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Variability on Seed Yield and Related Agronomic Traits in Mesoamerican Common Bean (*Phaseolus vulgaris* L.) Genotypes under Contrasting Environments at South Eastern Ethiopia

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ABSTRACT

The experiment was conducted during July-November, 2022 at Melkassa and Kulumsa Agricultural Research Center main station under rain fed condition to assess the extent of genetic variability and to identify potential candidate genotypes. A total of 64 small seeded common bean genotypes were evaluated for 18 quantitative traits using 8*8 triple lattice design. The analysis of variance showed that there was highly significant ($p \leq 0.01$) difference among genotypes for all studied traits at both individual locations. The genotypes variation for seed yield was ranged from 1685.09 kg ha^{-1} to 4499 kg ha^{-1} at Melkassa and from 1369.76 kg ha^{-1} to 4848.38 kg ha^{-1} at Kulumsa. High PCV and GCV were recorded for total number of seeds per plant, number of fertile pods and total number of pods plant^{-1} in both locations. Moderate to high value of GCV and broad sense heritability coupled with high GAM were obtained for seed per plant, dry pod yield per plant, fertile pods per plant, seed weight per plant, hundred seed weight and seed yield per hectare in both locations; indicating the importance of those traits in yield improvement of small seeded common bean. G-39, G-27, G-58, G-35, G-29, G-18, G-8, G-61, G-37 and G-33 showed yield advantage from 49% to 88.9% at Melkassa and G-33, G-8, G-4, G-12, G-58, G-11, G-45, G-13, G-36 and G-30 from 16% to 36% at kulumsa over the best standard check G-64. The existed variations implied the possiblity for further improvement of seed yield and atributing traits through utlizing selected potential genotypes and targeted hybridization schemes in breeding programs.

KEYWORDS: Crop improvement, genetic advance, genotype, heritability, variability

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1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the most important warm season food legume crop belongs to the fabaceae family (Anonymous, 2016). It is a global food legume crop grown on 34.8 mha of land with annual total production of over 27.5 mt (Anonymous, 2020). Common bean is the second most important food legumes in Africa next to faba bean as a source of dietary protein (Broughton et al., 2003). Currently in Ethiopia, common bean is the second major food legume crop after faba bean in terms of both area and total amount of production (Anonymous, 2019). The production and area allocation for common bean in Ethiopia is steadily increasing from time to time. In 2018/19 main cropping season more than 2.8 million smallholders are engaged in common bean production including red and white bean. It is grown on 288,637.23 ha of land with total production of 488,320.17 tons; which accounts for 17.81% of the total area covered by pulses and 16.21% of the total pulses production in the country in the main growing season (Anonymous, 2019).

It has great versatile purposes in the livelihood of the agricultural societies of the country. It serves as a source of food consumed as *Nifro* (boiled grain mixed with sorghum or maize), *Shirowat*, *soup*, *samosa* and the immature pods and seeds as a vegetable. The crop is also used as a rotational crop in cereal based cropping systems for sustainable production due to its pertinent atmospheric nitrogen fixing. In addition, common bean is important as a source of animal feed, cash to the farmers and foreign currency earning to the country.

Despite its huge importance in the country, the national average productivity of the crop (1.72 t ha^{-1}) (Anonymous, 2019) is low compared to the yield potential of the crop (3.5 t ha^{-1}) (Anonymous, 2017; Berhanu et al., 2018). These is primarily due to limited availability of source materials and improved varieties for stress tolerant such as biotic stresses like diseases, insect pests ,weeds and abiotic factors such as soil acidity, drought and, instability of cultivars across different agro-ecology, poor adaptation and poor crop management (Ketema and Thangavel, 2016; Berhanu et al., 2018).

On the other hand, currently, in Ethiopia the demand for improved common bean varieties especially for small red and white colored beans among producers are increasing as a result of the increasing demand of consumers and marketing industry (Frehiwot, 2010; Ephrem, 2016) even though the producers have varied preferences in different geographical regions of Ethiopia (Yonas, 2017). Hence, further development of desirable genotypes are essential through plant breeding program for selection of superior genotypes. These depend upon the extent of genetic variability and genetic advance in the base population with respect to desired traits.

There are many research studies have been conducted in Ethiopia on genetic variability in common bean (Ejigu et al., 2018, Aziza, 2019). However, limited research efforts have been done on genetic variability for genotypes of different seed size groups separately; while there are still numerous introduced and locally crossed common genotypes in which their genetic variability does not properly and systematically studied. In addition, information on genetic variability for small seeded genotypes considered in this study has not been generated so far. Therefore, the present study was conducted under contrasting environments (low and mid altitude areas) to estimate the extent of variability, heritability, and the expected genetic advance of important morpho-agronomic traits and to identify potential candidate genotypes to be used for future breeding activity.

2. MATERIALS AND METHODS

2.1. Experimental site

The experiment was conducted at two locations of South Eastern Ethiopia namely Melkassa and and Kulumsa Agricultural Research Center main station during the main cropping season in July–November 2022 under rain fed condition. The description of the test environments are shown in Table 1.

2.2. Experimental materials and design

Sixty-four small seeded common bean genotypes, including sixty-two breeding lines and two recently national released varieties were used for the study. List of common bean genotypes, code and origin are given in Table 2. The experiment was carried out using 8×8 triple lattice design; each replication containing eight incomplete blocks and each incomplete block containing eight genotypes. Each plot had four rows of 4 m length, with spacing of 40 cm between rows and 10 cm between plants. Each genotype was planted in a plot size of 6.4 m^2 with 3.2 m^2 for net harvesting.

