Hindawi
Advances in Agriculture
Volume 2023, Article ID 8697497, 9 pages
https://doi.org/10.1155/2023/8697497

Research Article

Genetic Variability and Association of Yield and Yield-Related Traits under Moisture Stress in Common Bean Genotypes (*Phaseolus vulgaris* L.) at Melkassa and Miesso, Ethiopia

Meseret Tola,[1] **Bulti Tesso**,[2] **and Berhanu Amsalu**[3]

[1]*Oromia Agricultural Research Institute (OARI), Bako Agriculture Research Center, Addis Ababa, Ethiopia*
[2]*College of Agriculture and Environmental Sciences, Haramaya University, Dire Dawa, Ethiopia*
[3]*Melkassa Agriculture Research Center, Nazareth, Ethiopia*

Correspondence should be addressed to Meseret Tola; meserettola342@yahoo.com

Received 26 September 2022; Revised 16 November 2022; Accepted 21 November 2022; Published 27 January 2023

Academic Editor: Othmane Merah

Twenty-five common bean genotypes were evaluated to assess the genetic variability, trait association, and determine the direct and indirect effects of traits on seed yield. The genotypes were grown in a lattice design at the research farm of the Melkassa Agricultural Research Center, Melkassa and Miesso, in the 2018 cropping season. Analysis of variance revealed that significant differences were observed among the genotypes at individual locations. The phenotypic coefficient of variation values were moderate for number of nodes, seeds per pod, plant height, and hundred seed weight at Melkassa. Moderate genotypic coefficient of variation values were obtained for pods per plant and seeds per pod. At Miesso, moderate phenotypic coefficients of variation values were recorded for number of nodes, hundred seed weight, and plant height. High heritability estimates were obtained for seed yield and hundred seed weight at Melkassa and for seed yield at Miesso, indicating that selection could be fairly easy and improvement is possible using these traits in a common bean breeding program. High genetic advances were obtained for seed yield and pods per plant at Melkassa, while moderate genetic advances as a percent of the mean were attained for plant height, hundred seed weight, and seeds per pod. Similarly, at Miesso, high and moderate genetic advances as percent of mean values were obtained for seed yield and hundred seed weight, respectively. Seed yield showed positive and significant phenotypic association with days to flowering, internode length, and pods per plant at Melkassa and had positive and significant phenotypic association with seeds per pod and hundred seed weight at Miesso. Hence, selection of those genotypes based on the traits with high genotypic coefficient of variability, heritability, genetic advance, and positive correlation coefficient and direct effect on seed yield can be recommended for further yield improvement at the respective location and at the national level in general.

1. Introduction

Common bean (*Phaseolus vulgaris* L.) is an annual leguminous plant that belongs to the genus *Phaseolus*, family Fabaceae, with pinnately compound trifoliate large leaves. Particularly in areas of sub-Saharan Africa (SSA), it is a nutritious crop that promotes food security. The annual per capita consumption of common bean is higher among low-income people who cannot afford to buy nutritious food stuff, such as meat and fish [1]. Dry beans, often called the "meat of the poor," provide micronutrients to over 300 million people in the tropics and are the second most important source of calories following maize [2]. Common bean (dry bean) is predominantly produced in Latin America and eastern and southern Africa where seasonal rainfall is erratic and soil moisture deficit often limits its yield production [3]. Dry beans that do not meet human food quality standards are used as feed for livestock.

The common bean could be grown as a seed legume in dry-land rotations with winter wheat to increase production diversity [4]. Beans are rich in a type of antioxidant called polyphenols [5]. Antioxidants fight the effects of free radicals, which are chemicals that affect a wide range of processes in the body, from physical aging to cancer and

inflammation. People who consume beans may be less likely to die of a heart attack, stroke, or other cardiovascular health problem. Health benefits of beans are generally acquired from their direct attributes, including their high content of proteins, dietary fibers, low saturated fat content, vitamins, minerals, and phytochemicals, as well as replacement in the diet, when they substitute for animal products [6]. In Ethiopia, common bean is most likely introduced by the Portuguese in the 16th century. There is a wide range of common bean types grown in Ethiopia, including mottled, red, white, and black varieties.

Beans grow well under average rainfall ranging from 500 to 1500 mm above sea level with an optimum temperature range of 16–24°C. Usually, high temperatures do not affect it if adequate soil water is present, although high night temperature will inhibit pollination [7]. They do poorly in very wet or humid tropical climate because of their susceptibility to bacterial and fungal diseases. According to [8], the current national average yield of common bean is 1.77 $t{\cdot}\text{ha}^{-1}$. However, this yield is far less than the attainable yield (2.5–3.6 $t{\cdot}\text{ha}^{-1}$) under good management conditions [9]. This low productivity is due to lack of high yielding varieties, poor cultural practices, and other impacts of climate change. The main challenges from climate change to agriculture and food production are the more frequent and severe droughts and floods and the higher pressure from insects and diseases. The most serious impediment in the production of common beans is intensive drought occurrence brought by climate change [10]. This problem is escalating from one year to another [11].

Climate change can change weather patterns, resulting in altered temperature and rainfall effects in different regions, which can have concomitant impacts on the suitability of crops for continued cultivation in climate change-impacted regions [12]. In particular, elevated temperatures (heat) and reduced rainfall (drought) can reduce crop yields [13]. Although it is documented that common bean is susceptible to moisture stress or water deficit, the production of this crop in many places of the world is carried out under moisture stress conditions due to insufficient water supply by rainfall and/or irrigation, which causes yield loses of more than >66% [14]. The adaptation strategies that will be necessary to implement at scale may be incremental (e.g., breeding new bean varieties or using agronomic practices such as irrigation) or transformational (e.g., involving changing to a different protein or high-value crop species or finding an alternative livelihood that is more climate-resilient) [15]. On the other hand, legume/common bean has a major role in mitigating climate change. These include lower fossil energy use than N-fertilized systems; lower greenhouse gas emissions than N-fertilized systems; contributing to C sequestration in soil; opportunities to replace petro problem ducts as a source of feedstock for biofuels and biorefineries [16].

