

Research Article

Genotypic Variation of Faba Bean (*Vicia faba* L.) for Agronomic Traits Under Low and High Soil Phosphorus Regimes

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Abstract

Faba bean (*Vicia faba* L.) is a multi-purpose crop owing to its immense economic and ecological benefits. Genetic variability assessment for agronomic traits is a crucial step in improving the yield and yield components of the crop. Phosphorus deficiency seriously affects the yield of faba bean. The present study was conducted to evaluate the genotypic variability of faba bean for agronomic traits. Twenty and 12 genotypes, in the field and greenhouse respectively, were planted under two P fertilizer regimes (0 and 46kg/ha). Analysis of variance indicated highly significant ($P < 0.01$) genotypic variation for most of the agronomic traits under both field and greenhouse; while grain yield (GY), days to fifty percent flowering (DFF), number of pods per plant (NPP) and days to 90% maturity (DNM) had significant genotype by location interaction. The agronomic performance of P-unfertilized (P-) treatments was significantly reduced; with the effect ranging from -4.6% for DNM to 20.3% for NPP in the field; and from -3.6% for DFF to 21.6% for shoot dry weight per plant (SDWP) in the greenhouse. Correlation analysis indicated that most traits were strongly correlated to one another; with consistently significant correlation among GY, DFF, and NPP. Biomass production per day (BPD), GY, SDWP, DNM, and NPP were the highest contributors to the genetic variation. Mean comparisons and biplot analysis results revealed that genotypes Moti, Gebelcho, Dosha, Tumsa, and Didea had superior agronomic performance under all conditions. The study revealed the availability of genotypic variation among the faba bean genotypes for agronomic traits.

Keywords

Faba Bean, Agronomic Traits, Genotypic Variability, Grain Yield, Phosphorus

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Received: 4 February 2025; Accepted: 9 May 2025; Published: 30 June 2025



1. Introduction

Faba bean is a cool-season grain legume crop originated in the Middle East [1]. With total production of 5.68 million tonnes from 2.57 million hectares of cultivated area, it ranked sixth globally among legume crops following common bean, field pea, chickpea, cowpea, and lentil [2]. China and Ethiopia are the world's largest producers of faba bean [2]. In Ethiopia, it occupies 31% of the total land cultivated and 34% of the total annual production of pulses produced in the country [3]. Faba bean is a good source of protein for many people in developing countries while it is mostly used for animal feed in the developed world [4]. The protein content of faba bean ranges from 24 to 35% of seed dry matter [4, 5]. Faba bean has also the highest and most efficient N₂ fixation capacity among the cool season grain legumes with up to 330 kg N/hm² [6, 7]. It is integrated into cropping systems in the form of crop rotation systems to minimize the occurrence of cereal nematodes and soil-borne diseases [8, 9], increase Nitrogen contribution for cereal due to N-fixation [6, 10], enhance soil microbial activity and its biological characteristics [11].

Despite the multi-faceted benefits of faba bean, its productivity has been declining in Ethiopia and the world at large [12, 13]. Lack of high-yielding genotypes suitable for different agro-climatic conditions, low yield potential of the existing genotypes, and scarcity of improved varieties tolerant/ resistant to various biotic and abiotic stresses are the major causes of the crop's yield reduction [12, 13]. In Ethiopia, while the yield potential of faba bean can be attained at more than 4 tons per hectare, its average yield is still around 2 t/ha [3, 12].

Agro-morphological variability characterizations of local germplasm is very important to better understand existing diversity, attain targeted genetic broadening of breeding populations, and transfer desired genes to enhance productivity [14, 15]. Grain yield improvement, as a primary breeding objective of the faba bean, should be made by evaluating the genetic variability of the crop so that high-yielding genotypes which are adapted to different agro-climatic conditions could be selected [16]. However, selection for superior genotypes based on yield alone is inefficient and ineffective due to the complexity of the yield and its dependence on other components and large genotype by environment interaction of the trait [17, 18]. Hence, the evaluation and identification of other agronomic traits are advisable [19].

Among the abiotic stresses, phosphorus deficiency, which is mostly a problem of soil in Sub-Saharan Africa (SSA), greatly reduces faba bean grain yield [20-22]. Phosphorus (P) plays an important role in nodule initiation, nitrogen fixation and other biochemical processes [23]. Farmers in SSA have limited resources and apply little to no P fertilizers [24, 25], which is mainly due to continuous price increases in phosphorus fertilizer [26]. Belachew et al., [27] reported that only half of faba bean fields were fertilized in Ethiopia in 2019. Hence, any effort aimed at assessing the genotypic variability

of the crop should consider soil with P-reduced or unapplied condition. Besides, it has been reported that abiotic stresses including P deficiency are capable of affecting genotypic variability of a crop [28, 29]; and thus it is important to investigate the extent of the variability under contrasting soil P regimes.

Genotypic variability for agronomic traits in faba bean has been reported in Ethiopia [30, 31]. However, detailed and systematic investigations on the genetic variability of the genotypes included in this study were not done in Ethiopia. Accordingly, the study was conducted to evaluate the genotypic variability of improved faba bean genotypes for their agronomic traits under contrasting phosphorus fertilizer regimes.

2. Materials and Methods

2.1. Description of the Study Areas

The study was carried out in 2015 at two field sites (Adadi and Holetta, in central Ethiopia) under rain-fed conditions and in 2016 at a greenhouse. Greenhouse experiment was done to validate results from the field experiment. The geographical coordinates, climatic and soil physicochemical properties of the sites used for the experiments are indicated in Table 1.