Table 1: Description of the test environments

Testing location	Altitude (m.a.s.l)	Latitude	Longitude	Annual Rainfall (mm)	Min.annual Temp. (°C)	Max.annual Temp. (°C)
Melkassa	1550	8°25' N	39° 20' E	763	16	28.8
Kulumsa	2200	80 01' 10"N	390 09'13"E	850	7.9	23.1

Table 2: List of genotypes used in the experiment

Code	Genotype	Source of origin	status	Code	Genotype	Source of origin	status
G-1	SSIN1148	CIAT	breeding line	G-33	NUA355	CIAT	breeding line
G-2	NUA648	CIAT	breeding line	G-34	SCAM15-21-124	CIAT	breeding line
G-3	SMR106	CIAT	breeding line	G-35	GENO363	MARC	breeding line
G-4	GENO110	MARC	breeding line	G-36	SMR126	CIAT	breeding line
G-5	SEC22	CIAT	breeding line	G-37	SSIN1347	CIAT	breeding line
G-6	SCAM15-21-348	CIAT	breeding line	G-38	GENO206	MARC	breeding line
G-7	GENO161	MARC	breeding line	G-39	SSIN1020	CIAT	breeding line
G-8	CB170064-5	MARC	breeding line	G-40	SCAM15-21-357	CIAT	breeding line
G-9	GENO188	MARC	breeding line	G-41	SMR44	CIAT	breeding line
G-10	CB170072-13	MARC	breeding line	G-42	GENO34	MARC	breeding line
G-11	SSIN939	CIAT	breeding line	G-43	CB170065-21-1	MARC	breeding line
G-12	SMR54	CIAT	breeding line	G-44	GENO 354	MARC	breeding line
G-13	GENO285	MARC	breeding line	G-45	SER347	CIAT	breeding line
G-14	GENO147	MARC	breeding line	G-46	SMR48	CIAT	breeding line
G-15	CB170058-11	MARC	breeding line	G-47	SCAM15-11-154	CIAT	breeding line
G-16	SCAM15-21-125	CIAT	breeding line	G-48	GENO126	MARC	breeding line
G-17	GENO158	MARC	breeding line	G-49	SSIN1358	CIAT	breeding line
G-18	CB170065-22-2	MARC	breeding line	G-50	SMR95	CIAT	breeding line
G-19	GENO245	MARC	breeding line	G-51	GENO418	MARC	breeding line
G-20	SMR123	CIAT	breeding line	G-52	SCAM15-21-381	CIAT	breeding line
G-21	SSIN1309	CIAT	breeding line	G-53	SMR103	CIAT	breeding line
G-22	GENO214	MARC	breeding line	G-54	SMR83	CIAT	breeding line
G-23	SSIN885	CIAT	breeding line	G-55	SSIN1313	CIAT	breeding line
G-24	GENO45	MARC	breeding line	G-56	GENO276	MARC	breeding line
G-25	CB170044-13-3	MARC	breeding line	G-57	GENO122	MARC	breeding line
G-26	GENO341	MARC	breeding line	G-58	CB170065-51-1	MARC	breeding line
G-27	SCAM15-21-430	CIAT	breeding line	G-59	SCAM15-21-227	CIAT	breeding line
G-28	SMR53	CIAT	breeding line	G-60	GENO331	MARC	breeding line
G-29	GENO263	MARC	breeding line	G-61	CB170044-91-1	MARC	breeding line
G-30	SMR46	CIAT	breeding line	G-62	GENO66	MARC	breeding line
G-31	SSIN956	CIAT	breeding line	G-63	RAZ42	MARC	Commercial variety
G-32	GENO186	MARC	breeding line	G-64	SCR15	MARC	Commercial variety

Where: MARC: Melkassa Agriculture Research Center; CIAT: International Center for Tropical Agriculture

2.3. Data collection

Data were collected on single plant and plot bases. On a plant basis, data were collected from ten randomly selected plants from each genotype in each replication, namely, plant height (PH) (cm), pod length (PL) (cm), pod diameter (PD) (mm), total number of pods per plant (TNPPP) (number), number of fertile pods plant^{-1} (NFPPP) (number), dry pod yield plant^{-1} (DPYPP) (g plant^{-1}), single pod dry weight (SPDW) (g pod^{-1}), number of seeds pod^{-1} (NSPP) (number), total number of seeds plant^{-1} (TNSPP) (number), and seed weight plant^{-1} (SWPP) (g plant^{-1}). While the data on plot basis were collected from the two central rows include stand count at emergence (SCE), days to 50% flowering (DF), days to 90% maturity (DM), stand count

at harvest (SCH), above ground biomass yield (BMYPH) (kg ha^{-1}), hundred seed weight (HSW) (gram), seed yield (SYPH) (kg ha^{-1}) and harvest index (HI) (%).

2.4. Data analysis

the analysis of variance was carried out using the procedure of triple lattice design for all traits to assess the significance of the difference among the genotypes by using lm function of stats package in R software version 4.1. The genotypic variance (σ^2g) and the environmental variance (σ^2e) were obtained directly from variance component table generated by the software using lmer function of the lme4 mixed model package in R software version 4.1.2 by considering the genotype in the linear mixed model as random and replication and block as fixed variable using Residual (restricted) maximum likelihood (REML) variance component estimation method. Other genetic parameters were calculated by Microsoft Excel using suggested equations by (Falconer and Mackay, 1996; Johnson et al., 1955).

