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Genetic Variation for Grain Yield of Common Bean (*Phaseolus vulgaris* L.) in Sole and Maize/Bean Intercropping Systems

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ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is grown in both sole and maize/bean intercrop systems in Ethiopia. Increasing bean yield partly requires developing cultivars that are adapted to both cropping systems. An experiment was carried out using 20 common bean genotypes in sole and maize/bean intercrop during 2012 main cropping season in Dilla, Ethiopia, to investigate genetic variances and broad-sense heritabilities and to estimate correlation coefficients for grain yield and yield related traits of bean in sole and maize/bean intercrop. Genetic variances for grain yield (g m^{-2}) and pods plant^{-1} in sole crop were greater than that of intercrop. Broad-sense heritability for grain yield, pods plant^{-1}, seeds pod^{-1} and 100-seed weight (g) was 0.91, 0.82, 0.71 and 0.90, respectively, for sole crop and its respective value for the intercrop was 0.79, 0.66, 0.67 and 0.91. Grain yield was positively correlated ($p<0.05$) with pods plant^{-1} ($rp = 0.50$, $rg = 0.59$) and 100-seed weight ($rp = 0.47$, $rg = 0.52$) in sole crop and pods plant^{-1} ($rp = 0.64$, $rg = 0.80$; $p<0.01$) in intercrop. This experiment suggests that grain yield per se or pods plant^{-1} would be used as a selection criterion to improve grain yield under both sole and intercropping systems. Moreover, genotypes DAB243 and DAB245 may be incorporated in the future breeding programs to develop high yielding cultivars in sole and intercropping systems.

Key words: Genetic variance, broad-sense heritability, correlations, intercrop, common bean, *Phaseolus vulgaris*

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is an important grain crop in Ethiopia and is mostly grown in intercrop with maize (*Zea mays* L.) (IAR, 1994). It coccupies over 331, 708 ha, i.e., 21% of the total crop area allocated to pulses and produces over 17% of the total pulses production (CSA, 2012). The low yield of common bean, averaging 1169 kg ha^{-1} (CSA, 2012), could be partly due to lack of improved cultivars adapted to both sole and intercropping systems. Intercropping also reduces common bean yield considerably while the associated maize yield is often not affected (Francis *et al.*, 1978a, b; Davis and Garcia, 1983).

The loss in grain yield of bean in association with maize would be minimized through selection of cultivars adapted to intercropping competitions. The earlier studies in common bean showed considerable genetic variation and correlations among agronomic traits under both sole crop and maize/bean intercrop (Francis *et al.*, 1978a, b; Atuahene-Amankwa and Michaels, 1997) indicating the possibility of improving grain yield and other important traits of this crop under both cropping systems.

The positive correlation between sole and intercropping systems for common bean yields would suggest that cultivars selected in sole crop will also show improved yields in intercrop (Francis *et al.*, 1978a, b; Davis and Garcia, 1983). However, the existence of significant genotype by cropping system interactions reported for bean (Francis *et al.*, 1978a, b; Atuahene-Amankwa and Michaels, 1997) would slow the progress in selection. The present experiment was carried out to investigate genetic variances and broad sence heritabilities and to estimate correlation coefficients for grain yield and yield related traits of bean in sole and maize/bean intercrop.

MATERIALS AND METHODS

This experiment was carried out in Dilla, 6°24′30″N and 38°18′36″E and 1700 m above sea level, during the main cropping season of 2012, on farm of School of Agricultural Science, Dilla University, Ethiopia. The average annual rainfall and temperature for Dilla are 1292 mm and 20.45°C, respectively. The monthly average rainfall for April to September of the experiment duration was 167 mm and that of average maximum and minimum temperature was 26.90 and 14.30°C, respectively. Analysis of the soil of experimental field at 0-30 cm depth revealed clay texture (clay 50%, sand 32%, silt 18%), pH 6.60 (in H_2O) and total nitrogen 0.30%.

