

# Genetic Variability on Grain Yield and Related Agronomic Traits of Faba Bean (*Vicia faba* L.) Genotypes Under Soil Acidity Stress in the Central Highlands of Ethiopia

Mesfin Tadele<sup>1,2,\*</sup>, Wassu Mohammed<sup>2</sup>, Mussa Jarso<sup>1</sup>

<sup>1</sup>Holetta Agricultural Research Center, Ethiopian Institute of Agricultural Research, Holetta, Ethiopia

<sup>2</sup>School of Plant Sciences, College of Agriculture and Environmental Sciences, Haramaya University, Haramaya, Ethiopia

## Email address:

mesfintadele64@gmail.com (M. Tadele)

\*Corresponding author

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**Abstract:** Faba bean is the leading in area coverage and total production of pulses in Ethiopia. However, soil acidity becomes the major production limiting factor of faba bean in the highlands of Ethiopia. Information on genetic variability and heritability of faba bean genotypes on different traits under soil acidity stress is scanty. Thus, this study was conducted to estimate genetic variability of faba bean genotypes on grain yield and related traits at soil of pH 4.66, 4.96 and 4.49 at Holetta, Watebecha Minjaro and Jeldu, respectively, during 2017 main cropping season. The experiment comprised 50 faba bean genotypes arranged in randomized complete block design with three replications. Data were collected on grain yield (g/5plants) and some other agronomic traits: days to 50% flowering, days to 90% maturity, grain filling period, plant height (cm), number of podding nodes/plant, number of pods/ podding node, number of pods/plant, chocolate spot disease (%) and 100-seeds weight (g). Analysis of variance for traits studied showed significant differences among genotypes, locations and their interaction ( $P \leq 0.01$ ) for all traits except number of pods/podding node for the interaction. Computed genotypic (GCV) and phenotypic coefficient of variation (PCV) values were ranged from 1.08-23.05 and 1.20-23.26%, respectively, whereas heritability ( $H^2$ ) and genetic advance as percent of the mean (GAM) ranged from 24.63 -98.22% and 2.0 - 47.13%, respectively. The highest values for all components were recorded for 100-seeds weight while lowest values except for  $H^2$  computed for days to 90% maturity. The observed PCV and GCV values were high for 100-seed weight and moderate for grain yield, number of podding node/plant and pod/plant. The values of PCV were higher than GCV for all traits. Hence, the high variation between PCV and GCV (6.78) for chocolate spot was due to environmental stress (soil acidity) besides the genetic constitution of tested genotypes. High  $H^2$  and GAM were observed for 100-seeds weight, number of pod/plant and podding node/plant. Traits with high  $H^2$  indicated that selection based on mean would be successful in improving the traits. Therefore, selection based on phenotypic performance of genotypes would be effective to improve traits that have high GAM coupled with high  $H^2$  estimates.

**Keywords:** Faba Bean, Genetic Advance, Grain Yield, Heritability, Soil Acidity, Variability

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## 1. Introduction

Faba bean (*Vicia faba* L.,  $2n=2x=12$ ) is produced throughout the world in different agro-ecological regions in which China followed by Ethiopia, Australia, United Kingdom, France and Egypt are the leading producers [1]. It is the leading pulse crops in Ethiopia [2]. It accounted for about 0.44 million ha (27.34%) and about 0.92 million tons

(30.95%) of the total pulse crops production. Oromia followed by Amhara Regional States are the largest producers of faba bean together accounting for about 83.20% of the country's production [3].

