

*Full Length Research Paper*

# Variation in genetic variability and heritability of agronomic traits in Faba bean (*Vicia faba* L.) genotypes under soil acidity stress evaluated with and without lime in Ethiopia

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Fifty faba bean is a multipurpose crop used as human food, animal feed, soil fertility restoration and income source for farmers and the country at large. However, the productivity of this crop is low as constrained by biotic and abiotic factors in which soil acidity takes the lions share in the highlands of Ethiopia. In order to estimate genetic variability on grain yield and related traits under soil acidity stress, 50 faba bean genotypes were evaluated in randomized complete block design with three replications at three locations, Holetta, Watebecha Minjaro and Jeldu with and without lime application in 2017. The combined analysis of variance (ANOVA) over locations for each lime level showed the presence of significant differences among genotypes for all agronomic traits except for the number of seeds per pod. The overall mean grain yields of tested faba bean genotypes were 62.93 (without) and 93.12 g/5plants (with lime) leading a yield reductions of 32.34% were encountered due to soil acidity stress through a varied number of genotypes over locations. Computed genotypic coefficient of variations (GCV) ranged from 1.08-23.05 and 0.94-23.88% and phenotypic (PCV) from 1.20-23.26 and 1.11-24.07%, while heritability ( $H^2$ ) ranged from 24.63-98.22 and 35.06-98.45% and genetic advance as percent of the mean (GAM) from 2.0-47.13 and 1.64-48.89% without and with the lime application, respectively. The highest values for all components were recorded for 100 seeds weight (HSW), whereas the lowest values except for  $H^2$  were computed for days to maturity. Under both lime levels medium to high estimates of GCV, PCV,  $H^2$  and GAM were computed for HSW and the number of pod per plant and selection based on phenotypic expression of genotypes is possible to improve these traits. Selection based on mean would be successful in improving traits that have high  $H^2$ . Furthermore, selection based on phenotypic performance of genotypes would be effective to improve traits that have high GAM coupled with high  $H^2$  estimates. Performances of variability components for different traits with and without lime application were performed differently and higher values were recorded with lime as optimum environments allow for better genetic expression. Hence soil acidity affects the production and variability components of faba bean.

**Key words:** Heritability, soil acidity, variability components, with lime, without lime.

## INTRODUCTION

Faba bean is an important pulse crop produced throughout the world in which Ethiopia is the second largest producer next to the People's Republic of China

(FAOSTAT, 2018). It is the leading pulse category of Ethiopia in terms of area coverage and volume of production, sharing 0.44 million ha (27.34%) area

coverage and about 0.92 million tons (30.95%) of the total pulse crops production (CSA, 2017/18). The crop is mainly cultivated in mid and high-altitude areas, with an elevation ranging from 1800 to 3000 m above sea level (Mussa and Gemechu, 2006).

Faba bean is used as a major source of protein rich foods in the developing countries for subsistence farmers (Asnahech et al., 2016; Mesfin, 2019) and as animal feed in industrialized countries (Duc et al., 2010; Tewodros et al., 2015). The crop is also a source of cash to the farmers and foreign currency to Ethiopia (Asnahech et al., 2016; Gemechu et al., 2016; Tewodros et al., 2015). Faba bean is widely used in rotation with cereals and other crops as it fixes atmospheric nitrogen (Gemechu et al., 2016; Mesfin, 2019; Tewodros et al., 2015). Realizing the potential importance of the crop, nationally 34 improved faba bean varieties have been released for production with appropriate management practices (Mesfin, 2019). Despite the diverse benefits and availability of high yielding faba bean varieties ( $>3 \text{ tha}^{-1}$ ) (MoALR, 2017), the national average yield of faba bean about  $2.11 \text{ tha}^{-1}$  in Ethiopia (CSA, 2017/18), which very low compared to Egypt and United Kingdom 3.47 and  $3.83 \text{ tha}^{-1}$ , respectively (FAOSTAT, 2018). However, the low average yield of this crop is attributed to its susceptibility to biotic (disease, weed and insects) and abiotic stresses such as waterlogging, low moisture stress, poor cultural practices and soil acidity (Gemechu et al., 2016). Currently, soil acidity is a major constraint of faba bean production in the highlands of Ethiopia as it associates with low nutrient availability (Endalkachew et al., 2018; Mesfin et al., 2019; Mesfin, 2020a, b). Hence, the productivity of acid soil needs to be improved as arable lands are shrinking and the demand of food and raw materials are increasing rapidly. Use of lime is a potential option for sustainable soil management for restoring soil health and fertility as a result it improves grain yield of faba bean (Mesfin, 2020a). However, the use of acid tolerant varieties remains the first option and low cost due to unaffordable cost of lime for poor smallholder farmers.

