

Evaluation of genetic variability, heritability, genetic advance, and association of yield and yield contributing traits of indeterminate climbing common bean (*Phaseolus vulgaris* L.) genotypes

Temesgen Asmare Molla

temesgen5778@gmail.com

Bahir Dar University

Tiegist Dejene Abebe

Bahir Dar University

Ephrem Worku Tesfa

University of Gondar

Andualem Muche Hiywotu

Debark University

Berhanu Amsalu Fenta

Ethiopian Institute of Agricultural Research (EIAR)

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Abstract

Despite the importance of common bean as a cash crop, research and development have given limited attention to the indeterminate climbing bean. As a result, its productivity has remained low due to a lack of improved varieties. Hence this study was undertaken to estimate the extent of genetic variability, heritability, genetic advance, and associations of yield and yield contributing to 12 quantitative traits of indeterminate climbing common bean genotypes. The study used forty-nine genotypes of indeterminate- climbing type of common beans with a 7x7 triple lattice design. Variance analysis revealed a highly significant difference among 49 genotypes of beans for twelve morphological traits (< 0.01) under study. The coefficient of variation, both at the phenotypic and genotypic levels, indicated significant differences among the genotypes for measured traits. The result revealed that estimates of heritability (%) in a broad sense for 12 traits studied, ranged from (23.73%) to (85.85%) for seed per plant and hundred seed weight respectively. Genetic advance estimation in this study revealed that plant height, pod per plant, branches per plant, biological yield, harvest index, 100-seed weight, and grain yield had high heritability estimates coupled with high genetic advance as a percentage of the mean. The correlation analysis revealed that grain yield had a highly significant and positive phenotypic correlation with plant height, pod length, pod per plant, seed per pod, seed per plant, branch per plant, hundred seed weight, biological yield, and significant positive phenotypic correlation with harvest index. Path coefficient analysis demonstrated that higher positive direct effects were exerted by biological yield harvest index and hundred seed weight on grain yield at phenotypic and genotypic levels. The study reveals significant genetic variability in indeterminate climbing common bean genotypes, highlighting the potential for selective breeding to enhance yield-related traits. By identifying high-performing genotypes, the research supports targeted breeding programs aimed at increasing productivity and benefiting smallholder farmers in Ethiopia.

1. INTRODUCTION

The common bean (*Phaseolus vulgaris* L.), also known as kidney bean, dry bean, or haricot bean, is a diploid and predominantly self-pollinated crop (Ibarra-Perez et al., 1997). It exhibits three growth habits: determinate bush, semi-indeterminate bush, and indeterminate climbing types. Globally, it is ranked as the second most important pulse after soybean (Gidago et al., 2011). The crop is cultivated across continents and serves as a direct food source for millions. It is estimated that about 300 million people in the tropics and roughly 100 million people in Africa depend on common beans as a staple (Sofi et al., 2011). Beyond being a dietary protein source, beans play an important role in household food security, livestock feed, and regional economies. While dry seeds are the major product, green pods are consumed as vegetables, leaves are eaten either fresh or cooked, and crop residues are used as animal fodder (Broughton et al., 2003).

In Ethiopia, common bean is one of the most widely grown pulse crops and holds significant economic importance. It is cultivated by smallholder farmers as a sole crop or intercropped with cereals. National surveys have identified it as a leading pulse crop in terms of area coverage and production volume. According to the 2020/21 Agricultural Sample Survey by the Central Statistical Agency (CSA), the crop was planted on about 311,584 hectares, yielding 552,564 metric tons with an average productivity of 1.77 t/ha (CSA, 2020/21). Major producing regions include Oromia, Amhara, SNNPR, and Benishangul-Gumuz (Frehiwot Mulugeta, 2010).

Indeterminate climbing beans are particularly valuable in Ethiopia, providing both food and income to smallholder farmers. Despite favorable agro-ecological conditions and farmers' long-standing experience with these beans, their cultivation has largely remained confined to homesteads and is often intercropped with cereals. Research and breeding efforts on climbing types have been limited, leaving considerable room for productivity improvement. Genetic enhancement through structured breeding programs offers an important opportunity to increase yields and expand their production potential.

The breeding process typically involves germplasm collection, hybridization, and subsequent selection to develop superior varieties. Among these steps, selection is especially critical, as it enables breeders to identify high-yielding genotypes based on variability in quantitative traits such as yield and its components. For selection to be effective, it is important to evaluate the magnitude of genetic variability and understand how different traits are interrelated. Genetic parameters such as heritability provide insights into the degree to which traits are transmitted from one generation to the next, while correlation analysis helps to reveal associations among traits that influence yield. Path coefficient analysis (Dewey and Lu, 1959) further refines this understanding by partitioning correlations into direct and indirect effects, thereby identifying traits that contribute most efficiently to yield improvement.

Despite its significance, few studies have comprehensively addressed genetic variability, heritability, and trait associations in indeterminate climbing beans in Ethiopia. Such information is essential for designing effective breeding strategies and enhancing seed yield. Therefore, the present study was conducted to evaluate the extent of genetic variability, heritability, and genetic advance in

indeterminate climbing common bean genotypes, and to examine the relationships among yield and yield-related traits using 49 genotypes.