Therefore, superior varieties generated through plant breeding are the most efficient approaches for agricultural production to increase or at the very least remain steady under new pressures from climate change. The study of genetic variability under moisture stress areas enables selection of drought-tolerant genotypes that would give better yields to ensure food security, especially for poor rural farmers. The choice of promising genotypes from a diverse genetic base and their subsequent utilization for hybridization is one of the strategies for improving the productivity of common beans [17]. Therefore, the assessment of variability parameters, viz., phenotypic and genotypic coefficients of variation, heritability, and genetic gain, is a prerequisite for the planning and execution of a breeding program for the improvement of different qualitative and quantitative traits in any [18]. Genetic variability studies have been conducted in Ethiopia by a considerable number of researchers on the common bean [19–21]. Moreover, even though several common bean varieties have been released for different agroecologies of Ethiopia, their level of drought tolerance has not been well documented. Indeed, only a few studies have tested breeding lines for drought stress and farmers perception of their drought tolerance [22, 23]. Therefore, keeping the above facts in view, the present study was carried out to understand the nature and extent of genetic variability, heritability, and genetic advance in some important traits of common bean genotypes under moisture stress. Thus, the main objectives were to assess the genetic variability of common bean genotypes for yield and yield-related traits, estimate association of traits, and determine direct and indirect effects of traits on yield.

2. Materials and Methods

2.1. Site Description. The experiment was conducted at the Melkassa Agricultural Research Center (MARC), Central Rift Valley, and at Miesso subsite of MARC of Ethiopia. MARC is 15 km southeast of Adama Town. However, Miesso (western Harargie) is located at 300 km East of Addis Ababa. Geographically, Melkassa is situated at an elevation of 1550 m above sea level at 8°30′ North latitude and 39°21′ East longitude. Miesso also found on 1332 m elevation, 9°28′ North latitude and 38°08′ East longitude. The place experienced 763.0 mm and 787.0 mm average rain fall for Melkassa and Miesso, respectively [24].

2.2. Experimental Design and Procedures. The experimental material comprising of 25 genotypes of common bean genotypes was obtained from the Melkassa Agricultural Research Center. The experiment was conducted using 5×5 triple lattice design on plot sizes of 3.2 m^2, each with 4 rows of 2 m length. The spacing was 0.4 m and 0.1 m between rows and plants, respectively. The spacing between replications was 1.5 m and 1 m between the incomplete blocks. Data were collected from the two central rows, leaving the plants at the ends of each row on both sides and the two outer rows for the border effect. All necessary cultural operations like weeding and hoeing were done as and when required during the growing period. In Table 1, the lists of the genotypes with their respective sources are presented.

2.3. Data Collection. Data were collected on single plant and plot bases. On a plant basis, data were collected from five randomly selected plants from each genotype in each

Table 1: List of common bean genotypes used in the study.

S. No.	Genotypes	Sources
1	DRKDDRB-65	MARC
2	DRKDDRB-70	MARC
3	DRKDDRB-81	MARC
4	DRKDDRB-78	MARC
5	DRKDDRB-35	MARC
6	DRKDDRB-48	MARC
7	DRKDDRB-66	MARC
8	DRKDDRB-55	MARC
9	DRKDDRB-96	MARC
10	DRKDDRB-46	MARC
11	DRKDDRB-77	MARC
12	DRKDDRB-80	MARC
13	DRKDDRB-38	MARC
14	DRKDDRB-32	MARC
15	DRKDDRB-33	MARC
16	DRKDDRB-34	MARC
17	DRKDDRB-93	MARC
18	DRKDDRB-101	MARC
19	DRKDDRB-94	MARC
20	DRKDDRB-55	MARC
21	DRKDDRB-100	MARC
22	DRKDDRB-49	MARC
23	DRKDDRB-37	MARC
24	DRKDDRB-36	MARC
25	Dark red kidney	MARC

replication, namely, plant height (cm), number of nodes on the main stem (count), internodes length (cm), number of pods per plant (count), and number of seeds per pod (count). While the data on plot basis were collected from the two central rows, leaving the two plants at the ends of each row on both sides, which include, days to 50% flowering, days to 90% maturity, grain filling period, hundred seed weight (g), and seed yield per plot (kg).

2.4. Data Analysis. Data were analyzed for estimation of genotypic and phenotypic coefficients of variation according to the methods suggested by [25]. Heritability in the broad sense was calculated following a method adopted by [26]. The expected genetic advance (GA) under selection was calculated assuming the selection intensity of 5% was calculated as proposed by [27]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per [25] (Table 2). Trait associations between yield and yield-related traits were computed using the method suggested by [30].

Path coefficient analysis was performed using the correlation coefficients to know the direct and indirect effects of yield components on grain yield using the general formula of [31].

$$GA = i\,\sigma p\,h^2, \tag{1}$$

where i = coefficient of selection which is 2.06 at 5% selection intensity, σp = phenotypic standard deviation, and h^2 = heritability in broad sense.

Genetic advance expressed as percentage over mean (GAM) in percent as suggested by Johnson et al. [27].

$$\text{GAM} = \frac{GA}{X} X100, \tag{2}$$

where GAM = genetic advance as percent of mean, GA = genetic advance, and X = genetic mean of the character.