Awareness about variability components, phenotypic (PCV) and genotypic coefficient of variation (GCV) helps to determine the type of breeding strategy to be followed. The magnitude of broad sense heritability ( $H^2$ ) also helps in predicting the behavior of succeeding generations by devising appropriate selection criteria and the genetic progress in the breeding program indicated by genetic gain expected from selection of the top 5% of the genotypes, as a percent of the mean (GAM) (Allard, 1960). The high GCV 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 (Ejigu et al., 2016). While, the higher PCV values than GCV implies greater influence of environmental factors for the phenotypic expression of these traits that make it difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the traits (Mesfin et al., 2019). Higher PCV values than GCV were reported for days to 90% maturity and plant height (Haridy and El-Said, 2016); for days to 50% flowering, days to 90% maturity and plant height (Sekhon et al., 2017); for days to 50% flowering and plant height (Hamza et al., 2017).

Traits with high to moderate  $H^2$  respond moderate to high for phenotypic selection (Singh and Ceccarelli, 1996). High estimates of  $H^2$  were reported for hundred seed weight and grain yield in faba bean genotypes at varied environments and a number of genotypes (Bakhiet et al., 2015; Gemechu and Mussa, 2009; Hamza et al., 2017; Million and Habtamu, 2012; Tafere et al., 2013; Sharifi, 2015). Also, high  $H^2$  was reported for chocolate spot disease (El-Badawy et al., 2012). High GAM in faba bean was reported for number of pod per plant (Bakhiet et al., 2015; Million and Habtamu, 2012) while low GAM for 100 seeds weight and grain yield (Hamza et al., 2017). Considering both the GAM and  $H^2$  of traits together helps to determine how much progress can be made through selection and selection based on phenotypic performance of genotypes would be effective to improve traits that have high GAM coupled with high  $H^2$  as high  $H^2$  will not always be associated with high GAM (Johnson et al., 1955).

The values of  $H^2$  and GAM did not show a similar trend under favorable and stressful environments (Gemechu et al., 2015; Singh, 2002). Favorable environments show higher estimates of  $H^2$  and GAM values than stress environment (Singh, 2002) as stressed condition masked  $H^2$  and GAM due to a greater genotype by environment interaction (Rosielle and Hambin, 1981). Genetic variability and  $H^2$  of faba bean genotypes for grain yield and other agronomic traits under soil acidity stress and non-stress environment are scanty. Therefore, genetic variability and  $H^2$  of traits under various environments is very important for breeders as 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 on grain yield and related agronomic traits of faba bean under soil acidity stress and non-stress environments.

## MATERIALS AND METHODS

### Description of the experimental site

The experiment was conducted at three locations in the central

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**Table 1.** Description of experimental locations.

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

highlands of Ethiopia during 2017 main cropping season under rain-fed condition. Descriptions of the experimental sites are given in Table 1.

### Treatment and experimental design

A total of 50 faba bean genotypes were used collected from Holetta and Kulumsa Agricultural Research Centers. Treatments were arranged in RCBD with three replications with and without lime using adjacent plot technique. The spacing between blocks was 2 m and within blocks 1.5 m. The experimental plots consisted of one row of 4 m length and 0.4 m row spacing continuously and 0.1 m between plants. Blended Fertilizer NPS was applied at the rate of 121 kg/ha at 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 recommendations.

### Data collection

Data were collected either from whole plot or from five sample plants from each plot. Days to 50% flowering, days to 90% physiological maturity, grain filling period, 100 seeds weight and chocolate spot disease severity were collected from whole plot. Plant height, number of podding nodes per plant, number of pods per podding node, number of pods per plant, number of seeds per pod, grain yield, economic growth rate and grain production efficiency were collected from five random sample plants from each plot. The mean values of these samples were utilized to estimate the performance of each genotype for the traits under consideration.

