

Research Article

Genetic Variability Analysis and Association of Traits in Common Bean (*Phaseolus vulgaris* L.) Landraces Collected from Ethiopia at Jimma

Eyuel Mesera,¹ Garome Shifaraw ,^{1,2} Sentayehu Alamerew,³ and Birhanu Amsalu⁴

¹South Agricultural Research Institute (SARI), Hawassa, Ethiopia

²Mettu University, Bedelle College of Agriculture and Forestry, Mettu, Ethiopia

³Jimma University, College of Agriculture and Veterinary Medicine, Jimma, Ethiopia

⁴Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia

Correspondence should be addressed to Garome Shifaraw; shifarawgarome@gmail.com

Received 8 July 2022; Revised 26 September 2022; Accepted 22 October 2022; Published 3 November 2022

Academic Editor: Othmane Merah

Copyright © 2022 Eyuel Mesera et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

This study was conducted on one hundred common bean landraces at the Jimma Agricultural Research Center, Melko, with the objective of assessing genetic variability and association of traits in common bean landraces collected from different parts of Ethiopia. The experiment was laid out in a simple lattice design with two replications. Analysis of variance showed significant differences among genotypes for all traits. This highly significant difference indicates the existence of large variability among genotypes. High phenotypic coefficients of variation and genotypic coefficients of variation were obtained for plant height (19.43, 11.73), pod length (11.27, 10.69), and 100-seed weight (15.42, 12.74). High heritability in the broad sense was found for days to 50% flowering (66.98), days to 90% maturity (87.43), pod length (90.03), pod width (78.23), harvest index (98.67), and 100-seed weight (68.31). High genetic advance as a percentage of mean with high heritability was obtained for pod length, pod width, harvest index, and hundred seed weight. Grain yield had a positive and significant association with pod length ($r_p = 0.153^*$, $r_g = 0.282^{**}$) and 100-seed weight ($r_p = 0.294^{**}$, $r_g = 0.492^{**}$). Hundred seed weight exerted the highest positive direct effect (0.294) on grain yield at genotypic level. The D^2 classified landraces into 7 clusters and one solitary, which makes them moderately divergent. The highest inter-cluster distance was observed between clusters VII and IV. The first five principal components with eigenvalues greater than one altogether explained about 79.56% of the total variation. In conclusion, the top high-yielding landraces, namely, P#1247, P#1092, P#1077, P#861, P#990, P#763, P#58, and P#857, should be included in the next breeding program. 100-seed weight had the highest direct effect and a positive significant association with grain yield. Thus, it should be considered as the selection criteria for further common bean yield improvement. However, the current result is merely indicative and cannot be used to draw definite conclusions. Therefore, the experiment should be replicated in different locations and seasons for greater consistency.

1. Introduction

Common bean (*Phaseolus vulgaris* L.) is also known as haricot bean, snap bean, navy bean, and kidney bean. It is seed propagated and true diploid ($2n = 22$). It is one of the most important pulse crops [1]. Common bean belongs to the genus *Phaseolus*, with pinnately compound trifoliolate large leaves. The genus consists of some 70 species [2]. This legume is an annual and self-pollinated crop [3],

which intensely grows throughout the entire tropical area and some temperate regions of the planet [4]. Common bean is the most cultivated and consumed legume throughout the world. It is the world's second most important pulse after soybean [5]. It is harvested as a dry grain and is one of the most important food grain legumes, occupying more than 41 million ha annually and providing food for more than 300 million people. It is regarded as “grain of hope” as it is an important

component of subsistence agriculture and feeds about 100 million people in the tropics alone [1].

Common beans are grown for local consumption and for export as cash crops. In Ethiopia, it is considered the major source of protein in the lowlands (mainly in eastern, southern, south western, and the rift valley areas of Ethiopia [6] where they are consumed as *Nifro*, *Wasa*, *Shirowat*, *Soup*, and *Samosa*). Additionally, common bean has health benefits being rich in protein content (about 23% for dried shelled beans and about 6% for green beans) and serves as a good source of iron and zinc (both of which are key elements for mental development) [6]. The crop is also a significant source of fiber, calories, and vitamins especially foliate. It is also used as a source of feed. Common bean can improve soil fertility through the fixation of atmospheric nitrogen (N_2) in symbiosis with rhizobia and decomposition of its residues [7]. Moreover, it is an increasingly important crop in the cropping systems since it is used for nitrogen [8].

In the world, the area covered by common beans was 41,712 000 hectares. Its production is 38.1 million tons. The world average yield was $1.09 t ha^{-1}$ [9]. The average annual production (tons) and yield ($kg ha^{-1}$) of common bean in major producing countries in Africa (Tanzania, Uganda, Kenya, and Rwanda) is 5.4 million tons and $1.623 t ha^{-1}$, respectively [9]. In Ethiopia, the area covered by common bean is about 357,299.89 ha with total production about $540238.94 t ha^{-1}$ with national average yield of $1.5 t ha^{-1}$ [6].

A common bean cultivar must combine desirable genotypes for several traits to be accepted by producers and consumers. For producers, it must have high grain yield, good plant architecture, resistance to the main pathogens, and a highly marketable grain type. However, consumers are interested only in the traits related to grain quality. Therefore, the main breeding programs that work with the common bean crop have devoted great efforts to obtaining lines that meet all the goals mentioned [10]. To improve the yield of common beans, it is necessary to generate sufficient variability to increase the probability of successful selection in common beans [11]. In common bean, architectural, phenological, and yield components collectively influence seed yield. The relationships between yield and yield contributing traits on the one hand and among themselves, on the other hand, are measured by the correlation coefficient. The knowledge of this relationship helps to identify traits on which selection can be based for the improvement of yield. Furthermore, the selection via highly correlated characters becomes easy if the contribution of different characters to the yield is quantified using path coefficient analysis. Path analysis splits the correlation coefficient into the direct and indirect effects of a set of independent variables on the dependent variable yield. This study aimed to estimate the genetic variability and association of quantitative traits among haricot bean landraces.

2. Materials and Methods

2.1. Description of Study Area. This study was conducted at the Jimma Agricultural Research Center (JARC). It is located at a $7^{\circ}40'N$ $36^{\circ}50'E$ / $7.667^{\circ}N$ $36.833^{\circ}E$ about 355 km away from the capital of Ethiopia, Addis Ababa, and it is found in Jimma Zone of the Oromia Region. The study area is 1753 m.a.s.l and receives an average rainfall of 1561 mm per annum. The maximum and minimum annual temperatures of the area are 28.8 and 11.8°C, respectively. The soil type of the study area was classified as Chromic Nito-soil and Cambi-soil with P^H of 5–6 and Cation exchange capacity (CEC) of 28.6 and nitrogen, organic carbon, and the available P of 0.25%, 2.96%, and 5 ppm, respectively.

2.2. Experimental Materials. For this study, 100 common bean landraces were obtained from Melkasa Agricultural Research Center (MARC) that are collected from different major common bean producing regions of Ethiopia (Table 1).

2.3. Experimental Design and Management. The experiment was laid out in a 10×10 simple lattice design in two replications with plot size of $0.8 m \times 2 m$. The total area of the experimental field was $701.8 m^2$. The distance between the block, plot, rows, and plants was 1 m, 50 cm, 40 cm, and 10 cm, respectively. The experiment was conducted during 2020/21 main growing season. Di-ammonium phosphate (DAP) was applied at the rate of $100 kg ha^{-1}$, and all other agronomic practices were applied as per the recommendations of the lowland pulse improvement program.

2.4. Data Collected. Five plants randomly taken from the two rows were considered for recorded plant and plot-based data and the average of the five plants was used for data analysis. To record those parameters, descriptors in [12] were used.

2.4.1. Data Collected on a Plant Basis. Plant base data collected from plant height and pod per plant.

2.4.2. Data Collected on a Plot Basis. Data on plot base were collected from days flowering, days to maturity ($g plot^{-1}$), hundred seed weight (gm), Biomass yield (Biological yield) ($kg ha^{-1}$), and Harvest index (%).

2.5. Data Analysis

2.5.1. Analysis of Variance (ANOVA). The data collected for each quantitative trait were subjected to analysis of variance (ANOVA).

Analysis of variance (ANOVA) was performed using Proc GLM procedures of SAS version 9.3 [13]. The mathematical model for simple lattice design is

$$Y_{ik}(j) = \mu + G_i + R_j + (Bk(j)) + \epsilon_{il}(j), \quad (1)$$

where $Y_{il}(j)$ is the observation of the i th genotype grown in the K^{th} block of the replication j , μ is the grand mean, G_i is the effect of the i th genotype, R_j is the effect of the j th replicate, Bk_j is the effect of k th block in the j th replicate and, and $\epsilon_{ik}(j)$ is the intra-block residual.

2.5.2. Analysis of Genetic Parameters

(1) Estimation of Phenotypic and Genotypic Coefficients of Variation. Phenotypic and genotypic variances and coefficients of variations were estimated as described in [14, 15].

Genotypic variance $\sigma^2_g = (MSg - MSe)/r$.

Phenotypic variance $(2p) = 2g + 2e$, where MSg = mean square due to genotypes, MSe = environmental variance (error mean square), and r = the number of replications.

$$\text{Phenotypic coefficients of variation (PCV)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100,$$

$$\text{genotypic coefficients of variation (GCV)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100. \quad (2)$$

(2) Heritability in a Broad Sense (h^2_b). Heritability in a broad sense for all characters was computed using the formula given in [16]. $h^2_b = 2g/2p \times 100$, where: h^2_b = heritability in a broad sense, $2g$ = genotypic variance, and $2p$ = phenotypic variance.

(3) Expected Genetic Advance under Selection (GA). Expected genetic advance for each character at 5% selection intensity was computed using the formulae described in [17].

$$GA = K * \sigma_P * hb, \quad (3)$$

where GA = expected genetic advance, K = constant (selection differential where $K = 2.056$ at 5% selection intensity), σ_P = phenotypic standard deviation on the mean basis, and h^2_b = heritability in a broad sense.