3. Results and Discussion

Highly significant differences among genotypes ($P \leq 0.01$) were observed for 10 traits studied at individual location (Table 3), indicating the presence of variability for further improvement for yield and yield components of common bean. Both at Melkassa and Miesso, days to flowering, hundred seed weight, and seed yield showed highly significant ($P \leq 0.01$) differences among the genotypes. At Melkassa, grain filling period, plant height, pods per plant, and seeds per pod showed significant differences ($P < 0.05$). On the other hand, days to maturity, internode length, and number of nodes per plant did not show significant differences. While at Miesso, plant height, days to maturity, and grain filling period showed a significant difference ($P < 0.05$). However, internode length, number of nodes per plant, number of pods per plant, and seeds per pod did not show significant variations among the tested genotypes (Table 3).

At Melkassa, the shortest days to flowering (35 days) were scored for genotype DRKDDRB-93 and only genotype DRKDDRB-34 matured earlier than the check. The plant height ranged from 36.67 cm for genotype DRKDDRB-49 to 55 cm for DRKDDRB-33 with a mean of 45.87 cm. The shortest internode length (2 cm) was found on genotypes (DRKDDRB-70, DRKDDRB-96, and DRKDDRB-66),

Table 2: Limits used for categorizing the magnitudes of different parameters.

Components	High (%)	Moderate (%)	Low (%)	References
GCV and PCV	More than 20	10–20	Less than 10	[28]
Heritability	60% and above	30–60	Less than 30	[29]
Genetic advance	20% and above	10–20	Less than 10	[27]

Table 3: Analysis of variance for various traits of the common bean genotypes at Melkassa and Miesso in the 2018 cropping season.

Traits	Melkassa					Miesso				
	Replication (d*f* = 2)	Genotypes (d*f* = 24)	Error (d*f* = 36)	Mean	CV %	Replication (d*f* = 2)	Genotypes (d*f* = 24)	Error (d*f* = 36)	Mean	CV %
DF	0.65	0.75**	0.14	36	1	1.08	2.26**	0.44	35.8	1.9
DM	4.44	0.52	0.37	80.3	0.8	13.32	6.92*	2.54	75.5	2.1
PH	41.33	68.83*	25.71	45.9	11.1	39	37.83*	15.04	43.4	8.9
GFP	1.69	0.75*	0.26	44.3	1.2	6.84	6.99*	2.55	39.8	4
INL	1.56	1.07	0.91	3.3	28.7	0.76	0.71	0.48	3.2	21.4
NN	3.88	0.59	0.88	4.2	22.6	1.29	0.3	0.38	4	15.4
PP	26.33	20.68*	7.92	11.3	24.8	50.68	6.44	5.65	9.6	24.7
SP	0.09	0.81*	0.25	3.8	13	0.04	0.54	0.4	2.7	23.6
HSW	8.41	44.67**	7.04	39.1	6.8	54.01	54.33**	14.51	40.1	9.5
SY	58239	219430.72**	26130	1431.7	11.3	38094.9	52738.94**	5798.21	552.4	13.8

***Significant at 1% and 5% probability levels, respectively. PH = plant height, DF = days to 50% flowering, DM = days to 90% maturity, GFP = grain filling period, INL = internode length, NN = number of node, PP = pod per plant, SP = seed per plant, HSW = hundred seed weight, and SY = seed yield.

which indicate that it has great contribution on yielding. A wide range was observed in pods per plant and highest pods per plant (17 pods) were scored for genotypes DRKDDRB 32. At Miesso, the shortest days to flowering (35 days) were scored for genotypes DRKDDRB-101, DRKDDRB-55, DRKDDRB-78, DRKDDRB-81, and DRKDDRB-65. The shortest days to maturity (72.67 days) also found for genotypes DRKDDRB-65, DRKDDRB-55, DRKDDRB-37, and DRKDDRB-70. Thus, they are recommendable for the area that faced moisture stress like Miesso. Generally, those genotypes which took shorter days to mature (early maturing genotypes) DRKDDRB-34, DRKDDRB-65, DRKDDRB-55, DRKDDRB-37, and DRKDDRB-70 can be recommendable for moisture stress area due to they need shorter rainy season and can scape moisture stress. Based on the results of the mean performance of the genotypes, seed yield showed wide variation (1163 kg·ha^{-1} to 2243.3 kg·ha^{-1}) with a mean value of 1431.67 kg·ha^{-1} at Melkassa and from 180 kg·ha^{-1} to 777 kg·ha^{-1} with a mean of 552.4 kg·ha^{-1} at Miesso. The highest yielding genotypes were DRKDDRB-32 (2243.3 kg·ha^{-1}), followed by DRKDDRB-80 (1948.7 kg·ha^{-1}) and DRKDDRB-55 (1752.3 kg·ha^{-1}) at Melkassa, while at Miesso, DRKDDRB-94 (777 kg·ha^{-1}), DRKDDRB-36 (775.67 kg·ha^{-1}), and DRKDDRB-66 (764 kg·ha^{-1}). Generally, yield performance was better at Melkassa than Miesso, indicating its potential for common bean production.