### Data analysis

#### 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 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 (Gomez and Gomez, 1984).

$$F - \text{ratio} = \frac{\text{larger MSE}}{\text{smaller MSE}}$$

#### Analysis of variance

Data were subjected to analyses of variance (ANOVA) and combined ANOVA over the environment for RCBD was performed using the SAS program (SAS Institute, 2010). The total variability for the traits was quantified using pooled analyses of variance over three locations with and without lime separately 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,  $B_i(M)_k$  = 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  $k$ ;  $e_{ijk}$  = the residual or effects of random error.

### Variance component

The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by (Johnson et al., 1955). 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 (1960).

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

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 locations.

Genetic advance in an absolute unit (GA) and percent of the mean (GAM), was estimated in accordance with the methods illustrated by Johnson et al. (1955). Genetic advance that is expected from selecting the top 5% of the tested genotype GAM was categorized as of low (0-10), moderate (10-20) and high (>20).

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

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

## RESULTS AND DISCUSSION

### Soil chemical properties of test locations

The physico-chemical properties of the soils from the

**Table 2.** Results of soil chemical analysis before and after liming at three locations.

Parameter	Holetta		Watebecha Minjaro		Jeldu		
	Before	After	Before	After	Before	After	
Texture (%)	Clay	47.50	-	70.00	-	40.00	-
	Silt	36.25	-	8.75	-	36.25	-
	Sand	16.25	-	13.75	-	23.75	-
pH	4.66	5.03	4.94	5.08	4.49	4.80	
TN (%)	0.14	0.14	0.14	0.21	0.29	0.30	
Avail. P	7.96	9.57	12.74	12.74	13.17	15.14	
CEC	18.18	19.04	17.38	18.80	20.24	20.42	
OC (%)	1.25	1.36	2.14	2.18	2.61	2.65	
Ex. Na (ppm)	0.03	0.03	0.03	0.03	0.02	0.03	
Ex.K (ppm)	0.57	0.58	0.53	0.54	0.14	0.23	
Ex.Mg (ppm)	2.35	2.46	1.25	1.26	0.50	0.58	
Ex.Ca (ppm)	9.43	10.89	9.30	10.95	6.35	11.82	
Ex. Al (ppm)	0.49	0.28	0.55	0.33	2.39	0.85	
Mn (ppm)	48.58	47.76	37.97	30.16	58.23	50.45	
Cu (ppm)	4.07	3.92	3.70	3.12	4.95	3.85	
Ext.Fe (ppm)	180.77	164.45	245.70	231.07	341.13	327.43	
Ext.Zn (ppm)	0.83	0.68	1.15	1.10	4.42	2.67	
Ex. Acidity	1.01	0.61	0.98	0.62	3.36	1.30	
Bulk density(gcm <sup>-3</sup> )	1.26	-	1.12	-	-	-	

CEC= cation exchange capacity, OC= organic carbon, TN= total nitrogen, Ex. = exchangeable, Ext=extractable.

three test locations showed a very strong acidic condition for all test locations with the pH values 4.49 to 4.94 (Table 2). It was observed little modification of pH and other soil parameters at each location in the lime treated blocks but the soil is still under very strong acidic category (pH<5.5) (Alemu et al., 2016) due to reduced basic cations. This may indicate that lime improves the chemical properties of soils but it needs more time to bring to the required level of change. Lime is slow acting, of long duration (Adane, 2014; Follet et al., 1981). At Jeldu, the values of exchangeable acidity, Al<sup>3+</sup>, Mn and other micronutrients were high and low for K, Ca, Mg and Na. The levels of exchangeable cations were increased at lime treated plots except Na<sup>+</sup> while decreased micronutrients. The level of soil P was increased at harvesting time except at Watebecha Minjaro (Table 2). All the three locations have clay soil and the high clay content at Watebecha Minjaro leads to high buffering capacity because the buffering capacity of the soil increases as the clay content increases; as a result high amount of lime will be required to alleviate acidity and increase the productivity of acid sensitive crops like faba bean.

Applied lime improved the physico-chemical properties of acid soil and improved the availability of P as it fixed in acid soil. Liming reduces soil acidity, Al toxicity and increases P availability, which have a role in root development and energy transfer in nodule formation (Endalkachew et al., 2018). Similarly, liming reduced Al<sup>3+</sup>

and H<sup>+</sup> ions as it reacts with water leading to the production of OH<sup>-</sup> ions to form Al(OH)<sub>3</sub> and H<sub>2</sub>O and the precipitation of Al<sup>3+</sup> and H<sup>+</sup> by lime causes the pH to increase which enhances microbial activity and nutrient availability (Onwonga et al., 2008).