Genotypic variance (σ^2 g)=(MSg-MSe)/r

Environmental variance (σ^2 e)=MSe

Phenotypic variance (σ^2 p)=σ^2 g+σ^2 e

Where: Msg=Mean squre of genotypes

Mse=Mean squre of error

r=Number of replication

Phenotypic and genotypic coefficients of variations of each trait were expressed as percentage of the corresponding phenotypic and genotypic standard deviations as described by Johnson et al. (1955) and expressed as follows:

PCV=$\sqrt{(\sigma^2 p/\bar{x})}\times100$

GCV=$\sqrt{(\sigma^2 g)/(\bar{x})}\times100$

Where: PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, σ^2p=Phenotypic variance, σ^2g=Genotypic variance, $\bar{x}$=mean value of the trait

According to Deshmukh et al. (1986) the PCV and GCV estimates classified as low, <10%, Moderate, 10–20%, High, >20%

Broad sense heritability values for all parameters (H^2B) were estimated based on the formula given by (Falconer and Mackay, 1996).

$H^2B=\sigma^2g/(\sigma^2 p)\times100$

Where: H^2B =Heritability in broad sense, σ^2g=Genotypic Variance, σ^2p=Phenotypic variance

Heritability estimates in broad sense was categorized as high (>60%), medium (30–60%) and low (<30%) (Dabholkar, 1992).

Genetic advance (GA) at 5% selection intensity was estimated as per formula given by (Johnson et al., 1955)

GA=K*$\sqrt{(\sigma^2 p)}$*H^2B

Where: GA=Genetic advance, K=Selection differential at 5% selection intensity which accounts to a constant value 2.063, σ^2p=Phenotypic variance, H^2B=Broad sense heritability

The genetic advance as percent of mean (GAM) was calculated using the following formula and was expressed in percentage (Johnson et al., 1955).

GAM=(GA/$\bar{x}$)*100

Where: GAM=Genetic advance as percent of mean, GA=Genetic advance at 5% selection intensity, $\bar{x}$= population Mean

According to Johnson et al. (1955), the GAM was classified as low if <10%, Moderate, 10–20% and High, >20%

3. RESULTS AND DISCUSSION

The analysis of variance showed the presence of highly significant *($p\leq0.01$)* difference among 64 common bean genotypes for all studied traits at both locations (Table 3 and 4). The presence of highly significant difference was an indication of the existence of considerable genetic variability in experimental materials for the studied traits, justified carrying out further genetic analysis. This will provide an opportunity for a breeder to select superior and desired genotypes for their better seed yield and other yield related traits for further improvement through exploiting the observed variations. Different researchers reported significant differences for one or more of the studied traits (Aziza, 2019; Abnet, 2020; Gebeyaw et al., 2021).

The present study indicated that there was a wide range of variation among the studied genotypes at both locations for most of traits including plant height, total number of pods plant^{-1}, number of seeds plant^{-1}, number of fertile pods plant^{-1}, dry pod yield plant^{-1}, seed weight plant^{-1}, hundred seed weight, harvest index, biological yield and seed yield ha^{-1} while other traits showed low to fairly high range value (Table 5 and 6). At Melkassa, days to 50% flowering ranged from 36.98 to 47.69 with a mean of 41.25. Accordingly, genotype G-14 took shortest (36.98) days whereas G-10 took longest (47.69) days to attain 50% flowering than the other common bean genotypes. Nearly 5 and 66% of genotypes flowered earlier than the standard check G-63 and G-64, respectively. The longest maturity period was recorded for G-35 while, the genotype G-11 took the shortesd days to mature. 47 and 72% of genotypes earlier mature than the standard check G-63 and G-64, respectively.

Twenty-four (37.5%) genotypes have matured in fewer days

Table 3: Mean square from the analysis of variance for 18 traits of 64 small seeded common bean genotypes tested at Melkassa in 2021/2022

Traits	Mean squares			Error		CV (%)	R^2 (%)	Efficiency relative to RCBD (%)
	Replication (df:2)	Block (Rep) (df:21)	Genotype (df:63)	Intra block (df:105)	RCBD (df:126)			
SCE	217.65	33.17	185.74**	22.03	23.94	7.53	85	108.4
DF	31.83	3.68	27.44**	2.73	2.89	4.00	87	105.9
DM	258.06	10.27	47.76**	5.01	5.89	2.64	88	117.6
PH	1280.49	90.90	379.65**	61.92	76.86	10.56	81	107.9
PL	4.87	0.54	2.84**	0.48	0.49	7.78	80	102.1
PD	1.13	0.29	0.79**	0.26	0.36	10.39	68	102.2
SCH	655.89	57.04	244.41**	35.47	39.65	10.53	83	110
TNPPP	119.26	13.49	54.75**	9.57	10.23	15.87	80	106.9
NFPPP	151.52	10.84	51.61**	10.48	10.54	17.99	77	100.6
NSPP	2.85	0.62	0.70**	0.20	0.41	8.28	75	134.6
TNSPP	4275.6	340.6	2084.8**	364.59	36.60	21.81	79	100
SPDW	0.14	0.04	0.09**	0.02	0.022	10.52	77	113.9
DPYPP	109.88	26.1	93.94**	16.61	18.19	16.90	79	109.5
SWPP	39.14	23.22	54.81**	12.19	14.03	17.97	76	115.1
HSW	3.129115	2.44	28.82**	1.50	1.66	5.38	92	110.6
HI	288.74	95.40	128.42**	43.64	52.28	13.87	70	119.8
BMYPH	30146363.4	1231420.5	3993747.4**	782177.5	857051.30	14.36	80	109.6
SYPH	13215426.22	711627.75	855919.79**	200764	285887.94	15.39	82	142.4