4. Genetic Variability Parameters

4.1. Estimates of Coefficient of Variation. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population [25] and are essential in opening a breeding program and in developing better varieties. At Melkassa, the phenotypic coefficient of variation (PCV) values ranged from 0.81% for days to maturity to 30.75% for pods per plant, whereas the genotypic coefficient of variation (GCV) ranged from 0.28% for days to maturity to 18.18% for pods per plant. Moreover, next to pods/plants, other traits with high PCV values include internodes length (29.53%) and grain yield (21.02%). A similar result was reported by [32] the regarding high PCV and GCV values of pods per plant. The values indicate the existence of variability in common bean genotypes for pods per plant, internodes length, and seed yield, indicating the possibility improvement for these traits through selection. However, internodes length had a low GCV (6.99%); thus, its relatively high PCV could be due to a high environmental effect, implying that there is limited scope for its improvement through selection. In addition to days to maturity, which had the lowest PCV and GCV values, other traits with low PCV include days to flowering (1.63%) and grain filling period (1.47%), while those with low GCV are plant height (8.27%), number of nodes (7.52%), and hundred seed weight (9.05%). It implies that those traits with low PCV and GCV values have limited scope for improvement through selection due to the high influence of the environment. PCV values were generally higher than their corresponding GCV values for all the traits considered at Melkassa (Table 4). This indicates that the apparent variation was not only due to genotypes but also due to the influence of the environment on the expression of the characters. This result agrees with what [33] reported.

At Miesso, the phenotypic coefficient of variability (PCV) values ranged from 2.65% for days to maturity to 26.51% for grain yield. On the other hand, the GCV values ranged from 1.60% for days to maturity to 22.64% for grain yield. Among all characters, high GCV and PCV were

Table 4: Estimate of range, mean, variance components, heritability, and genetic advance of common bean genotypes at MARC in 2018 cropping season.

Traits	Range	Mean ± SE	σ^2p	σ^2e	σ^2g	PCV (%)	GCV (%)	H^2 (%)	GA	GAM (%)
DF	35–37	35.97 ± 0.57	0.34	0.14	0.20	1.63	1.25	59.25	0.71	1.98
DM	79–82	80.28 ± 0.46	0.42	0.37	0.05	0.81	0.28	11.77	0.16	0.20
PH	35–55	45.87 ± 6.40	40.08	25.7	14.38	13.80	8.27	35.86	4.67	10.18
GFP	43–46	44.31 ± 0.69	0.42	0.26	0.16	1.47	0.91	38.09	0.51	1.15
INL	2–5	3.32 ± 6.56	0.96	0.91	0.05	29.53	6.99	5.61	0.11	3.40
NN	2–7	4.16 ± 13.04	0.68	0.58	0.10	19.89	7.52	14.29	0.24	5.84
PP	5–20	11.35 ± 14.31	12.17	7.92	4.25	30.75	18.18	34.96	2.51	22.10
SP	2–5	3.813 ± 7.50	0.43	0.24	0.19	17.26	11.35	43.21	0.58	15.33
HSW	32–51	39.133 ± 1.73	19.58	7.04	12.54	11.31	9.05	64.06	5.83	14.89
SY	989–2309	1432 ± 1.73	90563.59	26130.03	64433.56	21.02	17.73	71.15	440.21	30.75

PH = plant height (cm), DF = days to 50% flowering, DM = days to 95% maturity, GFP = grain filling period, INL = internodes length (cm), NN = number of node, PP = number of pod per plant, SP = number of seeds per pod, HSW = hundred seed weight (g), SY = seed yield per hectare (kg), SE = standard error mean, σ^2p = phenotypic component of variances, σ^2g = genotypic component of variances, σ^2e = environmental component of variances, PCV = phenotypic coefficient of variability, GCV = genotypic coefficients of variability, H = broad sense heritability, GA = expected genetic advance, and GAM% = genetic advance as percent of the mean.

observed for seed yield (22.64 and 26.51%, respectively). Moreover, high PCV values were obtained for pods per plant (25.23%), for seed per pod (24.96%), and for internode length (23.05%), suggesting sufficient variability and thus the possibility for genetic improvement of these traits through selection. The present finding is consistent with the report of [32]. Low GCV and PCV values were observed for days to flowering (2.18 and 2.86%), days to maturity (1.60 and 2.65%), grain filling duration (3.06 and 5.05 days), and also low GCV for hundred seed weight, indicating less scope of improvement through selection due to high environmental influence. This result disagrees with the finding of [19], who reported low phenotypic coefficients of variations for seeds per pod and internode length while agreed for, days to flowering and days to maturity. The rest of the traits had moderate GCV and PCV values. Generally, the PCV values were higher than their corresponding GCV values for all the traits considered (Table 5) similar to the results obtained at Melkassa. This indicated that most of the studied yield attributes were under the influence of the environment [34], which affects the growth and development of the crop [35].

4.2. Estimate of Broad Sense Heritability and Genetic Advance. Broad sense heritability (H^2) ranged from 5.61 to 71.15% at Melkassa and from 4.45 to 72.96% at Miesso (Tables 4 and 5). High heritability was observed for hundred seed weight (64.06%) and seed yield (71.15%) at Melkassa and only for seed yield (72.96%) at Miesso. Moderate heritability values were recorded for days to flowering (59.25%), seeds per pod (43.21%), grain filling period (38.09%), plant height (35.86%), and pods per plant (34.96%), whereas traits like number of nodes (14.29%), days to maturity (11.77%), and internodes length (5.61%) had low heritability at Melkassa. At Miesso, moderate heritability was observed for days to flowering (57.94%), hundred seed weight (47.77%), grain filling period (36.73%), days to maturity (36.46%), and plant height (33.56%), while internodes length (13.55%), seeds per pod (10.42%), number of nodes (7.46%), and number of pods per plant (4.45%) had low heritability and [36] also reported similar results for some of the traits in kidney bean.

