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Genetic variability of common bean (*Phaseolus vulgaris* L.) genotypes under sole and maize-bean cropping systems in Bako, Western Oromia, Ethiopia

Kassa Mammo^{1*}, Dagne Wegary², Dagnachew Lule¹ and Firew Mekbib³

¹Bako Agricultural Research Center, P. O. Box 03, West Shewa, Bako, Ethiopia.

²International Maize and Wheat Improvement Center (CIMMYT) Ethiopia, P. O. Box 5689, Addis Ababa, Ethiopia.

³Department of Plant Breeding and Genetics, Faculty of Agriculture, Haramaya University, P. O. Box 138, Dire Dawa, Ethiopia.

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Knowledge of the sources and magnitude of variability among genotypes plays a pivotal role in any crop improvement program to maximize gains from selection. This experiment was conducted at Bako Agricultural Research Center in 2011 cropping season with the objective of studying and estimating the extent of genetic variability in common bean genotypes under sole and mixed cropping systems. Meanwhile, the wider range of variability observed from the mean of various quantitative traits. The genotypes that varied by cropping system depicted the presence of high level of variability. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were recorded for hundred grain weight (29.56 and 35.46 g), biological yield (27.22 and 31.37) and grain yield (26.60 and 31.54 q/ha), whereas the lowest GCV and PCV values were recorded for days to maturity of sole common bean genotypes. Phenotypic variance in both sole and mixed cropping systems was higher than that of genotypic variances. This implies that, considerable contribution of environmental factors to the phenotypic expression of the genotypes. High broad sense heritability as observed under both sole and intercropping systems indicated that, genetic improvement can be obtained through further selection programme. Important agronomic traits: pods per plant, seeds per pod and branches per plant had positive and significant correlation with grain yield in most cases. Path coefficient analysis at genotypic level indicated that all traits except plant height, seeds per pod and hundred grain weights exerted their positive direct effect on grain yield. Hence, the current study identified the presence of wide variability between those common bean genotypes which can be used for further breeding program and selection can be made using those traits associated to yield.

Key words: Genotypic variance, heritability, intercropping, phenotypic variance, quantitative traits, sole cropping.

INTRODUCTION

Genetic diversity in crop plants arises as a consequence of evolutionary processes (mutations, selections,

migration and random genetic drift) and the influence of man through selection and domestication (Allard, 1960).

*Corresponding author. E-mail: fenerob@gmail.com.

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Genetic variability has been considered as an important factor which is also an essential prerequisite for crop improvement program for obtaining high yielding progenies (Tiwari and Lavanya, 2012). In this regard, variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised. This variability within or among populations can be genotypic, phenotypic or the interaction of these two factors (Falconer and Mackay, 1996). According to Welsh (1990) and Sharma (1998), genetic variability is due to genetic differences among individuals within a population, is the core of plant breeding.

Genetic variation is, therefore, the basis for crop improvement and plant breeders use this variation to direct and control evolutionary process by developing new varieties. This therefore has an immense importance to the breeder.

Heritability is important to plant breeders primarily as a measure of the value of selection for particular character in various types of progenies and as an index of transmissibility. Falconer and Mackay (1996) defined heritability as the heritable portion of phenotypic variance and is a good index of transmission of characters from parents to offspring. It is a property not only of a character being studied but also of a population being sampled, of the environmental circumstance to which the individuals are subjected, and the way in which the phenotype is measured (Dabholkar, 1992; Falconer and Mackay, 1996).

Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance, and epistatic variance, to the phenotypic variance whereas heritability in the narrow sense estimates only the additive portion of the total phenotypic variance and it expresses the extent to which phenotypes are determined by the genes transmitted from parents (Raiz and Chowdhry, 2003). Allard (1960) indicated that the heritability values for quantitative traits are low mainly due to their sensitivity to environment factors. Estimate of narrow sense heritability is not possible; thus, by estimating broad sense heritability along with genetic gain is usually more useful in selecting the best individual (Johnson et al., 1955).

Genetic advance measures the difference between genotypic values of generation obtained from the selected population over the mean value of the base population. Therefore, the utility of estimates of heritability is increased when heritability and genetic advance are used in conjunction with selection differential, the amount that the mean of the selected lines exceeds the mean of the entire group (Johnson et al., 1955). Heritability estimates and genetic advance should always be considered simultaneously, because high heritability will not be always associated with high genetic advance (Amin et al., 1992). Economic characters like grain yield are polygenic in nature and are often influenced by the environment and thus have low heritability (Raiz and

Chowdhry, 2003). If environmental variability is small in relation to genotypic differences, selection will be efficient and the selected trait will be transmitted to its progeny (Briggs and Knowles, 1967).

Furthermore, understanding of the genetic association of breeding materials could help to maintain genetic diversity and sustain long term selection gain. Correlation analysis suggested observations on rhizome yield and other such that the magnitude of genotypic correlation was morphological traits. The mean value of these is higher as compared to their corresponding plants computed and used for statistical phenotypic correlations indicating the inherent analysis. Analysis of variance to test the significant relationship among the characters studied (Prajapati et al., 2014). Hence, any breeding program aiming at increasing yield should consider association between yield and its attributes through estimation of genotypic and phenotypic correlation, which help a great deal in formulating selection indices to aid in selection programs. Knowing the variability existing in a crop is necessary to formulate and accelerate conventional breeding program. Therefore, the present study was initiated to assess the extent and pattern of phenotypic and genotypic variability of different common bean genotypes of the area.

MATERIALS AND METHODS

The study area

The experiment was conducted at Bako Agricultural Research Center (BARC) in 2011 cropping season. BARC is found in East Wellega zone, Oromia Regional State of Ethiopia. The center is located on 9° 6' N and 37° 09' E latitude and longitude, respectively. It is also characterized by sub-humid agro-ecology with an altitude of 1650 m.a.s.l and has a unimodal rainfall pattern and an annual rainfall of 1425.3 mm/annum. The rainy season extends from April to November, but maximum rainfall of 295.2, 224.0 and 294.6 mm was received during the growing months in June, July and August, respectively (Figure 1).