Faba bean has a potential to a good meat substitute in many parts of the world where there is demand for non-animal protein sources [4]. It is also used as animal feed in industrialized countries and source of cash to the farmers and

foreign currency to Ethiopia [5]. The crop is widely used in rotation with cereals because it fixes atmospheric nitrogen [5, 6, 7]. As a result, yield of cereal crops following faba bean is improved and it reduce the amount of artificial nitrogen fertilizer applications for subsistence farmers [8]. Despite its diverse benefits, the national average yield of faba bean (2.11 t ha<sup>-1</sup>) in Ethiopia has remained low compared to Egypt and United Kingdom 3.47 and 3.83 t ha<sup>-1</sup>, respectively [1]. The low average yield of the crop is attributed to susceptibility to biotic and abiotic stresses [6]. Soil acidity is among the major production limiting factors for this crop in the high lands of Ethiopia [7, 9, 10]. Therefore, utilization of soil acidity tolerant genotypes is an important strategy in improving bean yields and reducing cost of production [11]. As a result, the use of acid tolerant varieties remains the first option and low cost if the use of lime is beyond the reach of smallholder farmers. However, so far 34 faba bean varieties have been released nationally in Ethiopia [7] but none of them were not tested and recommended for areas with soil acidity stress.

The knowledge of phenotypic (PCV) and genotypic (GCV) coefficients of variation helps to determine the type of breeding strategy to be followed [12]. The close correspondence between the GCV and PCV variation in faba bean has been reported that variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors [13, 14]. The high phenotypic and genotypic coefficients of variation is an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding [15]. It was reported high environmental variance than genotypic variance for days to 90% maturity and plant height [16]. Similarly, high phenotypic variance reported for days to 50% flowering,

days to 90% maturity and plant height [17]. Likewise, high phenotypic variance reported for days to 50% flowering and plant height [14]. The magnitude of broad sense heritability ( $H^2$ ) also helps in predicting the behavior of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement [12]. High estimates of  $H^2$  reported for 100-seed weight and grain yield in faba bean genotypes at varied environments and number of genotypes [14, 18-20]. Also, high heritability reported for chocolate spot disease [21]. Thus, traits with high to moderate heritability may respond moderate to high for phenotypic selection [22]. The genetic gain expected from selection of the top 5% of the genotypes, as a percent of the mean (GAM) indicates the genetic progress that can be made in the breeding program [12]. High GAM was reported in faba bean for number of pods per plant [18, 20]. Low GAM was reported for 100-seed weight and grain yield [14].

Variability and heritability of faba bean genotypes for grain yield and other morpho-agronomic traits under soil acidity is scanty. Therefore, genetic variability and estimating  $H^2$  of traits is of paramount importance for breeders because the genetic advance achieved in each breeding cycle depends on how the additive gene effect is beneficial. Hence, this study was conducted to estimate genetic variability under soil acidity stress on grain yield and related traits of faba bean genotypes.

## 2. Materials and Methods

The experiment was conducted at three locations Holetta, Watebecha Minjaro and Jeldu during 2017 main cropping season under rain fed condition. Descriptions of the experimental sites have been given in Table 1 below.

*Table 1. Description of the study sites.*

Location	Latitude and longitude	Altitude (masl)	Annual rain fall (mm)	Temperature (°C)		Soil pH
				Min	Max	
Holetta	09° 00'N, 38° 30'E	2400	1072	6.6	24.1	4.66
Watebecha Minjaro	09° 05'N, 38° 36' E	2565	1100	8.7	23.3	4.94
Jeldu	09° 16'N, 38° 05'E	2800	1200	2.06	16.9	4.49

### 2.1. Treatment and Experimental Design

A total of 50 faba bean genotypes were used of which 22 were released varieties and 28 pipeline genotypes. The materials were collected from Holetta agricultural research center (Table 2). The experiment was arranged in Randomized Complete Block Design with three replications. The spacing between blocks was 1.5m. The experimental plots consisted of one row of 4m length and 0.4m row spacing continuously and

0.1m between plants. Undamaged clean seeds of each genotype were selected to a reasonably uniform size by hand sorting and whole set of genotypes were planted at each block. Blended Fertilizer was applied at the rate of 19 kg N, 38 kg P<sub>2</sub>O<sub>5</sub> and 7 SO<sub>4</sub> in the form of NPS 121kg/ha that can substitute DAP in each area during planting. One faba bean variety (Dosha) was planted as a border row in each block to avoid border effect. Weeding and other cultural practices were done as per the national recommendations of the crop.