df: Degrees of freedom; CV: Coefficient of variation; R^2: Coefficient of determination; SCE: Stand count at emergence; DF: Days to 50% flowering; DM: Days to 90% maturity; PH: Plant height; PD: Pod diameter; PL: Pod length; SCH: Stand count at harvest; TNPPP: Total number of pods plant^{-1}; NFPPP: Number of fertile pod plant^{-1}; NSPP: Number of seed pod^{-1}; TNSPP : Total number of seed plant^{-1}; SPDW: Single pod dry weight ; DPYPP: Dry pod yield plant^{-1}; SWPP: Seed weight plant^{-1}; HSW: Hundred seed weight; HI: Harvest index; BMYPH : Above ground biological yield ha^{-1}; SYPH: Seed yield ha^{-1}; **: Highly significant at (p=0.01) level of significance

than the grand mean (84.95) days from 64 genotypes to reach physiological maturity stage and these genotypes could be early maturing. Those genotypes which took shorter days to mature (early maturing genotypes) such as G-11, G-28, G-31, G-46, and G-55 can be recommendable for moisture stress area due to they need shorter rainy season and can scape moisture stress. The highest plant height was recorded by genotype G-6 (98.59 cm) followed by G-40 (93.77 cm) and G-54 (91.88 cm) while the lowest plant height was recorded in genotype G-55 (47.64 cm). A wide range was observed in number of fertile pods per plant varied from 10.05 to 29.35 with a grand mean of 17.99. The highest pods per plant (29.35 pods) were scored for genotypes G-35. A significant variation for number of seeds per plant ranged from 44.25 to 162.09 with a grand mean of 87.56. The maximum number of seeds per plant was obtained from G-35 whereas the check G-64 produced minimum number of seeds plant^{-1}. The maximum seed weight plant^{-1} (33.19 g plant^{-1}) was recorded from genotype G-35 whereas the minimum seed weight plant^{-1} (10.36 g plant^{-1}) was produced for G-53.

At Kulumsa, genotype G-41 took shortest (47.40) days whereas G-58 took longest (58.96) days to attain 50% flowering. The shortest maturity period (105.69) was recorded for G-39 while, the genotype G-58 took the longest days to maturity (119.04). Yohannes et al. (2020) reported a variation of days to maturity, ranged from 75 to 92 days in common bean. Genotypes which took longer days to mature (late maturing genotypes) such as G-58, G-43, G-61, G-53, G-54 and G-36 can be recommendable for non stress/potential/mid altitude areas like Kulumsa and similar agro-ecologies. The highest plant height was scored for G-5 (96.54) whereas the lowest plant height was recorded in genotype G-39 (42.55 cm). The highest

Table 4: Mean square from the analysis of variance for 18 traits of 64 small seeded common bean genotypes tested at Kulumsa in 2021/2022

Traits	Mean squares			Error		CV (%)	R^2 (%)	Efficiency relative to RCBD (%)
	Replication (df:2)	Block (Rep) (df:21)	Genotype (df:63)	Intra block (df:105)	RCBD (df:126)			
SCE	159.15	41.05	170.60**	29.02	31.02	7.91	80	106.89
DF	2.90	1.64	22.26**	1.55	1.56	2.4	89.9	100.65
DM	18.19	4.79	22.78**	3.25	3.51	1.6	82	108.00
PH	445.54	136.34	467.59**	64.69	76.6	10.64	83	118.41
PL	2.23	0.28	2.72**	0.099	0.128	3.74	94.6	129.29
PD	0.96	0.38	0.68**	0.186	0.219	14.16	73.1	117.74
SCH	28.35	43.80	192.70**	29.09	31.54	8.36	81	108.42
TNPPP	90.78	14.84	47.11**	8.12	9.24	14.82	80.2	113.79
NFPPP	88.26	17.21	45.18**	8.19	9.69	15.74	79.7	118.32
NSPP	0.59	0.31	0.76**	0.22	0.24	9.01	70.4	109.09
TNSPP	1476.27	735.92	1458.81**	220.54	306.4	17.85	82.6	138.93
SPDW	0.02	0.04	0.25**	0.028	0.029	11.1	85	103.57
DPYPP	71.01	25.13	48.51**	10.43	12.88	14.7	77.3	123.49
SWPP	71.19	20.98	27.97**	6.77	9.14	15.3	76.7	135.01
HSW	2.26	1.36	82.34**	0.73	0.83	4.03	98.6	113.70
HI	16.41	13.27	113.05**	16.51	15.97	8.43	81.1	96.73
BMYPH	3749084.5	1779683.4	3192655.4**	702364.5	881918	11.3	76.9	125.56
SYPH	663306.55	416944.48	1239857.6**	202802.2	238493	12.59	80.55	117.60