Generally, high heritability shows the reliability with which a genotype can be recognized by its phenotypic expression [37], mainly due to the major role of genotypic factors in the expression of the characters. However, heritability alone provides no indication of the amount of genetic improvement that would result from the selection of individual genotypes. Hence, knowledge about heritability coupled with genetic advance and genotypic coefficient of variations are most useful. In this study, the expected genetic advance as a percent of mean (GAM) ranged from 0.20% for days to maturity to 30.75% for grain yield at Melkassa. Pods per plant also had high GAM (22.10%) next to seed yield at Melkassa, while moderate GAM was observed for plant height (10.18%), hundred seed weight (14.89%), and seeds per pod (15.33%). At Miesso, GAM ranged from 1.99% for days to maturity to 39.77% for seed yield, while the moderate GAM value was obtained for hundred seed weight (12.92%). In the present study, high heritability coupled with high GAM was observed for seed yield at both locations, while high heritability coupled with moderate GAM was observed for hundred seed weight at Melkassa. Generally, high heritability together with GAM provides a better result than heritability alone and enables considerable improvement in the characters by selecting the best individuals and predicting the results [38].

5. Association among Traits

The analysis of the relationship among yield-related traits and their association with seed yield is essential to establish selection criteria [39]. The result at Melkassa indicated that seed yield showed positive and significant association with days to flowering, internodes length, and pods per plant. Therefore, any improvement of these traits can result in a substantial increment on seed yield. An author [40] also testified that seed yield was found to be positively correlated with number of pods per plant in common bean. The

Table 5: Estimate of range, mean, components of variance, heritability, and genetic advance of common bean genotypes at Miesso in 2018 cropping season.

Traits	Range	Mean ± SE	σ^2p	σ^2e	σ^2g	PCV (%)	GCV (%)	H^2 (%)	GA	GAM (%)
DF	35–39	35.76 ± 1.09	1.05	0.44	0.61	2.86	2.18	57.94	1.22	3.41
DM	70–78	75.52 ± 1.21	4.00	2.54	1.46	2.65	1.60	36.46	1.50	1.99
PH	35–55	43.4 ± 5.13	22.64	15.04	7.60	10.96	6.35	33.56	3.28	7.56
GFP	34–42	39.76 ± 2.30	4.03	2.55	1.48	5.05	3.06	36.73	1.52	3.81
INL	2–5	3.24 ± 12.35	0.56	0.48	0.08	23.05	8.48	13.55	0.21	6.42
NN	2–5	3.973 ± 8.89	0.33	0.30	0.02	14.41	3.93	7.46	0.09	2.21
PP	3–15	9.64 ± 14.26	5.92	5.65	0.26	25.23	5.32	4.45	0.22	2.31
SP	2–5	2.68 ± 13.62	0.45	0.40	0.05	24.96	8.06	10.42	0.14	5.35
HSW	28–53	40.07 ± 5.48	27.79	14.51	13.27	13.15	9.09	47.77	5.18	12.92
SY	156–869	552.4 ± 5.48	21445.12	5798.21	15646.91	26.51	22.64	72.96	219.68	39.77

PH = plant height (cm), DF = days to 50% flowering, DM = days to 95% maturity, GFP = grain filling period, INL = internodes length (cm), NN = number of node, PP = number of pod per plant, SP = number of seeds per pod, HSW = hundred seed weight (g), SY = seed yield per hectare (kg), SE = standard error mean, σ^2p = phenotypic component of variances, σ^2g = genotypic component of variances, σ^2e = environmental component of variances, PCV = phenotypic coefficient of variability, GCV = genotypic coefficients of variability, H = broad sense heritability, GA = expected genetic advance, and GAM% = genetic advance as percent of the mean.

Table 6: Phenotypic correlation coefficient between different yields-related traits at Melkassa during 2018 cropping season.

Traits	PH	DF	DM	GFP	INL	NN	PP	SP	HSW	SY
PH	1	0.11	0.09	0.02	−0.01	−0.07	0.11	0.20	0.23*	0.10
DF		1	0.49**	−0.35*	−0.03	−0.02	0.13	−0.01	0.04	0.28*
DM			1	0.65**	−0.13	0.01	−0.03	0.17	0.05	−0.03
GFP				1	−0.11	0.03	−0.14	0.19	0.01	−0.27*
INL					1	−0.2*	−0.11	0.24*	−0.06	0.23*
NN						1	0.16	0.01	0.09	0.01
PP							1	−0.29*	−0.03	0.24*
SP								1	−0.18	0.03
HSW									1	0.01
SY										1

PH = plant height (cm), DF = days to 50% flowering, DM = days to 95% maturity, GFP = grain filling period, INL = internode length (cm), NN = number of node, PP = number of pod per plant, SP = number of seeds per pod, HSW = hundred seed weight (g), and SY = seed yield per hectare (kg).

positive association of number of pods per plant with seed yield is in agreement with previous report by [41]. Moreover, [42] reported a significant positive correlation between the number of pods per plant and seed yield in pigeon pea. However, the grain filing period showed a significant and negative correlation with seed yield. On the other hand, at Miesso, seed yield showed a positive and significant phenotypic association with seeds per pod ($r = 0.40$) and hundred seed weight, indicating that any improvement/management that increases seeds per pod may result in improvement of seed yield to some extent.