2.2. Plant Materials and Experimental Method

Twenty faba bean genotypes were used for the field experiments while twelve genotypes were used in the greenhouse. The number of genotypes was reduced to 12 for the greenhouse experiment based on the preliminary performance of the genotypes under the field experiment and the availability of greenhouse space. The genotypes included were highly commercialized high-yielding varieties and the most promising breeding lines. The details of the germplasm are presented in Table 2. Seeds of these genotypes were obtained from the Holetta Agricultural Research Center. Undamaged, clean, and uniform-sized seeds of each genotype were used. Soil samples were collected for analysis, before planting, from 0-30 cm depth at each location from three different places within each block and mixed to form a composite. After air-drying, the soil was ground and sieved (2 mm) and analyzed for pH, texture [32], CEC and exchangeable bases [33], available P [34] and total phosphorus [35]. Total carbon (TC) and nitrogen (TN) were analyzed with an Elemental Analyzer-Isotope Ratio Mass Spectrometry (EA-IRMS) (20-20, SerCon, Crewe, UK). Table 1 shows the soil physicochemical characteristics of the experimental sites.

The experimental plots (rows for the field experiment) and pots (for the greenhouse experiment) were prepared in pairs where they received the same treatments except that one of the pair received phosphorus fertilizer (the recommended rate of

46 kg/ha of P_2O_5 , corresponding to 20g/row) and the second was devoid (0) of the fertilizer. This was meant to minimize the experimental error due to soil and other variations. For the field experiment, a plot is a single row of 4 m length spaced 0.4 m apart, with seeds planted 0.1 m apart in each row. Two seeds were planted per hill and thinned to one at one week after planting to achieve a plant population of 250,000 plants/ha. For the greenhouse study, each pot (40 cm diameter and 50 cm height) was filled with 5 kg of sterilized sand-soil

mixture (2: 1). Pots were watered to approximately 75% field capacity before planting. Four pre-germinated seeds were planted per pot and later thinned to three seedlings. Pots were watered daily till maturity. Glass mounted greenhouse's temperature and relative humidity were adjusted to 24°C and 90%, respectively. The experimental design for both field and greenhouse trial was a randomized complete block design (RCBD) with three replications.

Table 1. Description of the study areas.

Parameters	Field		Greenhouse
	Adadi	Holetta	Soil
Altitude (masl)	2520	2390	----
Latitude (N)	8.21	9.04	----
Longitude (E)	38.29	38.03	----
Temperature (°C)	8.5-23.5	6.4 -24.4	----
Rainfall (mm)	930.8	760.8	----
Soil type	Vertisol	Nitisol	Vertisol
Soil textural class	Clay	Clay	Clay
% Clay	61.18	46.42	66.58
% Silt	25.34	32.48	15.25
% Sand	12.54	20.17	15.45
pH (H ₂ O)	6.4	7.3	6.79
Available P (ppm)	15.94	23.67	19.92
Total N (%)	0.15	0.18	0.17
K (ppm)	37.35	25.79	31.56
Organic C (%)	1.16	0.738	1.17
CEC (Meq/100g)	25.13	23.05	18.17
EC (μS)	405.63	697.67	485.51

Table 2. Description of the faba bean genotypes used in the study

S.N.	Genotype	Pedigree	Year of Release	1000 seed weight	Altitude Range (masl)	Yield (t/ha)	
						Research Station	Farmer Field
1	Lalo	Selale Kasim 89-4	2002	325	2600-3000	3.6	--
2	Dagim	Girar Jarso 89-8	2002	299	2600-3000	3.5	--
3	CS20DK	CS20DK	1977	476	2300-3000	2.0-4.0	1.5-3.0
4	Obse	CS20DK x ILB4427	2007	821	1800-3001	2.5-6.1	2.1-3.5
5	Gebelcho	ILB4726 x Tesfa	2006	797	1800-3001	2.5-4.4	2.0-3.0

S.N.	Genotype	Pedigree	Year of Release	1000 seed weight	Altitude Range (masl)	Yield (t/ha)	
						Research Station	Farmer Field
6	Holetta-2	BPL 1802-2	2000	506	2300-3000	2.0-5.0	1.5-3.5
7	Hachalu	EH00102-4-1	2010	890	1900-2800	3.2-4.5	2.4-3.5
8	Wayu	Wayu 89-5	2002	312	2100-2700	1.8-3.2	1.0-2.3
9	Selale	Selale Kasim 91-13	2002	346	2100-2700	2.2-3.3	1.0-2.3
10	Didea	EH01048-1	2014	700	1800-2800	3.5-4.6	2.0-4.4
11	Gora	EK01024-1-2	2013	980	1800-2800	3.0-5.0	2.0-4.0
12	Dosha	Coll 155/00-3	2009	704	1800-3000	2.8-6.2	2.3-3.9
13	Walki	Bulga-70 x ILB4615	2008	676	1900-2800	2.4-5.2	2.0-4.2
14	NC58	NC58	1978	449	1800-3000	2.0-4.0	1.5-3.5
15	Moti	ILB4432 x Kuse 2-27-33	2006	781	1800-3000	2.8-5.1	2.3-3.5
16	Tumsa	Tesfa x ILB 4726	2010	737	1800-3000	2.5-6.9	2.0-3.8
17	EH06088-1	Advanced breeding lines	--	--	--	--	--
18	EH07015-7	Advanced breeding lines	--	--	--	--	--
19	EH06022-4	Advanced breeding lines	--	--	--	--	--
20	EH06006-6	Advanced breeding lines	--	--	--	--	--

2.3. Data Collection

Data were collected on five plants per plot for the field experiment and three plants per pot for the greenhouse experiment and the mean values were averaged per plant. The following traits were collected: early vigor (EV), average leaf area (ALA), biomass production per day (BPD), days to 50% flowering (DFF), shoot dry weight per plant (SDWP), number of pods per plant (NPP), days to 90% maturity (DNM), number of seed per pod (NSP), 100-seed weight (HSW), grain yield per plant (GY), total above-ground biomass dry weight (TAGB) and harvest index (HI). EV was recorded three times starting from 15 days after planting (DAP) till 45 DAP; with a 15-day interval. 1 to 5 scaling was used; with 1 being the least vigor and 5 being the most vigor. ALA and SDWP were recorded at 45 DAP and 90% physiological maturity. The leaf area was measured using a digital leaf area meter. GY was measured after harvest. TAGB was estimated by adding SDW and GY. HI was estimated as the proportion of TAGB that was grain; $HI = (GY / TAGB) \times 100$. BPD was calculated as, $BPD = TAGB / DNM$.