(4) Genetic Advance as a Percentage of Mean (GAM). The genetic advance as a percentage of mean was computed as described in [17].

$GAM = GA/\bar{X} \times 100$, where: GAM = genetic advance as percentage of mean, GA = genetic advance under selection, and \bar{X} = mean of the population in which selection was employed.

2.6. Phenotypic and Genotypic Correlations. Phenotypic and genotypic correlations between yield and yield-related traits were estimated using the formulae described in [18, 19] from the corresponding variance and covariance components as follows.

$$\text{Phenotypic correlation coefficients } (r_{p_{xy}}) = \text{pcov}(x, y) / \sqrt{(\sigma^2_{px} * \sigma^2_{py})}.$$

$$\text{Genotypic correlation coefficients } (r_{g_{xy}}) = \text{gcov}(x, y) / \sqrt{(\sigma^2_{gx} * \sigma^2_{gy})}.$$

TABLE 1: List of landrace accessions used in the study.

Serial	Accession
1	P#909
2	P#1285
3	P#1078
4	P#1070
5	P#1316
6	P#1107
7	P#882
8	P#1083
9	P#760
10	P#932
11	P#1315
12	P#1027
13	P#1097
14	P#1247
15	P#264
16	P#1176
17	P#1157
18	P#1250
19	P#1092
20	P#1232
21	P#1038
22	P#1057
23	P#1072
24	P#985
25	P#1275
26	P#831
27	P#864
28	P#1074
29	P#1187
30	P#1050
31	P#1046
32	P#14
33	P#1306
34	P#1212
35	P#1298
36	P#1086
37	P#1043
38	P#1300
39	P#772
40	P#1158
41	P#1182
42	P#40
42	P#1077
44	P#861
45	P#1063
46	P#1268
47	P#1124
48	P#990
49	P#1314
50	P#989
51	P#769
52	P#1063
53	P#1078
54	P#967
55	P#1139
56	P#82
57	P#984
58	P#763
59	P#1049
60	P#1094

TABLE 1: Continued.

Serial	Accession
61	P#906
62	P#1179
63	P#145
64	P#916
65	P#901
66	P#133
67	P#1055
68	P#986
69	P#1309
70	P#1103
71	P#934
72	P#1310
73	P#1211
74	P#1279
75	P#941
76	P#1227
77	P#1079
78	P#1095
79	P#859
80	P#157
81	P#945
82	P#1042
83	P#1071
84	P#1154
85	P#931
86	P#1270
87	P#93
88	P#1102
89	P#58
90	P#811
91	P#1150
92	P#857
93	P#1124
94	P#1127
95	P#999
96	P#13
97	P#1117
98	P#1283
99	P#989
100	P#872

The calculated phenotypic and genotypic correlation values were tested for their significance using t-test according to [20].

2.6.1. Phenotypic and Genotypic Path Coefficient Analysis. The direct and indirect effects of yield-related characters on yield and among themselves were computed using the following formulae suggested in [21].

$$rij = Pij + \Sigma rikpkj. \quad (4)$$

The residual effect = $\sqrt{1 - R^2}$, where R^2 is the residual factor, Pij is the direct effect of yield by i^{th} character, and rij is the correlation of yield of the i^{th} character.

2.7. Cluster Analysis. Clustering was performed using the proc cluster procedure of SAS version 9.3 [22] by employing the method of average linkage clustering strategy of the

observation. The number of clusters was determined by following the approach suggested by Copper and Milligan [23] by looking into three statistics, namely, pseudo-F, pseudo- t^2 , and cubic clustering criteria. The points where local peaks of the CCC and pseudo-F statistic join with small values of the pseudo- t^2 statistic followed by a larger pseudo- t^2 for the next cluster combination were used to determine the number of clusters. The dendrogram was also constructed by using the SAS software package based on the average linkage and Euclidean distance used to measure dissimilarity (the distance) technique.

2.7.1. Genetic Distance Analysis. Genetic divergence between clusters was determined using the generalized Mahalanobis D^2 statistics [24]. In matrix notation, the distance between any two groups was estimated from the following relationship.

$D^2_{ij} = ((xi - xj) S^{-1} (xi - xj))$, where D^2_{ij} = the squared distance between any two genotypes i and j .

X_i and X_j = the vectors of the values for i^{th} and j^{th} genotypes, respectively. S^{-1} = the inverse of the pooled covariance matrix within groups.

The D^2 values obtained for pairs of clusters were considered as the calculated values of chi-square (X^2) and tested against tabulated X^2 values at $n-1$ degree of freedom at 1% and 5% probability levels, where n = number of characters considered [15].

2.8. Principal Component Analysis (PCA). Principal component analysis was computed using the correlation matrix of SAS version 9.3 [22] to examine the relationships among the quantitative characters that are correlated with each other by converting them into uncorrelated characters called principal components. Below is the general formula to compute scores on the first component extracted (created) in a principal component analysis.

$PC_1 = b_{11}(x_1) + b_{12} + \dots + b_{1p}(x_p)$, where PC_1 = the subject's score on principal component 1 (the first component extracted); b_{1p} = the regression coefficient (or weight) for observed variable p , as used in creating principal component 1; and Xp = the subject's score on observed variable p .

3. Results and Discussion

3.1. Analysis of Variance. The mean square of the traits showed highly significant differences (0.01) among the tested genotypes (Table 2). This indicates the existence of sufficient variability among genotypes for all traits which can be exploited for common bean yield improvement. In agreement with these findings, the authors in [25, 26] reported the presence of genetic variability among common bean genotypes.

3.2. Range and Mean Values. Days to 50% flowering ranged from 45.5 to 54 days with a mean of 48.83 days. Days to 90% maturity ranged from 98.22 to 115.5 with a mean of 98.22

TABLE 2: Mean square values for the 10 characters of 100 haricot bean genotypes grown at Jimma (2020/21).

Traits	Replication (df = 1)	Genotype (df = 99)		Block (18)		Error		RE	CV%	Mean
		Un-adj	Adj	Intra (81)	RCBD (99)					
DF	1.62	8.32	8.25**	3.29	1.63	1.93	108.56	2.61	48.83	
DM	1.13	19.95	18.30**	2.05	1.23	1.38	104.58	1.12	98.23	
PH	677.57	243.57	225.44**	122.69	105.1	108.28	100.43	15.49	66.15	
NPP	73.62	15.30	14.32**	9.20	7.09	7.48	101.19	13.81	19.28	
NSP	352.77	375.90	274.67**	664.44	127	123.53	97.22	16.36	68.89	
PL	0.40	3.54	2.88**	0.17	0.15	0.15	100.19	3.55	10.92	
PW	0.001	0.05	0.03**	0.01	0.004	0.005	107.53	9.65	0.67	
HI	100.91	223.71	198.18**	1.78	1.32	1.41	101.56	3.32	34.55	
HWS	10.30	15.03	12.83**	3.91	2.42	2.69	104.01	8.67	17.91	
YLD	408402	963996	908976**	4846	4617	465849	100.04	20.17	3367.5	

** = highly significant at 0.01, df = degrees of freedom, DF = days to 50% flowering, DM = days to 90% maturity, PH = plant height, NPP = number of pods per plant, NSP = number of seeds per plant, PL = pod length, PW = pod width, HSW = hundred seed weight, and HI = harvest presence of genetic variability in common bean genotype efficiency of simple lattice to RCBD (complete randomized block design).

TABLE 3: Mean, minimum, and maximum values were recorded for ten quantitative variables in 100 common bean accessions from Ethiopia (2020/21).

Traits	Ranges	σ^2_g	σ^2_p	H ²	PCV	GCV	GA	GAM (%)	Mean \pm SEM
DTF	45.5–54	3.31	4.94	66.98	4.55	3.73	3.08	6.28	48.83 \pm 0.98
DTM	98.22–115.5	8.54	9.76	87.43	3.18	2.97	5.63	5.73	98.22 \pm 0.82
PH	57.45–99.26	60.18	165.26	36.42	19.43	11.73	9.64	14.58	66.14 \pm 7.4
NPP	12.9–27.4	3.61	10.71	33.75	16.97	9.86	2.27	11.80	19.28 \pm 1.9
NSP	50.4–108	73.81	200.86	36.75	20.57	12.47	10.73	15.57	68.89 \pm 7.6
PL	8.05–14.05	1.36	1.52	90.03	11.27	10.69	2.28	20.9	10.92 \pm 0.28
PW	0.45–1.24	0.015	0.02	78.23	20.67	18.31	0.22	33.32	0.66 \pm 0.05
HI	20.72–55.55	98.43	99.75	98.67	28.90	28.71	20.30	58.75	34.55 \pm 0.8
HWS	12.4–24.32	5.21	7.62	68.31	15.42	12.74	3.88	21.69	17.90 \pm 1.16
YLD	1645–263 2.1	223646	685330	32.63	24.58	14.04	556.52	16.53	3367.47 \pm 482.6

DTF = days to 50% flowering, DM = days to 90% maturity, PH = plant height, NPP = number of pods per plant, NSP = number of seeds per plant, PL = pod length, PW = pod width, HSW = 100-seed weight, HI = harvest index, and YLD = yield per hectare tone per hectare.

(Table 3). The wide range in days to 50% maturity indicated that early maturing variety can be developed for areas of the short rainy season (such as rift valley areas of Ethiopia) through selection. Additionally, late-maturing varieties could be evolved for areas with protracted rainy seasons through simple selection without hybridization. The values of plant height ranged from 57.45 (shortest) cm to 99.26 (tallest) cm with a mean of 66.14 (Table 3). In agreement with this study, the authors in [27, 28] reported various variations for plant height, days to 50% flowering, and days to 90% maturity (Table 3).