The correlation study also showed significant associations among the yield related traits. At the Melkassa location, days to flowering showed a highly significant positive correlation with days to maturity ($r = 0.49$), and similarly, highly significant positive correlations were observed between days to maturity and grain filling period ($r = 0.65$) and internodes length with seeds per plant ($r = 0.24$) (Table 6). While at Miesso (Table 7), positive and significant associations were observed between plant height and days to flowering ($r = 0.48$), days to flowering and days to maturity ($r = 0.28$), days to maturity and grain filling period ($r = 0.87$), and days to maturity and pods per plant ($r = 0.26$). As the result of path analysis showed that, internode length (0.243), pods per plant (0.216), and days to flowering (0.208) had high positive direct effects on seed yield at Melkassa (Table 8). A similar result was reported by [43]. These characters could be considered as main components of selection in a breeding program for obtaining higher seed yield. And also at Miesso (Table 8), days to maturity (0.245), seeds per pod (0.361), and hundred seed weight (0.211) showed a high positive direct effect on seed yield at the phenotypic level. However, grain filling period had a high positive indirect effect (0.214) through the days to maturity. Generally, the phenotypic residual values at Melkassa (0.089) and at Miesso (0.085) were low, indicating that the traits which were included in the phenotypic path analysis explained 91.1 and 91.5% of the variation in seed yield, and other factors not included in the study can explain only 8.9 and 8.5%, respectively. It is suggested that maximum emphasis should be given on the above traits in selecting common bean genotypes for seed yield in addition to the grain filling period at Miesso.

Table 7: Phenotypic correlation coefficient between different yields-related traits at Miesso during 2018 cropping season.

Traits	PH	DF	DM	GFP	INL	NN	PP	SP	HSW	SY
PH	1	0.48*	0.15	−0.10	0.20	0.12	−0.02	0.05	0.14	0.18
DF		1	0.28*	−0.23	0.07	−0.03	0.19	−0.03	−0.03	0.03
DM			1	0.87*	0.13	0.08	0.26*	0.02	−0.15	0.19
GFP				1	0.09	0.10	0.16	0.04	−0.14	0.18
INL					1	0.28	0.04	−0.14	0.02	0.17
NN						1	0.20	0.08	0.06	0.14
PP							1	0.16	0.03	0.13
SP								1	0.22	0.40*
HSW									1	0.23*
SY										1

PH = plant height (cm), DF = days to 50% flowering, DM = days to 95% maturity, GFP = grain filling period, INL = internode length (cm), NN = number of node, PP = number of pod per plant, SP = number of seeds per pod, HSW = hundred seed weight (g), and GY = grain yield per hectare (kg).

Table 8: Estimate of direct (bold diagonal) and indirect effects (off diagonal) of yield-related traits on seed yield at phenotypic level in 25 common bean genotypes tested at Melkassa and Miesso in 2018 cropping season.

	Melkassa					Miesso			
Traits	DF	GFP	INL	PP	Traits	DM	GFP	SP	SW
DF	**0.2084**	0.04923	−0.0076	0.02748	DM	**0.244546**	0.041066	0.00887	−0.03091
GFP	−0.0729	**−0.1407**	−0.0263	−0.0305	GFP	0.21386	**0.046958**	0.015439	−0.02863
INL	−0.0065	0.01522	**0.24313**	−0.0237	SP	0.006013	0.00201	**0.360719**	0.046457
PP	0.0264	0.01978	−0.0266	**0.21665**	SW	−0.0359	−0.00638	0.079589	**0.210557**
	Residual value = **0.089**					Residual value = **0.085**			

6. Conclusion

Since climate change can affect crop production, the study of genetic variability under moisture stress areas enables selection of drought-tolerant genotypes that would give better yields to ensure food security through the selection of traits based on high genetic parameters and keeping them for breeding purposes. Highly significant differences among genotypes ($P \leq 0.01$) were observed for ten traits studied at individual locations. However, the results at both locations were not consistent. Therefore, the recommendation of genotypes location-wise is crucial. Especially those genotypes which took shorter days to mature (early maturing genotypes) DRKDDRB-34, DRKDDRB-65, DRKDDRB-55, DRKDDRB-37, and DRKDDRB-70 could be recommendable for moisture stress area due to they need shorter rainy season and can scape moisture stress. The highest yielding genotypes were DRKDDRB-32 (2243.3 kg·ha^{-1}), followed by DRKDDRB-80 (1948.7 kg·ha^{-1}) and DRKDDRB-55 (1752.3 kg·ha^{-1}) at Melkassa, while at Miesso, DRKDDRB-94 (777 kg·ha^{-1}), DRKDDRB-36 (775.67 kg·ha^{-1}), and DRKDDRB-66 (764 kg·ha^{-1}) could be recommended for a breeding program or as breeding material. Generally, yield performance was better at Melkassa than Miesso, indicating its potential for common bean production. The experimental studies revealed that substantial amount of genetic variability among the genotypes under study. Genetic parameters in association with the correlation study indicated that primary emphasis should be given on days to flowering, internodes length, pods per plant, seeds per pod, and hundred seed weight for selection of superior genotypes. Hence, selection of those genotypes with high GCV, heritability, genetic advance, and positive correlation coefficient and direct effect on seed yield can be recommended for further yield improvement of common bean at respective location. Generally, legume/common bean has a major role in adaptation and mitigation of climate change because early maturing common bean has the chance to escape a rain shortage if they grow under moisture stress area.

Data Availability

The raw data and additional information are available from the corresponding author upon request.

Disclosure

An earlier version was submitted to Haramaya University as MSc Thesis titled "Genetic Variability and Association of Morphoagronomic Traits in Selected Common Bean (*Phaseolus vulgaris* L.) Genotypes Grown under Moisture Stressed Environments in Ethiopia."

Conflicts of Interest

The authors declare that there are no conflicts of interest.