2.4. Data Analysis

Data were checked for homogeneity of variance and transformed, where applicable, before statistical analysis. An

individual site and combined analysis of variance were performed using SAS 9.3 [36]. Multiple mean comparisons were performed using Duncan's New Multiple Range Test at a 0.05 level of probability. Relative reduction (RR) of the agronomic performance of the genotypes on the phosphorus untreated plot relative to their performance on the phosphorus treated plot was calculated as, $RR (\%) = 1 - (\text{performance without P} / \text{performance with P}) \times 100$; [37]. Pearson's correlation coefficients were estimated using the PROC CANCORR subprogram of SAS.

3. Results

3.1. Effect of Phosphorus Fertilizer Regimes, Locations, Genotype and Their Interactions on the Agronomic Performance of Faba Bean

Results of the ANOVA showed that the two P fertilizer regimes, the two locations and faba bean genotypes were highly significantly ($P < 0.01$) different for all agronomic traits; except for non-significant interaction for average leaf area (ALA) under greenhouse condition and harvest index (HI) under field condition (Table 3). Genotype by phosphorus interaction was non-significant for most agronomic traits; except for signifi-

cant interaction for ALA and hundred seed weight (HSW) at greenhouse and for ALA and grain yield (GY) at field. Phosphorus by location interaction was non-significant for all traits; except ALA and HSW. Genotype by location interaction was non-significant for half of the tested traits while it was significant for days to 50% flowering (DFF), days to 90% maturity (DNM), hundred seed weight (HSW), number of pod per plant (NPP) and GY. Genotype by location by phosphorus interaction was non-significant for all traits except NPP (Table 3).

Under both field and greenhouse conditions, mean values of the agronomic traits were higher under phosphorus (P)-fertilized than unfertilized treatment except for harvest index (HI), days to 50% flowering (DFF), days to 90% maturity (DNM (Table 4). The differences in performance under the two phosphorus fertilization regimes were reflected in the relative reduction (RR) values of the traits; with values ranging from -4.6% for DNM to 20.3% for number of pod per plant (NPP) in the field; and ranging from -3.6% for DFF to

21.6% for shoot dry weight per plant (SDWP) in the greenhouse (Table 4). The higher the RR values, the higher the trait's sensitivity to low soil P. Grain yield (GY), which is the main agronomic trait, was also drastically affected by the reduced phosphorus in the range of 13.8 to 18.9%. The negative RR values obtained for DFF and DNM are indicative of delay in flowering and maturity of the genotypes under low P. In the field, P-fertilized treatment attained 2.25 and 6.27 days earlier flowering and maturing duration than P-unfertilized treatment (Table 3).

With respect to the effect of location on the agronomic performance, the result showed that most traits had better performance at Adadi than Holetta; except for the better performance of ALA and NPP at Holetta than Adadi. The difference in performance at the two locations was largely attributed to a higher amount of rainfall at Adadi than Holetta during the growth season. The clayey soil type at Adadi may also contribute to better performance as compared to sandy soil at Holetta (Table 1).

Table 3. Mean and mean squares of the agronomic traits under field and greenhouse conditions.

Traits	ALA (cm ²)	BPD (mg/d)	SDWP (g/p)	AGBP (g/p)	NPP	HSW (g)	GY (g/p)	HI (%)	DFF	DNM
Field										
Mean	42.9	218.4	15.8	29.4	9.4	70.9	13.8	46.4	56.7	139.6
MS _G	25.3**	3047.8**	8.01**	17.51**	11.4**	1971.3**	2.57**	9.56**	165.3*	325.4**
MS _L	70.63**	1959.7**	15.66**	43.44**	6.14**	72.71*	6.97**	1.94ns	47.7**	8.82**
MS _P	2636.1*	87944.1*	404.8*	1278.1*	267.1*	1551.1**	243.0**	13.63*	33.0**	1664.1*
MS _{GxL}	7.59ns	152.17ns	0.60ns	1.79ns	3.31*	35.98**	0.61*	2.03ns	9.52**	13.28**
MS _{GxP}	9.45*	119.16ns	0.76ns	1.75ns	2.20ns	16.30ns	0.55*	2.35ns	0.33ns	0.82ns
MS _{PxL}	32.27*	117.60ns	0.51ns	1.75ns	5.28ns	339.15**	0.38ns	0.08ns	0.70ns	0.60ns
MS _{GxLxP}	3.13ns	43.31ns	0.46ns	0.72ns	3.63*	15.74ns	0.47ns	3.23ns	0.98ns	0.61ns
Greenhouse										
Mean	37.8	200.8	13.8	25.2	13.4	62.2	11.6	45.2	49.9	128.1
MS _G	2.53ns	536.90**	1.97**	8.86**	6.78**	533.40**	6.03**	30.1**	54.8**	123.2**
MS _P	693.1**	48319.1*	200.0**	604.9**	49.8**	274.95**	108.5**	11.84*	55.1**	304.2**
MS _{GxP}	5.54*	44.71ns	0.57ns	0.55ns	0.01ns	45.38**	0.17ns	3.70ns	0.88ns	2.16ns

ALA, Average leaf Area; BPD, Biomass production per day; SDWP, Shoot dry weight per plant; AGBP, above-ground biomass per plant; NPP, Number of pod per plant; HSW, Hundred seed weight; GY, Grain Yield per plant; HI, Harvest index; DFF, days to fifty percent flowering; DNM, days to ninety percent maturity; MS_G, MS_L, MS_P, MS_{GxL}, MS_{GxP}, MS_{PxL}, and MS_{GxLxP}, mean square of genotype, location, phosphorus, genotype by location, genotype by phosphorus, phosphorus by location, genotype by location by phosphorus, respectively; ns, *, and ** are non-significant, significant and highly significant, respectively.