The minimum, maximum and average air temperature of the center was 13.5, 27.3 and 20.4°C, respectively. Soil type of the study area is Alfisols, which is clay in texture and acidic in reaction (Negassa, 2001).

Experimental materials

Twenty-four common bean genotypes including one local variety which was frequently used by the farmers of the area were used as a planting material. These common bean genotypes were obtained from Melkassa Agricultural Research Center (MARC) and selected from the regional variety trials which were conducted at BARC during the 2009/2010 cropping season. The selection was made based on *per se* performance and adaptability of bean genotypes under sole cropping condition around Bako area (Table 1).

The hybrid maize variety used in this study was BH-540 which is the most popular maize variety around Bako and similar agro-ecologies of East Wellega and it has medium plant height and grouped within the medium maturing hybrid varieties.

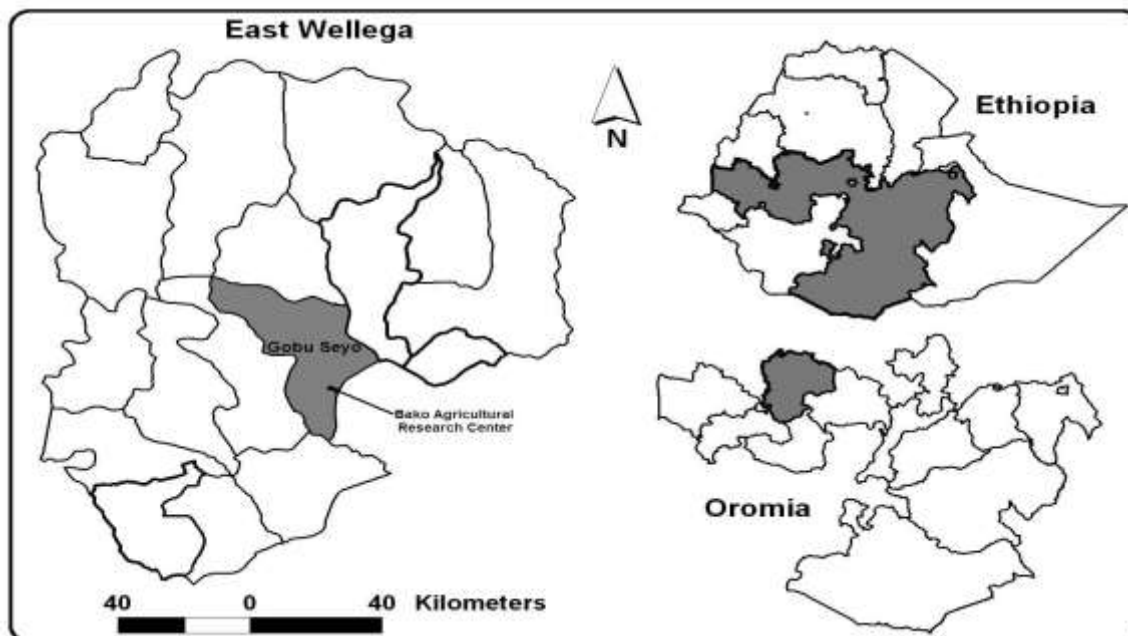


Figure 1. Study district in East Wellega Zone of Oromia, Ethiopia.

Table 1. List of common bean genotypes used.

Genotype	Genotype
SEN-4L	FEB-147 X EAP-4
SEN-46	ECAB-06-01
SEN-53	557-FIN-1
ICTAJU-95-56	DB-190-84-1
TB-94-02	UBR(92)25-13-1
AN-92=12123	BAT-1198 XBAT-1248
ICTAJU-95-1-07	MEXICO235 X PAN-182
AN-9123342	SK-93846
ICTAJU-95-28	MEXICO-23 X BAT-338-1C-10
FEB-190	BAT-1198 X BAT-1248-6
ROBA X FEB-147	BAT-448 X PAN-182-2
ATENDABA X EAP-4	Local check (Burree)

Experimental design and field management

The experiment comprised two separate activities, that is, sole common bean component and bean-maize intercropping which were used for compatibility study of common bean genotypes. Both experiments were laid out in 5x5 triple lattice designs with three replications. The sole common beans involved a total of twenty-five genotypes including one standard and local check and the bean-maize intercropping consisted of twenty-four genotypes and one maize plot grown without common bean as sole cropping. Each of the sole bean plots comprised four rows spaced at the distance of 0.40 m with 5.1 m length, and the space between individual plants within a row was 0.10 m. On the other hand, intercropped plot consisted of four rows of 5.1 m length and sown between 0.75 m spaced maize rows. Common bean genotypes were under sown

after twenty-one days at their optimum planting densities alike to that of sole cropping and later reduced to 50% of the plant population. Fertilizers were applied in the form of Urea and DAP with the rates of 18/46 kg ha⁻¹ N/P₂O₅ and 100/100 kg ha⁻¹ N/P₂O₅ for sole common bean and maize-bean intercropping plots, respectively. All the DAP fertilizer was applied at planting while urea was applied at two rates, half at planting and the remaining half side-dressed at knee height stage of maize.

Data collection

Data for all traits of beans and maize were collected from ten randomly selected plants of the two central rows for both sole and intercropped experiments. Grain yields of the two crops were

adjusted to 10 and 12.5% moisture level for bean and maize, respectively.

Date of emergence, days of flowering, days of maturity, plant height, number of pods per plant, number of seeds per pod, pod length, grain yield, number of plants per plot, 100 grain weight, biological yield and number of primary branches were data collected for bean crop whereas the number of ears per plant, ear length, thousand kernel weight and grain yield were data collected for maize crop.

Data analysis

Analysis of variance (ANOVA)

ANOVA for sole common bean was computed using Statistical Analysis System (SAS) computer software using SAS syntax for simple lattice design (SAS, 2004). Comparisons of the relative efficiency of lattice design to RCBD were done after data analysis due to the flexibility of lattice design (Cochran and Cox, 1957). The mean values and rank orders were calculated for each genotype. In addition, correlation coefficients were computed between each pair of the traits.