*Table 2. Description of experimental materials.*

No.	Genotypes	Year of release	Origin	No.	Genotypes	Year of release	Origin
1	Cool-0030	---	Collection	26	EKLS/CSR02017-3-4	---	Hybridization
2	Wolki	2008	Hybridization	27	Kasa	1980	Collection
3	EKLS/CSR02012-2-3	---	Hybridization	28	Cool-0025	---	Collection
4	Obse	2007	Hybridization	29	EH06070-3	---	Hybridization
5	NC58	1978	Collection	30	EKLS/CSR02010-4-3	---	Hybridization

No.	Genotypes	Year of release	Origin	No.	Genotypes	Year of release	Origin
6	Ashebeke	2015	Hybridization	31	Cool-0031	---	Collection
7	Hachalu	2010	Hybridization	32	Cool-0018	---	Collection
8	Degaga	2002	Introduction	33	EKLS/CSR02028-1-1	---	Hybridization
9	EH09031-4	---	Hybridization	34	EK 05037-4	---	Hybridization
10	Holetta-2	2001	Introduction	35	Cool-0035	---	Collection
11	EH09007-4	---	Hybridization	36	KUSE2-27-33	1979	Introduction
12	EH07023-3	---	Hybridization	37	EH07015-7	---	Hybridization
13	EK05006-3	---	Hybridization	38	Cool-0024	---	Collection
14	EKLS/CSR02014-2-4	---	Hybridization	39	Selale	2002	Collection
15	Numan	2016	Hybridization	40	Moti	2006	Hybridization
16	Bulga 70	1994	Collection	41	EH06027-2	---	Hybridization
17	EK05001-1	---	Hybridization	42	EKLS/CSR02019-2-4	---	Hybridization
18	Dosha	2008	Collection	43	EH09002-1	---	Hybridization
19	Gora	2012	Hybridization	44	Tumsa	2010	Hybridization
20	EH08035-1	---	Hybridization	45	Gebelcho	2006	Hybridization
21	Wayu	2002	Collection	46	EK05037-5	---	Hybridization
22	EKLS/CSR02023-2-1	---	Hybridization	47	Didi'a	2014	Hybridization
23	Mesay	1995	Hybridization	48	Cool-0034	---	Collection
24	EH09004-2	---	Hybridization	49	CS20DK	1977	Collection
25	EH06088-6	---	Hybridization	50	Tesfa	1995	Introduction

“---” pipeline genotypes

## 2.2. Data Collection

The following data were collected either from whole plot or from five sample plants from each plot. Mean values of these samples were utilized to estimate the efficiency of each genotype for the traits under consideration. The traits days to 50% flowering, days to 90% physiological maturity, grain filling period, 100- seeds weight, chocolate spot disease, plant height, number of podding nodes/plant, number of pods/plant, number of pod/podding node and grain yield were considered under this investigation.

## 2.3. Data Analysis

### 2.3.1. Homogeneity Test

Before proceeding with the analysis of variance for each variable, tests were made for homogeneity of error variance using the F-max method which is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error [23].

$$F - \text{ratio} = \frac{\text{Larger MSE}}{\text{Smaller MSE}}$$

### 2.3.2. Analysis of Variance

The data were subjected to analyses of variance and combined analysis of variance over environments for randomized complete block design was performed using the SAS program [24]. The total variability for the traits was quantified using pooled analyses of variance over three locations using the following model:

$$P_{ijk} = \mu + B_i(L_k) + G_j + L_k + (GL)_{jk} + e_{ijk}$$

Where  $P_{ijk}$  = phenotypic observation on genotype  $j$  in block  $i$  (at location  $k$ )  $G$ ,  $B$ , and  $L$  = number of genotypes, blocks and locations respectively,  $\mu$  = grand mean,  $B_i(L_k)$  = the effect of block  $i$  (within location  $k$ ),  $G_j$  = the effect of

genotype  $j$ ,  $L_k$  = the effect of location  $k$ ,  $(GL)_{jk}$  = the interaction effect between genotype  $j$  and location  $k$  and  $e_{ijk}$  = effects of random error.

