

Research Article

Correlations and path coefficient analysis of Grain yield and Grain yield related traits in Small seeded Common bean genotypes (*Phaseolus vulgaris* L.) at Goro and Ginnir, Southeast Ethiopia.Belay Asmare¹, Wassu Mohamed², Dagnachew Lule³**Abstract**

Common bean (*Phaseolus vulgaris* L.) is one of the crops produced by thousands of farmers in Bale. This study was conducted to assess the association of grain yield and grain yield related traits among small seeded common bean genotypes. Sixty-four common bean genotypes were evaluated in 8 X 8 simple lattice design at Goro and Ginnir in 2021. Results of analysis showed significant ($p < 0.05$) and positive strong correlation at phenotypic and genotypic levels for number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant with grain yield at both sites. These traits except number of seeds per plant had positive direct effects on Grain yield at genotypic level. The present study showed weak association of plant height and hundred seed weight with all the traits. The presence of non-significant correlations of the two variables indicated that the two traits are independent of each other or that genes concerned are located far apart on the same chromosome or they are located on different chromosomes. Days to flowering had negative and significant ($p < 0.01$) genotypic and phenotypic correlations with grain yield and the trait also exerted negative direct effect on grain yield at genotypic and phenotypic levels at both locations. This suggested that the importance of considering these traits during selection to improve grain yield in subsequent generations. In contrast, the negative direct effects of days to flowering and maturity as well as the negative indirect effects of these traits via other traits on grain yield suggested the need to select genotypes for early flowering and maturity for the study area.

Key words: common bean, Ethiopia, genotypic correlation, phenotypic correlation.

1. Introduction

Common bean is a major grain legume consumed worldwide; particularly in Sub-Saharan Africa (SSA). It is seed-propagated and diploid ($2n=22$) with a relatively small genome (650 Mb) (Broughton et al., 2003). It grows best in warm climate at optimum temperature of 18 to 24°C and between 1400 and 2000 m.a.s.l. (Teshale et al., 2006). As a result, it is an important crop for food security and nutrition (Margaret et al., 2014).

Common beans have two geographic centers of domestication, namely the Mesoamerican and Andean centers. The multiple centers of domestication of the crop have endowed it with relatively high diversity that is broadly classified into two gene pools, Mesoamerican and Andean (Gepts and Bliss, 1986); Singh et al., 1991).¹ The Andean lines have larger seeds in which 100 seed weight is above 30 grams while Mesoamerican lines have smaller seed size i.e.,

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their 100 seed weight is less than 30 grams (Gonzales et al., 2009). There are also variations in genotypes of common bean with different bean sizes and color. For instance, the small size genotypes vary from the small black wild type to the large white, brown, red or mottled seeds (Cobley and Steele, 1976).

For effective selection, information on characters' association with yield and among traits themselves, and the extent of environmental influence on the expression of these characters are necessary (Yagdi, 2009; Ejigu et al., 2017). Yield is the principal factor for determining improvement of a crop. Like other crops, seed yield in common bean is a quantitative character and influenced by a number of yields contributing traits. The selection of desirable types should therefore be based on yield and yield components. Information on mutual association between yield and yield components is necessary for efficient utilization of the genetic stock in the crop improvement program (Nechifor et al., 2011). To achieve significant progress in breeding programs, it is essential to know the relationship between seed yield and its components (Assady et al., 2005).

Correlation and path coefficient analysis could be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan et al., 2003). Although correlation estimates are helpful in determining the components of complex trait such as Grain yield, they do not provide an exact picture of the relative importance of direct and indirect influences of each of the component characteristics of the trait. Path coefficient analysis provides a more effective means of separating direct and indirect factors, permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. Correlation and path coefficient analysis of traits studies have been also conducted by considerable number of researchers on common bean, for instance, Kassaye, (2006), Karasu and Oz (2010), Salehi et al. (2010), Alamayehu, (2010), Daniel et al, (2015), and Barecha (2015), Ejara(2017).

Most of the studies on common bean correlation and path analysis of traits were conducted in other parts of the country. However, there are no reports on common bean under Bale zone (southeast Ethiopia) conditions, in where mono-cropping practice is a major crop production problem. Moreover, information is lacking on the potential of common bean genotypes in southeast Ethiopia in general and Ginnir, and Goro district of Bale zone. Hence the present study took place with the following objectives.