Estimation of components of variation

The genetic and phenotypic variability among genotypes and coefficient of variation of each trait under the study were calculated for common bean genotypes planted under sole and intercropping condition using the formula adopted by Johnson et al. (1955).

$$\sigma_g^2 = \frac{(MS_g - MSe)}{r}$$

Genotypic variance

Phenotypic variance $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Environmental variance (σ_e^2) = MS_e

where σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance, (σ_e^2) = environmental variance, MS_g = Mean square due to genotypes/accessions, MS_e = Error mean square, and r = number of replications.

The coefficients of variations at phenotypic and genotypic level were estimated using:

$$GCV = \frac{\sigma_g}{\bar{x}} \times 100$$

$$PCV = \frac{\sigma_p}{\bar{x}} \times 100$$

$$ECV = \frac{\sigma_e}{\bar{x}} \times 100$$

where σ_p = Phenotypic standard deviation, $(\sigma_g + \sigma_e)$ σ_g =

Genotypic standard deviation, σ_e = Environmental standard

deviation, and \bar{x} = Grand mean for the characteristic x ; PCV, GCV, and ECV = Phenotypic, genotypic and environmental coefficient of variation, respectively.

Estimate of heritability

Heritability (h^2) in broad sense for all characters was computed using the formula suggested by Allard (1960).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

$$\sigma_p^2 = \sigma_e^2 + \sigma_g^2$$

where σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance, and σ_e^2 = error variance.

Estimation of expected genetic advance

Genetic advance as percent of the mean (GA) for each character were computed using the formula by Allard (1960).

$$A = K \times \sigma_p \times h^2$$

$$GAM = \frac{GA}{\bar{x}} \times 100$$

where K = selection differential (2.056 at 5% selection intensity),

σ_p = Phenotypic standard deviation, h^2 = Heritability and \bar{x} = Grand mean.

Estimation of phenotypic and genotypic correlations

Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by Miller et al. (1958).

Phenotypic correlation coefficient:

$$r_{P_{xy}} = \frac{\sigma_{pxy}}{\sqrt{\sigma_{px}^2 \times \sigma_{py}^2}}$$

Genotypic correlation coefficient

$$r_{G_{xy}} = \frac{\sigma_{gxy}}{\sqrt{\sigma_{gx}^2 \times \sigma_{gy}^2}}$$

where $r_{P_{xy}}$ = phenotypic correlation coefficient between character x and y , $r_{G_{xy}}$ = genotypic correlation coefficients between character x and y , σ_{px}^2 = phenotypic variance for character x , σ_{gy}^2 = genotypic variance for character y , σ_{gx}^2 = genotypic variance for character x , and σ_{py}^2 = Genotypic variance for character y .

Table 2. Average mean values and percent reduction of grain yield of common bean genotypes grown as sole and intercropping, 2011.

Genotype	2011		RANK	% Reduction
	Sole	Mix	Sole	
SEN-4L	37.81	3.96	8	89.53
SEN-46	35.18	4.42	11	87.44
SEN-53	23.23	2.70	18	88.38
ICTAJU-95-56	30.13	2.61	15	91.34
TB-94-02	27.08	3.77	16	86.08
AN-92=12123	35.54	3.86	9	89.14
ICTAJU-95-1-07	20.16	1.74	21	91.37
AN-9123342	34.89	2.47	10	92.92
ICTAJU-95-28	6.81	3.37	24	50.51
FEB-190	36.92	2.13	7	94.23
ROBA X FEB-147	39.84	3.13	3	92.14
ATENDABA X EAP-4	34.67	3.09	14	91.09
FEB-147 X EAP-4	36.29	5.13	5	85.86
ECAB-O6-01	40.71	3.04	4	92.53
557-FIN-1	36.22	3.29	13	90.92
DB-190-84-1	39.29	3.80	6	90.33
UBR(92)25-13-1	39.06	8.51	2	78.21
BAT-1198 XBAT-1248	16.12	2.68	22	83.37
MEXICO235 X PAN-182	32.29	7.51	12	76.74
SK-93846	45.88	3.33	1	92.74
MEXICO-23 X BAT-338-1C-10	21.73	1.86	20	91.44
BAT-1198 X BAT-1248-6	22.81	3.21	19	85.93
BAT-448 X PAN-182-2	24.42	2.89	17	88.17
Local check	10.26	1.19	23	89.53

BYIE=Biological yield (g), BRPL=branch per plant, DF= days to flower, DM=days to maturity, HGW= hundred grain weight (g), HI= harvest index (%), PH=plant height (cm), POPL=pod per plant, PLEN=pod length (cm), SEPO=seed per pod, YLD=grain yield (Qt ha⁻¹)

Path coefficient analysis

The direct and indirect effects of the independent traits on grain yield per plot were estimated by formula described by Dewey and Lu (1959) and, it was analysed using the formula developed by Singh and Chaudhary (2004).

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

where r_{ij} = Mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient. p_{ij} = Component of direct effects of the independent character (i) and dependent (j) as measured by the

path coefficient, and $\sum r_{ik}p_{kj}$ = Summation of components of

indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k).

RESULTS AND DISCUSSION

ANOVA for sole and intercropped common bean genotypes

ANOVA indicated that highly significant differences ($P \leq 0.01$) between cropping systems for plant height, pods per plant, seeds per pod, pod length, biological yield, and harvest index, branches per plant and grain yield and highly significant differences ($P \leq 0.01$) were observed among genotypes for all traits except for pod length (Table 2).

Genotype \times cropping system interaction effect was highly significant ($P \leq 0.01$) for all traits except for days to flowering, seeds per pod and hundred grain weights. This indicates that the performances of the bean were not consistent across the cropping systems.

Most of the genotypes responded differently under various cropping systems. This could be mainly due to the difference in the genetic makeup of the genotype and the environment on which the genotypes were grown. In general, the significant difference observed among the

Table 3. Analysis of variance for yield and yield related traits of common bean varieties under sole and intercropping condition at Bako (2011).