Regarding seeds per plant, the minimum and maximum values were 50.4 and 108, respectively, with a mean of 68.89. The number of pods per plant ranged from 12.9 to 27.4, with a mean of 19.28. The mean value of the harvest index was 34.55, with minimum and maximum values of 20.72 and 55.55, respectively (Table 3). 100-seed weight ranged from 12.4 g to 24.32 g, with a mean value of 17.90 (Table 4). In agreement with these results, the authors in [1, 29, 30] reported the number of seeds per plant, the number of pods per plant, and the 100-seed weight. In agreement with this work, several authors reported a wide range in the number of pods per plant among common bean accessions from various parts of the world [1, 29, 31–33].

Pod length ranged from 8.05 cm to 14.05 cm with mean values of 10.92 cm. The pod width ranged from 0.45 to 1.24

with mean values of 1.24. The mean yield per hectare recorded was 3367 kg, with minimum and maximum values of 1642.1 kg and 5263 kg per hectare. The eight top yielder landraces were 14 (4526.0) kg per hectare, 19 (4528.4 kg ha⁻¹), 43 (5263.7 kg ha⁻¹), 44 (4682.2 kg ha⁻¹), 48 (4691.1 kg ha⁻¹), 58 (4800.0 kg ha⁻¹), 89 (4688.7 kg ha⁻¹), and 92 (4709.00 kg ha⁻¹). As observed in these findings, the genotype showed wide variation Tables 3 and 4. This implies that the common bean landraces of Ethiopia possess a tremendous genetic potential for use in future breeding programs to improve the seed yield of common beans. The authors in [34, 35] reported similar results in their previous studies.

3.3. Heritability Estimate in a Broad Sense (h^2_b). Heritability ranged from 32.63% for yield to 98.67% for the harvest index. According to Robinson et al. [36], heritability categorized as low (<30), medium (30 to 60), and high (above 60). Accordingly, days to 50% flowering (66.98), days to 90% maturity (87.43), pod length (90.03), pod width (78.23), harvest index (98.67), and 100-seed weight (68.31) showed high heritability values (Table 3). High heritability estimates for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment. Hence, the success of crop

TABLE 4: Mean performance of one hundred genotypes tested at Jimma during 2020/21.

Landraces	DTF	DTM	PH	NPP	NSP	PL	PW	HI	HSW	YLD
1	51a-f	94.5r-t	52.4q-w	16.8n-x	80.4b-r	13.05 b	0.515l-m	29.895x-z	16.510r-z	3444.9c-s
2	49.5d-i	98.5j-n	86.05a-f	18.4h-w	95.7a-e	13.05 b	0.905d-e	35.285s-u	17.525p-z	3203.5f-t
3	50 d-h	97.5l-p	56.8p-w	20.2b-s	61.6o-z	10.05l-o	0.705i-j	22.070n-q	16.350s-z	3631.2b-q
4	49.5d-i	96.5n-r	52.6q-w	25.3a-b	94.8a-f	13.15 b	0.6k-l	29.83x-z	16.065u-z	2753.0l-v
5	48.5f-k	97m-q	53.35q-w	15.5q-x	63.5n-z	11.55d-h	0.66i-k	54.055a-c	15.735v-z	3005.8h-u
6	54a	100.5f-j	61.95j-w	17m-x	56.1t-z	10.05l-o	0.515l-m	30.025x-z	18.330i-y	2832.3k-v
7	48g-l	99i-m	57.8n-w	19.1d-u	56t-z	12.05c-d	0.705i-j	50.19f-j	17.125p-z	2912.9i-v
8	45.5l	96o-s	67e-u	17.6k-x	38.6c	9.15p-s	0.705i-j	49.01i-j	18.360i-y	2659.1n-v
9	47i-l	99.5h-l	79.40a-l	17.5k-x	62.5n-z	11.1g-i	0.615k-l	44.18l-m	19.556e-r	4087.2a-l
10	53a-c	101.5d-h	99.26a	17.8j-x	58.2r-z	10.05l-o	0.615k-l	22.885l-q	16.730q-z	3571.2b-s
11	53.5a-b	102c-g	67.6d-t	21b-o	88.1a-m	12c-e	0.75f-i	28.435z	15.635w-z	3551.7b-s
12	49e-j	104.5 b	69.3d-r	19e-v	75.6b-w	11g-j	0.6k-l	49.9f-j	17.440p-z	3102.1g-u
13	52a-d	95q-t	76.3b-p	23.6a-h	84.6b-n	12.05c-d	1.1b-c	35.21s-u	12.405 l	3295.5f-t
14	48.5f-k	100.5f-j	77.9b-n	24a-f	77.7b-t	11g-j	0.7i-j	24.96g-l	18.165m-z	4526.0a-f
15	46.5j-l	96o-s	67.85d-t	21.3b-o	60.4o-z	13.05 b	0.605k-l	21.330p-q	16.900q-w	2839.6k-v
16	53.5a-b	100g-k	68.2d-s	19.4c-u	80.4b-r	11.15f-i	0.505l-m	21.835n-q	17.830n-z	4381.6a-g
17	49-j	103.5b-d	84.6a-i	17.5k-x	55.9t-z	12.1c-d	0.71i-j	30.55x-z	19.625e-q	3744.9b-p
18	53a-c	102c-g	65.7f-w	18.8f-v	64.2n-z	9.1q-s	0.515l-m	34.945s-u	13.680h-l	2549.4o-v
19	48g-l	95.5p-t	63.1j-w	20.6b-r	70.50h-z	13.15 b	0.705i-j	29.1y-z	18.735g-v	4528.4a-f
20	49e-j	101.5d-h	65.6g-w	22.9a-j	66.1l-z	9.05q-s	0.55k-m	39.855o-p	15.650v-z	2278.0r-v
21	49e-j	102c-g	85.2a-h	21b-o	69.6h-z	10.05l-o	0.61k-l	21.540o-q	18.020n-z	3279.0f-t
22	48g-l	93.5 t	47.8t-w	23.5a-i	74.2c-x	12c-e	1.1b-c	26.745d-i	14.925b-l	2253.1s-v
23	47i-l	98.5j-n	64.5i-w	20.6b-r	75c-w	12c-e	0.7i-j	33.715t-v	14.060g-l	3953.0a-n
24	47.5h-l	98.5j-n	67.3e-t	22.5a-l	80.9b-q	11.05g-j	0.81g-h	51.22d-i	14.680d-l	3023.5h-u
25	46.5j-l	96.5n-r	80.4a-j	17.2m-x	59.6p-z	11.9c-f	0.605k-l	50.8e-i	21.165b-m	3303.8f-t
26	49.5d-i	94s-t	51.3r-w	22.2a-m	69.9h-z	11.15f-i	0.72g-j	20.725q	15.275a-y	3235.9f-t
27	48g-l	95q-t	60.8j-w	18.9f-v	68.5i-z	10.05l-o	0.65i-k	30.86w-y	23.385a-c	3689.5b-p
28	48.5f-k	97.5l-p	78.3b-m	17.8j-x	68i-z	13.1 b	0.65i-k	24.59h-m	19.270f-t	2634.2n-v
29	50.5c-g	102.5b-f	79.9a-k	18.5g-w	61.7o-z	12.05c-d	1c-d	30x-z	17.385p-z	2853.9j-v
30	53.5a-b	102c-g	59.9k-w	20.4b-r	80.9b-q	12.1c-d	0.61k-l	30.89w-y	15.430a-y	3215.8f-t
31	53.5a-b	103b-e	72.3c-q	18.9f-v	55.4t-z	11.1g-i	0.605k-l	27.380c-f	16.465r-z	4128.9a-k
32	45.5l	97.5l-p	62.7j-w	15.4r-x	56.3t-z	10l-o	0.6k-l	33.2u-v	22.51a-e	4039.4a-m
33	49.5d-i	97.5l-p	58.7m-w	18.4h-w	69.3h-z	10.1l-o	0.6k-l	29.775x-z	17.400p-z	2827.1k-v
34	46.5j-l	99.5h-l	68.8d-r	23.2a-i	70.4h-z	11.05g-j	0.5l-m	27.04c-g	16.825q-w	2525.7o-v
35	51a-f	95q-t	66.3f-u	24.25a-e	82.7b-o	11.1g-i	0.605k-l	29.89x-z	17.210p-z	3946.3a-n
36	47i-l	98k-o	69.3d-r	27.4a	91.4a-h	10.05l-o	0.705i-j	37.025q-s	17.670p-z	3088.0g-u
37	51.5a-e	101e-i	64.1j-w	18.7g-v	73.4e-y	12.05c-d	0.61k-l	35.85s-u	18.530h-w	3785.0b-p
38	49.5d-i	97m-q	63.00j-w	19.9c-u	54.6x-z	9.1q-s	0.705i-j	43.715m-n	17.735o-z	3430.1c-s
39	50.5c-g	99.5h-l	58.9m-w	21.5b-n	66.7l-z	13b	0.5l-m	53.115b-d	16.805q-w	4345.0a-h
40	48g-l	96.5n-r	55.25q-w	22.7a-k	90a-j	11.15f-i	1.2a-b	50.05f-j	13.690h-l	3231.5f-t
41	51.5a-e	101.5d-h	45.65v-w	24.5a-c	98a-b	11g-j	0.5l-m	49.75h-j	13.610i-l	2811.1k-v
42	47i-l	95q-t	65.6g-w	20.2b-s	63.8n-z	12.1c-d	0.705i-j	55.55a	22.045a-f	3295.0f-t
43	49.5d-i	98k-o	60.4j-w	18.4h-w	67.9j-z	10.9h-k	0.515l-m	50.705e-i	20.070d-p	5263.7a
44	47.5h-l	95.5p-t	48.4s-w	18.4h-w	74.5c-w	14.05a	0.505l-m	41.455n-o	50.705a	4682.2a-e
45	47.5h-l	94s-t	60.55j-w	12.9x	50.5z	12.1c-d	0.605k-l	55.03a-b	18.205l-z	2691.2m-v
46	48g-l	94s-t	57.45w	17.1m-x	55u-z	11.75d-g	0.7i-j	23.91j-n	18.155m-z	3907.9b-n
47	46.5k-l	95.5p-t	52.85q-w	19.6c-u	73.6d-y	9.5n-q	1.25a	51.415d-h	21.620a-h	3412.1c-s
48	48.5f-k	97m-q	57.7n-w	17.5k-x	63.2n-z	12.55b-c	0.61k-l	42.865m-n	21.350a-k	4691.4a-d
49	50d-h	96.5n-r	64.85hw	22.57a-l	89.2a-k	11.95c-e	0.845e-g	36.995q-s	15.305a-y	3665.7b-p
50	50.5c-g	102c-g	69.8c-r	21.1b-o	96.6a-c	11.25e-i	0.65i-k	23k-q	15.705v-z	3668.0b-p
51	52a-d	99.5h-l	53.8q-w	17.5k-x	54.5x-z	12.15c-d	0.71i-j	30.105x-z	16.250t-z	4040.7a-m
52	48.5f-k	99i-m	63.3j-w	17m-x	65.7m-z	11.05g-j	0.505l-m	34.93s-u	15.670v-z	3114.2g-t
53	49e-j	99.5h-l	72.2c-q	17.4l-x	76.4b-v	11.1g-i	0.705i-j	25.000g-l	18.410i-x	3608.8b-r
54	49.5d-i	101.5d-h	69.95c-r	18.3i-w	61.2o-z	12.05c-d	0.6k-l	24.52i-m	16.325s-z	4242.6a-i
55	47i-l	96.5n-r	70.4c-r	15.4r-x	62.9n-z	10.15k-n	0.5 m	38.94p-q	15.685v-z	2023.6t-v
56	47i-l	97.5l-p	62.4j-w	19.4c-u	54.1x-z	8.05 t	0.55k-m	23.845j-n	16.570q-z	1751.8u-v
57	49e-j	97.5l-p	67.6d-t	20.9b-o	67.9j-z	9.05q-s	0.515l-m	27.06c-g	19.530e-r	3868.6b-o
58	46.5k-l	97m-q	68.6d-s	17m-x	64.4n-z	10.05l-o	0.515l-m	53.38a-d	23.060a-d	4800.0a-b
59	48g-l	99.5h-l	90.1a-c	16.2o-x	66.3l-z	13b	0.7i-j	34.14t-v	19.505e-r	4110.9a-k
60	50.5c-g	96.5n-r	68d-t	19.7c-u	57.2s-z	10.1l-o	0.605k-l	23.155k-o	18.545h-w	4218.5a-i