- (i) To determine associations among yield and yield related traits in small seeded common bean genotypes.
- (ii) To evaluate the direct and indirect effects of yield related traits on grain yield of small seeded common bean genotypes.

2. MATERIALS AND METHODS

2.1. Description of the Study Area

The experiment was conducted under field conditions at two potential areas of Bale and east Bale Zones. Both sites receive bimodal rainfall characterized as the main cropping season from July to October and short rain from March to May. The annual total rainfall of the area ranges between 806.9 and 1066.7 ppm and mean temperature ranges from 13.1–22.5°C (Bikila Mengistu et al. 2020).

Goro is located at 524km away from Addis Ababa in southeastern Ethiopia, 60 and 75 km from the near-by towns, Robe and Goba, respectively. The site is situated at 6° 59'20.97" N latitude and 40° 29'45.16" E longitude and elevation of 1771 meters above sea level. The soil is predominantly Vertisol in properties. The major crops grown widely in the area include cereal crops (barley, wheat, maize and teff), pulse crops (common bean, chickpea and lentil), spices (coriander, fenugreek) and vegetable crops (onion, potato, tomato and pepper) under rain fed and irrigation. Cereal crops are predominantly grown in the area (Taye and Abera, 2010; Amanuel et al., 2022).

Ginnir is located 599 km away from Addis Ababa. The site is situated at 7° 10'42.02"

N latitude and 40° 42' 58.64"E longitudes at 1972 m.a.s.l. The Vertisol soil type of Ginner district is suitable to produce cereal, pulse, oil and

horticultural crops (Wubishet et al., 2016; Amanuel et al., 2022).

Table1. Description of geographical positions and soil physico-chemical properties of the test locations.

Parameter	location	
	Goro	Ginner
Geographical position		
Latitude	6° 59' 20.97" N	7° 10' 42.02" N
Longitude	40° 29' 45.16" E	40° 42' 58.64" E
Altitude (m.a.s.l.)	1771	1972
Soil Property		
pH (1:2:5)	6.89	6.82
OC (%)	1.19	1.18
P _{avail} (ppm)	8.43	10.23
CEC (cmol.k8 (+) kg soil ⁻¹)	49.46	47.46
Soil texture		
Clay, %	46	52
Sand, %	20	21
Silt, %	34	27

Source: Sinana Agricultural Research Center, (2017/18) (unpublished data). OC = Organic Carbon, Pav = Phosphorus availability, CEC= Cation exchange capacity.