df: Degrees of freedom; CV: Coefficient of variation; R^2: coefficient of determination; SCE: Stand count at emergence; DF: Days to 50% flowering; DM: Days to 90% maturity; PH: Plant height; PD: Pod diameter; PL: Pod length; SCH: Stand count at harvest; TNPPP: Total no. of pods plant^{-1}; NFPPP: No. of fertile pod plant^{-1}; NSPP: No. of seed pod^{-1}; TNSPP: Total no. of seed plant^{-1}; SPDW: Single pod dry weight ; DPYPP : Dry pod yield plant^{-1}; SWPP: Seed weight plant^{-1}; HSW: Hundred seed weight; HI: Harvest index; BMYPH: Above ground biological yield ha^{-1}; SYPH: Seed yield ha^{-1}; **: Highly significant at (p=0.01) level of significance

pods plant^{-1} (26.8 pods) were scored for genotypes G-4. The maximum number of seeds plant^{-1} (142.60) and the highest seed weight plant^{-1} (23.85 g plant^{-1}) was recorded from G-44. Seed yield showed a wide range of variation (1685.09 kg ha^{-1} to 4499.61 kg ha^{-1}) with a mean value of 2911.04 kg ha^{-1} at Melkassa and from 1369.76 kg ha^{-1} to 4848.38 kg ha^{-1} with a mean of 3576.82.4 kg ha^{-1} at Kulumsa. In agreement with the present finding, Girum (2019) reported a significant difference in grain yield ha^{-1} ranged from 1668.8 kg ha^{-1} to 4014.7 kg ha^{-1} with a mean of 2863.7 kg ha^{-1} in thirty common bean genotypes. Abnet (2020) also found a wide range of variation in seed yield ha^{-1} which ranged from 2178 kg ha^{-1} to 5623.5 kg ha^{-1} among forty nine common bean genotypes.

The highest yielding genotypes at Melkassa were G-39(4499.61 kg ha^{-1}) followed by G-27(4157.1 kg ha^{-1}), G-58(3992.03 kg ha^{-1}), G-35(3868.8 kg ha^{-1}), G-29(3683.48 kg ha^{-1}), G-18(3631.18 kg ha^{-1}, G-8(3628.31 kg ha^{-1}),G-61(3595.21 kg ha^{-1}),G-37(3580.84 kg ha^{-1}) and G-33(3550.42 kg ha^{-1}). These genotypes showed from 49% to 88.9% yield advantage over the best standard check G-64. while the top high yielding genotypes at Kulumsa were G-33(4848.38 kg ha^{-1}), G-8(4730.12 kg ha^{-1}), G-4(4635.18 kg ha^{-1}),G-12(4431.71 kg ha^{-1}), G-58(4394.55 kg ha^{-1}), G-11(4365.80 kg ha^{-1}), G-45(4263.45 kg ha^{-1}), G-13(4157.19 kg ha^{-1}), G-36(4152.02 kg ha^{-1}) and G-30(4137.80 kg ha^{-1}). These genotypes also showed from 16% to 36% yield advantage over the best standard check G-64. Therefore; the above mentioned genotypes are promising which could be exploited in breeding program for further evaluation advanced to variety trial and or as a parent for improvement of yield and yield component traits. G-33, G-58 and G-8 gave higher mean grain yield consistently

Table 5: Range; mean and estimates of genetic parameters for 18 traits of small seeded common bean genotypes at Melkassa

Traits	Range	Mean±SE	σ^2g	σ^2p	GCV %	PCV %	H2B%	GA	GAM %
SCE	47.08-74.94	62.30±2.92	52.84	74.84	11.67	13.89	70.60	12.60	20.23
DF	36.98-47.69	41.25±1.03	8.4	11.15	7.03	8.09	75.34	5.19	12.58
DM	76.46-90.88	84.95±1.39	13.46	18.47	4.32	5.06	72.87	6.46	7.61
PH	47.64-98.59	74.48±4.90	109.68	171.75	14.06	17.60	63.86	17.27	23.18
PL	7.23-11.23	8.92±0.43	0.79	1.27	9.96	12.63	62.20	1.45	16.21
PD	3.31-6.31	4.89±0.32	0.16	0.42	8.18	13.25	38.10	0.51	10.42
SCH	38.54-71.69	56.55±3.71	72.01	107.54	15.01	18.34	66.96	14.33	25.33
TNPPP	10.95-30.99	19.50±1.93	15.2	24.76	19.99	25.52	61.39	6.30	32.32
NFPPP	10.05-29.35	17.99±2.02	13.65	24.12	20.54	27.30	56.59	5.73	31.87
NSPP	4.13-6.62	5.43±0.28	0.25	0.46	9.21	12.49	54.35	0.76	14.00
TNSPP	44.25-162.09	87.56±11.89	581.5	947.70	27.54	35.16	61.36	38.97	44.50
SPDW	0.96-1.83	1.33±0.09	0.03	0.04	11.95	15.92	56.31	0.25	18.50
DPYPP	12.90-43.21	24.11±2.54	26.11	42.78	21.19	27.13	61.03	8.24	34.16
SWPP	10.36-33.19	19.43±2.18	14.45	26.72	19.56	26.60	54.08	5.77	29.68
HSW	18.06-32.28	22.76±0.76	9.32	10.82	13.41	14.45	86.15	5.85	25.68
HI	33.76-64.88	47.63±4.12	30.5	73.99	11.59	18.06	41.22	7.31	15.36
BMYPH	3931.99-9204.89	6159.81±550.91	1072427	1858459	16.81	22.13	57.71	1622.9	26.35
SYPH	1685.09-4499.61	2911.04±279.11	225804	428411	16.32	22.48	52.71	711.71	24.45