TABLE 4: Continued.

Landraces	DTF	DTM	PH	NPP	NSP	PL	PW	HI	HSW	YLD
61	47.5h-l	101.5d-h	77.5b-o	22.2a-m	81.6b-p	10.05l-o	0.75f-i	25.6e-j	18.695g-w	2249.1s-v
62	49.5d-i	95.5p-t	51.55r-w	20.8b-p	88.4a-l	8.55s-t	0.8e-h	50.19f-j	12.945k-l	3031.7g-u
63	45.5l	94.5r-t	57.9n-w	20.2b-s	62.3n-z	13.05 b	0.61k-l	27.625b-e	23.975a-b	3200.7f-t
64	49.5d-i	96.5n-r	54.55q-w	19.8c-u	90.4a-i	10.65k-m	0.805e-h	24.635h-m	14.270f-l	2753.5l-v
65	49e-j	94.5r-t	58.05m-w	20.9b-o	77.1b-u	8.15 t	1.105b-c	26.65d-i	13.000j-l	4197.6a-j
66	47i-l	97m-q	66.5e-u	20.1b-t	53.6x-z	10.1l-o	0.515l-m	23.77j-o	16.690q-z	3346.7d-t
67	51.5a-e	100g-k	58.7m-w	22.6a-l	77.2b-u	8.6r-t	0.705i-j	52.72c-e	14.830c-l	3238.1f-t
68	47.5h-l	115.5a	70.9c-r	24.3a-d	72.56f-z	10.05l-o	0.61k-l	26.845c-h	19.230f-t	2284.2q-v
69	49.5d-i	95q-t	70.3c-r	20.7b-q	89.3a-k	9.35o-r	0.85e-f	29.845x-z	16.045u-z	3419.2c-s
70	47i-l	99i-m	66.6e-u	19.2d-u	48.8a-c	12.15c-d	0.61k-l	28.885y-z	17.680p-z	3054.0g-u
71	47i-l	96.5n-r	65.55g-w	17.2m-x	69.6h-z	9.05q-s	0.505l-m	29.745x-z	21.355a-k	3276.9f-t
72	50.5c-g	97.5l-p	94a-b	14.75u-x	66.9k-z	10.05l-o	0.805e-h	38.43p-q	17.885n-z	3385.2c-s
73	47.5h-l	100g-k	66.6e-u	16.2o-x	51.9x-z	12.05c-d	0.515l-m	25.25f-k	15.810u-z	3155.2g-t
74	47i-l	98k-o	79.4a-l	13.8v-x	57.6s-z	9.05q-s	0.7i-j	33.11u-w	20.780c-o	3156.5g-t
75	50.5c-g	97m-q	69.1d-r	17.9j-x	68.4i-z	12c-e	0.6k-l	35.88r-t	18.835g-u	3570.3b-s
76	48g-l	99i-m	58.6m-w	19.6c-u	59.6p-z	11.15f-i	0.71i-j	52.07c-g	15.170a-z	3846.4b-o
77	48g-l	95.5p-t	71.5c-r	16.2o-x	58.8q-z	11.05g-j	0.605k-l	28.165a-d	18.715g-w	3002.0h-u
78	48g-l	104b-c	86.8a-e	13.3w-x	46.9b-c	11.1g-i	0.61k-l	42.13m-o	21.285a-l	3475.2b-s
79	47i-l	97.5l-p	54.7q-w	20.3b-s	79.2b-s	9.1q-s	0.505l-m	49.83g-j	20.840c-n	3244.0f-t
80	47.5h-l	99i-m	67.3e-t	19.9c-u	56.8s-z	11.15f-i	0.65i-k	25.59e-j	16.100u-z	2248.0s-v
81	50d-h	97m-q	59.3l-w	18.6g-v	70.3h-z	8.05 t	0.55k-m	22.365m-q	18.310j-z	2814.5k-v
82	51.5a-e	101e-i	87.7a-d	18.3i-w	71.57g-z	10l-o	0.6k-l	22.805l-q	17.245p-z	3371.6c-t
83	48.5f-k	96.5n-r	70.4c-r	21.2b-o	90.1a-j	10.05l-o	0.91d-e	53.8a-c	16.730q-z	3503.6b-s
84	49e-j	101.5d-h	70c-r	17.2m-x	59.1q-z	9.05q-s	0.605k-l	22.390m-q	18.230l-z	3337.8e-t
85	47i-l	97.5l-p	60k-w	18.3i-w	57.9s-z	10.05l-o	0.605k-l	38.02p-r	21.365a-j	3171.4g-t
86	50d-h	96.5n-r	66f-v	18.4h-w	51.7y-z	11.1g-i	0.605k-l	43.405m-n	18.265k-y	3727.4b-p
87	47.5h-l	97.5l-p	53.2q-w	15.4r-x	55.9t-z	10.15k-n	0.65i-k	31.945v-x	21.415a-i	3251.6f-t
88	48g-l	97.5l-p	85.7a-g	19.5c-u	67.8j-z	10.05l-o	0.515l-m	30.12x-z	19.400f-s	4346.9a-h
89	47.5h-l	94.5r-t	70.1c-r	20c-u	53.7x-z	12.05c-d	0.6k-l	34.91s-u	21.700a-g	4688.7a-e
90	45.5l	95q-t	46.9u-w	20.8b-p	67.2k-z	10.05l-o	0.6k-l	27.22c-g	23.520a-c	3535.3b-s
91	49e-j	97m-q	62.5j-w	22.6a-l	108a	10.7k-l	0.7i-j	48.16j-k	16.195t-z	3308.7f-t
92	46.5k-l	94s-t	45.5w	17.8j-x	66.3l-z	11.1g-i	0.505l-m	40.215o-p	24.160a-b	4709.0a-c
93	46.5j-l	102.5b-f	76.4b-p	23.7a-g	93.4a-g	12c-e	0.8e-h	24.990g-l	14.520e-l	1642.1v
94	50d-h	97m-q	54.2q-w	14.9t-x	51.2y-z	10.05l-o	0.705i-j	24.105j-n	16.815q-w	2933.3i-v
95	50.5c-g	97.5l-p	77.8b-o	20.4b-r	96a-d	10.3k-m	0.9d-e	46.025k-l	15.120a-l	2728.0m-v
96	48g-l	96o-s	79.9a-k	15.6p-x	65.1n-z	9.9m-p	0.605k-l	29.775x-z	22.005a-f	3517.0b-s
97	50d-h	103b-e	76.2b-p	19.5c-u	66l-z	12.95 b	0.725f-j	23.425j-p	17.080p-z	3302.0f-t
98	47i-l	97m-q	59.4l-w	15.1s-x	50.4z	12.05c-d	0.75f-i	23.34j-p	17.985n-z	2483.3p-v
99	50.5c-g	96o-s	59.25l-w	16.5n-x	51.7y-z	10.15k-n	0.605k-l	22.825l-q	16.395s-z	2738.9l-v
100	45.5l	96.5n-r	51.2r-w	17.1m-x	66.6l-z	11.1g-i	0.505l-m	52.15c-f	23.475a-c	2946.6i-v
Mean	48.83	98.225	66.1486	19.2817	68.8923	10.9225	0.666749	34.5544	17.90786	3367.471
min	45.1973	93.5	45.5	12.9	38.6	8.05	0.4452	20.725	12.405	1642.08
Max	54.0298	115.5	99.26	27.4	108	14.05	1.2401	55.55	24.32	5263.66
LSD (0.05%)	2.54	2.2	20.39	5.29	22.42	0.77	0.12	2.28	3.09	1351.9
CV%	2.61	1.12	15.49	13.81	16.36	3.55	9.65	3.32	8.67	20.17

improvement through selection could be possible in the accessions. Lad et al. [37] reported high heritability values for days to 50% flowering and plant height. Yonas [38] also reported high heritability for days to 50% flowering and 100-seed weight. In this study, moderate heritability values were recorded for the number of plant heights (36.42), number of pods per plant (33.75), number of seeds per plant (36.75), and yield per hectare (32.63). For these traits, selecting superior individuals based on heritability estimates leads to genetic improvement. This result is in agreement with the report [39]. However, selecting superior individuals based on heritability estimates alone may not lead to genetic improvement; hence, heritability

estimates along with genetic advances would be more useful in predicting the effectiveness of selecting the best individuals [17].