Authors' Contributions

Meseret Tola initiated the research, wrote the research proposal, conducted the research, performed data entry and analysis, and wrote the manuscript. Bulti Tesso and Berhanu Amsalu were involved in analysis, methodology,

supervising, writing, reviewing, and editing of the research proposal and manuscript and also read and approved the final manuscript.

Acknowledgments

The authors would like to give special appreciation to Africa Center of Excellence for Climate Smart Agriculture and Biodiversity Conservation, Haramaya University, Ethiopia, for providing the financial support by the grant to do this study through ACE-II Project and Melkassa Agricultural Research Center especially lowland pulse team for endowment of experimental field and technical supports. Their appreciations go to AJPS for publishing abstract of the thesis.

References

[1] S. E. Beebe, I. M. Rao, M. W. Blair, and J. A. Acosta-Gallegos, "Phenotyping common beans for Adaptation to drought," *Frontiers in Physiology*, vol. 4, no. 35, pp. 35–20, 2013.

[2] Cgiar, "Consultative group on international agricultural research," 2016, http://www.cgiar.org/our-strategy/crop-factsheets/beans/.

[3] G. Urrea and S. Sabater, "Epilithic diatom assemblages and their relationship to environmental characteristics in an agricultural watershed (Guadiana River, SW Spain)," *Ecological Indicators*, vol. 9, no. 4, pp. 693–703, 2009.

[4] D. Svetleva, G. Pereira, J. Carlier, L. Cabrita, J. Leitão, and D. Genchev, "Molecular characterization of *Phaseolus vulgaris* L. genotypes included in Bulgarian collection by ISSR and AFLP™ analyses," *Scientia Horticulturae*, vol. 109, no. 3, pp. 198–206, 2006.

[5] A. Sharma, M. Kaur, J. K. Katnoria, and A. K. Nagpal, "Polyphenols in food: cancer prevention and apoptosis induction," *Current Medicinal Chemistry*, vol. 25, no. 36, pp. 4740–4757, 2018.

[6] V. Messina, "Nutritional and health benefits of dried beans," *The American Journal of Clinical Nutrition*, vol. 100, no. 1, pp. 437–442, 2014.

[7] E. Katungi, J. F. Chianu, L. Sperling, and S. Beebe, *Common Bean in East Africa: A Situation and Outlook Analysis*, ICRISAT, Hyderabad, India, 2009.

[8] W. Wondimu and T. Tana, "Yield response of common bean (*Phaseolus vulgaris* L.) varieties to combined application of nitrogen and phosphorus fertilizers at mechara, eastern Ethiopia," *Journal of Plant Biology and Soil Health*, vol. 4, no. 2, pp. 1–7, 2017.

[9] Csa (Central Statistical Authority), *Crop Production Forecast Sample Survey*, Green Library, Addis Ababa, Ethiopia, 2012.

[10] Bureau of Statistics, *Lesotho Agricultural Situation Report*, Ministry of Economics and planning, Maseru, Lesotho, 2014.

[11] J. Kihara, D. S. MacCarthy, A. Bationo et al., "Perspectives on climate effects on agriculture: the international efforts of AgMIP in Sub-Saharan Africa," *Handbook of Climate Change and Agroecosystems: The Agricultural Model Intercomparison and Improvement Project Integrated Crop and Economic Assessments*, vol. 3, 2015.

[12] D. K. Ray, J. S. Gerber, G. K. MacDonald, and P. C. West, "Climate variation explains a third of global crop yield variability," *Nature communications*, vol. 6, 2015.

[13] C. Rosenzweig, J. Elliot, D. Deryng et al., "The Global Gridded Crop Model Intercomparison: Data and modeling protocols for Phase 1 (v1.0)," *Geoscientific Model Development Discussions*, vol. 7, no. 4, pp. 4383–4427, 2014.

[14] P. Batel, H. Houchi, M. Daoust, N. Ramoz, M. Naassila, and P. Gorwood, "A h gene is associated with ad," *Alcoholism: Clinical and Experimental Research*, vol. 32, no. 4, pp. 567–572, 2008.

[15] L. Rickards and S. M. Howden, "Transformational adaptation: agriculture and climate change," *Crop and Pasture Science*, vol. 63, no. 3, pp. 240–250, 2012.

[16] E. S. Jensen, M. B. Peoples, R. M. Boddey et al., "Legumes for mitigation of climate change and the provision of feedstock for biofuels and biorefineries. A review," *Agronomy for Sustainable Development*, vol. 32, no. 2, pp. 329–364, 2012.

[17] H. Ali, M. A. Tiruneh, and H. Zelleke, "Estimation of better parent and economic heterosis for yield and associated traits in common beans," *Journal of Applied Biosciences*, vol. 71, no. 1, pp. 5706–5714, 2013.

[18] O. P. Meena and V. Bahadur, "Assessment of genetic variability, heritability and genetic advance among tomato (*Solanumly copersicum* L.) germplasm," *The Bioscan*, vol. 9, no. 4, pp. 1619–1623, 2014.

[19] G. Barecha, "Genetic variability and path coefficient analysis for yield and yield related traits in common bean (*Phaseolus vulgaris* L.) accessions at Haramaya University, MSc Thesis. Haramaya University, Haramaya, Ethiopia. Beans (*Phaseolus*spp) - model food legumes," *Plant and Soil*, vol. 252, pp. 55–128, 2015.

[20] G. Boru, *Genetic Variation and Characters Association Study for Drought Tolerance in Large white Seed Common Bean (Phaseolus vulgaris L.) Genotypes at Melkassa, Rift valley, Ethiopia*, MSc Thesis, Jimma University, Jimma, Ethiopia, 2014.