SE: Standard error; σ^2g: Genotypic variance; σ^2p: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H^2B: Broad sense heritability; GA: Genetic Advance; GAM: Genetic advance as percentage of mean; SCE: Stand count at emergence; DF: Days to 50% flowering; DM: Days to 90% maturity; PH: Plant height; PD: Pod diameter; PL: Pod length; SCH: Stand count at harvest; TNPPP: Total number of pods plant^{-1}; NFPPP: No. of fertile pod plant^{-1}; NSPP: No. of seeds pod^{-1}; TNSPP: Total no. of seeds plant^{-1}; SPDW: Single pod dry weight ; DPYPP: Dry pod yield plant^{-1}; SWPP: Seed weight plant^{-1}; HSW: Hundred seed weight; HI: Harvest index; BMYPH: Biological yield ha^{-1}; SYPH: Seed yield ha^{-1}

at both locations. In general, the yield performance was good at both locations. However, comparatively it was better at Kulumsa, indicating its potential for common bean production.

3.1. Phenotypic and genotypic coefficient of variation

Phenotypic coefficient of variation and genotypic coefficient of variation reveals the extent of variability present for different characters and used to measure the amount of genetic variation that exists in a given population but not the heritable portion of variability (Burton and Devane, 1953). The present study indicated that PCV value ranged from 5.06% for days to maturity to 35.16% for number of seed plant^{-1}, and GCV value ranged from 4.32% for days to maturity to 27.54% for number of seed plant^{-1} at Melkassa (Table 5). According to Deshmukh et al. (1986), the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) values can be categorized as low (<10%), moderate (10–20%), and high (>20%). Based on these categories, relatively high PCV and GCV values were recorded at Melkassa for number of seeds plant^{-1}, number of fertile pods plant^{-1}, dry pod yield plant^{-1}, total number of pods plant^{-1} and seed weight plant^{-1} (Table 5). Traits such as number of seeds plant^{-1}, hundred seed weight, number of fertile pods plant^{-1} and total number of pods plant^{-1} were showed relatively high PCV and GCV at Kulumsa (Table 6). These higher PCV and GCV values specified that the genotypes in this study had a wide genetic basis and high variability among themselves with respect to these traits. This indicated that selection may be effective based on these traits and their phenotypic expression would be a good indication of genotypic potential. In agreement with this result, Alemayehu (2010) reported high PCV and GCV for number of pods plant^{-1} and seed weight plant^{-1} in common bean. Panchbhaiya et al. (2017) observed high PCV and GCV for number of pods plant^{-1}, pod yield and seed weight plant^{-1}. Higher PCV and GCV value for number of pods plant^{-1} was also reported by (Wondwosen

Table 6: Range, mean and estimates of genetic parameters for 18 traits of Small seeded Common bean genotypes at kulumsa

Traits	Range	Mean±SE	σ^2g	σ^2p	GCV %	PCV %	H^2B %	GA	GAM %
SCE	48.42-80.50	68.1+3.56	47.6	76.79	10.13	12.87	61.99	11.19	16.43
DF	47.4-58.96	51.76+0.77	6.94	8.49	5.09	5.63	81.74	4.91	9.48
DM	105.69-119.04	112.79+1.12	6.67	9.92	2.29	2.79	67.24	4.36	3.87
PH	42.55-96.54	75.59+5.01	119.43	184.2	14.46	17.95	64.84	18.13	23.98
PL	6.52-10.40	8.42+0.196	0.89	0.99	11.20	11.81	89.99	1.84	21.90
PD	2.08-4.67	3.05+0.27	0.171	0.36	13.56	19.59	47.90	0.59	19.33
SCH	49.04-80.65	64.54+3.36	57.16	86.33	11.71	14.40	66.21	12.67	19.64
TNPPP	11.72-27.94	19.23+1.77	13.71	21.85	19.25	24.31	62.75	6.04	31.42
NFPPP	9.03-26.8	18.18+1.78	12.37	20.57	19.35	24.95	60.14	5.62	30.90
NSPP	3.79-6.37	5.23+0.29	0.17	0.39	7.88	11.94	43.59	0.56	10.72
TNSPP	32.27-142.60	83.2+9.25	430.43	651.82	24.94	30.69	66.04	34.73	41.74
SPDW	1.11-2.68	1.5+0.10	0.078	0.11	18.62	21.71	73.58	0.49	32.90
DPYPP	10.02-31.62	21.99+2.01	12.92	23.43	16.35	22.01	55.14	5.50	25.00
SWPP	8.14-23.85	17+1.62	6.81	13.62	15.35	21.71	50	3.80	22.36
HSW	14.50-47.13	21.19+0.53	27.58	28.31	24.78	25.11	97.42	10.68	50.39
HI	29.88-59.02	48.2+2.53	30.59	47.1	11.47	14.24	64.95	9.18	19.05
BMYPH	7869.84-9725.31	7417.36+522.05	919702	1626433	12.93	17.19	56.55	1485.58	20.03
SYPH	1369.76-4848.38	3576.82+280.52	355439	559831	16.67	20.92	63.49	978.60	27.36