Source	Df	50%DF	DM	PH	POPL	SEPO	POLEN	HGW	BYIE	HI	BRPL	YLD
REP	2	93.44	48.38	317.26	11.96	0.39	0.92	30.14	258.43	20.54	2.65	6.82
Cropping system (A)	1	52.90 ^{ns}	3.86 ^{ns}	11665.13**	5119.17**	12.43**	11.20**	31.21 ^{ns}	1159063.93**	562.93**	359.90**	25.903.13**
Error A	2	134.25	29.55	129.76	12.87	0.27	0.42	83.96	139433.34	7.21	5.48	28.02
Genotype (B)	23	31.91**	316.88**	3533.66**	60.80**	2.84**	4.53 ^{ns}	292.72**	171413.06**	312.2**	5.80**	177.37**
A x B	23	11.59 ^{ns}	73.88**	777.74**	36.45**	0.43 ^{ns}	0.60**	29.34 ^{ns}	111254.25**	158.23**	4.42**	136.98**
Error B	46	10.65	16.42	135.16	7.78	0.16	0.35	15.47	41531.20	50.66	1.16	22.06
R2	-	0.85	0.90	0.97	0.95	0.90	0.92	0.90	0.91	0.90	0.91	0.97
CV	-	6.86	5.50	12.61	22.05	8.66	6.36	19.73	30.10	13.43	16.25	27.55
LSD	-	3.15	5.55	10.15	3.16	0.56	0.63	5.18	251.89	6.72	1.42	5.41
Relative reduction*	-	-3.3	-0.7	22.9	64.9	9.0	7.2	7.6	56.5	14.7	34.0	88.5

*Percent relative reduction due to intercropping ($1 - V_{\text{mixed}}/V_{\text{sole}}$), negative values indicate an increase under intercropping in that particular trait; V_{mixed} and V_{sole} , indicate trait mean values under intercropping and sole cropping condition, respectively. BYIE= biological yield (g), BRPL= branch per plant, DF= Days to flower, DM=days to maturity, HGW= hundred grain weight (g), HI= Harvest index (%), PH=plant height (cm), POPL=pod per plant, POLEN=pod length (cm), SEPO= Seed per pod, YLD =Grain Yield (Qt ha^{-1}), **, * and ns = Highly significant at ($P \leq 0.05$), significant and non-significant, respectively.

genotypes in the two cropping systems indicated that there is an apparent phenotypic and genotypic variation among the genotypes and which could be exploited in breeding program (Table 3).

Components of variation for sole and intercropped bean genotypes

As per the analysis for intercropped beans shown in Table 4, the highest genotypic and phenotypic coefficient of variations were recorded for plant height (50.22 and 52.8), grain yield (45.04 and 51.40), hundred grain weight (33.23 and 40.85) and pod per plant (32.13 and 37.0), respectively, whereas the lowest genotypic and phenotypic coefficient of variation was recorded for the days to maturity (6.65 and 8.84). Similarly, when the two cropping systems are compared based on the GCV and PCV values of respective traits, the highest GCV and PCV values were exhibited for similar traits, that is, hundred grain weight, grain

yield and pod per plant, for both sole and intercropping conditions. Moreover, the GCV and PCV values for plant height for both sole cropping and intercropping were considered as the highest value. Generally, the PCV values were greater than the GCV values in both cropping systems which indicated the influence of environmental factor greater than genotypic factor. In addition, the PCV values exhibited for most of the traits under intercropping condition were greater than the PCV values exhibited under sole cropping condition except for days to maturity and branch per plant. Pooja et al. (2015), also indicated that, PCV values were higher than GCV values, which indicate the effect of environment on the expression of characters. Characters showed considerable difference between PCV and GCV values, to be number of pods per plant and number of ovules per pod. It indicates more environment influenced variation rather than due to genotype, so these traits may be misleading in selection procedure. Similar to the PCV values,

the GCV values recorded for most of the quantitative traits under intercropping condition were greater than the PCV values recorded under sole cropping condition except for days to maturity, pod length, biological yield and branch per plant. The greater difference in PCV and GCV value of the traits and the variability of genotypes under sole and intercropping condition for most of the traits implicated that the presence of phenotypic and genotypic variation between genotypes and these variations were more pronounced under intercropping than the sole cropping. Kassaye (2006) reported that the highest values of PCV and GCV were recorded for most of the traits and the lowest PCV and GCV values were recorded for days to maturity. Similarly, Samal et al. (1995) also examined the performance, variability and correlation and co-heritability estimates in Rajmash and found out that all the traits except branches per plant and pod length exhibited wide range of variability. He also reported that the phenotypic and genotypic

Table 4. Values for components of variation and range for sole and intercropped bean at Bako (2011).

Trait	GVs	GVMi	PVs	PVMi	EVs	EVMi	GCVs	GCVMi	PCVs	PCVMi	Range Mi
DM	57.65	33.51	67.36	59.36	9.71	25.85	8.78	6.65	9.49	8.84	71.0-104.33
PH	291.05	914.68	423.92	1010.90	132.87	96.22	21.84	50.22	26.35	52.80	26.33-156.33
POPL	13.90	4.18	26.12	6.34	12.22	2.16	20.59	32.13	28.23	39.58	2.73-8.53
SEPO	0.42	0.60	0.59	0.81	0.17	0.21	11.13	14.68	13.21	17.03	2.8-6.27
PLEN	0.87	0.57	1.11	0.99	0.25	0.42	10.41	9.07	11.80	11.98	6.8-10.47
HGW	52.44	54.02	73.04	66.87	20.60	12.85	30.24	33.23	35.69	36.97	13.67-49.67
BYIE	49581.26	7678.14	102181.74	20282.30	52600.48	12604.16	22.70	20.52	32.58	33.35	233.3-900.0
HI	78.84	35.72	96.62	90.47	17.78	54.75	19.58	14.55	21.68	23.15	21.87-60.67
BRPL	1.81	0.66	3.58	1.06	1.77	0.40	14.91	13.66	20.95	17.29	3.93-7.33
YLD	62.56	2.47	90.97	3.21	28.41	0.75	26.10	45.04	31.48	51.40	1.19-8.52