For the ease of discussing the results with respect to the effect of genotype and its interaction with other factors on the performance of agronomic traits, we categorized the traits in

to three; namely, *vegetative* traits which include average leaf area (ALA), biomass production per day per plant (BPD), shoot dry weight per plant (SDWP) and TAGB; *reproductive*

traits comprising NPP, HSW, GY, and HI; and *phenological* traits consisting DFF and DNM.

3.1.1. Vegetative Traits (ALA, SDWP, BPD and AGBP)

In the field, faba bean genotypes Dagim, CS20DK and Hachalu had the highest average leaf area (ALA); while EH06006-6 and NC58 had the lowest ALA. In the greenhouse, genotype Dosha had the highest ALA, although difference among the genotypes for the trait was not significant (Table 4). Under P fertilized field treatment, faba bean genotypes Tumsa and Hachalu had the highest average leaf area (ALA); while EH06006-6 and NC58 had the lowest ALA (Table 4). Under without-P treatment, Dagim, Holetta-2 and CS20 DK had the highest ALA values, with the lowest values obtained for EH06006-6 (35.7 cm²) and NC58 (36.4 cm²) (Table 4).

The highest shoot dry weight per plant (SDWP) was produced by Gora (16.7 g/plant), followed by Dosha (16.6 g/plant) and Moti (16.6 g/plant) and Tumsa (16.6 g/plant), while the lowest was produced by Selale and EH06088-1. In the greenhouse, Hachalu and Selale had the highest SDWP; while Walki and Moti had the lowest SDWP values (Table 4).

Biomass production per day (BPD) of the genotypes, under field trial, ranged from 188.9 mg/plant/day for EH06088-1 to 240.9 mg/plant/day for Moti; while it ranged from 183.9 mg/plant/day for Walki to 211.9 mg/plant/day for Gora under greenhouse condition (Table 4).

In the field, the highest total above-ground biomass weight (AGBP) was obtained for Moti, Gebelcho and Dosha; while Hachalu and Dosha had the highest AGBP under greenhouse condition (Table 4).

3.1.2. Reproductive Traits (NPP, HSW, GY and HI)

The number of pods per plant (NPP) of the genotypes, at field, ranged from 7.8 for EH06022-4 to 11.8 for Moti; while it ranged from 11.4 for Selale to 14.2 for Gebelcho under greenhouse trial (Table 4). At Holetta, Gebelcho (12.0 pods/plant), Moti (11.6 pods/plant), Dosha (11.3 pods/plant) and Tumsa (10.9 pods/plant) had the highest NPP. At Adadi, Moti (11.4 pods/plant), Hachalu (10.3 pods/plant), Gebelcho (10.1 pods/plant) and Walki (9.9 pods/plant) had the highest number of pods. Selale and NC58 had the lowest values for this trait at Holetta while EH06088-1 and EH06022-4 had the least number of pods per plant at Adadi (Figure 1).

Under field trial, the highest hundred seed weight (HSW) was obtained for Moti (83.8 g), Tumsa (82.8 g), and EH06022-4 (82.3 g) (Table 4). At Holetta, genotypes Moti, Gebelcho, Tumsa and Obse had the highest HSW; while genotypes EH06006-6, EH06022-4, Holetta-2 and Moti had the highest HSW at Adadi (Figure 1). For the greenhouse trial, the highest HSW were obtained by Tumsa and Didea; while Selale and Obse had the lowest HSW (Table 4).

Grain yield per plant (GY) of the genotypes, at field, ranged from 13.0 g/plant for EH06022-4 to 14.6 g/plant for Moti;

while it ranged from 10.4 g/plant for Tumsa to 13.1 g/plant for Moti under greenhouse condition (Table 4). In the greenhouse, the highest GY was observed for Moti (13.1 g/plant), Dosha (13.0 g/plant), Hachalu (12.8 g/plant) and Gebelcho (12.7 g/plant); while it was lowest for Tumsa (10.4 g/plant) and Selale (10.7 g/plant) (Table 4). With regard to the influence of locations on GY of the genotypes, Gebelcho, Dosha and Moti with grain yield of 14.4 g/plant each had superior performance at Holetta; while Moti (14.8 g/plant), Hachalu (14.7 g/plant) and Gebelcho (14.2 g/plant) had the highest GY at Adadi (Figure 1). Among the genotypes, Moti, Gebelcho, Dosha and Hachalu showed consistently higher GY at both field locations and in the greenhouse; indicating the stability of the genotypes across different environmental conditions.

In the field, the highest Harvest index (HI) ranged from 45.2% for Gora to 48.7% for EH06088-1. The result indicated that most genotypes had values statistically similar to the highest genotype; indicating that most genotypes had an efficient distribution of assimilates to their seeds. In the greenhouse, HI ranged from 42.6% for Selale to 50.8% for Moti (Table 4).

3.1.3. Phenological Traits (DFF and DNM)

In the field trial, the number of days to 50% flowering (DFF) ranged from 49.9 days for Gebelcho to 63.9 days for Dagim (Table 4). The highest (latest flowering) and lowest (earliest flowering) DFF under greenhouse trial were recorded for Selale (51.8 days) and Moti (42.8 days) respectively (Table 4). DFF of most genotypes were similar at both field and greenhouse; which means most early flowering genotypes at field also flowered early at greenhouse suggesting that the trait is less influenced by environment. In the field, the significant genotype x location interaction obtained for DFF resulted in late flowering of Dagim, CS20 DK, Selale and EH06022-4 at Holetta; while Dagim, Selale, Walki and Dosha flowered late at Adadi (Figure 1).

The number of days to ninety percent maturity (DNM) of the genotypes ranged from 130.5 days for Moti to 148.0 days for Dagim. Genotypes Dagim, NC58, Lalo, Selale, EH06006-6 and EH06088-1 had one of the highest (later maturing) DNM; while it was lowest (earlier maturing) for Moti, Gebelcho, Tumsa, Dosha, and Obse (Table 4). In the greenhouse, DNM of the genotypes ranged from 119.5 days for Selale to 134.0 days for Moti (Table 4). Similar to DFF, location has significantly affected DNM of the genotypes. However, in the two field locations days to maturity of a particular genotype is more or less similar irrespective of the location. For instance, at Holetta site, NC58, Dagim, EH06022-4 and Selale were late maturing; while Dagim, NC58, Lalo and Selale were late maturing genotypes at Adadi (Figure 1).