### 2.3.3. Variance Components

The coefficients of variations at phenotypic and genotypic levels were estimated using the adopted formula [25]. The PCV and GCV values were categorized as low for values ranged from 0-10%, moderate 10- 20% and high for values greater than 20%.

$$PCV = \frac{\sqrt{\text{phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$GCV = \frac{\sqrt{\text{Genotypic Variance}}}{\text{Grand mean}} \times 100$$

Broad-sense heritability ( $H^2$ ) was estimated for pooled analysis over three locations using the formula adopted by Allard [12].

$$H^2 = \sigma_g^2 / [\sigma_g^2 + \sigma_{gl}^2/L + \sigma_e^2/RL] \times 100$$

Where:  $H^2$  = heritability in broad sense,  $\sigma_g^2$  = genotypic variance,  $\sigma_{gl}^2$  = genotype by location interaction effects,  $\sigma_e^2$  = error variance,  $R$  = number of replication and  $L$  = number of location.

Genetic advance in absolute unit (GA) and percent of the mean (GAM), was estimated in accordance with the methods illustrated [25]. Genetic advance that is expected from selecting the top 5% of the tested genotypes as percentage of the mean (GAM) was categorized as low (0-10), moderate (10-20) and high (>20).

$$GA = k \cdot \sigma_p \cdot h^2 \text{ and } GA \text{ (as \% of the mean)} = \frac{GA}{\bar{x}} \times 100$$

Where,  $k$  = selection differential (at 5% selection intensity with value 2.06)  $\sigma_p$  = phenotypic standard  $h^2$  = heritability;  $\bar{x}$  = Grand mean.

### 3. Results and Discussion

#### 3.1. Analysis of Variance

Mean squares due to locations were highly significant ( $P < 0.01$ ) for all traits under consideration, indicating that there are differences between the three environments which are significant enough to see the genetic performance of faba bean genotypes. Also, it is evident from the results that mean squares due to genotypes (572.51) were highly significant for grain yield, indicating the existence of enough genetic variability for grain yield. The two-way interaction (genotype x location) had significant effects on all 10 traits except number of pods per podding node (Table 3). The effect of G x L being significant on most of the traits over location indicated the differential performance of genotypes in different locations. In line with this result it was reported significant genotypic differences in faba bean genotypes for days to flowering, plant height, number of pod/plant and hundred seed weight [26]. Significant effect of locations on

100-seed weight of faba bean has been reported [27]. Many reports also showed the presence of significant effects of G x L interaction on grain yield in faba bean in different sets of environments in Ethiopia [18, 28]. Contrary to the current result, non-significant interaction effect of chocolate spot disease due to environmental variance was observed [28].

The significant effects of G x L interaction indicated that the genotypes had differential performance over locations for agronomic traits. Due to performance inconsistency of genotypes over locations such as with significant effects of G x L, selection of genotypes for superior efficiency under one set of environments may not perform consistently under different environment. This implies that recommendation of genotypes for all locations is hardly possible based on better performance of genotypes at one location. Likewise, it was reported that, under significant G x L selection of genotypes that perform best under all sets of environments becomes impractical [29].

**Table 3.** Mean squares for 10 traits of 50 faba bean genotypes evaluated over three locations in 2017 cropping season.

Trait	Rep (d.f=6)	Genotype (G) (d.f=49)	Location (L) (d.f=2)	G x L (d.f=98)	Error (d.f=294)	CV (%)
DF	11.54	22.67**	4730.67**	4.45**	1.22	2.05
DM	20.56	27.38**	4012.56**	5.20**	2.69	1.12
GFP (day)	28.59	37.51**	4401.98**	8.22**	3.69	2.09
PH (cm)	1855.06	175.01**	277083.56**	79.32**	31.67	5.06
PNP	8.19	5.90**	242.89**	1.20**	0.78	13.49
PP	4.62	21.55**	309.31**	2.86**	1.52	14.75
PPN	0.11	0.09**	0.13**	0.02	0.02	11.16
HSW (g)	110.15	2395.51**	715.23**	42.72**	11.99	4.94
CS (%)	1451.75	482.59**	2502.76**	344.07**	143.28	36.29
GY (g)	430.05	572.51**	15788.37**	190.83**	58.96	12.20

\*, \*\* significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively, Rep = replication, CV (%) = coefficient of variation in percent, DF = days to 50% flowering, DM = days to 90% maturity, GFP = Grain filling period, PH = plant height, PNP = Number of podding node/plant, PP = Number of Pod/Plant, PPN = Number of pod/podding node, HSW = 100-seed weight, CS = Chocolate spot disease (%) and GY = Grain yield (g/5 plants).