BYIE=Biological yield (g), BRPL=branch per plant, DF= days to flower, DM=days to maturity, HGW=hundred grain weight (g), HI=harvest index (%), PH=plant height (cm), POPL=pod per plant, PLEN=pod length (cm), SEPO= seed per pod, YLD =grain yield (Qt ha⁻¹), GV, PVs, EVs, GCVs, and PCVs =genotypic variance, phenotypic variance, environmental variance, genotypic coefficient of variation and phenotypic coefficient of variation for sole cropping, respectively. GVMi, PVMi, EVMi, GCVMi and PCVMi =genotypic variance, phenotypic variance, environmental variance, genotypic coefficient of variation and phenotypic coefficient of variation for intercropping, respectively.

Table 5. Heritability, genetic advance as percent mean, mean and coefficient of variation of eleven traits for sole and intercropped bean.

Trait	Heritability		Genetic advance		GA as percent of mean		Grand mean		CV (%)	
	Sole	Mixed	Sole	Mixed	Sole	Mixed	Sole	Mixed	Sole	Mixed
DM	85.59	56.45	14.44	8.94	16.70	10.26	86.51	87.11	3.60	7.16
PH	68.66	90.48	29.06	59.14	37.20	98.21	78.13	60.22	14.75	17.30
POPL	53.21	65.91	5.59	3.41	30.89	53.63	18.10	6.36	19.30	21.55
SEPO	71.02	74.31	1.12	1.37	19.29	26.02	5.80	5.28	7.10	8.63
PLEN	77.86	57.36	1.69	1.17	18.88	14.12	8.94	8.30	5.50	7.81
HGW	71.79	80.78	12.62	13.58	52.68	61.40	23.95	22.11	18.95	16.20
BYIE	48.52	37.85	318.90	110.84	32.50	25.95	981.13	427.08	23.40	21.50
HI	65.29	42.83	39.99	26.74	45.89	35.97	87.14	74.33	20.14	21.26
BRPL	50.61	62.39	1.97	1.32	21.80	22.17	9.03	5.96	14.70	10.6
YLD	68.77	76.79	13.49	2.82	44.51	81.15	30.30	3.48	17.59	24.76

BYIE=Biological yield, BRPL=branch per plant, DM=days to maturity, HGW=hundred grain weight, HI=harvest index, PH=plant height, POPL=pod per plant, PLEN=pod length, SEPO=seed per pod, YLD=yield quintal per hectare, CV(%)=coefficient of variation for mixture.

variances were maximum for yield per plant and minimum for branches per plant.

Heritability in broad sense and genetic advance of common bean under sole and intercropping condition

Heritability estimates for all traits varied from 50.6 branches per plant to 85.6% for days to maturity for the sole cropping. Most of the traits recorded the highest percentage of heritability, which included days to maturity (85.59), pod length (77.86), hundred grain weight (71.79), seed per pod (71.02), grain yield (68.77), plant height (68.66) and harvest index (65.29) (Table 5). The lowest heritability value was recorded for days to flowering

(30.19) indicating that selection may be difficult to improve this character due to the masking effect of environment on the genotypic effect. Some of the traits that have higher heritability estimate also have high to moderate GCV and PCV values which indicated that improvement of these characters could easily be achieved because of close association between genotype and phenotype.

Likewise, the heritability estimates for intercropped bean genotypes revealed that the highest heritability estimate was recorded for plant height (90.48) followed by hundred grain weight (80.78) and grain yield (76.79) and the least heritability estimate was recorded for biological yield (37.85) and harvest index (42.83) under bean intercropping condition. Most of the traits under this cropping system exhibited the highest heritability, GCV

Table 6. Genotypic correlation among traits in common bean under sole cropping systems (the upper most of the table) and maize-bean intercropping (below diagonal) when analysed separately.

Correlation	DF	DM	PH	POPL	SEPO	PLEN	HGW	BYIE	HI	BRPL	YLD
DF		0.669**	0.501*	-0.128	0.319	0.328	-0.385	-0.113	-0.125	-0.122	-0.020
DM	0.59		0.706**	0.376	0.397	-0.372	-0.549**	0.289	-0.156	-0.086	0.197
PH	0.593**	0.895*		-0.087	0.326	0.038	-0.127	0.194	-0.080	-0.469*	0.094
POPL	0.460*	0.767**	0.759**		0.341	-0.556**	-0.536**	0.179	0.217	0.740**	0.549**
SEPO	0.339	0.428*	0.192	0.266		-0.271	-0.486*	0.426*	0.390	0.064	0.543**
PLEN	0.177	0.014	0.147	-0.251	-0.159		0.696**	-0.311	0.101	-0.309	-0.131
HGW	0.210	-0.089	0.129	-0.127	-0.730**	0.637**		-0.468*	0.309	-0.266	-0.142
BYIE	0.139	0.368	0.366	0.397	0.063	0.171	0.210		-0.139	-0.052	0.444*
HI	-0.005	0.584**	0.693**	0.588**	0.300	-0.008	-0.063	0.306		0.297	0.72**
BRPL	0.043	0.317	0.356	0.353	-0.227	0.083	0.288	0.559**	0.304		0.414*
YLD	0.029	0.831**	0.906**	0.829**	0.221	0.100	0.088	0.589**	0.795**	0.419	

BYIE=Biological yield (gm), BRPL=branch per plant, DF=days to flower, DM=days to maturity, HGW=hundred grain weight (g), HI=harvest index (%), PH=plant height (cm), POPL=pod per plant, PLEN=pod length (cm), SEPO= Seed per pod, YLD =Grain Yield (Qt ha⁻¹),

and PCV estimates that could be used during selection through these characters because of the better association between the genotype and phenotype. The higher genetic advances were recorded for biological yield (110.8 and 318.9) followed by plant height (59.14 and 37.2) and the least was recorded by branch per plant (1.32) and seed per pod (1.2) for sole and intercropped beans, respectively. Whereas, the highest genetic advance as a percent of mean were recorded for plant height (98.21), grain yield (81.15), hundred grain weight (61.4) and pod per plant (53.6) according to their order of importance. Generally, 98, 81, 61, and 53% of improvement can be made in selection through these characters for intercropped beans.