3.4. Genetic Advance (GA) and Genetic Advance as a Percentage of Mean (GAM). The value of expected genetic advance and advance as a percentage of the mean is presented in Table 3. High values of GAM indicate additive gene action, whereas low values indicate non-additive gene action [40]. In this study, the genetic advance as a percentage of the mean ranged from 5.73 days to 90% maturity to 58.75% for the harvest index (Table 3). According to Johnson et al. [41],

genetic advance as a percent of mean categorized as low (<10), moderate (10 to 20), and high (above 20). Based on these values, high genetic advance as a percentage of mean was found for pod length (20.9), pod width (33.32), harvest index (58.750), and 100-seed weight (21.69) (Table 3). The selection based on these traits will improve the performance of the landraces for the traits. Lad et al. [37] reported high GAM for pod length and pod width. Moderate GAM was found for plant height, the number of pods per plant, and the number of seeds per plant. Low GAM was obtained for days to 50% flowering (6.28) and days to 90% maturity (5.73) (Table 3). This low estimate of genetic advance as a percentage of the mean arises from a low estimate of phenotypic variance and heritability. High heritability estimates along with the high genetic advance are usually more helpful in predicting gain under selection than heritability estimates alone [17]. This would probably indicate additive gene action for the inheritance of these traits and simple selection would be effective for improving these traits. Lad et al. [37] reported high GAM coupled with high heritability for pod length, pod width, harvest index, and yield.

3.5. Phenotypic and Genotypic Correlation

3.5.1. Phenotypic and Genotypic Relationships of Grain Yield with Other Traits. Grain yield had a positive and significant association with 100-seed weight and pod length ($rg = 0.492^{**}$ and $rg = 0.282^{**}$) at the genotypic level, respectively (Table 5). At the phenotypic level, it had a positive and significant correlation with 100-seed weight ($rp = 0.294^{**}$) and pod length ($rp = 0.153^{*}$). Generally, a positive and significant correlation of different traits with grain yield indicates the presence of component interactions in which conditioning in one trait will influence another traits. Kassaye [28] reported similar results in the common bean that grain yield significantly correlated with pod length. Additionally, Ejigu et al. [42] reported a significant and positive association between thousand seed weights and grain yield in common bean. Further, the authors in [27, 43–45] reported a similar result in that yield had a significant positive correlation with 100-seed weight. This relationship is caused by genetic and non-genetic factors. Kassa et al. [46] also reported a significant and positive association of 100-seed weight with grain yield in common beans.

3.5.2. Phenotypic and Genotypic Correlations among Yield-Related Traits. At phenotypic level, days to 50% flowering had a significant and positive association with hundred seed weight ($rp = 0.362^{**}$), days to maturity ($rp = 0.269^{**}$), and the number of seeds per plant ($rp = 0.204^{**}$) (Table 5). The association of those characters shows that genotypes with early flowering would tend to mature early and genotypes that take longer to mature also have taller plant height, whereas it had a negative and significant association with harvest index ($rp = -0.182^{**}$ and $rg = -0.223^{*}$). This result agrees with the findings of Barecha and Ejigu et al. [25, 42]. According to Laura et al. [47], days to 50% flowering were

positively correlated with days to maturity, pod length, and the number of seeds per pod. Genotypically days to 50% flowering had significant and positive correlation with days to 90% maturity ($rg = 0.311^{**}$) and number of seed per plant ($rg = 0.269^{**}$). It also had a negative correlation with the harvest index ($rg = -0.223^{*}$) and hundred seed weight ($rg = -0.688^{**}$) (Table 5). The current result agrees with the previous works reported in [29, 39, 48, 49]. Similarly, Sadeghi et al. [44] reported a similar significant negative correlation between days and 50% flowering and harvest index.

The result further indicated that days to 90% maturity positively correlated with plant height ($rp = 0.317^{**}$) and hundred seed weight ($rp = -0.147^{*}$) at the phenotypic level; similarly, it had a significant positive correlation with plant height ($rg = 0.557^{**}$) at genotypic level. This suggests that genotypes with taller plant height took many days for maturity to produce the maximum number of seeds per plant. However, the seeds were small. The current finding is supported by Loko et al. [50] who reported a positive and significant association between days and flowers with days to 50% flowering and the number of seeds per plant. Plant height negatively correlated with harvest index ($rp = -0.1699^{*}$) and pods per plant ($rg = -0.247^{*}$) at phenotypic level, whereas it had a negative association with harvest index ($rg = -0.258^{**}$) at genotypic level. This result concurred with those reported in previous studies, in which plant height correlated with the number of pods per plant and harvest index [28, 38, 42, 43]. The number of pods per plant was positively and significantly associated with the number of seeds per plant ($rp = 0.637^{**}$), pod width ($rp = 0.1948^{**}$), and hundred seed weight ($rp = -0.283^{**}$) at genotypic level.

Number of pod per plant exhibit positive and significant correlation with number of seed per pod (0.629) and pod width (0.389) (Table 5). The correlation between seed per pod and the number of pods per plant is interesting to the breeder because this character is relatively easy to determine the yield substantially. This result agrees with the reports of several scholars [27, 43–45]. The number of seeds per plant positively correlated with pod width ($rp = 0.282^{**}$) and seed weight ($rp = -0.271^{**}$) at phenotypic level and significantly correlated with pod width ($rg = 0.425^{**}$) and hundred seed weight ($rg = -0.511^{**}$) at genotypic level. The pod width correlated with hundreds of seed weights ($rp = -0.324^{**}$) and genotypically correlated with hundreds of seed weights ($rg = -0.370^{**}$). Zewdu [27] reported the same scenario.

3.6. Path Coefficient Analysis. Path analysis is the breakdown of correlations in the direct and indirect effects of independent characters and explanatory variables on a basic main variable and its estimations obtained by regression equations, in which the variables are previously determined [50]. Genotypic path coefficient analysis for yield and yield component of common bean is revealed in Table 6. The 100-seed weight that had a significant genotypic correlation with yield had the highest direct effect (0.294). This justifies that the correlation explains

TABLE 5: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients of 100 common bean genotypes were tested at Jimma (2020/021).

Character	DTF	DTM	PH	NPP	NSP	PL	PW	HI	HSW	YLD
DTF	1	0.269**	0.091	0.106	0.204**	0.016	0.028	-0.18**	0.362**	0.102
DTM	0.311**	1	0.317**	0.096	0.029	-0.018	-0.129	-0.134	-0.147*	-0.135
PH	0.184	0.557**	1	-0.117	-0.051	-0.006	-0.03	-0.169*	-0.007	0.132
NPP	0.074	0.153	-0.247*	1	0.637**	0.004	0.194**	-0.02	-0.28**	-0.001
NSP	0.269**	0.032	-0.072	0.629**	1	0.038	0.28**	0.093	-0.27**	-0.009
PL	0.013	-0.009	0.018	0.008 ^{NS}	0.071	1	0.008	-0.003	-0.324	0.153*
PW	0.004	-0.187	0.038	0.389**	0.425**	0.015	1	0.092	0.324**	-0.101
HI	-0.223*	-0.146	-0.258**	-0.049	0.131	-0.008	0.097	1	0.088	0.083
HSW	-0.688**	-0.177	0.018	-0.617**	-0.51**	0.045	-0.37**	0.117	1	0.294**
YLD	0.124	-0.213*	-0.292**	-0.396**	-0.145	0.282**	-0.159	0.157	0.492**	1

** = highly significant, * = significant, Ns = non-significant, DTF = date to flowering, DTM = date to maturity, PH = plant height, NPP = number of pods per plant, NSD = number of seeds per pod, PL = pod length, PW = pod width, HI = harvest index, HSW = hundred seed weight, and GYD = grain yield.

the true relationship and that direct selection through this trait is effective. Another direct effect was recorded from the number of pods per plant (0.025) and plant height (0.005). The results agreed with Wright [51] who reported the positive direct effect of the number of pods per plant and plant height on grain yield. In this respect, many researchers have found positive direct effects on yield for plant height [42, 43, 52, 53]. However, the trait days to 90% maturity and pod length had a negative direct effect on grain yield. These negative direct effects will not be considered for selection in a breeding program [15].

At the phenotypic level, the highest direct effect was exerted by 100-seed weight (Table 7). The correlation it had with yield was positive and significant. This indicates the true relationship between the two traits. Thus, 100-seed weight could be considered in indirect selection criteria for yield improvement. A similar finding was reported in [54]. The residual effect at genotypic path coefficient was 51% which suggests that the traits included in path analysis explain 49% of the variation in yield. In this regard, Johnson et al. [41] found high residual effects at both phenotypic (45.82%) and genotypic (51.3%) levels.

3.7. *Cluster Analyses.* Clustering is the partition of data into a group of similar or dissimilar data points and each group is a set of data points called clusters [55]. The more divergent the two genotypes are, the more will be the probability of improvement through selection and hybridization. Hence, to develop a sound hybridization program, the genotypes must be genetically divergent, especially for quantitative characters that contribute toward yield [56]. The distribution of accessions into 7 clusters and one solitary is presented in Table 8 and Figure 1. Cluster II was the largest containing 33 genotypes followed by cluster IV which consists 19 genotypes. Whereas cluster I and III consist 16 genotypes, Cluster V consists 7 genotypes, cluster VI consists 6 genotypes, cluster VII consists 2 genotypes, and one solitary (un-grouped genotype). These indicate considerable variability among the genotypes under study. Kassaye [28] grouped 114 common bean genotypes into nine clusters, which

TABLE 6: Genotypic direct and indirect effects of different traits on grain yield.