#### 3.2. Estimates of Phenotypic and Genotypic Coefficient of Variation

The values of genotypic (GCV) and phenotypic (PCV) coefficients of variations for agro-morphology traits fall in the range between 1.08 and 23.05 and between 1.20 and 23.26%, respectively. The lowest and highest values of GCV and PCV were calculated for days to 90% maturity and 100-seed weight, respectively. The differences between PCV and GCV values were in the range between 0.12 - 6.78 for days to 90% maturity and chocolate spot disease, respectively (Table 4). The high variation between PCV and GCV for chocolate spot was because of environmental stress. Similarly, narrow PCV and GCV variation in faba bean have been reported by various authors and they stated that variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors [13, 14]. However, traits like chocolate spot that have high PCV values than GCV implies greater influence of environmental factors for the phenotypic expression of these traits that make difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the

traits.

The PCV and GCV values were high for 100-seed weight moderate for number of podding node/plant, number of pod/plant and grain yield. The high to moderate PCV and GCV for the mentioned traits suggested that the traits were less influenced by environmental factors and selection based on phenotypic expression of the genotypes could be applied as breeding method. Likewise, it was reported that, high PCV and GCV values were an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding [15]. The PCV values were moderate and GCV values were low (<10%) for chocolate spot and the values were low for both parameters for days to 50% flowering, days to 90% maturity, plant height and grain filling period (Table 4). This implies greater influence of environmental factors for the phenotypic expression of these traits that make difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the traits. In close agreement with this result, high environmental variance than genotypic variance were reported for days to 90% maturity and plant height [16]. Likewise, high environmental variance reported for days to 50% flowering

and plant height [14, 17].

**Table 4.** Estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance for 9 traits of 50 faba bean genotypes based on the analysis of variance over three locations in 2017 cropping season.

Traits	Range	Mean	$\sigma^2_g$	$\sigma^2_{ph}$	GCV	PCV	H <sup>2</sup>	GA K=5%	GAM
DF	51.44-58.89	54.06	2.02	2.52	2.63	2.94	80.37	2.63	4.87
DM	142.11-149.00	145.86	2.46	3.04	1.08	1.20	81.01	2.91	2.00
GFP	87.22-95.33	91.80	3.26	4.17	1.97	2.22	78.10	3.29	3.58
PH	100.78-119.00	111.24	10.63	19.45	2.93	3.96	54.68	4.97	4.47
PNP	5.11-8.33	6.54	0.52	0.66	11.06	12.38	79.74	1.33	20.37
PP	5.56-12.67	8.36	2.08	2.39	17.24	18.52	86.71	2.77	33.12
HSW	35.39-93.92	70.13	261.42	266.17	23.05	23.26	98.22	33.06	47.13
GY	40.72-79.56	62.93	42.41	63.61	10.35	12.67	66.67	10.97	17.43
CS	26.17-43.69	34.39	5.27	21.41	6.68	13.46	24.63	2.35	6.84

$\sigma^2_g$  = Genotypic variance,  $\sigma^2_p$  = phenotypic variance, GCV = Genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H<sup>2</sup> = broad sense heritability, GA = Genetic advance, GAM = Genetic advance as percentage of mean, DF = days to 50% flowering, DM = days to 90% maturity, GFP = Grain filling period, PH = plant height, PNP = Number of podding node/plant, PP = Number of Pod/Plant, HSW = 100-seed weight, CS = Chocolate spot disease (%) and GY = Grain yield (g/5 plants)