In agreement with the present study, Alemineh (2009) indicated that, heritability of the different traits measured under drought stressed and non-stress condition. Days to 50% flowering showed the lowest (31.74%) heritability under non-stressed whereas chlorophyll content had the lowest heritability under stressed treatments. Kassaye (2006) also reported high heritability estimate coupled with high genetic advance as percent of mean for 100-seed weight, plant height and number of nodes on the main stem.

Mesele (1997) also indicated that almost all the characters studied showed higher heritability percentage for pods per plant, pod length, seeds per plant and yield per plant than other characters. According to Sintayehu (1997), higher heritability estimate was recorded for 100-seed weight and moderately higher heritability estimates for pod length, yield per plant and days to maturity.

Most of yield and yield related traits in both cropping systems show the largest heritability estimates which enable the breeders to improve bean genotypes through better heritable traits. Similarly, the genetic advance as a percent mean also implicated that greater possibility of genotype improvement which could be made through

these characters.

Association of characters

Genotypic correlation coefficient for intercropped beans in comparison with sole cropping

Seed yield is a complex trait whose production is influenced by its component traits directly or indirectly. Breeder is certainly interested in investigating the extent and type of association of such traits for they contribute valuable information in breeding for yield. The correlation coefficient result for bean intercropping, below diagonal of the Table 6, indicated that grain yield was found to be positively and significantly correlated with days to maturity ($rg=0.83^{**}$), plant height ($rg=0.91^{**}$), pod per plant ($rg=0.83^{**}$), biological yield ($rg=0.59^{**}$) and harvest index ($rg=0.80^{**}$). Similarly, days to maturity with plant height ($r=0.89^{**}$), pod per plant with days to maturity ($rg=0.77^{**}$) and plant height ($rg=0.76^{**}$), hundred grain weight with pod length ($rg=0.64^{**}$), harvest index with days to maturity ($rg=0.58^{**}$), plant height ($rg=0.69^{**}$) and pod per plant ($rg=0.59^{**}$) and branch per plant with biological yield ($rg=0.56^{**}$) positively and significantly correlated.

There was also positive and significant correlation observed between pods per plant and days to maturity and days to flowering, and between seeds per pod and days to maturity. In contrast to this result there was negative and highly significant correlation observed between seeds per pod and hundred grain weight ($rg = -0.73^{**}$). Grain yield exhibited positive and highly significant genotypic correlation with harvest index ($rg=0.71^{**}$ and $rg=0.80^{**}$), pod per plant ($rg=0.55^{**}$ and $rg=0.83^{**}$) and biological yield ($rg=0.44^{**}$ and $rg=0.59^{**}$) under both sole and intercropping condition, respectively.

Table 7. Combined analysis of correlation coefficient among traits in common bean sole and intercropping condition.

Trait	DF	DM	PH	POPL	SEPO	PLEN	HGW	BYIE	HI	BRPL	YLD
DFMIX	0.409*	0.448*	0.372	-0.007	0.149	0.224	-0.175	0.196	-0.204	-0.114	0.020
DMMIX	0.612**	0.662**	0.646**	0.134	0.474*	0.077	-0.212	0.306	0.234	-0.173	0.424*
PHMIX	0.561**	0.554**	0.675**	0.015	0.312	0.297	0.112	0.079	0.323	-0.293	0.338
POPLMIX	0.501*	0.623**	0.454*	0.349	0.318	-0.104	-0.151	0.092	0.361	0.125	0.393
SEPOMIX	0.356	0.509*	0.388	0.252	0.761**	-0.401	-0.748**	0.527**	-0.065	0.038	0.227
PLENMIX	-0.013	-0.245	0.238	-0.725**	-0.308	0.776**	0.451*	-0.248	-0.362	-0.554**	-0.527**
HGWMIX	-0.211	-0.433*	-0.116	-0.597**	-0.643**	0.809**	0.822**	-0.398	-0.035	-0.319	-0.322
BYIEMIX	-0.322	-0.100	0.067	-0.141	0.165	0.323	0.267	0.319	0.388	0.030	0.410
HIMIX	0.248	0.348	0.621**	-0.070	0.331	0.096	0.085	0.075	0.467*	-0.250	0.333
BRPLMIX	0.020	-0.095	0.051	0.045	-0.134	0.224	0.302	0.028	0.271	0.140	0.286
YLDMIX	0.369	0.482*	0.649	-0.007	0.321	0.241	0.133	0.078	0.442*	-0.193	0.391

BYIE=Biological yield (g), BRPL=branch per plant, DF=days to flower, DM=days to maturity, HGW=hundred grain weight (g), HI=harvest index (%), PH=plant height (cm), POPL=pod per plant, PLEN=pod length (cm), SEPO=seed per pod, YLD=grain yield (Qt ha⁻¹), DFMIX=days to flower in mixture, DMMIX= days to maturity in mixture, PHMIX=plant height in mixture, POPLMIX=pod per plant in mixture, SEPOMIX=seed per pod in mixture, PLENMIX=pod length in mixture, HGWMIX=hundred grain weight in mixture, BYIEMIX=biological yield in mixture, HIMIX=harvest index in mixture, BRPLMIX=branch per plant in mixture, YLDMIX=grain yield in mixture.

The comparison of variables between sole and bean maize cropping systems and the association of some of the characters is shown in Table 7. The result indicated that, among the tested variables, days to maturity ($rg=0.66^{**}$), plant height ($rg=0.68^{**}$), seed per pod ($rg=0.76^{**}$), pod length ($rg=0.78^{**}$), and hundred grain weight ($rg=0.82^{**}$) showed positive and highly significant correlation between the two cropping systems.