	DTM	PH	NPP	PL	HSW	rg
DTM	-0.2719	-0.0027	0.16896	-0.05578	-0.0522	-0.2136*
PH	-0.4877	0.00537	0.0942	0.08987	0.00531	-0.29294*
NPP	0.12062	0.0024	0.02594	-0.3634	-0.1817	-0.39605*
PL	-0.0092	0.28342	-0.0016	-0.0031	0.01322	0.28272*
HSW	-0.0088	0.01275	-0.03	0.22445	0.29406	0.49247*

Residual = 0.51, NPP = number of pod per plant, PL = pod length, HSW = hundred seed weight, HI = harvest index, rg = genotypic correlation coefficient.

TABLE 7: The phenotypic direct and indirect effects of different traits on grain yield.

	PL	HSW	rp
PL	0.14038	0.01352	0.154
HSW	0.00660	0.28770	0.294

Residual = 89.

makes them divergent. Furthermore, Getachew [57] grouped 36 common bean accessions into five clusters.

Accessions in clusters CI and CII were characterized by medium mean values for all traits (Table 9). Accession in cluster CIII is characterized by the lowest mean value of the number of seeds per plant. Accessions in cluster CIV are characterized by the highest mean values of days to 50% flowering and pod width. Accessions in cluster CV are characterized by the lowest value of days to 90% maturity and the highest mean values of pod length and 100-seed weight. Accession in cluster CVI is characterized by the highest value of days to 90% maturity. Accessions in CVII are characterized by the lowest mean value of days to 50% flowering, pod length, harvest index, 100-seed weight, and yield, whereas the highest mean values of plant height, the number of pods per plant, and the number of seeds per plant are recorded.

3.8. *Genetic Distance Analysis.* Cluster formation and finding out intra and inter-cluster divergence provide a basis for selecting genetically divergent parents and it may be useful to produce crosses between genotypes belonging to

TABLE 8: The cluster of 100 common bean genotypes based on the qualitative traits under study (2020/21).

Cluster	No. of genotypes	Proportion (100%)	Name of genotypes
1	16	16	P#264, P#1250, P#1074, P#1187, P#1306, P#1212, P#1070, P#1182, P#1063, P#1107, P#916, P#1083, P#945, P#999, P#1283, P#989
2	33	33	P#872, P#1027, P#1097, P#1285, P#1038, P#985, P#1275, P#831, P#1050, P#1086, P#1158, P#40, P#1316, P#1063, P#1179, P#145, P#133, P#1055, P#882, P#1103, P#934, P#1310, P#1211, P#1279, P#1079, P#859, P#1042, P#1154, P#931, P#93, P#1150, P#1127, P#1117
3	16	16	P#1176, P#1072, P#1046, P#14, P#1298, P#772, P#1268, P#769, P#967, P#984, P#1049, P#1094, P#901, P#1227, P#1102, P#760, P#772
4	19	19	P#909, P#1315, P#932, P#1157, P#864, P#1078, P#1043, P#1300, P#1124, P#1314, P#989, P#1078, P#1309, P#941, P#1095, P#1071, P#1270, P#811, P#13
5	7	7	P#1247, P#1092, P#861, P#990, P#763, P#58, P#857
6	6	6	P#1232, P#1057, P#1139, P#906, P#986, P#157
7	2	2	P#82, P#1124
8	1	1	P#1077

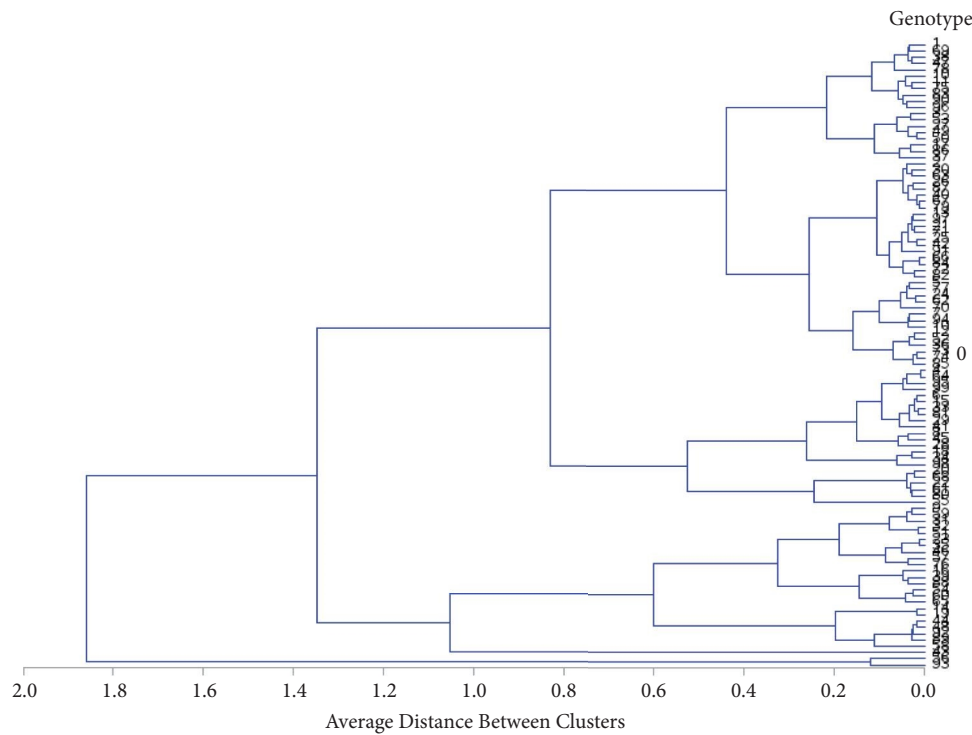


FIGURE 1: Dendrogram of eight clusters of traits for 100 genotypes tested at Jimma during 2020/21.

the clusters separated by large estimated distances [58]. This finding showed the existence of an accepted difference among all clusters, and the genetic divergences between all pairs were highly significant (0.01), except between clusters CII and CIV (Table 10). Regarding the inter-cluster distance, the maximum distance was found between cluster CVII and CV ($D^2 = 616.64$), followed by CVI and CV ($D^2 = 423.83$). The presence of high inter-cluster distance between different clusters indicates wider genetic diversity (Table 10), which creates an opportunity for genetic recombination through hybridization, which is the basis for the identification of important recombinants in the segregating population. This result indicate that, crossing the genotype of cluster VII and

V might be rewarding for improving the common bean yield by developing superior inbred lines from the segregated generations. According to [59–61], the cross between genotypes with maximum genetic distance would bring maximum heterosis (Table 10).

3.9. Principal Component Analysis (PCA). Yield is a polygenic trait that is directly or indirectly influenced by several other traits. Therefore, a technique must identify and prioritize the important traits by minimizing the number of traits for effective selection and genetic gain. PCA is a well-known data reduction technique that identifies the

TABLE 9: Mean value of 10 traits for the eight clusters of 100 common bean genotypes.

Traits	Clusters						
	I	II	III	IV	V	VI	VII
DTF	49.35	48.45	49.35	49.64**	47.53	47.78	46.42*
DTM	97.97	98.11	98.28	98.18	96.28*	101.25**	100
PH	63.58	66.31	67.59	68.29	61.61*	66.58	69.4**
NPP	19.11	19.12	19.20	18.91	19.33	21.36	21.55**
NSP	68.17	69.63	65.35*	71.33	67.18	69.03	73.75**
PL	10.94	10.82	11.06	10.83	11.99**	10.41	10.03*
PW	0.65	0.67	0.64	0.71**	0.59	0.67	0.69
HI	32.53	37.21	32.19	33.78	38.13	30.59	24.42*
HWS	16.76	17.79	17.52	18.54	21.64**	16.71	15.55*
YLD	2718.43	3182.44	4103.85	3576.37	4660.81**	2222.65	1696.94*

* = lowest values, ** = highest values, DTF = days to 50% flowering, DTM = days to 90% maturity, PH = plant height, NPP = number of pods per plant, NSP = number of seeds per plant, PL = pod length, PW = pod width, HSW = hundred seed weight, HI = harvest index, and YDKPHA = yield per hectare tone per hectare.

TABLE 10: Pair-wise generalized squared distance (D²) among 100 common bean genotypes in seven clusters (2020/21).

Cluster	I	II	III	IV	V	VI	VII	VIII
I	—	16.41*	135.84**	49.17**	269.62**	20.53**	75.75**	465.44**
II		—	59.44**	9.73 ^{NS}	155.03**	68.28**	156.44**	309.78**
III			—	23.91**	25.83**	250.97**	403.08**	101.6**
IV				—	91.48**	126.72**	240.87**	216.72**
V					—	423.83**	616.64**	31.25**
VI						—	19.82**	663.56**
VII							—	901.22**
VIII								—

* and ** indicate significant at 0.05 and highly significant at 0.01 probability levels, respectively.

TABLE 11: The principal component of 100 common bean genotypes in five components (2020/21).