3.2. Correlation Among Agronomic Traits

Pearson's correlation analysis among agronomic traits showed that most of the traits were positively and signifi-

cantly correlated ($P < 0.05 - 0.001$) to one another; while days to 50% flowering (DFF) and days to 90% maturity (DNM) were negatively correlated to other traits and positively correlated to each other (Figure 2). Correlation between most traits had comparable values under both field and greenhouse; indicating repeatability of the result. Relationships among pairs of traits that are consistent under different environments conditions can be exploited more readily than those which are considerably influenced by environmental conditions.

The pairs of traits with high correlations at both field and greenhouse are BPD vs SDWP, NPP ($r = 0.73 - 0.90$) and NPP vs GY, AGBP ($0.57 - 0.76$). Correlation between DFF vs DNM was high in the greenhouse (0.76 for P+ and 0.61 for P-) and moderate in the field (0.51 for P+ and 0.48 for P-). The traits with consistent significant correlation with GY across both environments were DNM, DFF, BPD, HI, AGBP and NPP; suggesting that the traits are key components in determining grain yield of the crop.

Table 4. Agronomic performance of the faba bean genotypes under field and greenhouse conditions.

Genotypes	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
Field										
Lalo	43.3ad	192.6hi	14.6fg	27.9gi	8.2gi	51.3f	13.3dh	47.8ac	55.5ef	145.6c
Dagim	44.5a	198.9gi	15.7be	29.2cg	9.3dh	52.2f	13.6cf	46.5cf	63.9a	148.0a
EH06088-1	42.2be	188.9j	13.8g	26.9i	7.9i	78.1bc	13.1fh	48.7a	58.2d	143.5de
CS20DK	44.2ac	207.8ef	15.6ce	29.4bf	9.8df	63.5de	13.8bc	47.1bd	61.8b	142.7f
Obse	43.9ad	219.2cd	15.5ce	29.3cg	9.4dg	81.0ac	13.7cd	46.8cf	54.8fg	134.9j
Gebelcho	43.0ae	235.1ab	16.4ac	30.9a	11.3ab	82.0ac	14.5a	47.0be	49.9k	132.7l
Holetta-2	43.1ae	199.8fh	14.8ef	28.5eh	9.6df	81.0ac	13.7ce	48.3ab	55.0fg	143.5de
Hachalu	44.3ab	233.1ab	16.4ac	30.7ab	10.2bd	66.1d	14.3ab	46.6cf	55.0fg	132.9l
Wayu	42.4ae	205.1fg	15.0ef	28.2fh	8.8ei	50.6f	13.2eh	47.0be	58.3d	138.5i
Selale	42.0ce	193.0hj	14.5fg	27.6gi	8.3gi	50.3f	13.1gh	47.6ac	59.8c	143.9d
Didea	42.2ae	217.4cd	16.4ac	30.1ad	9.6df	77.6bc	13.7ce	45.5df	51.1j	139.7h
Gora	43.7ad	215.0ce	16.7a	30.5ac	10.1cd	77.3c	13.8cd	45.2f	55.8e	142.9ef
Dosha	42.5ae	231.3b	16.6ab	31.0a	11.1ac	66.3d	14.4a	46.6cf	58.3d	135.3j
EH07015-7	42.9ae	213.3de	16.1ad	29.7be	9.4dg	79.6ac	13.6cg	45.6df	56.0e	140.5g
EH06022-4	41.8de	200.7fh	15.6be	28.6dh	7.8i	82.3ac	13.0h	45.4ef	58.8d	143.6de
Walki	41.9ce	222.1c	16.5ab	30.4ac	10.2bd	60.8e	13.9bc	45.7df	58.2d	138.2i
NC58	39.7fg	190.8ij	14.6fg	27.9gi	8.7fi	50.4f	13.3dh	47.7ac	53.7i	147.1b
Moti	41.0ef	240.9a	16.6ab	31.1a	11.8a	83.8a	14.6a	46.9be	48.4i	130.5m
Tumsa	43.8ad	230.1b	16.6ab	30.5ac	10.0ce	82.8ab	13.9bc	45.6df	54.7h	133.7k
EH06006-6	38.6g	200.7fh	15.4df	28.7dh	8.1hi	81.9ac	13.3dh	46.4cf	54.8fg	143.9d
Location	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
Holetta	43.4a	209.0b	15.5b	28.9b	9.5a	67.8b	13.4b	46.5a	55.7a	139.9b
Adadi	42.4b	214.7a	16.0a	29.8a	9.2b	68.9a	13.8a	46.3a	56.6b	140.3a
P Regime	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
P+	46.2a	231.0a	17.1a	31.7a	10.4a	70.9a	14.6a	46.1b	56.5a	137.5b
P-	39.6b	192.7b	14.5b	27.1b	8.3b	65.8b	12.6b	46.6a	55.8b	142.7a
RR (%)	14.3	18.0	15.3	14.6	20.3	7.2	13.8	-1.1	-4.1	-4.6
Greenhouse										