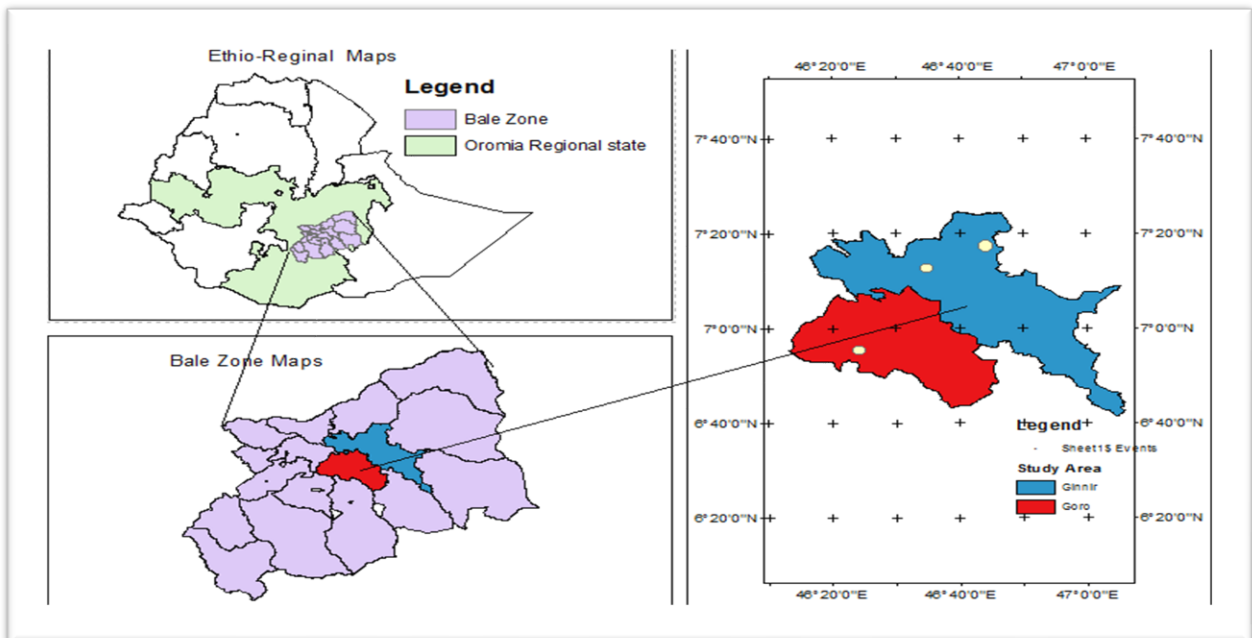


Figure 1 Map of Ethiopia showing the experimental sites.

2.2. Plant Materials

A total of 64 small-seeded common bean genotypes, of which 60 genotypes and two released varieties were obtained from the Melkasa Agricultural Research Center (MARC)

and two released varieties from Sinana Agricultural Research Center (SARC), which were used as standard checks. The small seeded common bean genotypes and released varieties are listed in Table 2.

Table 2. List of Common bean genotypes and varieties test at the study sites.

No	Genotypes	Seed Color	Origin	No	Genotypes	Seed Color	Origin
1	CB170087-39-2	Red	MARC	33	CB170008-6	Red	MARC
2	CB170065-22-1	Red	MARC	34	CB1615-11-72-2	Red	MARC
3	CB170025-3	White	MARC	35	CB170002-10	White	MARC
4	CB170060-8	Red	MARC	36	CB170052-23	Red	MARC
5	CB170038-15	White	MARC	37	CB170064-10-3	White	MARC
6	CB170065-40-1	Red	MARC	38	CB170046-8-2	Red	MARC
7	CB170046-5-2	Red	MARC	39	CB170001-20-2	White	MARC
8	CB170052-30-3	Red	MARC	40	CB170044-57-1	Red	MARC
9	CB170065-59-2	White	MARC	41	CB170003-21	White	MARC
10	CB170044-55-1	White	MARC	42	CB170037-18	Red	MARC
11	CB170001-17	Red	MARC	43	CB170038-36-3	White	MARC
12	CB170044-44-2	White	MARC	44	CB170008-3	White	MARC
13	CB170001-3-2	Red	MARC	45	CB170008-4	White	MARC
14	CB170044-88-3	White	MARC	46	CB170001-5-3	White	MARC
15	CB170024-5-1	Red	MARC	47	CB170038-11-3	White	MARC
16	CB170066-6	White	MARC	48	CB170052-3-2	White	MARC
17	CB170044-46	Red	MARC	49	CB170058-3-1	White	MARC
18	CB170044-31-3	Red	MARC	50	Geno418	White	MARC
19	CB170003-24-1	Red	MARC	51	CB170003-17	White	MARC
20	CB170046-5-1	White	MARC	52	CB170001-18	Red	MARC
21	CB170044-89-2	Red	MARC	53	CB170065-59-1	White	MARC
22	CB170002-11-1	Red	MARC	54	CB170064-3-2	White	MARC
23	CB170065-56	White	MARC	55	CB170001-9-4	White	MARC
24	CB170044-31-1	White	MARC	56	CB170003-16	White	MARC
25	CB170003-28	Red	MARC	57	CB170046-42	Red	MARC
26	CB170044-41-3	Red	MARC	58	CB170003-20	Red	MARC
27	CB170002-1	White	MARC	59	CB170001-11	White	MARC
28	CB170064-10-2	Red	MARC	60	CB170003-19	White	MARC
29	CB170003-23-1	White	MARC	61	SeR119	Red	MARC
30	CB170051-7	White	MARC	62	Awash-2	White	MARC
31	CB170058-10	White	MARC	63	Gobu	White	SARC
32	CB170051-3-1	Red	MARC	64	Wabero	White	SARC

The genotype and the variety listed from 1 to 62 were obtained from Melkasa Agricultural Research Center (MARC) and the two varieties listed as No. 63 and 64 were obtained from Sinana Agricultural Research Center (SARC).