2. MATERIALS AND METHODS

2.1. Description of the study area

The experiment was conducted at Finoteselam Agricultural Research Subcenter during the 2019/2020 G.C main cropping seasons under rain fed conditions. Finoteselam is located 176 km from Bahir Dar, at 10.41'N Latitude, at 37.15'E Longitude, and an altitude of 1956 m.a.s.l. The average annual rainfall of the area is 884 mm and the maximum and minimum annual mean temperatures are 28.4°C and 12.6°C, respectively (Jabetena District Agricultural Office). The soil type of the site is Nitosoil.

2.2. Experimental materials and design

Forty-eight genotypes of indeterminate climbing common bean (*Phaseolus vulgaris* L.) obtained from Melkassa Agricultural Research Center which was introduced from *CIAT* (*International Center for Tropical Agriculture*) with one check, a total of forty-nine genotypes were used for this experiment. The experiment was laid out in a 7x7 triple lattice design and plot size of 4mx1.6m. Each plot consisted of four rows with 4m length and 40 cm inter-row and 10 cm intra-row spacing. The spacing between plots, blocks, and replications were 40cm, 1m, and 1.5m, respectively. The total experimental area was 34mx 43.8m. A seed rate of 90 to 100 kg ha⁻¹ was used. The recommended rates of 100 kg ha⁻¹ and 50 kg ha⁻¹ NPS and Urea respectively were applied.

Table 1.1
Designation of indeterminate common bean (*Phaseolus vulgaris* L.) genotypes

Number	Name of genotypes	Source	Number	Name of genotypes	Source
1	NUV187	CIAT	26	16371	CIAT
2	NUV100	CIAT	27	NUV140	CIAT
3	NUV1142	CIAT	28	NUV77	CIAT
4	NUV131	CIAT	29	NUV180	CIAT
5	16525	CIAT	30	NUV85b	CIAT
6	Local seed	Local market	31	NUV173	CIAT
7	228080	CIAT	32	16378	CIAT
8	16361	CIAT	33	211278	CIAT
9	NUV90	CIAT	34	211350	CIAT
10	NUV159	CIAT	35	NUV21	CIAT
11	NUV102	CIAT	36	NUV182	CIAT
12	214662	CIAT	37	NUV30	CIAT
13	208639	CIAT	38	NUV54	CIAT
14	16364	CIAT	39	215050	CIAT
15	21136	CIAT	40	211320	CIAT
16	NUV20	CIAT	41	16367	CIAT
17	NUV27	CIAT	42	NUV40	CIAT
18	NUV115	CIAT	43	207933	CIAT
19	9213	CIAT	44	212978	CIAT
20	213319	CIAT	45	NUV42	CIAT
21	211336	CIAT	46	NUV160	CIAT
22	NUV56	CIAT	47	NUV76	CIAT
23	NUV219-9	CIAT	48	15996	CIAT
24	215048	CIAT	49	201940	CIAT
25	211331	CIAT			

2.3. Data Collected

The following data were collected from the middle two rows of each plot on both a plot and plant basis.

Data recorded on a plant basis

Data were recorded following the standard procedures outlined by Debouck et al. (1986).

Plant height (cm)

Measured at the pod-filling stage from the ground level to the tip of the main stem on five randomly selected plants and the average were taken.

Number of primary branches

Counted as the number of branches arising from the main stem, recorded on randomly sampled plants, and expressed as the average per plant.

Pod length (cm)

Measured at harvest as the mean length of five pods sampled from each selected plant.

Number of pods per plant

Total pods per plant were counted on pre-marked, randomly chosen plants and expressed as the average value.

Number of seeds per pod

Determined as the mean number of seeds from five plants divided by the total number of pods harvested from the same plants.

Number of seeds per plant

Calculated as the average number of seeds per plant from randomly selected samples.

Data recorded on a plot basis

The following traits were measured using standard procedures described by Debouck et al. (1986):

Days to 50% flowering

The number of days from sowing to the point when approximately half of the plants in a plot had produced flowers.

Days to maturity

Recorded as the number of days from planting until about 90% of the plants in a plot reached physiological maturity, as indicated by yellowing of leaves and stems.

Grain yield (GY)

Measured after harvesting, threshing, and cleaning the seed. Grain weight per net plot was taken using an electronic balance and converted to kilograms per hectare after adjusting for seed moisture content.

Hundred-seed weight (HSW)

Determined by counting 100 seeds from each plot and weighing them using an electronic balance.

Above-ground dry biomass (AGDB)

Total dry matter (biological yield) per plot was measured and recorded after harvesting.

Harvest index (HI)

Calculated as the ratio of seed yield to biological yield for each plot, i.e., $HI = \text{seed yield (kg)} / \text{biological yield (kg)}$.

2.4. Data analyses

2.4.1. Analysis of variance

The collected data was subjected to statistical analysis according to the procedure of triple lattice design. SAS computer software version 9.2 (SAS, 2008) was used for data analysis. The relevant values generated on plot and plant basis were subjected to analysis of variance (ANOVA) using the linear model implemented in SAS software version 9.2.

The Mathematical Model for Triple Lattice Design is: $Y_{ijk} = \mu + GI + Bk(j) + Rj + Eljk$

Where,

Y_{ijk} = Phenotypic effect of i th genotype under j th replication and k th incomplete block within replication j ,

μ = grand mean,

G_i = effects of i th genotype,

$B_k(j)$ = the effect of incomplete block within replication j

R_j = the effect of replication j ,

E_{ijk} = the plot residual effect or effect of random error.

2.4.2 Estimation of phenotypic and genotypic variances

The phenotypic and the genotypic variations were estimated according to the method suggested by Mirza et al. (2011) as follows.