This experiment was carried out using 20 bush bean genotypes obtained from Hawassa Agricultural Research Centre, Hawassa, Ethiopia and a commonly grown maize hybrid, BH140. The experimental design was a split plot with three replications. The cropping system (sole bean and maize/bean intercrop) constituted the main plots and the 20 bean genotypes were the sub-subplots. Bean genotypes were planted on April 20, 2012, in four rows with 2 m long separated by 40 cm, with 10 cm between plants (after thinning excess plants per hill). The space between main plots was 1.5 m and that between replications was 2 m. For intercrop, simultaneous planting of maize was done (20×80 cm spacing) in between two outer bean rows so that the two central bean rows are in between the two maize rows. In addition, the sole maize was grown in three replications and four rows to compare its yield with intercrop maize. The 25 kg ha^{-1} N and 60 kg ha^{-1} P_2O_5 were apphed in the form of diammonium phosphate at the time of planting. Weeds were controlled with frequent hand weeding throughout the experiment.

Days to flowering and maturity, 100-seed weight (g), pods plant^{-1} (average of six random plants at maturity), seeds pod^{-1} (average for ten random pods) and grain yield (g m^{-2}) by using the two central rows were recorded. Grain yield and 100-seed weight were determined after oven drying the grain samples to constant weight at 65°C. Analysis of variance and correlations were done using SAS software (SAS, 1996).

Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance as:

$$h^2 = \sigma^2_g / \sigma^2_p$$

where, σ^2_g the genotypic variance [(MSG-MSE)/r], σ^2_p the phenotypic variance (genotypic variance plus error variance), σ^2_e error variance (MSE/r), MSG mean square of genotypes, MSE mean square of error and r are number of replications.

The genotypic and phenotypic coefficients of variation were computed according to the methods of Burton and Devance (1952) and Kumar *et al.* (1985) as:

$$GCV = (\delta^2_g)^{0.5}/z \times 100$$

$$PCV = (\delta^2_p)^{0.5}/z \times 100$$

where, GCV and PCV are the genotypic and phenotypic coefficient of variation, respectively and σ^2_g the genotypic variance, σ^2_p the phenotypic variance and z the general mean of a trait.

Genetic and phenotypic correlation coefficients between pairs of traits were calculated using estimates of variances and covariances according to Kibite and Evans (1984) as:

$$r_g = COV_{gxy}/ (\sigma^2_x \times \sigma^2_y)^{0.5}$$

where, r_g is the genetic correlation coefficient, COV_{gxy} the genetic covariance between traits x and y and σ^2_x and σ^2_y are the genetic variances for traits x and y, respectively. Similar analyses were made for phenotypic correlation coefficients (r_p) using the phenotypic variances and covariances.

RESULTS

Cropping system significantly affected grain yield, pods plant^{-1} and seeds pod^{-1}. The effect of genotype and genotype×cropping system interaction was significant for these traits including days to flowering and maturity and 100-seed weight. The effect of genotype was also significant for grain yield and yield related traits under both sole and intercrop systems (Table 1).

Table 1: Significance of mean squares for six grain yield and yield related traits of common bean for two cropping system (sole and maize/bean intercrop) and 20 genotypes

Sources of variation	df	GY	DTF	DTM	Pods plant^{-1}	Seeds pod^{-1}	SW
Replication	2	5393ns	1.20*	0.51ns	6.56ns	0.14ns	0.62ns
Cropping system (C)	1	343210**	0.21ns	26.13ns	443.52**	1.63*	0.14ns
Error (a)	2	850	0.03	2.41	3.44	0.06	0.61
Genotype (G)	19	9604**	26.44**	51.83**	8.79**	0.60**	81.46**
G×C	19	5939**	3.24*	7.50*	4.67**	0.26*	19.18**
Error (b)	76	928	1.66	3.63	1.46	0.12	4.92
CV (a) (%)		8.89	0.44	2.43	20.65	6.65	1.81
CV (b) (%)		9.29	3.07	2.99	13.48	9.58	5.14
Sole crop							
Replication	2	1488ns	0.52ns	2.45ns	3.03ns	0.18ns	0.01ns
Genotype	19	11472**	10.61**	24.45**	10.49**	0.40**	46.58**
Error	38	1014	1.96	5.29	1.90	0.11	4.74
CV (%)		8.34	3.33	3.65	12.65	8.82	5.06
Intercrop							
Replication	2	4755**	0.12ns	0.47ns	6.97**	0.02ns	1.22ns
Genotype	19	4070**	19.07**	34.88**	2.98**	0.45**	54.06**
Error	38	842	0.92	1.98	1.03	0.14	5.10
CV (%)		10.55	2.28	2.20	14.40	10.63	5.25