2.3. Experimental Design and Management of the Experiment

The field experiment was laid out in 8*8 Simple Lattice Design. The plot size was 4.8 m² (4 rows of 3m long) with plant-to-plant and row-to-row distances were maintained at 10 and 40 cm, respectively. The genotypes were assigned to plots randomly within each incomplete block of each replication. All other crop management and protection practices were applied uniformly to all genotypes as recommended for the crop.

3.4. Data Collection

Data on phenology and yield were registered on plot basis while data on growth traits and yield components were collected from 10 randomly taken sample plants as described in descriptors of *Phaseolus vulgaris* (IBPGR, 1982) and Handbook on evaluation of *Phaseolus* Germplasm (Cuadrado et al., 2001).

3.4.1. Data collected on plot basis

At individual plot level data on Days to 50% of flowering, Days to maturity, Seed yield per hectare (kg) and 100 seed weight (g) were collected.

3.4.2. Basic parameter data collection

Plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant (NSPL), number of seeds per pod (NSPP).

3.5. Phenotypic and Genotypic Correlation Coefficients

The phenotypic and genotypic correlation coefficients were computed using the formula suggested by Singh and Chaudhury (1996).

$$\text{Phenotypic coefficient of correlation (rp)} \quad r_p = \frac{P_{covxy}}{\sqrt{(\sigma^2_{px} \cdot \sigma^2_{py})}}$$

$$\text{Genotypic Coefficient of Correlation (rg)} \quad r_g = \frac{G_{covxy}}{\sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})}}$$

Where

r_p = Phenotypic correlation coefficient, r_g = Genotypic correlation coefficient

P_{covxy} = Phenotypic covariance between variables x and y

G_{covxy} = Genotypic covariance between variables x and y

σ^2_{gx} = Genotypic variance for trait X, σ^2_{gy} = Genotypic variance for trait Y

σ^2_{px} = Phenotypic variance for trait X, σ^2_{py} = Phenotypic variance for trait Y

3.6. Path Coefficient Analysis

The path coefficient obtained by using the general formula of Wright (1921) by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient.

$$r_{ij} = p_{ij} + \sum r_{ik} \cdot p_{kj}$$

Where; r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficient, p_{ij} components of direct effects of the independent character (i) on the dependent variable (j) as measured by the genotypic path coefficient; and $\sum r_{ik} \cdot p_{kj}$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent character (k)

The coefficient of correlations at phenotypic level was tested for their significance by comparing the value of correlation coefficient with tabulated *t*-value at *g*-2 degrees of freedom. However, the coefficient of correlations at genotypic level was tested for their significance using the formula described by Robertson (1959) indicated below:

$$t = \frac{(rg_{xy})}{SEg_{xy}}$$

the calculated 't' value was compared with the tabulated 't' value at *g*-2 degrees of freedom at 5% level of significance, where *g* = number of genotypes

$$SEg_{xy} = \sqrt{\frac{(1-r^2_{g_{xy}})}{2h_x h_y}}$$

Where: SEg_{xy} = Standard error of genotypic correlation coefficient between character *x* and *y*
 h_x = Heritability value of character *x*
 h_y = Heritability value of character *y*

The calculated absolute *t* value was tested against the tabulated *t*-value at *g*-2 degrees of freedom for both phenotypic and genotypic correlations. Environmental correlation coefficients were tested at [(*g*-1) (*r*-1)-1] degrees of freedom, where *g* is the number of genotypes.

The contributions of the remaining unknown factors (effects) were measured as the residual effect (RE) is calculated as:

$$\sqrt{1 - R^2}, \quad R^2 = \sum pijri$$

3. RESULTS AND DISCUSSION

3.1. Genotypic and Phenotypic Correlation Coefficients of Grain Yield with other Traits

Estimates of genotypic and phenotypic correlation coefficients were computed for different characters at Ginir (Table 3) and at Goro (Table 4). The computed characters include number of secondary branches, pods per plant, seeds per pod and seeds per plant at genotypic and phenotypic levels at two locations Grain yield

had positive and highly significant ($P < 0.01$) correlations with number of primary branches. Reports by (Ejara et al., 2017; Kassa et al., 2019; and Chaudhary et al., 2020) revealed positive and significant relationships of grain yield with number of primary branches, number of secondary branches, Number of pods per plant and total number of seeds per plant.