SE: Standard error; σ^2g: Genotypic variance; σ^2p: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H^2B: Broad sense heritability; GA: Genetic Advance; GAM: Genetic advance as percentage of mean; SCE: Stand count at emergence; DF: Days to 50% flowering; DM: Days to 90% maturity; PH: Plant height; PD: Pod diameter; PL: Pod length; SCH: Stand count at harvest; TNPPP: Total no. of pods plant^{-1}; NFPPP: No. of fertile pod plant^{-1}; NSPP: Number of seeds pod^{-1}; TNSPP: Total number of seeds plant^{-1}; SPDW: Single pod dry weight ; DPYPP: Dry pod yield plant^{-1}; SWPP: Seed weight plant^{-1}; HSW :Hundred seed weight; HI: Harvest index; BMYPH: Biological yield ha^{-1}; SYPH: Seed yield ha^{-1}

and Abebe, 2017; Ghimire and Mandal, 2019). Similarly, higher PCV for number of seeds per plant was reported by many researchers (Yonas, 2017; Abnet, 2020; Temesgen, 2020) but the authors found moderate GCV contradicting with the present result. The difference among the present result and the previous studies for GCV with respect to this trait may be differences in genotype. At Melkassa, seed yield and biological yield ha^{-1} were recorded high PCV and moderate GCV values. Seed weight plant^{-1}, single pod dry weight, dry pod yield plant^{-1} and Seed yield ha^{-1} had high PCV and moderate GCV values at kulumsa. In line with these finding different researchers reported high PCV and moderate GCV for seed yield ha^{-1} (Ejigu et al., 2018) and for biological yield ha^{-1} (Aziza, 2019; Kefelegn et al., 2020).

Moderate PCV and GCV (10–20%) values were observed in harvest index, stand count at emergence, plant height and stand count at harvest at both locations (Table 5 and 6). These moderate values indicated the existence of enough genetic variation on the studied genotypes to perform selection for improvement. Similar results have been noted by different authors such as Alemayehu (2010) and Wondwosen and Abebe (2017) for hundred seed weight, Aziza (2019) for harvest index, Bagheri et al. (2017) and Ghimire and Mandal (2019) for plant height, Panchbhaiya et al. (2017) and Jhanavi et al. (2018) for single pod weight.

However, days to 50% flowering and days to 90% maturity showed lower GCV and PCV values. The low value of this variation indicates that selection is not effective for these traits, because of the narrow range of variations even though it showed less influence of environmental effect on the expression of these traits at both locations. In order to improve those traits there is a requirement of creation of genetic variation through hybridization and or induced mutagenesis followed by selection. Yonas (2017) and Ejigu et al. (2018) reported low GCV and PCV for days to 50% flowering and days to 90% maturity in common bean genotypes. In addition, Abnet (2020) also observed low PCV and GCV values for days to 50% flowering and days

to maturity in forty nine common bean genotypes similar to the present result.

Moderate PCV and low GCV values were recorded by pod length, and pod diameter at Melkassa and number of seeds per pod at both Melkassa and Kulumsa. This would indicate the presence of environmental influence on the phenotypic expression of these traits and low range of genetic variation. Hence, these traits also lower responsive for selection. Aziza (2019) reported moderate PCV and low GCV for pod length and pod diameter. Moderate PCV and low GCV estimate of number of seeds pod^{-1} was reported by Yonas (2017) and Ejigu et al. (2018) similar to the current finding. The lowest PCV and GCV (2.79, 2.29%) was recorded for days to 90% maturity and the highest (30.69, 24.94%) for number of seeds plant^{-1} at Kulumsa respectively (Table 6).

Similar GCV and PCV patterns were observed in both locations for number of seeds plant^{-1}, number of fertile pods plant^{-1}, total number of pods plant^{-1}, seed yield ha^{-1}, harvest index, stand count at emergence, plant height, stand count at harvest, number of seeds pod^{-1}, days to 50% flowering and days to 90% maturity. Generally, in the present study, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) at both locations for all traits although the differences were not large for most of traits. This would be due to the fact the variation at the phenotypic level was due to the effect of genotypes and influence of environment. PCV values for most of the traits at Melkassa were higher than that observed at Kulumsa. This could be due to high environmental influence for phenotypic expression of those traits at Melkassa. Consistently higher PCV and GCV values were observed in both environments for number of seeds plant^{-1}, number of fertile pods plant^{-1} and total number of pods plant^{-1}.

3.2. Estimates of heritability (H^2B) in a broad sense

Broad sense heritability gives an idea about portion of observed variability attributable to genetic difference. The broad sense heritability values were ranged from moderate to high at both locations (Table 5 and 6). It was ranged from 38.10% for pod diameter to 86.15% for hundred seed weight at Melkassa (Table 4) and from 43.59% for number of seeds pod^{-1} to 97.42% for hundred seed weight at Kulumsa (Table 5). Heritability estimates in broad sense was categorized as high (>60%), medium (30–60%) and low (<30%) (Dabholkar, 1992). Based on this classification, most of the traits have shown consistently high heritability values in both locations such as stand count at emergence, days to 50% flowering, days to 90% maturity, plant height, pod length, stand count at harvest, total number of pods plant^{-1}, number of seeds plant^{-1} and hundred seed weight (Table 5 and 6). At Kulumsa, pod length, number of fertile pods plant^{-1}, single pod dry weight, harvest index and seed yield per hectare also scored high heritability. Higher heritability estimates for those traits indicated that the variation observed was mainly under genetic control and was less influenced by environment. In supporting of this finding different researcher reported high broad sense heritability for hundred seed weight, pods per plant, days to maturity and days to flowering (Alemayehu, 2010; Panchbhaiya et al., 2017; Wondwosen and Abebe, 2017).