### Analysis of variance

The pooled analysis of variance over three locations with and without lime indicated the presence of significant differences ( $P \leq 0.01$ ) among genotypes and locations for most of the traits studied like days to 50% flowering (DF), days to 90% maturity (DM), grain filling period (GFP), plant height (PH), number of podding node per plant (PNPP), number of pod per plant (PPP), number of pod per podding node (PPPN), chocolate spot (CS), 100 seed weight (HSW), grain yield (GY), grain production efficiency (GPE) and economic growth rate (EGR). Conversely, number of seed per pod (SPP) was not significantly different under both lime levels (Table 3). This may show lack of sufficient genetic variation for these traits among the tested genotypes. The highly significant differences for GY with and without lime application indicated the existence of variations among genotypes under acid soil and limed condition. Similarly, a previous study on Ethiopian faba bean germplasm accessions also indicated that SPP often showed non-significant differences among genotypes (Gemechu et al.,

**Table 3.** Mean squares from combined analysis of variance without (above) and with lime application (below) over three locations for 13 traits of 50 faba bean genotypes in 2017 main cropping season.

Trait	Without lime application							
	Rep (6)	Genotype (G) (49)	Location (L) (2)	G x L (98)	Error (294)	CV (%)	R <sup>2</sup>	Mean
DF (day)	11.54	22.67**	4730.67**	4.45**	1.22	2.05	0.96	54.01
DM (day)	20.56	27.38**	4012.56**	5.20**	2.69	1.12	0.92	145.86
GFP (day)	28.59	37.51**	4401.98**	8.22**	3.69	2.09	0.90	91.80
PH (cm)	1855.06	175.01**	277083.56**	79.32**	31.67	5.06	0.97	111.24
PNPP	8.19	5.90**	242.89**	1.20**	0.78	13.49	0.78	6.54
PPP	4.62	21.55**	309.31**	2.86**	1.52	14.75	0.81	8.36
PPPN	0.11	0.09**	0.13**	0.02 <sup>ns</sup>	0.02	11.16	0.54	1.28
SPP	0.016	0.027 <sup>ns</sup>	0.029 <sup>ns</sup>	0.015 <sup>ns</sup>	0.020	4.74	0.33	2.98
CS (%)	1451.75	482.59**	2502.76**	344.07**	143.28	36.29	0.56	34.39
HSW (g)	110.15	2395.51**	715.23**	42.72**	11.99	4.94	0.97	70.13
GY (g)	430.05	572.51**	15788.37**	190.83**	58.96	12.20	0.81	62.93
GPE (g)	2359.41	1858.03**	113609.25**	683.50**	207.49	13.26	0.85	108.61
EGR (g/day)	490.21	700.33**	27756.57**	232.64**	72.07	12.31	0.83	68.95
<b>With lime application</b>								
DF (day)	15.00	13.25**	4567.41**	4.12**	1.27	2.08	0.96	54.05
DM (day)	15.27	23.54**	4438.82**	6.61**	2.31	1.04	0.93	145.92
GFP(day)	17.08	28.50**	5922.11**	9.26**	2.51	1.72	0.95	91.87
PH(cm)	1489.31	144.10**	243555.95**	85.82**	34.54	4.58	0.97	128.20
PNPP	3.64	6.04**	100.70**	1.33*	0.94	12.00	0.70	8.08
PPP	5.55	35.50**	237.27**	4.30**	2.24	12.84	0.79	11.66
PPPN	0.10	0.14**	3.69**	0.04**	0.02	10.15	0.73	1.44
SPP	0.027	0.037 <sup>ns</sup>	0.027 <sup>ns</sup>	0.027 <sup>ns</sup>	0.033	6.16	0.31	2.97
CS (%)	873.28	573.40**	9065.48**	357.20**	78.09	32.17	0.74	30.64
HSW(g)	137.61	2690.63**	2305.57**	41.76**	12.96	5.01	0.97	71.83
GY(g)	376.50	1032.64**	1028.45**	281.20**	87.03	10.02	0.74	93.12
GPE(g)	2182.34	3853.17**	106043.51**	1069.63**	304.37	10.87	0.83	160.55
EGR(g/day)	347.55	1176.61**	3771.96**	330.84**	103.57	10.02	0.75	101.57

\*and\*\*, significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively ns=non-significant. Numbers in parenthesis represent degree of freedom for the respective source of variation. Rep= replication, CV (%) = coefficient of variation in percent, DF= days to flowering(days), DM = days to maturity(days), GFP = grain filling period(days), PH = plant height(cm), PNPP = number of podding node per plant, PPP = number of pod per plant, PPPN = number of pod per podding node, SPP= number of seed per pod, CS = chocolate spot disease(%), HSW = hundred seed weight(g), GY = grain yield per 5 plants(g), GPE = grain production efficiency(g), EGR = economic growth rate(g/day).