The presence of highly significant ($P < 0.01$) and positive correlation of these traits with grain yield at genotypic and phenotypic levels indicate prime importance of these traits in selection program to identify common bean genotypes with high grain yield. The estimate of genotypic correlation is higher than their respective phenotypic correlations for most of the traits except for number of secondary branches indicating strong inherent relationship between the traits. Direct selection only for higher grain yield could be misleading because many factors interact to determine grain yield of crops. Selections for separate grain yield traits which are less influenced by the environment than grain yield itself are useful to acquire genotypes with better grain yield abilities (Gatti et al., 2005). Phenotypic correlation measures the extent to which the two observed traits are linearly related while genotypic correlation measures the degree of the same genes or closely linked genes cause co-variation (simultaneous variations) in two different traits (Singh and Chaudhary, 1977; Falconer and Mackay 1996; Sharma, 1998). The inherent or heritable association between two variables is a genotypic correlation but phenotypic correlation varies at different environments and lessened by the significant interaction of environment (Kumar and Reddy, 2014).

Grain yield had negative and highly significant ($P < 0.01$) associations with days to flowering at genotypic and phenotypic levels at both Ginir and Goro Vertisol locations (Table 3 and Table 4). The negative and highly significant ($p < 0.01$) association of this trait with grain yield suggested the importance of giving attention to days to flowering in the process of the selection of common bean genotypes for high grain yield. The presence of non-significant correlations of the two variables indicated that the two traits are independent of each other or that

genes concerned are located far apart on the same chromosome or they are located on different chromosomes. In plant genetics and breeding studies, correlated traits are of prime importance because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes can be brought in correlated traits either by a natural or/and artificial selection (Singh, 1993; Falconer et al., 1990; Sharma, 1998). Ketema and Geleta (2022) reported that days to maturity and plant height had negative and non-significantly correlated with grain yield at genotypic and phenotypic level. Simon et al. (2020) reported that positive and non-significant phenotypic and genotypic correlation coefficients of hundred seeds weight with grain yield of common bean genotypes. Simon et al. (2020) reported that positive and non-significant phenotypic and genotypic correlation coefficients of hundred seeds weight with grain yield of common bean genotypes

The coefficients of genotypic and phenotypic variations were generally low for days to maturity and plant height which could be due to limited variability in the genetic materials studied. Ejara et al. (2017) and Kassa et al. (2019) reported that grain yield had non-significant and negative correlation with days to maturity and plant height. Ketema and Geleta (2022) also reported negative and non-significant association of days to maturity and plant height with grain yield of common bean genotypes. Ejara et al. (2017) reported that early flowering and maturing genotypes produce a higher grain yield than the late ones in most situations. In contrast, Bagheri et al. (2017) reported positive and significant association of days to flowering with grain yield in common bean. Simon et al. (2020) also reported positive and significant association days to flowering and days to maturity with grain yield.

3.2. Genotypic and Phenotypic Correlation Coefficients among Yield Related Traits

Positive and significant ($p < 0.05$) correlations among phenology parameters (days to flowering and days to maturity) were observed at phenotypic level, while positive and non-significant at genotypic level. Days to maturity

with plant height at genotypic and phenotypic levels showed positive and non-significant correlations. Days to flowering with number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant showed negative and significant ($P < 0.05$) correlations at genotypic and phenotypic levels. Days to maturity had negative and non-significant genotypic and phenotypic associations with number of primary branches, secondary branches, pods per plant, seeds per pod and hundred seed weight at Ginnir and Goro (Table 3 and Table 4). The presence of non-significant correlations of these traits with days to maturity indicated that they are independent of each other.

Number of primary branches showed positive and highly significant ($p < 0.01$) association with number of secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant. The number of secondary branches showed positive and significant ($p < 0.05$) correlation at genotypic and phenotypic level with number of pods per plant, number of seeds per pod and number of seeds per plant. The number of pods per plant also showed positive and significant ($p < 0.05$) correlation with the number of seeds per pod and number of seeds per plant at Goro (Table 3 and Ginnir (Table 4).