Ejigu et al. (2018) and Temesgen (2020) obtained high heritability for seeds plant^{-1} and plant height, respectively. Kefelegn et al. (2020) also found high heritability values for pod plant^{-1}, pod length, plant height, days to 50% flowering, days to maturity and hundred seed weight in their study in common bean which support the present findings.

Whereas, consistently moderate heritability values (30-60%) was recorded for pod diameter, number of seeds pod^{-1}, seed weight plant^{-1} and biological yield ha^{-1} at both locations as indicated in (Table 5 and 6). Number of fertile pods plant^{-1}, single pod dry weight, seed weight plant^{-1}, harvest index and seed yield ha^{-1} had a moderate heritability at Melkassa. Aziza (2019) observed moderate heritability for traits like number of seeds pod^{-1} (44.7%), pod diameter (43.8%), biological yield (54.6%) and seed yield (49.9%) in common bean genotypes in agreement with the present result. However, the author found moderate heritability (30-60) estimate for number of seeds plant^{-1} (57.3%) and hundred seed weight (46.2%) opposing to the current heritability estimates. Kefelegn et al. (2020) also reported high heritability values for seed pod^{-1} (71%) and biological yield (73%) in their study in common bean contradicted with the present findings. The difference among the present result and the aforementioned authors may be differences in genotype and environment often bring about differences in the results of different studies.

3.3. Estimates of genetic advance as percent of mean

Genetic advance as percent of mean (GAM) ranged from low to high at both locations (Table 5 and 6). It was ranged from 7.61% for days to maturity to 44.50% for number of seeds per plant at melkassa and from 3.87% for days to maturity to 50.39% for hundred seed weight at Kulumsa. According to Johnson et al. (1955) genetic advances as a percentage of the mean (GAM) are classified high (>20%), moderate (10–20%) and low (<10%). Based on this delineation, consistently high GAM values were observed in both locations for most of traits including plant height, total number of pods plant^{-1}, number of fertile pods plant^{-1}, number of seeds plant^{-1}, seed weight plant^{-1}, dry pod yield plant^{-1}, hundred seed weight , biological yield and seed yield ha^{-1}. A result of high GAM indicated the maximum control of characters by additive gene action and the high possibility of using this trait for genetic improvement through

selection. In harmony with present finding, high GAM for number of seeds plant^{-1}, number of pods plant^{-1}, plant height and seed yield has been reported by Anunda et al. (2019), Aziza (2019) and Kefelegn et al. (2020). However, days to 90% maturity showed lower GAM values. In addition, days to 50% flowering also showed low GAM in Kulumsa. This implies selection of genotype based on these traits will not make any improvement in new population. Similarly, low GAM for days to maturity was reported by other researchers (Yonas, 2017; Ejigu et al., 2018; Abnet, 2020).

Since high heritability does not always indicate a high genetic gain, heritability with genetic advance, considered together, should be used in predicting the ultimate effect of selecting superior varieties (Johnson et al., 1955). Accordingly, in the present study, most of the traits coupled moderate to high heritability with moderate to high genetic advance as a percent of mean except days to 90% maturity (at both locations) and days to 50% flowering (at Kulumsa) coupled with high heritability and low genetic advance indicating the presence of non-additive gene action and hence, heterosis breeding may be recommended for the improvement of these traits than selection. The present result is in agreement with Anunda et al. (2019) who reported high heritability coupled with high genetic advance for plant height, number of pods plant^{-1}, number of seeds plant^{-1} and hundred seed weight. This indicating most likely the heritability is due to additive gene effects and selection may be effective for further improvement. Similarly, high heritability coupled with low genetic advance for days to maturity was also reported by Yonas (2017).

In addition, estimating genotypic coefficient of variation along with heritability plus genetic advance as a percent of mean are crucial to improve traits of interest by understanding the type of gene action involved in the expression of traits especially for polygenic traits (Anunda et al., 2019) and thus to provide better information and to reach more concrete conclusion than single parameters alone (Denton and Nwangburuka, 2011). Based on this fact, high GCV with moderate to high heritability coupled with high GAM were observed for number of fertile pods plant^{-1}, number of seeds plant^{-1} and total number of pods plant^{-1} at both locations. Dry pod yield and seed weight per plant at Melkassa and hundred seed weight at Kulumsa also showed high GCV with moderate to high heritability coupled with high GAM values in the present study which indicates that the traits were simply inherited in nature and possessed additive gene effects. In agreement to the present result, Topwal and Gaur (2016) and Bagheri et al. (2017) found higher GCV with high heritability coupled with high GAM for number of pods plant^{-1}, number of seeds plant^{-1} and pod weight plant^{-1} respectively.

Traits such as stand count at emergence, plant height, stand count at harvest, single pod dry weight, above ground biological yield, seed yield ha^{-1} and harvest index exhibited moderate GCV coupled with moderate to high heritability and Genetic advance as a present of mean even though they don't showed similar trend of patterns in both locations. It indicates that the phenotype of an individual in the current population is a good indicator of the genotypes, or it may mean that most of the variation in this trait observed in the present population is caused by variation in genotypes. This reflected the involvement of additive gene action in the expression of these traits.

4. CONCLUSION

The phenotypic coefficient of variation was higher than genotypic coefficient of variation; indicated the variation at the phenotypic level was due to the effect of genotypes and influence of environment. Most of traits exhibited moderate to high GCV, heritability and GAM association, implying the importance of those traits for improving yield and associated traits. The present study generally indicated considerable genetic variability among the genotypes. Thus, there is enormous opportunity for improving yield and atributing traits through direct selection and or hybridisation.

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