GY: Grain yield (g m^{-2}), DTF: Days to flowering, DTM: Days to maturity, SW: 100-seed weight (g), *, **: Significant at p<0.05 and p<0.01, respectively; ns: Not significant

Table 2: Estimates of variances, coefficients of variations and broad-sense heritability (h^2) for 20 common bean genotypes under sole crop (S) and maize/bean intercrop (I)

Traits	ð^2_p	ð^2_g	ð^2_e	PCV	GCV	h^2
Grain yield (g m^{-2})						
S	3824.00	3486.00	338.00	16.21	15.48	0.91
I	1357.00	1076.00	281.00	13.42	11.95	0.79
Days to flowering						
S	3.54	2.89	0.65	4.48	4.04	0.82
I	6.36	6.05	0.31	6.01	5.87	0.95
Days to maturity						
S	8.15	6.39	1.76	4.51	3.99	0.78
I	11.60	10.90	0.66	5.31	5.16	0.94
Pods plant^{-1}						
S	3.49	2.86	0.63	17.10	15.50	0.82
I	0.99	0.65	0.34	14.10	11.40	0.66
Seeds pod^{-1}						
S	0.14	0.10	0.04	9.76	8.37	0.71
I	0.15	0.10	0.05	10.90	9.13	0.67
100-seed weight (g)						
S	15.50	13.90	1.58	9.13	8.65	0.90
I	18.00	16.30	1.70	9.82	9.34	0.91

The ð^2_g values were much higher than that of ð^2_e for grain yield and yield related traits (Table 2). Both phenotypic and genotypic coefficients of variation were high for grain yield and pods plant^{-1} compared to days to flowering and maturity and seeds pod^{-1} and 100-seed weight under both sole and intercrop systems. The decrease in values of phenotypic and genotypic coefficients of variation for grain yield and pods plant^{-1} and the increase for days to flowering and maturity, seeds pod^{-1} and 100-seed weight were obtained in intercrop. Broad-sense heritability values for grain yield, days to flowering, days to maturity, pods plant^{-1}, seeds pod^{-1} and 100-seed weight were 0.91, 0.82, 0.78, 0.82, 0.71 and 0.90, respectively, for sole crop and 0.79, 0.95, 0.94, 0.66, 0.67 and 0.91, respectively, for intercrop.

There were considerable differences among genotypes for grain yield and yield related traits in both sole crop and intercrop. Grain yield ranged from 283(genotype DAB269) to 472 gm^{-2} (genotype DAB393) in sole crop and 197 g m^{-2} (genotype DAB269) to 348 g m^{-2} (genotype DAB236) in intercrop. Genotype DAB243 and DAB245 gave high yield in both sole and intercrop systems whereas genotypes DAB258 and DAB393 gave low yield in intercrop despite their high yield in sole crop. Pods plant^{-1} ranged from 6.70 (genotype DAB237) to 15.10 (genotype DAB245) in sole crop and 5.47 (genotype DAB246) to 9.60 (genotype DAB243) in intercrop. Genotypes also showed considerable variations for days to flowering and maturity, seeds pod^{-1} and 100-seed weight (Table 3).