2005; Gemechu and Mussa, 2009; Million and Habtamu, 2012); significant for DF, PH, PPP and HSW (Kumar et al., 2017), significant effect ( $P \leq 0.05$ ) of locations for HSW (Ashenafi and Mekuria, 2015).

The two way interaction G x L had significant effects on most of the traits both with and without lime application except for PPPN and SPP without lime and for SPP with lime (Table 3). The significant effects of G x L interaction indicated that the genotypes had differential performance over locations for agronomic traits and the effects of experimental plots with lime and without lime applications also exerted differential effects over locations on the performance of genotypes. Due to performance inconsistency of genotypes over locations such as with significant effects of G x L interactions, selection of genotypes for superior performance under one set of environment may perform poorly under different environment. This implies that recommendation of genotypes for all locations and managements of soil acidity is hardly possible based on better performance of genotypes at one location and management. This result partially agrees with the report for significant difference for PH and GY and non-significant difference for PPP, SPP and HSW as a result of lime application on acid soils of western highlands of Ethiopia (Abebe and Tolera, 2014). Many reports also showed the presence of significant effects of G x L for GY in faba bean in different sets of environments in Ethiopia (Gemechu and Mussa, 2009; Million and Habtamu, 2012; Tamene et al., 2015). Contrary to the current result a non-significant interaction effect for chocolate spot disease resistance was reported due to environmental variance (Tamene et al., 2015).

The overall mean grain yield of tested faba bean genotypes was 62.93 without and 93.12 g with lime that resulted a mean grain yield reduction of 32.34% due to soil acidity stress through varied number of genotypes over locations. Moreover, the result suggested the importance of lime for yield improvement. Soil acidity associates with low nutrient availability and major yield-limiting factor for pulse production (Fageria et al., 2012).

## Estimates of variability component

### *Phenotypic and genotypic coefficients of variation*

The genotypic coefficient of variation (GCV) values fall in the range between 1.08 and 23.05 and 0.94 and 23.88% and phenotypic coefficient of variation (PCV) values between 1.20 and 23.26% and 1.11 and 24.07% without and with lime application, respectively. The lowest and highest values of GCV and PCV were calculated for days to 90% maturity (DM) and hundred seed weight (HSW), respectively, for both GCV and PCV for both without and with lime application.

The differences between PCV and GCV were in the

range between 0.12 to 6.78 and 0.17 to 7.04 for DM and chocolate spot disease (CS) for all traits without and with lime, respectively (Table 4). The differences between traits without and with lime application were in the range between 0.14 and 3.54% for GCV and 0.09 and 3.8% for PCV (Table 4). The low differences between PCV and GCV under two managements over locations may indicate the less influence of environmental factors in the expression of traits. Similarly, narrow PCV and GCV variation in faba bean have been reported by various authors (Hamza et al., 2017; Mostafa et al., 2017; Solieman and Ragheb, 2014) and they stated that variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors.

According to Johnson et al. (1955), the values of PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Accordingly, both the PCV and GCV values were high for HSW both with and without lime applications. The values of both genetic parameters were moderate for number of podding node per plant (PNPP), number of pod per plant (PPP), grain yield (GY), grain production efficiency (GPE) and economic growth rate (EGR) without lime and moderate for PPP, GPE and CS with lime. Almost all the traits fall under high and moderate PCV and GCV under stress (without lime) and non-stress (with lime) over locations (Table 4). 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. Ejigu et al. (2016) reported high PCV and GCV as 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.

The PCV values were moderate and GCV values were low (<10%) for GY and EGR with lime and for CS without lime and the values were low for both parameters for DF, DM, PH and GFP for both managements (Table 4). This implies greater influence of environmental factors for the phenotypic expression of these traits that make it difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the traits. In close agreement with this result it was reported that higher PCV than GCV exist for DM and PH (Haridy and El-Said, 2016); for DF, DM and PH (Sekhon et al., 2017), and higher PCV for DF and PH (Hamza et al., 2017).