Traits	PC							
	PC1	PC2	PCA3	PCA4	PCA5	PCA6	PC7	PC8
DF	-0.28	-0.08	0.61	0.08	0.1	-0.21	0.65	-0.12
DM	0.36	0.34	-0.07	-0.09	-0.39	0.18	0.43	0.52
PH	0.18	0.52	0.08	0.26	0.23	0.34	0.15	-0.55
NPP	0.045	0.48	0.12	-0.17	0.66	-0.1	-0.14	0.35
NsPS	0.47	-0.22	0.13	0.46	0.1	-0.14	-0.25	-0.08
PL	0.48	-0.26	0.15	0.33	0.18	-0.1	0.17	0.28
PW	0.05	-0.01	-0.72	0.09	0.21	-0.39	0.46	-0.19
HI	0.29	-0.28	0.11	-0.64	0.3	-0.18	0.07	-0.10
HWS	-0.06	-0.42	-0.15	-0.03	0.32	0.76	0.22	0.06
YLD	-0.46	-0.052	-0.09	0.39	0.26	-0.1	-0.02	0.40
Eigenvalue	2.28	1.62	1.22	2.54	2.75	2.66	2.56	2.65
% of the total variance explained	22.75	16.23	12.22	9.89	9.55	8.92	6.62	6.12
The cumulative percentage of total variance explained	22.75	38.98	51.2	61.09	70.64	79.56	86.18	92.3

DF = days to 50% flowering, DM = days to 90% maturity, PH = plant height, NPP = number of pods per plant, NSP = number of seeds per plant, PL = pod length, PW = pod width, HSW = hundred seed weight, HI = harvest index, and YDTPHA = yield per hectare tone per hectare.

minimum number of traits, which contributes to maximum variability [62]. The first eight principal components with eigenvalues greater than one altogether explained about 92.3% of the total variation among the 100 common bean genotypes based on 10 quantitative traits (Table 11). The variation in PC1 (22.75%) was chiefly due to pod length (0.4790), seeds per pod (0.47), days to 90% maturity (0.360), and yield (-0.45). The current finding agrees with the former studies that reported the maximum contribution of 100-seed weight, seeds/plant, and pod length [63–65].

The second principal component accounts for about 16.22% of the total variation. The major contributing traits to the variation were plant height (0.519), the number of pods per plant (0.476), seed weight (-0.422), and pod length (-0.2652). The third principal component accounted for 12.22% of the total variation. The traits that had a major contribution were days to 50% flowering (0.612) and pod length (0.145), pod width (-0.71), and hundred seed weight (-0.15). The character contributing to the maximum loading for variation should be given greater emphasis. The authors

in [26, 37] also used principal component analysis in the genetic variability study of common beans. The fourth principal component accounts for 9.89% of the total variation, and traits that contribute to this component were the number of seeds per pod (0.45) and yield (0.38), harvest index (−0.63), and the number of pods per plant (−0.17). The fifth principal component accounts 9.55% of the total variation. The contributing traits for this PC were the number of seeds per pod (0.66), hundred seed weights (0.31), and days to 90% maturity (−0.39). Positive and negative loadings show variation. The sixth PC contributes to 8.92% of the total variation. This study showed that Ethiopian common bean germplasm showed variation for the characters studied. This trait diversity evident among the accessions suggests the presence of opportunities for genetic improvement through selection directly from the accessions and/or selection of diverse parents for hybridization programs and conservation of the germplasm for further usage. Such an existence of broad agro-morphological genetic diversity among common bean germplasm is in agreement with the results of previous studies [1, 30, 34, 59, 60].

4. Summary and Conclusions

The present study indicated the presence of genetic variability among the tested genotypes which can be exploited in further common bean improvement. The presence of variability among the tested genotypes for quantitative traits shows the chance of selecting parental genotypes to develop hybrid varieties. The top eight landraces, namely, P#1247, P#1092, P#1077, P#861, P#990, P#763, P#58, and P#857, performed better than all other landraces. Therefore, for common bean yield improvement, direct selection of those genotypes will be rewarding. In general, the presence of genetic variability creates enormous opportunities for the improvement of common bean genotypes. Therefore, considering the above findings, grain yield improvement could be achieved through a direct selection of high-yielding genotypes or by crossing genotypes from a different cluster. However, this study was conducted for one season at one location. Thus, further studies should be conducted over locations and seasons to make more reliable conclusions and recommendations. Additionally, this genetic variability study of the present genotypes should be supported with molecular analysis techniques.

Data Availability

The data supporting the findings of this study are available on request from the corresponding author.

Conflicts of Interest

The authors declare that they have no conflicts of interest regarding the publication of this paper.

References

- [1] A. Asfaw, M. W. Blair, and C. Almekinders, "Genetic diversity and population structure of common bean (*Phaseolus vulgaris* L.) landraces from the East African highlands," *Theoretical and Applied Genetics*, vol. 120, pp. 1–12.
- [2] G. F. Freytag and D. G. Debouck, *Taxonomy, Distribution, Andecology of the Genus Phaseolus (Leguminosae-Papilionoideae) in North America, Mexico and Central America*, Journal of the Botanical Research Institute of Texas (BRIT Press), Ft. Worth, TX, 2002.
- [3] J. J. Ferreira, E. Álvarez, M. A. Fueyo, A. Roca, and R. Giraldez, "Determination of the outcrossing rate of *Phaseolus vulgaris* L. using seed protein markers," *Euphytica*, vol. 113, pp. 259–263, 2000.
- [4] R. C. Coelho, M. A. Faria, J. Rocha, A. Reis, M. B. P. P. Oliveira, and E. Nunes, "Assessing genetic variability in the germplasm of *Phaseolus vulgaris* L collected in Northern Portugal," *Scientia Horticulturae*, vol. 122, no. 3, pp. 333–338, 2009.
- [5] C. M. Paredes, V. V. Becerra, and J. U. Tay, "Inorganic nutritional composition of common bean (*Phaseolus vulgaris* L.) genotypes race Chile," *Chilean Journal of Agricultural Research*, vol. 69, no. 4, pp. 486–495, 2009.
- [6] Central Statistics Agency (Csa), vol. pp I, Central Statistics Agency, Addis Ababa, Ethiopia, Report on area and production of major crops, vol. 2016.
- [7] M. Kermah, A. C. Franke, S. Adjei-Nsiah, B. D. K. Ahiabor, R. C. Abaidoo, and K. E. Giller, "N₂-fixation and N contribution by grain legumes under different soil fertility status and cropping systems in the Guinea savanna of northern Ghana," *Agriculture, Ecosystems & Environment*, vol. 261, pp. 201–210, 2018.
- [8] D. W. Israel, "Investigation of the role of phosphorus in symbiotic dinitrogen fixation," *Plant Physiology*, vol. 84, no. 3, pp. 835–840, 1987.
- [9] Faostat, "Databases: soybean production and trade data," 2019, <https://www.fao.org/faostat/en/#data>.
- [10] H. S. Pereira, V. M. d. Almeida, L. C. Melo et al., "Influência do ambiente em cultivares de feijoeiro-comum em cerrado com baixa altitude," *Bragantia*, vol. 71, no. 2, pp. 165–172, 2012.
- [11] S. P. Singh and C. A. Urrea, "Inter-and intraracial hybridization and selection for seed yield in early generations of common bean *Phaseolus vulgaris* L." *Euphytica*, vol. 81, no. 2, pp. 131–137, 1995.
- [12] IBPGR, *Descriptors for Phaseolus Coccineus*, IBPGR, Rome, 1983.
- [13] O. Gómez, *Evaluation of Nicaraguan Common Bean (Phaseolus vulgaris L.) Landraces*, Doctor's dissertation, 2004.
- [14] G. W. Burton and E. H. Devane, "Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material¹," *Agronomy Journal*, vol. 45, no. 10, pp. 478–481, 1953.
- [15] R. K. Singh and B. D. Chaudhary, *Biometrical Methods in Quantitative Analysis*, Kalayani Publishers, New Delhi, India, 1985.
- [16] D. S. Falconer, *Introduction to Quantitative Genetics*, p. 438p, Editora Longman, London, 1989.
- [17] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of genetic and environmental variability in soybeans 1," *Agronomy Journal*, vol. 47, no. 7, pp. 314–318, 1955.
- [18] P. A. Miller, J. C. Williams, H. F. Robinson, and R. E. Comstock, "Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection¹," *Agronomy Journal*, vol. 50, no. 3, pp. 126–131, 1958.
- [19] P. Kashiani, G. Saleh, N. A. P. Abdullah, and S. N. Abdullah, "Variation and genetic studies on selected sweet corn-inbred