Environmental variance (δ^2_e) = MSE (square)

Genotypic variance (δ^2_g) = $Msg - Mse/r$

Phenotypic variance (δ^2_p) = $\delta^2_g + \delta^2_e$

Where,

Msg = mean square due to genotype;

Mse = Environmental variance

r = number of replications

2.4.2. Estimation of genotypic and phenotypic coefficient of variability

Phenotypic and genotypic coefficients of variation are helpful to estimate the magnitude of variability present in a population. According to Singh (2001), the phenotypic and genotypic coefficients of variances are expressed by the following formula.

Phenotypic coefficient of variation (PCV) = $\sqrt{\sigma^2 P} / X * 100$

Genotypic coefficient of variation (GCV) = $\sqrt{\sigma^2 g} / X * 100$

Where;

X = Mean value of the trait.

$\sqrt{\sigma^2 g}$ = Genotypic standard deviations

$\sqrt{\sigma^2 P}$ = phenotypic standard deviations

2.4.3. Estimation of heritability and genetic advance

Heritability provides the degree of transmissibility of a trait and indicates the effectiveness of selection. Further, estimates of heritability have to be considered in conjunction with genetic advances to find the expected genetic gain in the next generation (Shukla et al., 2006). Broad sense heritability (H^2_b) shall be expressed as the percentage of the ratio of the genotypic variance (δ^2_g) to the phenotypic variance (δ^2_p) and were estimated on genotype mean basis as described by Allard and Hansche (1964) as:

$H^2_b = \delta^2_g / \delta^2_p * 100$ Where;

H^2_b = heritability in broad sense δ^2_p = phenotypic variance δ^2_g = genotypic variance

The genetic advances for selection intensity (k) at 5% (2.06) were estimated by the formula of Johnson et al. (1955) Genetic advance (GA) = $H^2_b * K * \delta_p$ and Genetic advance as percent of the mean (GAM) = $\frac{GA}{X}$

Where:

δp = Phenotypic standard deviation;

H^2b = heritability in a broad sense and k = selection intensity

$\bar{X}$ = Grand mean

2.4.4. Estimation of phenotypic and genotypic correlation coefficients

Correlation studies help to find the degree of interrelationship among various traits and to evolve selection criteria for improvement. Phenotypic correlation is the relationship between two variables, which includes both genotypic and environmental effects while genotypic correlation is the inherited association between two variables. Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Dewey and Lu (1959) from corresponding variance and co-variance components;

$$\text{phenotypic correlation} = r_p(xy) = \frac{COV_p(xy)}{\sqrt{V_p(x)} \times \sqrt{V_p(y)}}$$
$$\text{Genotypic correlation} = r_g(xy) = \frac{COV_g(xy)}{\sqrt{V_g(x)} \times \sqrt{V_g(y)}}$$

Where; $COV_p(xy)$ and $COV_g(xy)$ are phenotypic and genotypic covariance between x and y traits.

$V_p(x)$ and $V_g(x)$ represent variances of x traits at phenotypic and genotypic levels $V_p(y)$ and $V_g(y)$ denote variance of y traits at phenotypic and genotypic levels, respectively.

2.4.5. Path coefficient analysis

Path coefficient analysis was carried out to separate the observed correlation coefficients into direct and indirect effects of yield-related traits on grain yield. This approach helps to identify whether a trait contributes to yield primarily through its own direct influence or indirectly through its association with other traits. The analysis followed the method proposed by Dewey and Lu (1959), which applies standardized partial regression coefficients to estimate direct effects. Indirect effects were obtained by multiplying the correlation of an independent trait with an intermediate trait by the direct effect of that intermediate trait on yield. The residual effect was calculated to determine the proportion of variation in grain yield not explained by the traits included in the model.

$$\text{varvecr} \text{varveci} \text{varvecj} = \text{varvecP} \text{varveci} \text{varvecj} + \sum \text{varvecr} \text{varveci} \text{varveck} \text{varvecP} \text{varvecj} \text{varveck}$$

Where

$\text{varvecr} \text{varveci} \text{varvecj}$ = mutual association between independent variable (i) and dependent variable (j) as measured by phenotypic and genotypic correlation coefficient.

$\text{varvecP} \text{varveci} \text{varvecj}$ = component of a direct effect of independent variable (i) as measured by the phenotypic and genotypic path coefficient.

$\sum \text{varvecr} \text{varveci} \text{varveck} \text{varvecP} \text{varvecj} \text{varveck}$ = summation of components of an indirect effect of a given independent variable (i) on a given dependent variable (j) via all other independent traits(K).

3. RESULTS AND DISCUSSION

3.1. Analysis of Variance (ANOVA)

The analysis of variance revealed highly significant differences ($p < 0.01$) among the 49 bean genotypes for all twelve morphological traits studied (Table 3.1). This demonstrates the presence of substantial genetic variability, providing an opportunity to identify superior genotypes for future breeding and improvement programs.

Similar results have been reported in previous studies. Ghimire and Mandal (2019) found significant variation among bean genotypes for traits such as flowering time, maturity, plant height, pod number, seed traits, seed weight, and grain yield. Bulyaba et al. (2020) likewise observed strong genotypic effects on flowering and maturity duration, plant height, pods per plant, seeds per pod, biomass, harvest index, branch number, and yield. In addition, Msolla and Mduruma (2007) reported marked differences in flowering time, maturity, and yield-related traits in common bean lines, further supporting the present findings.