Genotypes	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
Field										
Genotypes	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
Obse	37.3a	188.5ef	13.3bd	24.7de	11.9cd	48.3e	11.3de	46.1cf	49.1ef	131.0b
Hachalu	37.2a	210.8ab	14.f	27.2a	14.0a	67.2b	12.8a	47.2bd	46.8g	129.0c
ILB4358	37.5a	197.4de	14.0ab	25.6bd	12.0cd	57.9d	11.6cd	45.4df	48.6f	130.3bc
Selale	38.1a	211.3ab	14.5a	25.2cd	11.4d	44.0f	10.7ef	42.6g	55.5a	119.5f
Didea	38.0a	201.2bd	13.9ac	26.1ac	14.0a	73.0a	12.1bc	46.5be	48.2f	130.0bc
Gora	37.5a	211.9a	14.3a	26.4ab	13.8a	68.5b	12.1bc	45.9cf	49.2df	125.3e
Dosha	39.3a	209.6ac	14.1ab	27.1a	14.0a	61.7c	13.0a	48.1b	50.4cd	129.5bc
Walki	37.4a	183.9f	13.0cd	24.0e	12.5bc	57.9d	11.0df	45.8df	51.3bc	130.8b
Moti	37.8a	192.9df	12.7d	25.8bd	13.9a	70.5ab	13.1a	50.8a	42.8h	134.0a
Tumsa	37.5a	200.5cd	13.4bd	23.8e	12.0c	73.3a	10.4f	44.1fg	51.8b	118.8f
Gebelcho	37.0a	208.8ac	13.9ac	26.6ab	14.2a	67.0b	12.7ab	47.9bc	48.4f	127.4d
Wayu	37.3a	198.8d	14.3ab	25.8bd	12.8b	69.0b	11.6cd	44.8ef	49.9de	130.3bc
P Regime	ALA	BPR	SDWP	AGBP	NPP	HSW	GY	HI	DFF	DNM
P+	40.9a	226.3a	15.5a	28.5a	13.8a	64.3a	13.0a	45.6b	48.5b	126b
P-	34.7b	174.5b	12.1b	22.7b	12.2b	60.4b	10.6b	46.5a	50.2a	130.1a
RR (%)	15.2	22.7	21.6	20.6	12.1	6.1	18.9	-1.5	-1.4	-3.3

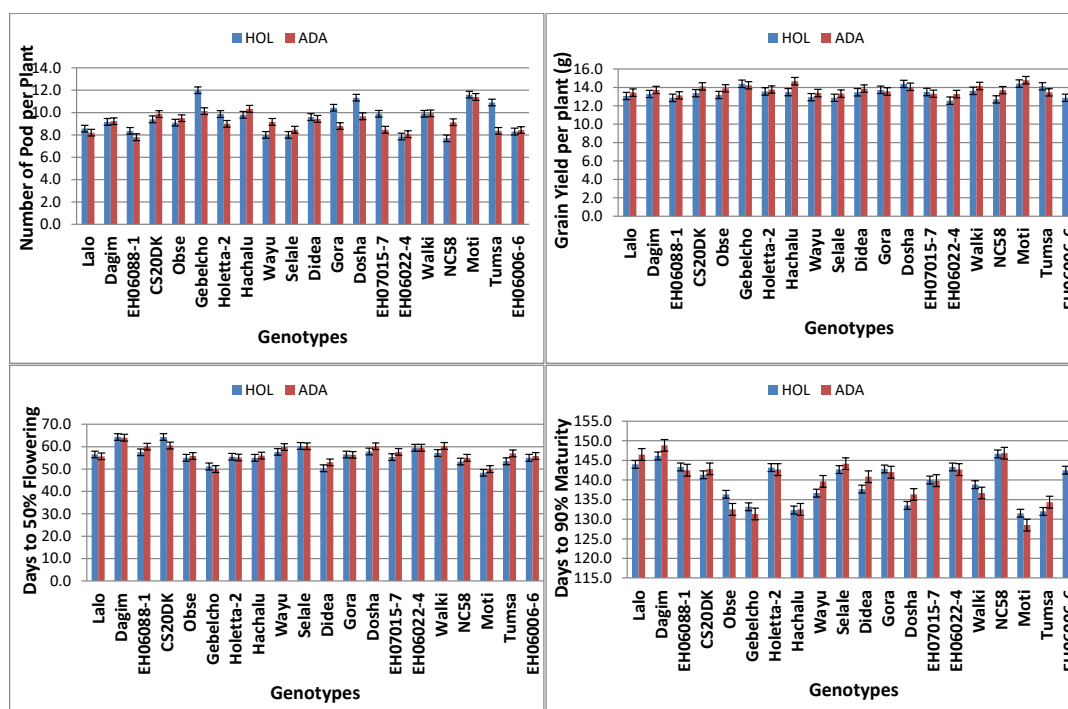


Figure 1. Number of pod per plant, Grain yield, days to 50% flowering and days to 90% maturity of the faba bean genotypes at Holetta (HOL) and Adadi (ADA).

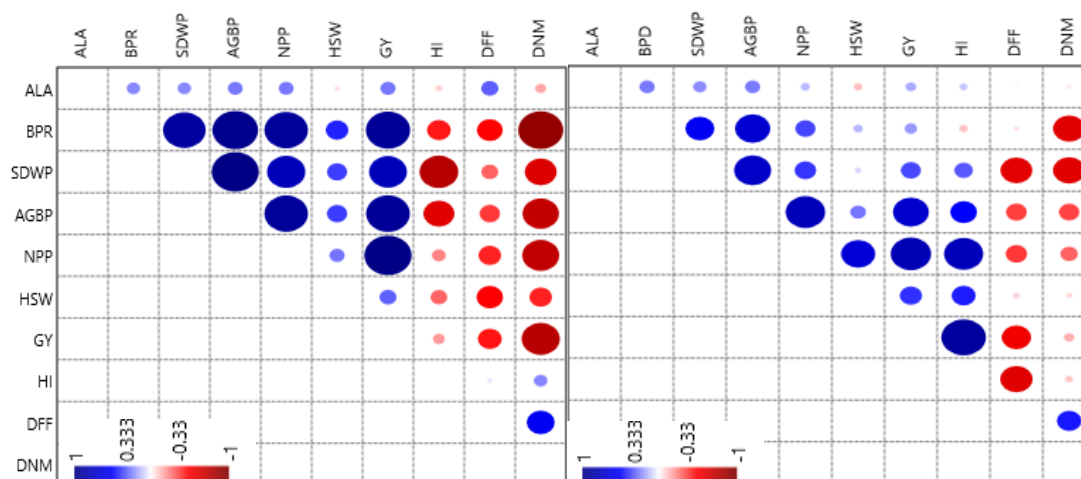


Figure 2. Correlation analysis among the faba bean agronomic traits at field (left) and greenhouse (right).