Similarly, days to 50% flowering ($rg=0.41^*$) and harvest index ($rg=0.14^*$) showed positive and significant correlation between sole and intercropping. The result of the present study agreed with the report of Santalla et al. (2001) who indicated that significant and high correlations of bean yields between sole cropping and intercropping with maize.

According to Woagyehu (2008), grain yield of common bean genotypes under sole cropping has shown a positive correlation with yield under intercropping ($rg=0.55$). Similarly, he stated that, positive correlation between grain yield between the two-cropping system. Some of yield and yield related traits, that is, branch per plant, biological yield, pods per plant and grain yield revealed insignificant correlation between the sole and inter cropping conditions. It is worth mentioning that there was no negative association between variables of the two cropping systems.

Similarly, Mesele (1997) indicated the relationship between seed yield and number of pods per plant was highly significant at phenotypic and genotypic level. He also reported that yield per plant was highly and significantly correlated with number of seeds per plant both at phenotypic and genotypic levels.

Most of the traits showed highly significant variation between the two cropping systems revealing the insignificant correlation between sole and intercropping.

Therefore, as per the combined analysis of variance, there was an apparent variation between genotypes, cropping system and genotype \times cropping system interaction.

However, the correlation coefficient can be affected by the test genotypes and environments at which the genotypes are raised, correlations among the quantitative traits are very important for selecting genotypes and/or populations having multiple associated characters.

Direct and indirect effects of characters on grain yield at genotypic level for sole cropped common bean

Every component character can exert a direct and indirect effect on grain yield. Path coefficient analysis offered a much more realistic interpretation of the factors involved. The use of this technique requires a cause and effect situation among the variables. Based on the effects exerted by characters on the grain yield, one can consider that the possibility of improving the crop through these characters.

The direct and indirect effects of various traits on seed yield per plant among genotypes are shown in Table 8. Among the eleven characters studied, ten quantitative traits assumed to be the causal factors exerted their direct or indirect effects on grain yield. Of these traits, all exerted their positive direct effects on grain yield except seed per pod and hundred grain weight. Harvest index (0.96) and biological yield (0.62) recorded the highest direct effect on grain yield and followed by days to maturity, branch per plant, days to 50% flowering and pod length.

This indicated that, selection of high yielding genotypes

Table 8. Genotypic path analysis (direct and indirect effect) of ten quantitative traits studied for sole cropping.

	DF	DM	PH	POPL	SEPO	PLEN	HGW	BYIE	HI	BRPL	rg
DF	0.191	0.173	0.130	0.085	0.085	-0.040	-0.097	0.023	0.075	-0.024	-0.020
DM	0.128	0.259	0.083	0.046	0.049	-0.047	-0.063	0.037	-0.038	-0.005	0.197
PH	0.096	0.182	0.117	0.001	0.003	0.000	-0.001	0.002	-0.003	-0.004	0.094
PL	0.063	0.102	-0.009	0.007	-0.107	0.162	0.153	0.059	0.076	-0.210	0.549
EPO	0.063	0.107	0.035	0.004	-0.278	-0.072	-0.113	0.084	0.045	0.033	0.468
LEN	-0.029	0.103	0.002	0.006	0.112	0.175	-0.052	0.025	0.005	0.026	-0.131
GW	0.072	-0.140	-0.015	-0.005	0.175	0.133	-0.680	-0.311	0.166	-0.220	-0.142
BYIE	-0.017	0.081	0.023	0.002	-0.131	-0.065	0.035	0.615	-0.113	0.007	0.444
HI	0.056	-0.084	-0.032	0.003	-0.070	0.014	-0.019	-0.073	0.957	0.078	0.718
RPL	-0.018	-0.011	-0.052	0.008	-0.052	-0.067	0.025	0.004	0.357	0.207	0.4414

U=0.2132. BYIE= biological yield (g), BRPL= branch per plant, DF= Days to flower, DM=days to maturity, HGW=hundred grain weight (g), HI= Harvest index (%), PH=plant height (cm), POPL=pod per plant, PLEN=pod length (cm), SEPO=Seed per pod, YLD=Grain Yield (Qt ha⁻¹), rg=genotypic correlation, U=Residual.

either separately or in combination of these traits would result in increasing grain yield. Harvest index through number of branches per plant (0.36), seed per pod through hundred grain weight (0.18) and days to maturity through plant height (0.18) recorded the highest positive indirect effect on grain yield.

Even though pod per plant showed significant genotypic correlation with grain yield ($rg=0.55^{**}$), it exerted very low positive direct effect value on grain yield. On the other hand, all quantitative traits except pod per plant, hundred grain weight and harvest index and branch per plant exerted their positive indirect effect on grain yield via plant height. Conversely, seed per pod (-0.28) and hundred grain weight (-0.07) recorded their negative direct effects on grain yield. But this negative direct effect of the traits is compensated by the indirect effect exhibited by these traits as they interact each other, that is, seed per pod through hundred grain weight (0.175) exerted moderate to higher indirect effect on grain yield as compared to other quantitative traits.

Incongruent to the present study, Sintayehu (1997) reported 100-seed weight, had the highest direct effect on grain yield followed by pod per plant and number of seeds per pod. Similarly, Mesele (1997) also noted that seed per plant had the highest degree of favorable influence on seed yield followed by days to maturity and days to flowering exerted negative direct influence on seed yield on the other direction.

According to Kassaye (2006), days to flowering and maturity had positive direct effect on seed yield. In contrast, these phenological traits contributed their negative indirect effects through 100- seed weight.

Conclusion

Genetic variability studies provide basic information regarding the genetic properties of the population based

on which breeding methods are formulated for further improvement of the crop. The present study was also aimed to investigate about the nature and extent of variability that can be attributed to characters that can be observed and realized in practical breeding.