Table 3.1
Mean square for quantitative traits of bean genotypes

Trait	Treatment (Df = 48)	Rep (Df = 2)	Block (Df = 18)	CV (%)	R ²	Error	Mean
DF	68.94**	2.71	25.84	9.58	0.58	26.80	54.71
DM	162.00**	61.76	10.81	3.79	0.85	18.58	111.15
PH	1681.46**	366.24	148.18	10.69	0.87	144.85	111.99
PL	3.39**	0.36	0.22	8.88	0.75	0.72	9.09
PPP	62.47**	12.75	7.12	15.68	0.86	5.52	15.44
SPP	1.16**	0.06	0.22	10.17	0.65	0.36	5.72
SPPL	319.05**	309.14	105.55	27.24	0.53	165.03	46.83
BPP	0.87**	0.11	0.07	13.96	0.79	0.14	2.57
HSW	158.14**	12.72	7.79	12.34	0.92	8.24	22.75
BY	2933236.00**	96403.00	264222.00	10.46	0.89	192636.00	4181.38
GY	1182013.00**	44171.00	69038.00	15.07	0.90	75325.00	1821.81
HI	260.54**	23.72	26.66	13.84	0.80	36.41	42.91
Note: DF = days to flowering; DM = days to maturity; PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPL = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha ⁻¹); GY = grain yield (kg ha ⁻¹); HI = harvest index (%), CV% = coefficient of variation; and R ² = R-square.							

3.2. Mean and range of measured traits

The mean, minimum, and maximum values of the 12 traits are presented in Table 3.2, showing wide variation among the 49 bean genotypes. This variability reflects the presence of substantial genetic differences across the genotypes studied. Yohannes and Berecha (2015) also reported considerable ranges in traits such as seed yield per plant, hundred-seed weight, seeds per pod, and flowering time, supporting the present findings.

Days to 50% flowering ranged from 44 to 73.66 days, while days to maturity ranged from 98.66 to 125.33 days. The latest maturing genotype was 16525 (125.33 days), and the earliest was 211320 (98.66 days). Such variation provides opportunities to classify genotypes into early- and late-maturing groups, which is valuable for breeding programs targeting contrasting environments such as moisture-deficit areas and high-rainfall regions.

Plant height ranged from 63.93 cm (NUV160) to 158.2 cm (208639), with a mean of 111.99 cm. Pod length varied between 5.8 and 11.07 cm, while pods per plant ranged from 5.13 to 25.66, with a mean of 15.43. Hundred-seed weight was highest in genotype 208639 (49.19 g) and lowest in 212978 (13.22 g), consistent with the variation reported by Yohannes and Berecha (2015). Grain yield ranged from 387.7 kg ha⁻¹ (NUV173) to 3246.9 kg ha⁻¹ (16525), which aligns with the results of Raffi and Nath (2004). The highest harvest index (60.86) was recorded in NUV140, while the lowest (13.24) was found in NUV173. Biological yield was also highest in genotype 16525 and lowest in 15996.

Overall, the wide range of variation observed across genotypes provides a strong basis for selection. The presence of such diversity indicates good prospects for identifying and improving superior genotypes through breeding.

Table 3.2
Range and mean values for 12 traits of 49 bean genotypes

Trait	Min	Genotype	Max	Genotype	Mean	Range
DF	44	214662	73.667	NUV30	54.71429	29.67
DM	98.667	211320	125.333	16525	111.1497	26.66
PH	63.933	NUV160	158.2	208639	111.9852	94.27
PL	5.8	NUV173	11.0667	208639	9.085714	5.27
PPP	5.133	201940	25.667	211350	15.43673	20.54
SPP	3.8	201940	7.1333	NUV219-9	5.722449	3.33
SPPL	17.27	201940	64.47	211350	46.82993	47.2
BPP	1.4667	15996	3.4667	NUV30	2.57415	2
HSW	13.22	212978	49.187	208639	22.74639	35.97
BY	2234	15996	7733.5	16525	4181.376	5499.5
GY	387.7	NUV173	3246.9	16525	1821.805	2859.2
HI	13.235	NUV173	60.862	NUV140	42.91218	47.62
Note: DF = days to flowering; DM = days to maturity; PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPL = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha ⁻¹); GY = grain yield (kg ha ⁻¹) and HI = harvest index (%).						

3.3. Phenotypic and Genotypic Variations

The phenotypic and genotypic variances, along with the coefficients of variation (PCV and GCV), for yield and related traits are presented in Table 3.3. Following the classifications of Sivasubramaniam and Madhava Menon (1973) and Deshmukh et al. (1986), coefficients of variation were categorized as low (< 10%), moderate (10–20%), or high (> 20%).

Both PCV and GCV values revealed substantial variability among the genotypes. In line with the findings of Bashir et al. (2014), PCV values were generally higher than GCV values, indicating that environmental factors contributed to the observed variation.

High GCV estimates were recorded for plant height, pods per plant, hundred-seed weight, biological yield, grain yield, and harvest index. These results are consistent with Singh (2001), who reported high genetic variance for seed yield and related traits in common bean. Traits such as pod length, seeds per plant, and branches per plant showed moderate GCV, suggesting that improvement through selection is feasible. In contrast, days to flowering and days to maturity exhibited low GCV values, implying that these traits are strongly influenced by the environment and thus less responsive to selection.