Grain yield was positively correlated with pods plant^{-1} (rp = 0.50, rg = 0.59; p<0.05) and 100-seed weight (rp = 0.47, rg = 0.52; p<0.05) in sole crop and with pods plant^{-1} (rp = 0.64, rg = 0.80; p<0.01) in intercrop. Seeds pod^{-1} had negative correlation with pods plant^{-1} (rg = -0.52; p<0.05) and 100-seed weight (rp = -0.60, rg = -0.75; p<0.01). in intercrop and with 100-seed weight (rp = -0.46, rg = -0.54; p<0.05) in sole crop. Moreover, there was positive correlation between

Table 3: Mean values for six grain yield and yield related traits for 20 common bean genotypes grown under sole crop (S) and maize/bean intercrop (I)

Genotypes	GY		DTF		DTM		Pods plant^{-1}		Seeds pod^{-1}		SW	
	S	I	S	I	S	I	S	I	S	I	S	I
DAB221	347	264	41	40	63	61	12.60	7.47	3.70	3.40	45	45
DAB228	347	272	41	40	62	63	9.90	6.33	3.77	3.50	40	44
DAB230	301	263	40	41	60	63	11.00	7.53	3.53	3.40	47	47
DAB236	424	348	41	40	62	63	12.40	8.53	3.87	3.27	49	50
DAB237	346	291	40	41	61	61	6.70	6.27	3.60	4.47	42	36
DAB238	309	275	41	41	63	64	11.47	6.47	3.73	3.70	42	41
DAB239	368	305	43	41	63	62	11.07	8.27	4.07	3.43	44	40
DAB243	452	319	41	40	62	62	11.87	9.60	3.73	3.33	44	49
DAB245	466	312	40	40	59	64	15.10	7.60	4.00	3.90	39	41
DAB246	332	259	41	40	62	60	8.73	5.47	4.17	4.50	35	36
DAB247	393	283	40	41	60	62	10.87	7.80	3.23	3.30	42	41
DAB253	406	328	45	43	68	66	11.67	6.90	3.67	3.43	45	44
DAB258	467	216	45	47	68	69	12.47	5.70	3.30	3.37	48	42
DAB269	283	197	41	40	62	61	9.80	6.53	3.87	3.60	38	36
DAB273	295	269	41	42	62	63	10.07	6.60	3.53	3.13	43	42
DAB280	375	238	45	42	66	65	11.00	6.93	3.80	3.13	41	47
DAB354	386	284	40	41	62	64	7.27	7.00	4.80	3.67	41	46
DAB360	465	273	44	46	68	69	11.27	7.07	3.23	3.07	45	41
DAB393	472	239	44	47	66	71	11.73	6.00	3.43	3.30	52	48
DAB404	397	257	45	47	67	72	11.00	7.00	4.10	3.57	42	48
Mean	382	275	42	42	63	64	10.90	7.05	3.76	3.52	43	43
SE	8.56	5.79	0.28	0.34	0.44	0.46	0.28	0.18	0.06	0.06	0.55	0.59

GY: Grain yield (g m^{-2}), DTF: Days to flowering, DTM: Days to maturity, SW: 100-seed weight (g), SE: Standard error

cropping systems for days to flowering (rp = 0.82, rg = 0.92; p<0.01), days to maturity (rp = 0.76, rg = 0.88; p<0.01) and 100-seed weight (rp = 0.62, rg = 0.68; p<0.01) (Table 4).