At both genotypic and phenotypic levels, the number of seeds per pod also showed positive and highly significant ($p < 0.01$) association with number of primary branches, number of secondary branches, number of pods per plant and number of seeds per plant at both Goro and Ginnir aite. The number of seeds per plant also showed positive and highly significant ($p < 0.01$) genotypic and phenotypic association with number of primary branches, number of secondary branches and number of pods per plant. On the other hand. The hundred seed weight had negative and non-significant genotypic and phenotypic association with days to flowering, days to maturity and plant height. This negative association of hundred seed weight with those traits indicates a compensatory relationship between them. More late flowering and maturing could result in the reduction of the seed size because of competition among seeds for limited food reserves (Dewey and Lu, 1959). The

correlation results of the present study had showed that the genotypic correlation coefficient in most cases was higher than their corresponding phenotypic correlation coefficient. This suggests that there was an inherent relationship between these traits and the possibility of effective phenotypic selection (Choyal et al., 2018).

Correlation coefficient is a statistical measure commonly used to find out the degree of relationship between two or more variables and changes brought about by a natural or artificial selection among correlated traits. The genotypic correlation coefficients having similar sign and nature to the corresponding phenotypic correlation coefficient bring similar changes among correlated traits either by a natural or artificial selection (Falconer et al., 1990; Sharma, 1998). Therefore, any pairs of traits that had positive correlation of the present common bean genotypes indicated the possibility of correlated response to selection. Unlike positive correlation, negative correlation between two desirable traits may make it impossible to achieve the simultaneous improvement of those traits along with each other.

Ejara et al. (2017) reported that number of branches showed positive correlation with number of Seeds per pod, number of seeds per plant and grain yield at genotypic and phenotypic levels. Razvi et al. (2018) also reported number of pods per plant showed significant ($P < 0.05$) and positive correlation with number of branches, number of seeds per pod and grain yield in common bean. However, the present study showed weak association of plant height and hundred seed weight with all the traits. Such disagreement can be explained as reported by Falconer and Mackay (1996) indicating that the genetic and environmental variations influenced those traits through different physiological mechanisms. The occurrence of positive or negative genetic correlation is due to pleiotropy or genetic links among the genes responsible for these characteristics (Ghobary and Abd Allah, 2010).

3.3. Genotypic and Phenotypic Path Analyses of Yield and other Traits

The correlation coefficient indicates the association of variables' total effect that does not show the direct effect and indirect effects of variables. The path analysis is the portioning of the total correlation into direct and indirect effects of independent variable(s) on dependent variable (Singh and Chaudhary, 1977; Dabholkar, 1992). According to Wright (1921), path coefficient analysis provides a better knowledge of direct and indirect causes of associations, and it permits a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor.

The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 5 and Table 6 at Goro and Ginnir. respectively. While, phenotypic path coefficient analysis of grain yield with other traits are presented in Table 7 at Goro and Table 8 at Ginnir,. Number of primary and secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant had positive and highly significant ($P < 0.01$) correlation. Days to flowering had showed negative and highly significant ($P < 0.01$) genotypic and phenotypic correlation at Goro (Table 3) and Ginnir Table 4).

In the present study, only characters that had significant relationship with grain yield were included in the path analysis (Dewy and Lu, 1959). Number of primary branches, number of pods per plant and number of seeds per pod had high positive direct effects of grain yield at genotypic and phenotypic levels, at both Goro and Ginnir. The results of this study revealed that the number of secondary branches had a small positive direct effect on grain yield, which can be counter balanced by high direct effect through number of primary branches, number of pods per plant and number of seeds per pod. Number of primary branches, number of pods per plant and number of seeds per pod had significant ($P < 0.05$) and positive association with grain yield. Therefore,

Table 3. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient at Ginnir among 15 traits of 64 Small seeded Common bean genotypes evaluated in 2021

Trait	DF	DM	NPB	NSB	NPPP	NSPP	NSPL	PHT	HSW	GY
DF	1	0.37	-0.93**	-0.78**	-0.92**	-0.92**	-0.94**	-0.05	-0.23	-0.95**
DM	0.33*	1	-0.31	-0.3	-0.26	-0.31	-0.28	0.26	-0.04	-0.34
NPB	-0.90**	-0.22	1	0.86**	0.92**	0.89**	0.93**	0.1	0.23	0.96**
NSB	-0.72**	-0.2	0.81**	1	0.79**	0.80**	0.81**	0.16	0.19	0.85**
NPPP	-0.90**	-0.2	0.88**	0.71**	1	0.90**	0.98**	0.12	0.24	0.92**
NSPP	-0.85**	-0.24	0.81**	0.71**	0.85**	1	0.96**	0.05	0.21	0.93**
NSPL	-0.91**	-0.23	0.88**	0.74**	0.96**	0.93**	1	0.07	0.23	0.94**
PHT	-0.03	0.21	0.09	0.1	0.1	0.04	0.06	1	-0.13	0.07
HSW	-0.2	-0.02	0.2	0.17	0.22	0.19	0.22	-0.12	1	0.24
GY	-0.93**	-0.29	0.92**	0.77**	0.90**	0.87**	0.92**	0.06	0.22	1