## Estimates of heritability and expected genetic advance

The broad sense heritability ( $H^2$ ) values ranged from 24.63 to 98.22% and 35.06 to 98.45% and the genetic

**Table 4.** Estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance for 11 and 12 traits of 50 faba bean genotypes based on the analysis of variance without (above) and with lime (below) over three locations in 2017.

Traits	Range	Mean	Without lime				GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA K=5%	GAM
			$\sigma^2g$	$\sigma^2p$	$\sigma^2l$	$\sigma^2gl$					
Days to 50% flowering (days)	51.44-58.89	54.06	2.02	2.52	31.51	1.03	2.63	2.94	80.37	2.63	4.87
Days to 90% maturity(days)	142.11-149.00	145.86	2.46	3.04	26.72	0.73	1.08	1.20	81.01	2.91	2.00
Grain filling period(days)	87.22-95.33	91.80	3.26	4.17	29.29	1.36	1.97	2.22	78.10	3.29	3.58
Plant height(cm)	100.78-119.00	111.24	10.63	19.45	1846.70	6.61	2.93	3.96	54.68	4.97	4.47
Number of podding node plant <sup>-1</sup>	5.11-8.33	6.54	0.52	0.66	1.61	0.11	11.06	12.38	79.74	1.33	20.37
Number of pod plant <sup>-1</sup>	5.56-12.67	8.36	2.08	2.39	2.04	0.44	17.24	18.52	86.71	2.77	33.12
Chocolate spot disease (%)	26.17-43.69	34.39	5.27	21.41	6.00	25.80	6.68	13.46	24.63	2.35	6.84
Hundred seed weight(g)	35.39-93.92	70.13	261.42	266.17	4.48	9.78	23.05	23.26	98.22	33.06	47.13
Grain yield(g/5plants)	40.72-79.56	62.93	42.41	63.61	103.98	42.18	10.35	12.67	66.67	10.97	17.43
Grain production efficiency(g)	60.46-138.01	108.61	130.50	206.45	752.84	148.32	10.52	13.23	63.21	18.74	17.25
Economic growth rate(g/day)	46.98-90.52	68.95	51.97	77.81	183.49	51.43	10.45	12.79	66.78	12.15	17.63
<b>With lime</b>											
Days to 50% flowering (days)	52.33-58.11	54.05	1.01	1.47	30.42	0.90	1.86	2.24	68.88	1.72	3.19
Days to 90% maturity(days)	142.67-148.78	145.92	1.88	2.62	29.55	1.34	0.94	1.11	71.92	2.40	1.64
Grain filling period(days)	87.67-96.00	91.87	2.14	3.17	39.42	2.20	1.59	1.94	67.50	2.48	2.70
Plant height(cm)	119.00-137.11	128.20	6.48	16.01	1623.10	9.72	1.99	3.12	40.45	3.34	2.60
Number of podding node plant <sup>-1</sup>	6.56-9.56	8.08	0.52	0.67	0.66	0.13	8.95	10.14	77.91	1.32	16.30
Number of pod plant <sup>-1</sup>	8.44-16.00	11.66	3.47	3.94	1.55	0.67	15.97	17.03	87.89	3.60	30.88
Number of pod podding nod <sup>-1</sup>	1.25-1.72	1.44	0.01	0.02	0.02	0.00	7.59	8.79	74.45	0.19	13.50
Chocolate spot disease (%)	18.95-43.84	30.64	9.81	27.97	25.44	40.19	10.22	17.26	35.06	3.83	12.48
Hundred seed weight(g)	36.67-98.50	71.83	294.32	298.96	15.09	9.36	23.88	24.07	98.45	35.12	48.89
Grain yield(g/5plants)	61.60-115.10	93.13	83.49	114.74	4.98	62.80	9.81	11.50	72.77	16.08	17.27
Grain production efficiency(g)	92.70-201.14	160.57	309.28	428.13	699.83	244.15	10.95	12.89	72.24	30.84	19.20
Economic growth rate(g/day)	69.48-127.88	101.59	93.97	130.73	22.94	74.05	9.54	11.25	71.88	16.96	16.69

$\sigma^2g$ - Genotypic variance,  $\sigma^2p$ - phenotypic variance,  $\sigma^2l$ - location variance,  $\sigma^2gl$ -genotype by location interaction 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.

advance as percent of mean (GAM) values ranged from 2.0 to 47.13% and 1.64 to 48.89% without and with lime, respectively, over locations.