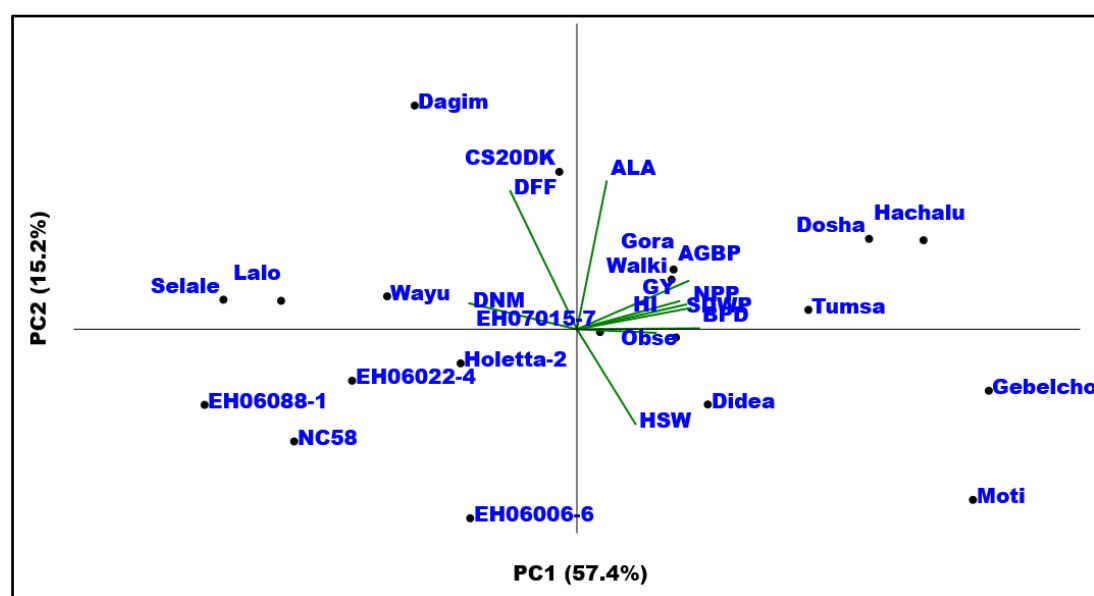


Figure 3. GT biplot analysis for the agronomic traits of the faba bean genotypes.

3.3. Biplot Analysis

Results from the genotype by trait (GT) biplot analysis showed that the first two principal components accounted for 72.6% of the total variation (Figure 3). The result displayed in the GT biplot is interpreted based on the principles described in [38]. Accordingly, five traits had longer vectors and are responsible for large genetic divergence in the PC1. The traits include biomass production per day (BPD) (+0.402), total above-ground biomass weight (AGBP) (+0.397), Grain Yield (GY) (+0.374), shoot dry weight per plant (SDWP) (+0.373) and number of pod per plant (NPP) (+0.371). ALA and HSW were the least contributors for the genetic variation (Figure 3).

Out of the ten agronomic traits, most of them formed acute

angles to one another and thus had positive correlation among each other (Figure 3). As shown in the figure, Grain Yield (GY), a main trait of the crop's breeding objective, was positively correlated to all traits except for its negative correlation with days to 50% flowering (DFF) and days to 90% maturity (DNM). These associations could be confirmed from Pearson correlation coefficients between any two traits (Figure 2).

As observed in the biplot, vectors of the genotypes Moti, Gebelcho, Hachalu, Tumsa and Dosha formed acute angles with traits such as GY, AGBP, NPP, HSW and BPD and thus had above-average performance for the traits. On the other hand, vectors of genotypes such as Wayu, Dagim, Selale and EH06022-4 formed obtuse angle with the traits and had below-average performance for the traits (Figure 3).

4. Discussions

The response to selection in any crop improvement program depends on the degree of genetic variability. The present study assessed the genotypic variability of the faba bean genotypes for agronomic traits under contrasting phosphorus (P) fertilizer application and revealed significant genotypic variation for all the tested traits. The study also showed that the performances of the agronomic traits were negatively affected under P-unfertilized treatments as compared to P applied treatments (Table 4). In corroboration with the present study, [21, 22, 39] reported lower performance of faba bean agronomic traits under reduced P application. Higo et al., [40] also indicated that plant growth & development was significantly higher under high P than low P soil.

Reduced soil P had increased days to 50% flowering (DFF) and days to 90% maturity (DNM) by 4.1 and 4.6%; in the field, respectively. The shorter DFF and DNM with phosphorus fertilization can be explained by the role of phosphorus fertilizer in shortening days to flowering and physiological maturity as reported by [39, 40]. Similar to our study, [21, 22] also reported that HI was higher under low P than at higher soil P. El Mazlouzi et al., [22] argued that P allocation from shoots to grains in plants on low P soil was more than that on high P soil that higher grain P under low P may lead to increased grain yield relative to shoot yield resulting in higher HI under low P. It was also reported that P resulted in higher relative increase in shoot dry matter weight than it resulted in grain yield which ultimately reduced HI under high P soil [41].

With regard to the effect of genotype on the agronomic performance of faba bean, previous studies supported the results of our study. Studies conducted by [16, 39, 42] reported that agronomic traits of faba bean were significantly different for different genotypes; indicating the potential to improve the crop for the agronomic traits. Furthermore, in agreement with our results, comparable average leaf area (ALA), biomass production per day (BPD) & total above-ground biomass (TAB) values were reported for faba bean [30, 39, 43]. Similarly, other studies reported number of pods per plant (NPP) and shoot dry weight (SDW) for faba bean within the range reported in this study [43-45]. Another study showed that NPP of faba bean is an important selection criterion for the development of high yielding genotypes and is strongly influenced by the environment [46].