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ probability level respectively DF =days to flowering, DM = days to maturity, NPB = number of primary branches, NSB = number of secondary branches, NPPP = number of pod per plant, NSPP = number of seed per pod, NSPL = number of seed per plant, PHT = Plant height, HSW = Hundred seed weight, and GY = grain yield.

Table 3 Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient at Goro among 15 traits of 64 Small seeded Common bean genotypes evaluated in 2021

Trait	DF	DM	NPB	NSB	NPPP	NSPP	NSPL	PHT	HSW	GY
DF	1	0.39	-0.93**	-0.81**	-0.3	-0.83**	-0.84**	0.22	-0.23	-0.98**
DM	0.31*	1	-0.33	-0.15	-0.28	-0.34	-0.43*	0.32	-0.08	-0.35
NPB	-0.87**	-0.23	1	0.74**	0.31	0.81**	0.81**	-0.17	0.15	0.94**
NSB	-0.71**	-0.08	0.64**	1	0.17	0.68**	0.66**	-0.14	0.28	0.83**
NPPP	-0.25	-0.23	0.24	0.13	1	0.14	0.52**	-0.01	-0.09	0.90**
NSPP	-0.77**	-0.31*	0.72**	0.59**	0.06	1	0.88**	-0.3	0.22	0.85**
NSPL	-0.78**	-0.38**	0.74**	0.57**	0.49**	0.85**	1	-0.24	0.12	0.85**
PHT	0.21	0.28	-0.14	-0.1	-0.02	-0.28	-0.23	1	-0.14	-0.19
HSW	-0.22	-0.04	0.13	0.25	-0.08	0.2	0.11	-0.14	1	0.23
GY	-0.96**	-0.29	0.90**	0.75**	0.86**	0.78**	0.80**	-0.19	0.22	1

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ probability level respectively DF =days to flowering, DM = days to maturity, NPB = number of primary branches, NSB = number of secondary branches, NPPP = number of pod per plant, NSPP = number of seed per pod, NSPL = number of seed per plant, PHT = Plant height, HSW = Hundred seed weight, and GY = grain yield

important consideration should be given while practicing selection aimed at the improvement of grain yield

The trait that has positive correlation with grain yield and has large and positive direct effect is considered as an important component of grain yield (Dabholkar, 1992). In this study, the observed positive and significant correlations of number of primary branches, number of secondary branches and number of pods per plant with grain yield were the true relationship suggesting that the direct selection of genotypes for yield through these traits will be effective.

Days taken to flowering and number of seeds per plant had negative direct effects at genotypic and phenotypic level, and indirect effects via number of primary branches, number of secondary branches, number of pods per plant and number of seeds per pod, whereas other traits had positive indirect effects at Goro and Ginnir. The indirect effects via most other traits were negligible. Therefore, the phenotypic correlation with grain yield was eagerly due to the direct effect. The number of primary branches had a positive direct effect at genotypic and phenotypic level on grain yield at both Goro and Ginnir,

likewise, the significant and positive correlation between number of primary branches and grain yield might be due to considerable indirect effect of number of primary branches via number of secondary branches, number of seeds per pod and number of pods per plant. Daniel et al. (2015) had reported that path coefficient at genotypic level showed that number of pods per plant had positive direct influence on grain yield while days to flowering and number of seeds per plant had showed negative direct effect on grain yield. Mukerem et al. (2019) also reported similar results for days to flowering had exerted negative direct effect on grain yield of common bean.

Residual effect in genotypic path analyses at Goro and Ginnir was 0.261 and 0.401 Table 5 and Table 6, respectively, showing that 97.39% and 95.99% of the variability in grain yield was explained by the component factors at genotypic levels. The remaining 2.63 and 4.01 % could be explained by other traits, not considered in this study. While at phenotypic level residual effect was 0.1024 and 0.816, at Goro and Ginnir, respectively, indicating that 89.76% and 91.84% of variability was explained by component factors (Table 7 and Table 8).