Accordingly, in this experiment, common bean genotypes showed high significant variability for all the traits considered, that is, days to maturity, plant height, pod per plant, seed per pod, pod length, hundred grain weight, biological yield, harvest index, branch per plant and grain yield quintal per hectare, but there was no apparent variation for days to flowering. Quantitative traits that showed the maximum significant variation between genotypes were plant height, pod per plant, seed per pod, biological yield, harvest index and grain yield.

The PCV values of all of the traits considered in this study were greater than their GCV values. These results could be indication of other environmental factors played a great role on the variation observed. Whereas, the highest genetic advance as a percent of mean recorded for plant height (98.21), grain yield (81.15), hundred grain weight (61.4) and pod per plant (53.6) according to their order of importance. Generally, 98, 81, 61, and 53% of improvement can be made in selection through these characters for intercropped beans.

Based on the genotypic correlation coefficient analysis of the present study, about 70% of the traits revealed positive and significant correlation with grain yield. Among which, harvest index, pod per plant, seed per pod and biological yield showed highly significant correlation with grain yield. This correlation could be either due to pleiotropic gene action or linkage or more likely due to both phenomena. Furthermore, the qualitative traits studied for path coefficient analysis at genotypic level, most of the traits exerted their direct effect on grain yield except seed per pod and hundred grain weight.

From this study, one can conclude that, utilizing the

variability of those traits which have significant and positive correlation with grain yield and those that have direct or indirect influence on the productivity of the genotypes is very much decisive.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

- Alemineh M (2009). Evaluation of Common Bean (*Phaseolus Vulgaris* L.) Varieties Intercropped With Maize (*Zea Mays* L.) for Double Cropping at Alemaya Aand Hirna Aareas, Eastern Ethiopia. MSc thesis, Haramaya University, Addis Ababa.
- Allard RW (1960). Principles of Plant Breeding. John Wiley and Sons. Inc. New York pp. 99-108.
- Amin MR, Barma NCD, Razzaque MA (1992). Variability, heritability, genetic advance and correlation study in some quantitative characters in durum wheat. *Rachis* 16(12):30-32.
- Briggs FN, Knowles PF (1967). Introduction to Plant Breeding. Reinhold publishing cooperation New York, Amsterdam, London.
- Cochran WG, Cox M (1957). Experimental designs. John Wiley and Sons, Inc, New York 611 p.
- Dabholkar AR (1992). Elements of Biometrical Genetics. Concept Publishing Company, New Delhi 110059. P 431.
- Dewey DR, Lu H (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal* 51:515-518.
- Falconer DS, Mackay TF (1996). Introduction to Quantitative Genetics 4th ed. Longman Group Limited Malaysia P 438.
- Johnson HW, Robinson HF, Comstock RE (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47:314-318.
- Prajapati KN, Patel MA, Patel JR, Joshi NR, Patel AD, Patel JR (2014). Genetic Variability, Character Association and Path Coefficient analysis in Turmeric (*Curcuma longa* L.). *Electronic Journal of Plant Breeding* 5(1):131-137.
- Kassaye N (2006). The studies on genetic divergence in common bean (*Phaseolus vulgaris* L.) introductions of Ethiopia. MSc thesis, Addis Ababa University, Addis Ababa. *Electric Journal of Plant Breeding* 5(1):131-137, ISSN 0975-928X.
- Mesele A (1997). Genetic variation and Interrelationships of Agronomic Traits in Cow pea (*Vigna unguiculata* (L) Walp). A Thesis Submitted to the Department of Plant Science School of Graduate Studies. Alemaya University.
- Miller PA, Williams C, Robinson HF, Comstock RE (1958). Estimates of genotypic and Environmental variances and co-variances in upland cotton and their implications in selection. *Agronomy Journal* 50:126-131.
- Negassa W (2001). Assessment of important physicochemical properties of Dystric Udalf (Dystric Nitosols) under different management systems in Bako area, Western Ethiopia. Alemaya University, School of Graduate Studies, (McS Thesis), Ethiopia. 93p.
- Pooja P, Neeraj S, Monisha R (2015). Study of Genetic Variation, Heritability And Correlation In Vegetable Pea (*Pisum Sativum* L.) An International Quarterly Journal of Life Sciences pp.2131-2133.
- Singh RK, Chaudhary BD (2004). Biometrical Methods in Quantitative genetic Analysis. Kaliyani Publishers pp. 39-72.
- Raiz R, Chowdhry A (2003). Estimation of variation and heritability of some physiomorphic traits of wheat under drought condition. *Asian Journal of Plant Science* 2(10):748-755.
- Samal KM, Senapati N, Lenka D, Nandi A, Tripathy P (1995). Varietal performance, genetic variability and correlation in rajmash (*Phaseolus vulgaris* L.). *Legume Research* 18:223-227.
- SAS (2004). SAS User's Guide. Released 9.1 editions. SAS Institute Inc, Cary, NC, USA. https://support.sas.com/documentation/onlinedoc/91pdf/sasdoc_91/ets_ug_7314.pdf
- Sharma JR (1998). Statistical and biometrical techniques in plant breeding. New Age International (P) Limited Publishers, New Delhi 432 p.
- Sintayehu A (1997). Variability and association of some agronomic characters with seed yield in common bean (*Phaseolus vulgaris* L.). A Thesis Submitted to the Department of Plant Science School of Graduate Studies. Alemaya University.
- Santalla M, Rodino AP, Casquero PA, De Ron AM (2001). Interactions of bush bean intercropped with field and sweet maize. *European Journal of Agronomy* 15(3):185-196.
- Tiwari G, Lavanya GR (2012). Genetic variability, character association and component analysis in F4 generation of fieldpea (*Pisum sativum* var. *arvense* L.). *Karnataka Journal of Agricultural Science* 25(2):173-175.
- Welsh JR (1990). Fundamentals of Plant Genetic and Breeding. John Wiley and Sons. New York.
- Woagyehu W (2008). Evaluation of common bean (*Phaseolus vulgaris* L.) Genotypes of Diverse Growth Habit under sole and intercropping with maize (*Zea mays* L.) in Southern Ethiopia. *Journal of Agronomy* 7(4):306-313.