Hundred seed weight (HSW) remained the most stable trait of a genotype at both field locations and greenhouse as witnessed by the comparable values observed in Table 4. In agreement with our study, [47, 48] also reported that seed size is among the most stable yield components in faba beans and least affected by changes in the environment. Despite a general consideration of faba bean as a large-seeded crop, its seed size varies greatly among varieties and within a genotype depending on the position of the pod on the stem [20, 49]. Plant breeders have been breeding for the trait for years due to

the fact that large seeds have more food reserves which help germinate faster, have better vigor and higher yield than smaller seeds [50, 51]. However, smaller seeds can significantly reduce the production costs by lowering the seed rate [45]. The study also showed that recently released varieties had larger seed than the older ones; which is in line with [12] who reported that faba bean breeding in Ethiopia has resulted in 34-47% seed size increment as compared to the older ones.

The grain yield per hectare of the faba bean genotypes obtained in the present study (3.2 to 4.2 t/ha) was in the range of 1.6 to 5.2 t/ha reported by [31, 49, 52]. Besides, in accordance with our results, previous studies by [17, 18, 31] indicated that faba bean grain yield was greatly influenced by genotype, environment and the interaction of the two. Hence, breeding of genotypes adapted to specific climatic zones is very important in order to increase yield stability. The study also indicated that the HI of all faba bean genotypes were less than or equal to 50% in both the field and greenhouse, which is in agreement with the results of [21, 53] who reported average HI value of 45%.

Time of flowering is a key trait in faba bean breeding. The induction of flowering is a critical process determining the final yield [54]. Hence, in order to minimize exposure to critical stress such as frost, high temperature and/or low moisture early flowering is a better than late flowering [55]. The present study showed that genotypes Gebelcho, Didea, Moti, NC58 and Tumsa were early flowering genotypes. It was also observed that most early flowering genotypes were also high yielders. Alharbi et al., [56], also reported that flowers developed earlier in the growth stage had a faster and higher pod formation rate (41–43%) than those formed later and contributed more to yields. Genotypic variation in faba bean genotypes for DFF was also reported by [16, 20, 42]. Dewangan et al. [57] (2022) reported DFF ranging from 41.67 to 96.33 for faba bean. Olle et al. [58] reported DFF ranging from 46.3 to 55.8 in *Vicia faba* L. minor varieties. Photoperiod and temperature play a critical role in plant flowering and the response to these factors varies considerably among genotypes suggesting that DFF is genotype dependent and possibility of improving the trait [59].

Early maturity is one of the breeding objectives of faba bean. In Ethiopia, about 66.4% of the farmers preferred early maturing varieties [60]. The study also revealed that early maturing genotypes such as Moti, Gebelcho, Tumsa, Dosha, and Obse were also among the highest yielding genotypes. In accordance with our results, early maturity correlated with high yielding in faba bean [57] and soybean [61]. Dewangan et al., [57] reported that the days to maturity in faba beans ranged from 95.00 to 118.30 days. Olle et al., [58] also reported days to maturity ranging from 113 to 132 for *Vicia faba* L. minor varieties, which falls within the range reported in this study.

Correlation analysis showed that most agronomic traits were strongly correlated to one another and to the grain yield. Out of all the traits, DFF (early flowering) and NPP were consistently and significantly correlated to GY at both field and greenhouse

conditions; indicating that the two traits are important yield components and could be inherited simultaneously. Similar correlation results were also reported by [62-65] for faba bean and other legume crops. The observed correlations among some of the measured agronomic traits have clear implications for faba bean improvement. Since strongly correlated traits may possibly be controlled by the same genes or have pleiotropic effects, one trait can be used to select for the other; thereby reducing cost and time of breeding [66, 67].

Biplot analysis showed that biomass production per day (BPD), total above-ground biomass weight (TAGB), number of pod per plant (NPP), Grain Yield (GY) and shoot dry weight per plant (SDWP) contributed the largest to the genetic variation among the genotypes. The GT biplot also showed the trait profiles of the genotypes that Moti, Gebelcho, Hachalu, Tumsa and Dosha formed acute angles with the most important traits such as GY, NPP and HSW and thus had above-average performance for the traits. Genotypes excelling in a particular trait were plotted closer (acute angle) to the vector line and further in the direction of that particular vector, often on the vertices of the convex hull [38]. Similar results of biplot analysis for the traits were also reported by [65, 68].

Based on the traits profile of the genotypes, breeding objectives can easily be determined [69]. For instance, Gebelcho and Moti had larger seed size, higher grain yield and lower HI; while Lalo and Selale had smaller seed size, lower grain yield and higher HI. Hence, higher HI of the genotypes can be transferred to the high yielding genotypes. Based on the length of the genotype vector, Gebelcho, Moti, Tumsa, and Holetta-2 are the best while Wayu, Lalo, Selale and NC58 are the poorest genotypes for most traits including grain yield. GT biplot is also used to identify redundant traits and culling of genotypes. Genotypes that have below average values can be discarded. Culling based on multiple traits can achieve high selection intensity [69, 70].

5. Conclusions

Understanding and characterization of the extent of agro-morphological genetic diversity within a germplasm is very important in order to attain the targeted genetic improvement of a crop. This study revealed the existence of a significant genetic variation in the faba bean genotypes for most of the agronomic traits measured under both field and greenhouse conditions. The study revealed that traits such as early flowering, biomass production per day, number of pod per plant and shoot dry weight per plant were the determinants of grain yield performance of the crop. The trend of performance for most genotypes at both field and greenhouse was similar that genotypes Moti, Gebelcho, Dosha, Tumsa, and Didea had superior agronomic performance under both conditions and hence can be used as potential parents for improving grain yield and other agronomic traits of the crop. Comprehensive studies involving larger number of genotypes and environments and using advanced genomic tools are suggested.

Abbreviations

CEC	Cation Exchange Capacity
CSA	Central Statistical Agency
FAO	Food and Agriculture Organization of the United Nations
PC	Principal Component
SAS	Statistical Analysis Software

Acknowledgments

The authors would like to thank every individual who took part in the research undertakings. We are particularly grateful for African Union for funding the research.

Conflicts of Interest

The authors declare no conflicts of interest.

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