High PCV values were observed for plant height, pods per plant, seeds per plant, branches per plant, hundred-seed weight, biological yield, grain yield, and harvest index. Moderate PCV values were recorded for days to flowering and pod length, while days to maturity exhibited the lowest PCV (< 10%). Similar trends were reported by Yohannes and Berecha (2015), who found higher PCV values for plant height, biological yield, pods per plant, harvest index, and seed weight, while traits like flowering time and seeds per pod showed moderate variation.

The relatively large differences between PCV and GCV for traits such as seeds per plant, flowering time, and branch number suggest strong environmental influence, making direct selection less reliable for these traits. However, the smaller differences observed for most other traits indicate that genetic factors were the main source of variation, making them dependable targets for selection in breeding programs.

3.4. Heritability

Broad-sense heritability estimates for the 12 traits are summarized in Table 3.3, ranging from 23.73% for seeds per plant to 85.85% for hundred-seed weight. High heritability was recorded for plant height, hundred-seed weight, biological yield, grain yield, harvest index, branches per plant, days to maturity, and pods per plant. These results suggest that the expression of these traits is largely governed by genetic factors with minimal environmental influence, making phenotypic selection effective. Moderate heritability estimates were

observed for seeds per pod and days to flowering, while seeds per plant exhibited low heritability, indicating greater environmental influence and reduced effectiveness of direct selection.

Comparable findings have been reported in previous studies. Mallu et al. (2014) found high heritability for grain yield and hundred-seed weight, and Ghimire and Mandal (2019) reported heritability above 60% for seed weight, pod length, pod number, maturity period, yield, and plant height. Similarly, Wondwosen and Abebe (2017) observed strong heritability for yield, seed weight, and maturity-related traits, while Raffi and Nath (2004) documented values exceeding 60% for maturity, yield, seed weight, pod length, and plant height. More recently, Langat et al. (2019) reported high heritability (> 60%) for flowering, maturity, seeds per pod, hundred-seed weight, and grain yield under stress conditions. In French bean, Aklade et al. (2018) also reported high heritability for flowering, maturity, pod length, hundred-seed weight, and seeds per pod. Similarly, Ali et al. (2010) identified high heritability for biomass, grain yield, seed weight, and pod number, noting that these traits are reliable for selecting high-yielding genotypes.

3.5. Genetic Advance

Genetic advance estimates are presented in Table 3.3. Traits including plant height, pods per plant, branches per plant, biological yield, harvest index, hundred-seed weight, and grain yield showed high heritability combined with high genetic advance as a percentage of the mean. This indicates strong additive gene action, suggesting that these traits can be effectively improved through direct selection. In contrast, days to maturity, pod length, seeds per pod, and seeds per plant exhibited moderate genetic advance, while days to flowering showed low values, reflecting limited genetic variability and reduced potential for selection.

These findings are consistent with Mohammed et al. (2019), who reported high genetic advance as a percentage of the mean (GAM) for grain yield, biomass yield, pods per plant, and hundred-seed weight, but lower GAM values for maturity, flowering, and seeds per pod.

Table 3.3
Estimates of variances and coefficients of variability, heritability, and genetic advance of the 12 traits of 49 bean genotypes

Traits	σ^2_e	σ^2_g	σ^2_p	PCV%	GCV%	H ²	GA	GAM
DF	26.80	14.05	40.84	11.68	6.85	34.39	4.53	8.28
DM	18.58	47.81	66.39	7.33	6.22	72.01	12.09	10.87
PH	144.85	512.20	657.05	22.89	20.21	77.95	41.16	36.76
PL	0.72	0.89	1.61	13.95	10.39	55.50	1.45	15.95
PPP	5.52	18.99	24.50	32.07	28.23	77.49	7.90	51.18
SPP	0.36	0.27	0.63	13.84	9.03	42.62	0.70	12.15
SPPL	165.03	51.34	216.37	31.41	15.30	23.73	7.19	15.35
BPP	0.14	0.24	0.38	23.97	19.13	63.68	0.81	31.44
HSW	8.24	49.97	58.21	33.54	31.08	85.85	13.49	59.32
BY	192636	913533.4	1106169	25.15	22.86	82.59	1789.29	42.79
GY	75325	368896	444222	36.58	33.34	83.04	1140.18	62.58
HI	36.41	74.71	111.12	24.56	20.14	67.24	14.60	34.02

Note: DF = days to flowering; DM = days to maturity; PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPL = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha⁻¹); GY = grain yield (kg ha⁻¹) and HI = harvest index (%); σ^2_e = environmental variance; σ^2_g = genotypic variance; σ^2_p = phenotypic variance; H² = broad sense heritability; GA = genetic advance and GAM% = Genetic advances as percent of the mean.

3.6. Correlation of grain yield with other traits and correlation among traits

3.6.1. Phenotypic correlation

Phenotypic correlation coefficients among the studied traits are shown in Table 3.4. Grain yield displayed strong and positive associations with plant height, pod length, pods per plant, seeds per pod, seeds per plant, branch number, hundred-seed weight, and

biological yield. A significant positive relationship was also observed with harvest index. These results suggest that selection based on these traits could indirectly enhance grain yield. Similar positive associations between yield and traits such as seeds per plant (Cokkizgin et al., 2013), seeds per pod (Roy et al., 2006), hundred-seed weight (Karasu and Oz, 2010), and branch number (Kulaz and Ciftci, 2012) have been reported in previous studies. Positive correlations of grain yield with days to flowering were also noted by González et al. (2016) and Bagheri et al. (2017). Conversely, yield exhibited a non-significant but positive correlation with days to maturity, indicating limited potential for indirect improvement through this trait.