### 3.3. Estimates of Heritability and Expected Genetic Advance

The broad sense heritability (H<sup>2</sup>) and genetic advance as percent of mean (GAM) values ranged from 24.63 to 98.22% and 2.0 to 47.13%, respectively, over locations. Heritability values can be categorized as low (<30%), moderate (30-60%) and high (>60%) and genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%) [25]. Hence, low and high heritability values were calculated for chocolate spot disease and 100-seed weight, respectively. Also, low and high GAM computed for days to 90% maturity and 100- seed weight, respectively (Table 4). In contrary to the current result, it was reported high GAM for seed yield (35.46%) [18].

It was suggested that the importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much progress can be made through selection [25]. In this study, high heritability accompanied with high to moderate genetic advance was observed for number of podding node/plant, number of pod/plant, 100-seed weight and grain yield. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the traits. Therefore, selection based on phenotypic performance of genotypes would be effective to improve traits that have high genetic advance as percent of mean coupled with high heritability estimates. The traits with high to moderate heritability, indicates that it may respond moderate to high for phenotypic selection [22]. The high H<sup>2</sup> and GAM value of traits indicates the high possibility of transferring traits from parents to the next progeny. In agreement with this result, high estimates of broad sense heritability for 100-seed weight and grain yield in faba bean genotypes were reported at varied environments and number of genotypes [14, 18, 19]. Likewise, high GAM was reported for number of pod/plant [18, 20]. In contradict to this finding low GAM reported for 100-seed weight and grain yield [14]. Low GAM values were calculated for chocolate spot. Low heritability coupled with low GAM was calculated for

chocolate spot (Table 4). The result indicated that low heritability values for chocolate spot limit possibility of improvement for this trait through selection. In contradict to this result it was reported high H<sup>2</sup> for chocolate spot disease [21].

Generally, 100-seed weight had high PCV, GCV, H<sup>2</sup> and GAM values which indicated that this trait is controlled by genetic factor and higher chance to improve this trait through selection. The probable reason for the variation of traits low to high GAM and vice versa with this result and others were due to the difference of growing environments and genetic makeup of the evaluated genotypes. Thus, under stressed environments H<sup>2</sup> and GAM values may be masked due to a greater genotype by environment interaction [30]. In contrary, H<sup>2</sup> and GAM values influenced by the nature of the genetic material evaluated rather than the growing environment [31].

## 4. Conclusion

Faba bean is an important legume crop in Ethiopia mainly cultivated in the mid to high altitude areas with elevations 1800-3000 meter above sea level. The crop is a major source of protein for highland inhabitants those who cannot afford animal products and restores soil fertility. However, the highlands of Ethiopia are characterized by high soil acidity which becomes the major production constraints of faba bean. The mean squares due to genotypes showed the presence of significant (P < 0.01) differences for all agronomic traits. Similarly, the mean squares due to G x L were significant for all traits except number of pod/podding node. The results indicated the presence of genetic variability in faba bean genotypes for most of agro-morphology traits that could be exploited in breeding programs. The significant differences among locations, G x L interactions on grain yield and other traits showed the differential response of genotypes over locations and the test locations were different each other.

The computed GCV values ranged from 1.08-23.05 and PCV between 1.20-23.26% whereas H<sup>2</sup> ranged from 63-98.22% and GAM from 2.0 - 47.13%. The highest values for all components obtained for 100-seeds weight while all

lowest values except for  $H^2$  obtained for days to 90% maturity. Medium to high estimates of GCV, PCV,  $H^2$  and GAM computed for 100- seeds weight and number of pod/plant suggested selection based on phenotypic expression of genotypes is possible to improve the traits. However, traits with high PCV values than GCV the  $H^2$  and GAM values will be low due high environmental factors which limit improvements of these traits. The high PCV values than GCV for all traits were because of environmental variation attributed by soil acidity. Therefore, the results allows conclude that the presence of genetic variability among the evaluated faba genotypes is a good opportunity to identify genotypes of interest.

## Conflict of Interest

All the authors do not have any possible conflicts of interest.

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