Table 5. Genotypic path analysis of the direct (bold) and indirect effect of yield related traits on grain yield of 64 common bean Genotypes at Goro, 2021

Traits	DF	NPB	NSB	NPPP	NSPP	NSPL	GY
DF	-1.0183	0.3278	-0.2123	-0.6675	-2.6655	3.2558	-0.98**
NPB	0.9470	-0.3525	0.1940	0.6898	2.6013	-3.1395	0.94**
NSB	0.8248	-0.2608	0.2621	0.3783	2.1838	-2.5582	0.83**
NPPP	0.3055	-0.1093	0.0446	2.2251	0.4496	-2.0155	0.9**
NSPP	0.8452	-0.2855	0.1783	0.3115	3.2114	-3.4109	0.85**
NSPL	0.8553	-0.2855	0.1730	1.1571	2.8261	-3.8760	0.85**

Residual = 0.026

Table 6. Genotypic path analysis of the direct (bold) and indirect effect of yield related traits on grain yield of 64 common bean Genotypes at Ginnir, 2021

Trait	DF	NPB	NSB	NPPP	NSPP	NSPL	Rg
DF	-0.27	-0.41	-0.06	-0.36	-0.45	0.61	-0.95
NPB	0.26	0.45	0.07	0.36	0.43	-0.60	0.96**
NSB	0.21	0.38	0.08	0.31	0.39	-0.52	0.85**
NPPP	0.25	0.41	0.06	0.39	0.44	-0.63	0.92**

NSPP	0.25	0.40	0.06	0.35	0.49	-0.62	0.93**
NSPL	0.26	0.41	0.06	0.38	0.47	-0.65	0.94**

Residual = 0.040

Table 7. Phenotypic path analysis of the direct (bold) and indirect effect of yield related traits on grain yield of 64 Common bean Genotypes at Goro, 2021

Trait	DF	NPB	NSB	NPPP	NSPP	NSPL	rg
DF	-0.5480	-0.2662	-0.1310	-0.5117	-1.9882	2.3970	-0.96**
NPB	0.4767	0.3060	0.1181	0.4913	1.8591	-2.2741	0.9**
NSB	0.3890	0.1959	0.1845	0.2661	1.5234	-1.7517	0.75**
NPPP	0.1370	0.0734	0.0240	2.0470	0.1549	-1.5058	0.86**
NSPP	0.4219	0.2203	0.1089	0.1228	2.5821	-2.6122	0.78**
NSPL	0.4274	0.2265	0.1052	1.0030	2.1948	-3.0731	0.8**

Residual = 0.102

Table 8. Phenotypic path analysis of the direct (bold) and indirect effect of yield related traits on grain yield of 64 Common bean Genotypes at Ginnir, 2021

Trait	DF	NPB	NSB	NPPP	NSPP	NSPL	Rg
DF	-0.35	-0.27	-0.04	-0.02	-0.10	-0.15	-0.93**
NPB	0.31	0.30	0.04	0.02	0.09	0.15	0.92**
NSB	0.25	0.25	0.05	0.02	0.08	0.13	0.77**
NPPP	0.31	0.27	0.04	0.03	0.10	0.16	0.90**
NSPP	0.29	0.25	0.04	0.02	0.12	0.16	0.87**
NSPL	0.31	0.27	0.04	0.02	0.11	0.17	0.92**

Residual=0.082

4. CONCLUSION

Grain yield showed positive and highly significant ($p < 0.01$) correlation with numbers of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant at genotypic and phenotypic level. On the other hand, grain yield had showed negative and highly significant ($p < 0.01$) correlation with days to flowering at genotypic and phenotypic level at both Goro and Ginnir. Number of primary branches, number of secondary branches, number of pods per plant and number of seeds per pod had positive direct effect on grain yield at genotypic and phenotypic levels at Goro and Ginnir suggesting that the direct selection of genotypes for these traits will be effective to identify genotypes for high grain yield. Days to flowering and number of seeds per plant exerted negative direct effect on grain yield at genotypic and phenotypic levels. Therefore, much attention

should be given to these traits as they are helpful for indirect selection to improve grain yield in small seeded common beans.

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