Pod length showed highly significant and positive correlations with seeds per pod, seeds per plant, and branches per plant, hundred-seed weight, biological yield, grain yield, and harvest index. This implies that improvement in pod length could lead to simultaneous gains in these traits, making it a useful selection criterion. However, pod length had a significant negative association with days to maturity, consistent with findings by Roy et al. (2006).

Harvest index exhibited strong positive correlations with pod length, pods per plant, seeds per pod, seeds per plant, branch number, hundred-seed weight, biological yield, and grain yield, as well as a positive association with plant height. In contrast, it showed a significant negative correlation with days to maturity and a non-significant negative correlation with days to flowering. These patterns suggest that genotypes with higher values for positively correlated traits are likely to achieve greater harvest index.

In general, the predominance of positive and significant phenotypic correlations indicates that many traits can be improved simultaneously through selection. Negative correlations, however, may constrain the possibility of achieving simultaneous improvement for certain trait combinations.

3.6.2. Genotypic correlations

Genotypic correlation coefficients among yield and yield-related traits are presented in Table 3.4. Grain yield showed highly significant and positive correlations with plant height, pod length, pods per plant, seeds per pod, seeds per plant, branches per plant, hundred-seed weight, biological yield, and harvest index. Seeds per plant were positively associated with several traits including pod length, branches per plant, biological yield, seeds per pod, harvest index, and pods per plant, indicating that these traits tend to improve together. Pod length also exhibited strong positive correlations with seeds per pod, seeds per plant, branches per plant, hundred-seed weight, biological yield, grain yield, and harvest index. Likewise, biological yield was strongly correlated with nearly all yield-related traits, underscoring its central role in influencing productivity.

These findings are consistent with earlier reports. Agrawal et al. (2000) and Yohannes et al. (2020) documented strong genotypic correlations of grain yield with traits such as biological yield, pods per plant, seeds per pod, stem diameter, and leaf area index. In the current study, biological yield recorded the highest genotypic correlation with grain yield, which aligns with their findings. By contrast, grain yield showed non-significant but positive correlations with days to flowering ($r_g = 0.15$) and days to maturity ($r_g = 0.05$), suggesting limited potential for improving yield through these traits.

Correlation analysis also revealed that days to flowering had significant positive associations with days to maturity and biological yield, while its relationships with pod length, pods per plant, seeds per pod, seeds per plant, branches per plant, and grain yield were positive but non-significant. Negative correlations were detected with plant height and harvest index. Similarly, days to maturity was significantly and positively correlated with days to flowering, biological yield, and pods per plant, while its associations with plant height, branches per plant, grain yield, and hundred-seed weight were positive but non-significant. Negative but non-significant relationships were observed with seeds per plant and pod length.

In general, the predominance of positive and significant genotypic correlations suggests that many traits can be improved simultaneously through selection. However, negative correlations highlight potential trade-offs, which may limit the scope of simultaneous trait improvement.

Table 3.4
Estimates of genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients among 12 traits in 49 bean genotypes

Variable	DF	DM	PH	PL	PPP	SPP	SPPI	BPP	HSW	BY	GY	HI
DF	1	0.25**	-0.01	0.05	0.11	0.06	0.01	0.09	-0.06	0.24**	0.09	-0.11
DM	0.36*	1	0.19*	-0.16*	0.26**	-0.31**	-0.01	0.06	0.12	0.32**	0.05	-0.32**
PH	-0.01	0.21	1	0.20*	0.06	0.1	0.16	0	0.50**	0.32**	0.34**	0.21*
PL	0.13	-0.23	0.26	1	0.04	0.62**	0.35**	0.44**	0.53**	0.37**	0.53**	0.52**
PPP	0.18	0.30*	0.04	0.06	1	0.18*	0.54**	0.23**	-0.01	0.34**	0.37**	0.27**
SPP	0.09	-0.34*	0.15	0.80**	0.23	1	0.45**	0.18*	0.23**	0.15	0.35**	0.49**
SPPI	0.13	-0.07	0.19	0.48**	0.65**	0.59**	1	0.28**	0.12	0.35**	0.45**	0.39**
BPP	0.18	0.07	-0.03	0.49**	0.30*	0.32*	0.44**	1	0.21*	0.54**	0.53**	0.31**
HSW	-0.07	0.1	0.55**	0.61**	-0.02	0.30*	0.14	0.22	1	0.45**	0.57**	0.43**
BY	0.34*	0.36*	0.35*	0.42**	0.36*	0.18	0.43**	0.62**	0.48**	1	0.82**	0.25**
GY	0.15	0.05	0.39**	0.60**	0.40**	0.43**	0.59**	0.58**	0.61**	0.87**	1	0.74*
HI	-0.1	-0.37**	0.28	0.63**	0.33*	0.63**	0.59**	0.34*	0.48**	0.35*	0.76**	1

Note: DF = days to flowering; DM = days to maturity; PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPI = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha⁻¹); GY = grain yield (kg ha⁻¹) and HI = harvest index (%).