- lines," *Asian Journal of Crop Science*, vol. 2, no. 2, pp. 78–84, 2010.
- [20] J. R. Sharma, *Statistical and Biometrical Techniques in Plant Breeding*, New Age International, New Delhi, India, 1998.
- [21] D. R. Dewey and K. H. Lu, "A correlation and path-coefficient analysis of components of crested wheatgrass seed production 1," *Agronomy Journal*, vol. 51, no. 9, pp. 515–518, 1959.
- [22] SAS Institute Inc, *Statistical Analysis System*, Cary, North Carolina, USA, 2014.
- [23] M. C. Copper and G. W. Milligan, "The effect of error on determining the number of clusters proceeding of international workshop on data analysis, decision support and expert knowledge representation in marketing and related areas of research," *In Data, expert knowledge and decisions*, pp. 319–328, Springer, Berlin, Heidelberg, 1988.
- [24] P. C. Mahalanobis, *On the Generalized Distance in Statistics*, National Institute of Science of India, India, 1936.
- [25] G. Barecha, *Genetic Variability and Path Coefficient Analysis for Yield and Yield-Related Traits in Common Bean (Phaseolus vulgaris L.)*, Haramaya University, MSc Thesis, Haramaya University, Haramaya, Ethiopia, 2015.
- [26] A. Panchbhayia, D. K. Singh, and P. V. J. Verma, "Genetic analysis of French bean (*Phaseolus vulgaris* L.) germplasm through principal component analysis and D2 cluster analysis," *Journal of Pharmacognosy and Phytochemistry*, vol. 6, no. 3, pp. 537–542, 2017.
- [27] Z. Zewdu, "Evaluation of agronomic traits of different haricot bean (*Phaseolus Vulgaris* L.) lines in the Metekel zone, North Western part of Ethiopia," *Wudpecker Journal of Agricultural Research*, vol. 3, no. 1, pp. 39–43, 2014.
- [28] N. Kassaye, "Studies on genetic divergence in a common bean (*Phaseolus vulgaris* L.), Introductions of Ethiopia," Msc.thesis submitted to the school of graduate studies of Addis Ababa university in partial fulfillment Of the Requirements for the Degree of Master of Science in Applied Genetics (Biology), Addis Ababa University, Addis Ababa, pp. 1–109, 2006.
- [29] M. W. Blair, L. F. González, P. M. Kimani, and L. Butare, "Genetic diversity, inter-gene pool introgression and nutritional quality of common beans (*Phaseolus vulgaris* L.) from Central Africa," *Theoretical and Applied Genetics*, vol. 121, no. 2, pp. 237–248, 2010.
- [30] M. L. Burle, J. R. Fonseca, M. José del Peloso, L. C. Melo, S. R. Temple, and P. Gepts, "Integrating Phenotypic evaluations with a molecular diversity assessment of a Brazilian collection of common bean landraces," *Crop Science*, vol. 51, no. 6, pp. 2668–2680, 2011.
- [31] M. Kwak and P. Gepts, "Structure of genetic diversity in the two major gene pools of common bean (*Phaseolus vulgaris* L., Fabaceae)," *Theoretical and Applied Genetics*, vol. 118, no. 5, pp. 979–992, 2009.
- [32] F. K. Awan, Y. M. Khurshid, and O. Afzal, "Agro-morphological evaluation of some exotic common bean genotypes under rainfed conditions in Islamabad, Pakistan," *Pakistan Journal of Botany*, vol. 46, no. 1, p. 259, 2014.
- [33] O. Dennis, T. Phinehas, K. James et al., "The genetic diversity and population structure of common bean (*Phaseolus vulgaris* L.) germplasm in Uganda," *African Journal of Biotechnology*, vol. 13, pp. 2935–2949, 2014.
- [34] N. Gujaria-Verma, L. Ramsay, A. G. Sharpe et al., "Gene-based SNP discovery in tepary bean (*Phaseolus acutifolius*) and common bean (*P. vulgaris*) for diversity analysis and comparative mapping," *BMC Genomics*, vol. 17, no. 1, p. 239, 2016.
- [35] K. S. Dinesh, P. Kumar, and A. K. Bhardwaj, "Evaluation of agronomic management practices on farmers' fields under the rice-wheat cropping system in northern India," *International Journal of Agronomy*, vol. 2014, Article ID 740656, 2014.
- [36] H. F. Robinson, R. E. Comstock, and P. H. Harvey, "Estimates of heritability and the degree of dominance in corn 1," *Agronomy Journal*, vol. 41, no. 8, pp. 353–359, 1949.
- [37] D. B. Lad, N. Longmei, and U. M. Borle, "Studies on genetic variability, association of characters and path analysis in French bean (*Phaseolus vulgaris* L.)," *International Journal of Pure & Applied Bioscience*, vol. 5, no. 6, pp. 1065–1069, 2017.
- [38] M. G. Yonas, "Genetic diversity in speckled bean (*Phaseolus vulgaris* L.) genotypes in Ethiopia," *Journal of Plant Breeding and Crop Science*, vol. 9, no. 11, pp. 200–207, 2017.
- [39] S. Ahmad and Kalamuddin, "Correlation and path analysis for agromorphological traits in rajmash beans in Baramulla-Kashmir region," *African Journal of Agricultural Research*, vol. 8, no. 18, pp. 2027–2032, 2013.
- [40] P. Singh and S. S. Narayanan, *Biometrical Techniques in Plant Breeding*, p. 43, Kalyani Publishers, New Delhi, India, 1993.
- [41] E. Johnson, P. N. Miklas, J. R. Stavelly, and J. C. Martinez-Cruzado, "Coupling- and repulsion-phase RAPDs for marker-assisted selection of PI 181996 rust resistance in common bean," *Theoretical and Applied Genetics*, vol. 90, no. 5, pp. 659–664, 1995.
- [42] E. Ejigu, M. Wassu, and A. Berhanu, "Genetic variability, heritability and expected genetic advance of yield and yield-related traits in common bean genotypes (*Phaseolus vulgaris* L.) at Abaya and Yabello, Southern Ethiopia," *African Journal of Biotechnology*, vol. 17, no. 31, pp. 973–980, 2018.
- [43] A. Karasu and M. Oz, "A study on coefficient analysis and association between agronomical characteristics in a dry bean (*Phaseolus vulgaris* L.)," *Bulgarian Journal of Agricultural Science*, vol. 16, no. 2, pp. 203–211, 2010.
- [44] A. Sadeghi, K. Cheghamirza, and H. R. Dorri, "The study of morphoagronomic relationship in a common bean (*Phaseolus vulgaris* L.)," *Biharean Biologist*, vol. 5, no. 2, pp. 102–108, 2011.
- [45] A. Z. A. M. Negahi, M. R. Bihamta, Z. A. H. R. A. Negahi, and M. O. H. A. M. M. A. D. Alidoust, "Evaluation of genetic variation of some agronomical and morphological traits in the Iranian and exotic common bean (*Phaseolus vulgaris* L.)," *Agricultural Communications*, vol. 2, no. 3, pp. 22–26, 2014.
- [46] M. Kassa, W. Dagne, L. Dagnachew, and M. Firew, "Genetic variability of common bean (*Phaseolus vulgaris* L.) genotypes under sole and maize-bean cropping systems in Bako, Western Oromia, Ethiopia," *African Journal of Agricultural Research*, vol. 14, no. 7, pp. 419–429, 2019.
- [47] Laura Estelle Laboratory of Applied Entomology, Faculty of Sciences and Technology of Dassa (FAST-Dassa), National University of Sciences Technologies Engineering and Mathematics of Abomey (UNSTIM), BP 14 Dassa-Zoumé, Benin.
- [48] K. B. Bhushan, S. Jadli, O. Verma, and A. K. Goswami, "Plant characteristics correlation and path coefficient analysis of seed yield in exotic French bean (*Phaseolus vulgaris* L.) germplasm," *International Journal of Agriculture Sciences*, vol. 4, no. 2, pp. 667–669, 2008.
- [49] V. Kumar, S. Sharma, S. Kero et al., "Assessment of genetic diversity in common bean (*Phaseolus vulgaris* L.) germplasm using amplified fragment length polymorphism (AFLP)," *Scientia Horticulturae*, vol. 116, no. 2, pp. 138–143, 2008a.
- [50] E. Y. L. Laura, O. Azize, A. Arlette et al., "Morphological characterization of common bean (*Phaseolus vulgaris* L.) landraces of Central region of Benin Republic," *Journal of*

- Plant Breeding and Crop Science*, vol. 10, no. 11, pp. 304–318, 2018.
- [51] S. Wright, “Correlation and causation,” *Journal of Agricultural Research*, vol. 20, pp. 557–585, 1921.
- [52] B. D. Singh, *Plant Breeding*, Kalayani publisher, Varanasi, Ludhiana, New Delhi, Hindu university, 2000.
- [53] Ö. Mustafa, K. Ali, and C. Ercan, “Correlation and path analysis for yield and yield components in common bean genotypes (*Phaseolus vulgaris* L.),” *Ratarstvo i Povrtarstvo*, vol. 50, no. 2, pp. 14–19, 2013.
- [54] G. D. de Lima, M. A. Barelle, de.T. C. Oliveira, and P. R. J. conducts Santo, “Gentic correlation and path analysis of common bean collected from Brazil,” *Ciência Rural*, vol. 08, Article ID e20160815, 2017.
- [55] A. V. Jiman and P. H. K. Khanuja, “Literature survey: clustering technique,” *IJCATR*, vol. 5, no. 10, pp. 671–674, 2016.
- [56] B. D. Singh, *Plant Breeding Principles and Methods*, p. 506, Kalyani Publisher, New Delhi, India, 1983.
- [57] E. Getachew, *Phenotypic Diversity in Haricot Phaseolus Vulgaris L.) Germplasm a Thesis Submitted to the School of Graduate Studies, Jimma University College of Agriculture and Veterinary Medicine, Jimma*, 2010.
- [58] G. M. Bhatt, “Path coefficient analysis in determining character association,” *Euphytica*, vol. 22, pp. 383–393, 1973.
- [59] M. Khodadadi, M. H. Fotokian, and M. Miransari, *Genetic Diversity of Wheat (Triticum aestivum L.) Genotypes Based on Cluster and Principal Component Analyses for Breeding*, 2011.
- [60] A. Rahim, A. M. Ranjha, and E. W. Rahmatullah, “The effect of phosphorous application and irrigation scheduling on wheat yield and phosphorous use efficiency,” *Soil & Environment*, vol. 29, pp. 15–22, 2010.
- [61] R. Ali, M. J. Khan, and R. A. Khattak, “Response of rice to different sources of sulfur (S) at various levels and its residual effect on wheat in the rice-wheat cropping system,” *Soil and Environment*, vol. 27, pp. 131–137, 2008.
- [62] G. Avinash, S. K. Srivastava, and D. Singh, “The effect of copper on various phytochemical in sorghum bicolor,” *International Journal of Communication Systems*, vol. 6, no. 5, pp. 2235–2243, 2018.
- [63] S. O. Park, D. P. Coyne, G. Jung et al., “Mapping of QTL for seed size and shape traits in common bean,” *Journal of the American Society for Horticultural Science*, vol. 125, no. 4, pp. 466–475, 2000.
- [64] A. Cristina Gonçalves Ceolin, M. Celeste Gonçalves-Vidigal, P. Soares Vidigal Filho, M. Vinicius Kvitschal, A. Gonela, and C. Alberto Scapim, “Genetic divergence of the common bean (*Phaseolus vulgaris* L.) group Carioca using morpho-agronomic traits by multivariate analysis,” *Hereditas*, vol. 144, pp. 1–9, 2007.
- [65] S. P. Mishra, U. Sarkar, S. Taraphder et al., “Multivariate statistical data analysis-principal component analysis (PCA),” *International Journal of Livestock Research*, vol. 7, no. 5, pp. 60–78, 2017.