Low and high H<sup>2</sup> values were calculated for CS and HSW, respectively, with and without lime applications over locations. Also low and high

GAM computed for DM and HSW, respectively, under both managements (Table 4). This result implied that H<sup>2</sup> and GAM values were higher

under stress free condition than stressed environments. In contrary to the current result moderate GAM were reported for number of seeds per plant (12.32%) and high for GY (35.46%) (Million and Habtamu, 2012).

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 accompanied with high to moderate genetic advance was observed for number of podding node per plant, number of pod per plant, hundred seed weight and grain yield under both managements. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the traits. Thus, 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. Likewise, traits with high to moderate heritability may respond moderate to high for phenotypic selection (Singh and Ceccarelli, 1996). The high  $H^2$  and GAM value of traits indicates the high possibility of transferring traits from parents to the next progeny. Many authors (Bakhiet et al., 2015; Gemechu and Mussa, 2009; Hamza et al., 2017; Million and Habtamu, 2012; Tafere et al., 2013; Sharfi, 2015) also reported high estimates of broad sense heritability for hundred seed weight and grain yield in faba bean genotypes at varied environments and number of genotypes. In agreement with this result high GAM were reported for number of pod per plant (Bakhiet et al., 2015; Million and Habtamu, 2012). In contradict to this finding low GAM was reported for hundred seed weight and grain yield (Hamza et al., 2017).

Low GAM values were calculated for days to 50% flowering, days to 90% maturity, grain filling period and plant height under lime and additionally for chocolate spot without lime applications over locations. Low heritability coupled with low GAM was calculated for chocolate spot without lime application over locations (Table 4). The result indicated that low heritability values for chocolate spot limit possibility of improvement for this trait through selection. In contrast to this result, high heritability for chocolate spot disease was reported (Asnakech, 2014; El-Badawy et al., 2012). 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 in the genetic makeup of the evaluated genotypes.

Generally, medium to high estimates of GCV, PCV,  $H^2$  and GAM were computed for hundred seed weight and number of pod per plant under both lime levels. Traits with high PCV, GCV,  $H^2$  and GAM indicated that these traits are controlled by genetic factor and a higher chance for improvement of these traits through selection. The present results showed that heritability and genetic advance values did not show a definite trend with and without limed applications. For most of the traits heritability under lime free condition is less than limed

condition while genetic advance is in contrasting direction. It was reported that favorable environments show higher estimates of heritability and genetic advance values than unfavorable environment (Singh, 2002). Hence, heritability and genetic advance value may be masked due to a greater genotype by environment interaction under unfavorable conditions (Rosielle and Hambin, 1981). Likewise, it was reported that heritability and genetic advance values varied in the presence or absence of phosphorus in chick pea (Gemechu et al., 2015). Contrarily, to the current result and the reports of others, heritability and genetic advance values were influenced by the nature of the genetic material and was not evaluated by the growing environment (Ceccarelli and Grando, 1996).

## Conclusion

This research was conducted to estimate genetic variability in faba bean genotypes under soil acidity stress and non-stress conditions. As soil acidity becomes one of the major production constraints of faba bean in the highlands of Ethiopia. As a result of this stress the tested genotypes encountered a mean grain yield reduction of 32.34%; suggesting the importance of lime application on acid soil for yield improvement. The computed variability components were ranged between 1.08-23.05 and 0.94-23.88% for GCV, between 1.20-23.26 and 1.11-24.07% for PCV, between 24.63-98.22 and 35.06 - 98.45% for  $H^2$  and between 2.0-47.13 and 1.64 - 48.89% for GAM without and with lime application, respectively. The result indicated that the performance of variability components will not follow similar trends for different traits with and without lime. However, for all variability components higher values were recorded in the presence of lime. The results, allowed to conclude that the presence of variability in faba genotypes with wide genetic distance both under lime and without lime application which is a good opportunity to identify genotypes of interest. The differential performances of traits evaluated with and without lime application indicate a future breeding activity to identify soils acid tolerant genotypes.

## CONFLICT OF INTERESTS

The authors declare that they have no conflict of interests.

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