3.7. Path coefficient analysis

Path coefficient analysis partitioned the correlations of different traits with grain yield into their direct and indirect effects. At the phenotypic level, biological yield, harvest index, and 100-seed weight exerted the strongest positive direct effects on yield, suggesting that direct selection for these traits would be effective. Conversely, traits such as plant height and pod number displayed negative direct effects but contributed indirectly through positive associations with yield components like biological yield and seed weight. The residual effect of 0.14 indicated that the variables included explained about 86% of the yield variation. At the genotypic level, biological yield and harvest index again showed the largest positive direct effects, followed by seed weight and seed number per plant. Negative direct effects were observed for plant height, pod length, and pods per plant, though these were compensated by positive indirect contributions. The residual value of 0.045 suggested that the considered traits explained more than 95% of yield variation at the genotypic level.

3.7.1. Phenotypic direct and indirect effects of various traits on grain yield

At the phenotypic level, biological yield exerted the strongest direct effect on grain yield, followed by harvest index and hundred-seed weight. Traits showing strong direct positive effects can be used as effective selection criteria in breeding programs. Although pod number and plant height showed negative direct effects, they contributed positively to yield through strong indirect effects mediated by seed number, biological yield, and harvest index.

Plant height and seeds per pod both had negative direct effects on yield but showed positive indirect effects through hundred-seed weight, biological yield, and harvest index. Similar results were reported by Espósito et al. (2009). Pods per plant also exhibited a negative direct effect on grain yield but remained positively correlated with it overall, as the negative effect was offset by strong positive indirect effects via seeds per plant, biological yield, and harvest index. This agrees with the findings of Huque et al., (2012).

Other traits, such as pod length and branches per plant, also recorded negative direct effects on yield. In such cases, direct selection is unlikely to be effective; instead, improvement may be achieved indirectly through traits that compensate for their effects, such as biological yield and harvest index.

Overall, the phenotypic path analysis highlighted biological yield, hundred-seed weight, and harvest index as the most influential contributors to grain yield. Indirect contributions from traits like pod number and plant height further emphasize the importance of considering both direct and indirect effects when designing selection strategies.

Table 3.5
Estimation of direct (bold diagonal) and indirect effects (off-diagonal) of 9 traits on grain yield at phenotypic level in common bean genotypes

Traits	PH	PL	PPP	SPP	SPPI	BPP	HSW	BY	HI
PH	-0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.22	0.12
PL	0.00	-0.02	0.00	-0.02	0.01	-0.01	0.02	0.25	0.31
PPP	0.00	0.00	-0.02	-0.01	0.01	0.00	0.00	0.23	0.16
SPP	0.00	-0.01	0.00	-0.04	0.01	0.00	0.01	0.10	0.29
SPPI	0.00	-0.01	-0.01	-0.02	0.02	0.00	0.00	0.24	0.23
BPP	0.00	-0.01	0.00	-0.01	0.00	-0.01	0.01	0.37	0.18
HSW	-0.01	-0.01	0.00	-0.01	0.00	0.00	0.04	0.31	0.25
BY	0.00	-0.01	-0.01	-0.01	0.01	-0.01	0.02	0.68	0.15
HI	0.00	-0.01	0.00	-0.02	0.01	0.00	0.02	0.17	0.59

Residual effect = 0.14; Note: PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPI = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha⁻¹) and HI = harvest index (%).

3.7.2. Genotypic direct and indirect effects of various traits on grain yield

Genotypic path analysis (Table 3.6) showed that biological yield had the strongest direct positive effect on grain yield, followed by harvest index, hundred-seed weight, and number of seeds per plant. The high correlations of biological yield ($r = 0.87$) and harvest index ($r = 0.76$) with yield were largely explained by these direct contributions, underscoring their importance as selection criteria. These findings agree with Korat et al. (2010), who reported similar positive direct effects of harvest index, seed weight, and biological yield on seed yield.

Seeds per pod had a small positive direct effect but contributed more strongly through indirect effects via seed number, hundred-seed weight, biological yield, and harvest index. Hundred-seed weight also exhibited modest direct influence but reinforced yield through its indirect associations with the same traits.

In contrast, plant height and pod number per plant exerted negative direct effects on grain yield. However, their overall influence remained positive due to strong indirect pathways, especially through hundred-seed weight, biological yield, and harvest index. Comparable results were reported by Mammo et al. (2019) and Ambachew et al. (2015), who noted negative direct effects of pod number and seed weight on yield that were offset by indirect contributions. Conversely, Mesele (1997) found that seed number per plant was the most favorable contributor, while maturity and flowering time had negative direct effects. In the present study, pod length also showed a negative direct effect but was compensated by positive indirect influences through seed number, seed weight, biological yield, and harvest index.

In general, the direct effects of traits did not always correspond with their correlation coefficients, highlighting the complexity of inter-trait relationships. The low residual effect (0.045) indicated that the traits included in the model accounted for about 95.5% of the variation in grain yield, leaving only 4.5% unexplained.