[21] D. Ambachew, F. Mekbib, A. Asfaw, S. E. Beebe, and M. W. Blair, "Trait associations in common bean genotypes grown under drought stress and field infestation by BSM bean fly," *The Crop Journal*, vol. 3, no. 4, pp. 305–316, 2015.

[22] A. Asfaw, M. W. Blair, and P. C. Struik, "Multienvironment quantitative trait loci analysis for photosynthate acquisition, accumulation and remobilization traits in common bean under drought stress. G3: Genes," *G3 Genes*, vol. 2, no. 5, pp. 579–595, 2012.

[23] Y. Rezene, S. Gebeyehu, and Z. Habitamu, "Morpho-physiological response to post- flowering drought stress in small seeded common bean (*Phaseolus vulgaris* L.) genotypes," *Journal of Plant Studies*, vol. 2, pp. 36–41, 2013.

[24] MoA (Ministry of Agriculture), *Agro-Ecological Zones of Ethiopia*, Natural ResourceManagement and Regulatory Department, Addis Ababa, Ethiopia, 2000.

[25] G. W. Burton and E. H. Devane, "Estimating heritability in tall Fescue (*Festucaarundinacea).* from replicated clonal material," *Agronomy Journal*, vol. 45, no. 10, pp. 478–481, 1953.

[26] R. W. Allard, *Principles of Plant Breeding*, John Willey and Sons, Inc, New York, NY, USA, 1960.

[27] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of genetic and environmental variability in soybeans," *Agronomy Journal*, vol. 47, no. 7, pp. 314–318, 1955.

[28] S. N. Deshmukh, M. S. Basu, and P. S. Reddy, "Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut," *Indian Journal of Agricultural Sciences*, vol. 56, pp. 816–821, 1986.

[29] H. F. Robinson, R. E. Comstock, and P. H. Harvey, "Estimates of heritability and the degree of dominance in corn," *Agronomy Journal*, vol. 41, no. 8, pp. 353–359, 1949.

[30] P. A. Miller, J. C. Williams, H. F. Robinson, and R. E. Comstock, "Estimates of genotypic and environmental variances and c in upland cotton and their implications in selection," *Agronomy Journal*, vol. 50, no. 3, pp. 126–131, 1958.

[31] D. R. Dewey and K. H. Lu, "A correlation and path coefficient analysis of components of crested wheatgrass seed production," *Agronomy Journal*, vol. 51, no. 9, pp. 515–518, 1959.

[32] A. S. Kamaluddin, "Variability, correlation and path analysis for seed yield and yield related traits in common beans," *Indian Journal of Horticulture*, vol. 68, no. 1, pp. 61–65, 2011.

[33] M. Syed, P. A. Sofi, M. N. Khan, N. R. Sofi, and Z. A. Dar, "Genetic diversity variability and character association in local common Bean (*Phaseolus vulgaris* L.) germplasm of Kashmir," *Electronic Journal of Plant Breeding*, vol. 3, no. 3, pp. 883–891, 2012, http://sites.google.com/site/ejplantbreeding.

[34] K. P. Ghosh, A. K. Islam, M. A. Mian, and M. M. Hossain, "Variability and character association in F2 segregating population of different commercial hybrids of Tomato (Solanumlycopersicum L.)," *Journal of Applied Sciences and Environmental Management*, vol. 14, no. 2, pp. 91–95, 2010.

[35] A. S. Gerrano, P. O. Adebola, W. S. Jansen van Rensburg, and S. M. Laurie, "Genetic variability in cowpea (Vigna unguiculata (L.) Walp.) genotypes," *South African Journal of Plant and Soil*, vol. 32, no. 3, pp. 165–174, 2015.

[36] K. M. Samal, N. Senapati, and A. Sahu, "Varietal performance and genetic variability in kidney bean (*Phaseolus vulgaris L*)," *Indian Journal of Agricultural Sciences*, vol. 67, no. 8, pp. 328-329, 1997.

[37] J. L. Lush, "Inter-sire correlation and regression of offspring on damasasa method of estimating heritability characters," *Proceedings of the Australian Society of Animal Production*, vol. 33, pp. 293–301, 1940.

[38] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Genotypic and phenotypic correlations in *soybeans* and their implications in selection," *Agronomy Journal*, vol. 47, no. 10, pp. 477–483, 1955.

[39] K. Darkwa, D. Ambachew, H. Mohammed, A. Asfaw, and M. W. Blair, "Evaluation of common bean (*Phaseolus vulgaris* L.) genotypes for drought stress adaptation in Ethiopia," *The Crop Journal*, vol. 4, no. 5, pp. 367–376, 2016.

[40] K. B. Singh, G. Bejiga, and R. S. Malhotra, "Associations of some characters with seed yield in chickpea collections," *Euphytica*, vol. 49, no. 1, pp. 83–88, 1990.

[41] B. B. Singh, R. D. Mohan, R. L. K. Dashie, and L. E. N. Jackai, *Origin, Taxonomy and Morphology of (VignaunguiculataL. Walp)*, Co-publicatin of Intrnational Institute of Tropical Agriculture (IITA) and Japan International Research Center for Agricultural Sciences (JIRCAS) IITA, Ibadan, Nigeria, 1997.

[42] F. K. Padi, "Correlation and path coefficient analyses of yield and yield components in p," *Pakistan Journal of Biological Sciences*, vol. 6, no. 19, pp. 1689–1694, 2003.

[43] N. Rai, P. K. Singh, A. Verma, P. K. Yadav, and T. Choubey, "Hierarchical analysis for genetic variability in pole type French bean," *Indian Journal of Horticulture*, vol. 67, pp. 150–153, 2010.