DISCUSSION

In the present experiment, grain yield (average of 4383 g m^{-2}) of maize was not significantly varied between sole and intercrop systems as well as in association with different bean genotypes (data not shown). This is in consistent with previous maize/bean intercropping studies for climbing (Francis *et al.*, 1978a) and bush beans (Francis *et al.*, 1978b). In the present experiment, the existence of genotype×cropping system would suggest that the inference of intercrop performance based on sole crop performance may not always be successful. The presence of genotype×cropping system interaction effect has also been reported in earlier study in common bean (Francis *et al.*, 1978a; Zimmermann *et al.*, 1984b; Atuahene-Amankwa and Michaels, 1997). The reduction in grain yield due to intercropping observed in present experiment agrees with the previous studies in common bean (Francis *et al.*, 1978a, b; Atuahene-Amankwa and Michaels, 1997) and would indicate poor competitive ability of bean in association with maize. This reduction was mainly due to the reduction in pods plant^{-1} as it was reported in previous studies (Atuahene-Amankwa and Michaels, 1997). The high grain yield was obtained under both sole crop and intercrop for genotypes DAB243 and DAB245 suggesting that these genotypes may be used in future breeding programs to improve grain yield in sole and intercrop systems.

Table 4: Phenotypic and genetic correlation coefficients among six common bean traits under sole crop (above diagonal) and maize/bean intercrop (below diagonal) and correlation between cropping systems for 20 common bean genotypes

Traits	1	2	3	4	5	6
Grain yield (g m^{-2})						
rp		0.41ns	0.43ns	0.50*	-0.18ns	0.47*
rg		0.48*	0.53*	0.59*	-0.26ns	0.52*
Days to flowering						
rp	-0.33ns		0.94**	0.21ns	-0.23ns	0.38ns
rg	-0.35ns		1.00**	0.21ns	-0.32ns	0.40ns
Days to maturity						
rp	-0.25ns	0.95**		0.16ns	-0.24ns	0.40ns
rg	-0.27ns	0.99**		0.15ns	-0.32ns	0.45*
Pods plant^{-1}						
rp	0.64**	-0.35ns	-0.24ns		-0.31ns	0.35ns
rg	0.80**	-0.44ns	-0.30ns		-0.35ns	0.38ns
Seeds pod^{-1}						
rp	0.03ns	-0.30ns	-0.40ns	-0.38ns		-0.46*
rg	0.11ns	-0.36ns	-0.51*	-0.52*		-0.54*
100-seed weight (g)						
rp	0.28ns	0.26ns	0.43ns	0.47*	-0.60**	
rg	0.29ns	0.29ns	0.45*	0.60**	-0.75**	
Sole vs. Intercrop						
rp	0.27ns	0.82**	0.76**	0.37ns	0.40ns	0.62**
rg	0.31ns	0.92**	0.88**	0.48*	0.65**	0.68**

*, **: Significant at p<0.05 and p<0.01, respectively; ns: Not significant

In the present experiment, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation but in some cases the two values differed only slightly, indicating small environmental effects in estimating these traits. On the other hand, the high broad-sense heritability observed in the present experiment suggests the feasibility of selection to improve bean grain yield under sole and intercrop systems. However, heritability is a value of a character only for the population and the environment to which the genetic materials are subjected (Falconer, 1989). Thus, value of heritability depends on the magnitude of all the components of variance and a change in any of these will affect it. As to the present experiment, the increase in broad-sense heritability in sole crop system for grain yield and pods plant^{-1} (Atuahene-Amankwa and Michaels, 1997) and grain yield (Zimmermann *et al.*, 1984b) has also been reported in previous studies in common bean which could be because sole crop allows greater expression of yield potential (Francis *et al.*, 1978b). Rosielle and Hamblin (1981) also reported that heritabilities are generally higher in nonstress than stress environments.

As to the present experiment, the positive correlation between pods plant^{-1} and grain yield in both cropping systems has been reported in previous studies (Atuahene-Amankwa and Michaels, 1997). This would suggest that either grain yield per se or pods plant^{-1} may be used to improve grain yield in both conditions. However, the use of pods plant^{-1} as the selection criterion may be complicated due to its negative genetic correlation (rg = -0.52, p<0.05) with seeds pod^{-1} in intercrop. On the other hand, lack of correlation between cropping systems for grain yield, despite previous studies in beans (Francis *et al.*, 1978a, b; Davis and Garcia, 1983; Zimmermann *et al.*, 1984a) suggests that selection under sole crop may not always serve to improve grain yield in intercrop system.

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