Table 3.6
Estimation of direct (bold diagonal) and indirect effects (off-diagonal) of 9 traits on grain yield at genotypic level in common bean genotypes

Traits	PH	PL	PPP	SPP	SPPI	BPP	HSW	BY	HI
PH	-0.04	-0.02	0	0	0.01	0	0.05	0.25	0.15
PL	-0.01	-0.09	0	0.01	0.02	-0.01	0.06	0.29	0.33
PPP	0	-0.01	-0.04	0	0.03	-0.01	0	0.25	0.17
SPP	-0.01	-0.07	-0.01	0.01	0.03	-0.01	0.03	0.13	0.33
SPPI	-0.01	-0.04	-0.03	0.01	0.05	-0.01	0.01	0.3	0.31
BPP	0	-0.04	-0.01	0	0.02	-0.02	0.02	0.43	0.18
HSW	-0.02	-0.06	0	0	0.01	0	0.09	0.34	0.25
BY	-0.01	-0.04	-0.02	0	0.02	-0.01	0.04	0.7	0.18
HI	-0.01	-0.06	-0.01	0.01	0.03	-0.01	0.04	0.25	0.52

Residual effect = 0.045; Note: PH = plant height (cm); PL = pod length (cm); PPP = pod per plant; SPP = seed per pod; SPPL = seed per plant; BPP = branch per plant; HSW = hundred seed weight (g); BY = biological yield (kg ha⁻¹) and HI = harvest index (%).

4. CONCLUSIONS

This study demonstrated substantial genetic variation among the 49 climbing common bean genotypes across 12 quantitative traits, confirming the availability of a broad genetic base for improvement. Yield-related traits such as grain yield, pods per plant, and hundred-seed weight exhibited particularly wide variability, highlighting their potential as priority targets for breeding.

High heritability coupled with notable genetic advance was observed for several traits, including plant height, pods per plant, branches per plant, biological yield, harvest index, hundred-seed weight, and grain yield. These results suggest that additive genetic effects play a major role in the expression of these traits, making direct selection an effective strategy. Grain yield, pod number, biomass, and seed weight were especially important because they combined strong heritability with high genetic advance values.

Genotypic correlations were generally stronger than phenotypic ones, indicating that genetic factors were more influential than environmental effects in shaping trait associations. Grain yield showed significant positive correlations with multiple traits, including pod length, plant height, branch number, seeds per pod, seeds per plant, pods per plant, hundred-seed weight, biological yield, and harvest index. This implies that simultaneous improvement of yield and related traits is feasible through selection.

Path coefficient analysis further identified biological yield and hundred-seed weight as the most important direct contributors to grain yield, reinforcing their relevance as key selection criteria for developing high-yielding indeterminate climbing bean genotypes.

In general, the results highlight the presence of valuable genetic diversity in Ethiopian climbing common beans and demonstrate the potential for achieving substantial genetic gains through targeted selection. The identification of promising genotypes provides opportunities for their advancement and eventual release, thereby contributing to improved productivity and supporting smallholder farmers.

However, the study was conducted at a single site and within one growing season, which may limit the broader applicability of the results. Multi-location and multi-season trials are needed to validate trait stability under diverse environments. Furthermore, molecular approaches such as marker-assisted selection were not applied but could provide additional insights into the genetic basis of yield and related traits, supporting more efficient breeding strategies.

Declarations

Data availability statement

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

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Declaration of Interest's statement

The authors declare no competing interests.

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Figures

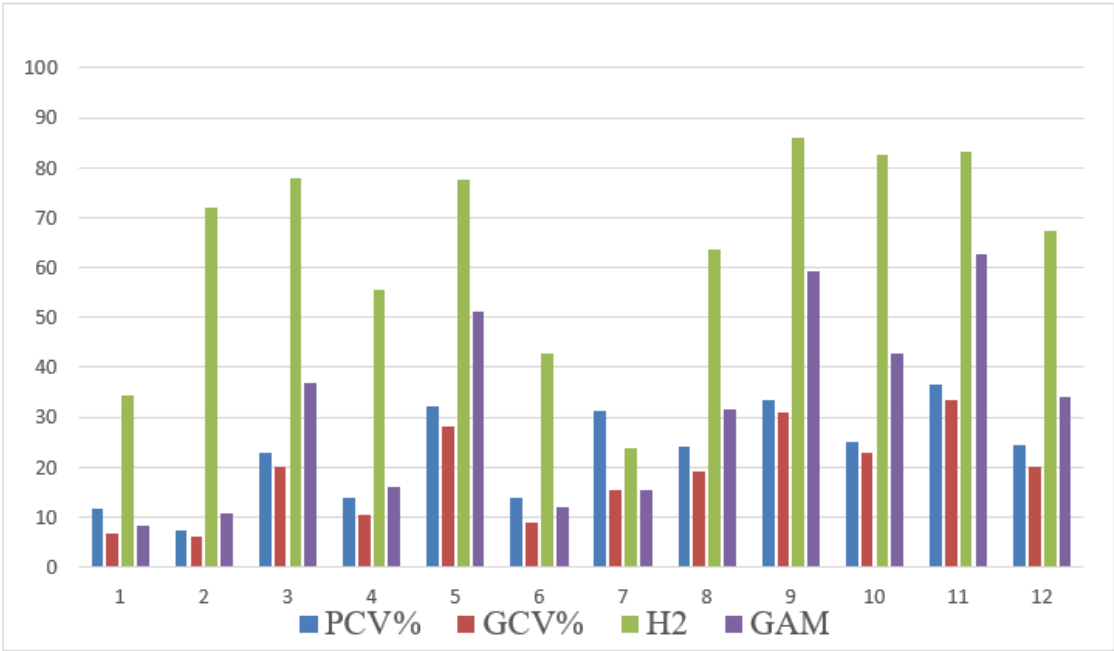


Figure 1

Figure 3.1 plots of the figure show genotypic and phenotypic variances, heritability, and genetic advance as the percent of the mean and genetic parameters discussed in common bean genotypes studied with 12 traits.