be effective. Direct negative effects on seed yield have been reported for plant height [29, 30]; number of leaves per plant [41]; number of days until flowering [33, 41]. In general if correlation between dependent and independent characters is due to the direct effect of a character, it reflects a true relationship between them. Therefore, selection can be done to improve the dependent character. The residual effect shows how much the explanatory variables represent the variability of the dependent variable [11]. The residual effect in our study on the genotypic path coefficient was 0.0041, indicat-



ing that the traits studied explain 99 % of the variability in seed yield [42].

**Table 11.** Genotypic path coefficient analysis of haricot bean varieties tested in YeroSekoru and Inkure Sekoru district of the Jimma zone in 2020.

	PH	PB	SBPP	DTF	DTM	PPP	PL	SPP	DBY	HSW	rg
PH	-0.045	-0.001	-0.019	0.001	0.005	0.07	0.119	0.064	0.319	0.007	0.91**
PB	-0.009	-0.005	-0.006	-0.001	0.001	0.032	0.03	0.004	0.114	-0.011	0.30 <sup>ns</sup>
SBPP	-0.028	-0.001	-0.031	0.001	0.007	0.058	0.101	0.044	0.177	0.002	-0.71*
DTF	0.038	-0.001	0.012	-0.001	-0.015	-0.042	-0.079	-0.047	0.136	0.019	-0.65*
DTM	0.009	0.001	0.009	-0.001	-0.024	-0.017	-0.042	-0.025	0.224	-0.003	-0.35 <sup>ns</sup>
PPP	-0.042	-0.002	-0.023	0.001	0.005	0.077	0.12	0.063	0.436	0.001	0.97**
PL	-0.046	-0.001	-0.026	0.001	0.008	0.078	0.119	0.067	0.362	0.003	0.98**
SPP	-0.045	-0.001	-0.02	0.001	0.009	0.073	0.119	0.067	0.376	0.005	0.95**
DBY	-0.023	-0.001	-0.008	-0.001	-0.008	0.052	0.067	0.039	0.646	0.012	0.48 <sup>ns</sup>
HSW	0.009	-0.001	0.002	0.001	-0.002	-0.002	-0.008	-0.009	-0.198	-0.038	-0.01 <sup>ns</sup>

R=-0.0041

When, PH= plant height, PB=primary branch, SBPP=secondary branch per plant, DTF=days to 50% flowering, DTM=days to maturity, PPP=pods per plant, PL=pod length, SPP=seeds per pod, DBY = dry biomass yield, HSW = hundreds of seed weight

## 4. Conclusion and Recommendation

The purpose of this study was to evaluate the yield and related traits of the released and one local common bean variety in two locations in the Sekoru district of the Jimma zone, in the south western of Ethiopia, with the objective of identifying the best performing varieties for the study area. To accomplish the evaluation process, twelve common bean varieties were selected and tested using a randomized complete block design with three replications under rain-fed conditions in Sekoru agro ecology of two locations, namely Yerosekuru and Inkure. The results showed that the genotypes were highly significant for all traits in both locations. This indicates the presence of valuable variation among genotypes that help for breeding purposes. Highly significant G x L interactions were observed for combined data of all traits except for plant height, dry biomass yield, and hundred seed weight. This indicates that the genotypes responded differently for the traits in the two locations. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation, indicating that the influence of the environment is higher than the genotypic influence on the expression of these traits. The results of this research showed that a high phenotypic coefficient of variation was observed for traits such as hundred seed weight, dry biomass yield, pod length, pods per plant, harvest index and seed yield, and a high genotypic coefficient of variation was observed for the traits

hundred seed weight and pods per plant. In this study, high heritability with high genetic advance was observed for the traits hundred seed weight, seeds per pod, primary branches per plant. The correlation coefficient was used to generate information on the association of characteristics and observed a positive phenotypic significant correlation with seed yield per hectare for all traits except primary branches per plant, days to 80% physiological maturity and days to 50% flowering, which showed a negative significant and nonsignificant correlation with seed yield per hectare at the phenotypic level. Genotypic path coefficient analysis indicates that the traits studied that showed a positive direct effect on seed yield per hectare were dry biomass yield, pod length, seeds per pod and pods per plant and also those traits that showed a negative direct effect on seed yield per hectare were plant height, primary branches and secondary branches per plant, days to 50% flowering, days to 80% physiological maturity, and 100 seed weight. Among the varieties studied, Ser119 and Ser125 showed a higher seed yield performance in two of the test locations, Yerosekuru Ser119 (2870.7 kg/ha), Ser125 (2696.7/ha) and Inkure Ser119 (2859.7kg/ha), Ser125 (2701.7kg/ha) and also their average yield performance in the area was Ser119 (2865.2 kg/ha) followed by Ser125 (2699.2 kg/ha) and also these varieties showed good adaptation with good stand. Based on this fact, introducing these varieties for the study areas with medium altitudes will result in best productivity, even though repeating this experiment for another one more year is required.

## Abbreviations

GCV: Genotypic Coefficient of Variation  
PCV: Phenotypic Coefficient of Variation  
H<sup>2</sup>: Heritability in Broad Sense

## Data Availability Statement

Data supporting the findings of this study were included in the manuscript.

## Conflicts of Interest

The authors declare no conflicts of interest.

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