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Genetic Variability on Seed Yield and Related Traits of Elite Faba Bean (*Vicia faba* L.) Genotypes

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Abstract: Faba bean is one of the most important cool season crops in the highlands of Ethiopia and the country is considered as the secondary center of diversity. This study was conducted at Haramaya, Boreda and Hirna districts of Eastern Hararghe from 2006 to 2008 cropping season using twenty five elite genotypes of faba bean to determine the extent and pattern of genetic diversity for seed yield and related traits. The treatments were arranged in a randomized complete block design with three replications. The data were subjected to the analyses of variance using the SAS program. The mean squares due to genotypes were highly significant for seed yield (p<0.01) indicating the existence of sufficient genetic variability for seed yield. Mean squares due to the interaction between year and location were highly significant for all the traits studied (p<0.01). High genotypic coefficient of variation (10093.53%) was observed for seed yield followed by number of seeds per plant (325.45%). The estimated values of phenotypic variances were in the range of 0.60 for number of seeds per pods to 196564.64 for seed yield. Genetic gains that expected from selecting the top 5% of the genotypes, as a percent of the mean, varied from 12.32% for number of seeds per plant to 35.46% for seed yield. The average linkage technique of clustering produced a more understandable portrayal of the 25 faba bean genotypes by grouping them into five clusters. The maximum distance was found between cluster three and five ($D^2 = 691.47$). Thus, the materials tested in the entire experiment will be maintained for further breeding program.

Key words: Genetic variability, seed yield, genetic gains, genetic distance, *Vicia faba*

INTRODUCTION

Faba bean (*Vicia faba* L.) is a grain legume cultivated for multiple usages because of its high nutritional value excellent source of protein ranges from 27-34% (Duc, 1997; Haciseferogullari *et al.*, 2003). Ethiopia is the second largest faba bean producing countries in the world (Hebblethwaite *et al.*, 1993). According to Duc *et al.* (2010), faba bean is spread from the principal center to Ethiopia and from Mediterranean region to Europe to form a third center of importance. They also reported about 1118 faba bean *ex situ* collection in Ethiopia in 2008 which were mostly contains improved cultivars and farmers' population. The crop is well grown in the highlands of Ethiopia ranged from 1800-3000 m.a.s.l. with annual rain fall of 700-1000 mm (Yohannes, 2000). It was planted to 3.88% of the grain crop area with total annual grain production of 3.43% of the country (CSA, 2011). It is the main food source that supplements a low cost alternative to animal protein subsistent farmers by providing 18-32% protein (Hanelt and Mettin, 1989). It also cash source for local farming community in particular and foreign currency for the country in general. Moreover, the crop can be used as break crops where cereal based mono-cropping system is dominated, replenish soil nutrients through biological nitrogen fixation and reduce biological pests (Chintalapati, 2001).

The crop prevails high degree of genetic variability due to the fact that the presence of high percentage of out crossing (Polignano and Zeuli, 1985; Hanelt and Mettin, 1989). A large genetic variability has already been identified in faba bean in terms of floral biology, seed size and composition, yield potential efficiency of symbiotic nitrogen fixation and tolerance to several biotic and a biotic stresses (Duc *et al.*, 2010). It is obvious that genetic gain from selection depends on the extent of genetic variation and on the magnitude of the heritable portion of these variations. To this effect, having the information on the degree of genetic variability exist in the faba bean is critical to design effective breeding program.

Therefore, this piece investigation was conducted to determine the extent and pattern of genetic diversity for seed yield and related traits and to establish fundamental genetic facts such as heritabilities and covariances of traits of interest for further improvement of faba bean.

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MATERIALS AND METHODS

The field experiment was conducted at three locations: Haramaya, Boreda and Hirna during 2006, 2007 and 2008 main cropping seasons. Haramaya has an altitude of 1980 m above sea level. It was in semi-arid sub-tropical belt of eastern Ethiopia. The area receives an average annual rainfall of 870 mm. The soil is characterized as a fluvisol with a pH of 7.4 (Solomon, 2006). While Hirna situated under 9°13'N and 41°6'E has an altitude of 1763 m above sea level and Boreda has an altitude of 2800 m above sea level average rain fall of 1064 mm and annual temperature of 16-28°C.

Treatment and experimental design: Twenty five elite genotypes of faba bean along with a commercial variety (Tesfa) and a local check were considered in this study. Treatments were arranged in a randomized completely block design with three replications. Seeding was done in a plot of four rows with four meter length and regular spacing of 10 cm between plants and 40 cm between rows. The layout and randomization were as per the standard procedure set by Cochran and Cox (1957). Weeding and other cultural practices were done as per the recommendations adopted for the respective sites.

Collected data: The following data were collected either from whole plot or from ten sample plants from each plot. Mean values of these samples were utilized to estimate the performance of each germplasm accession for the traits under consideration. The traits number of pods per plant, number of seeds per plant, number of seeds per pod and seed yield per plot were considered under this investigation.

Statistical analysis
Homogeneity test: Before proceeding with the analysis of variance for each variable, tests were made for homogeneity of variances using the F_{max} test as given by the following formula:

$$F_{max} = \frac{Largest\ Mse}{Smallest\ Mse}$$

and tested at $[(g-1)\ (r-1)]$ degree of freedom of mean square where g and r are the number of genotypes and replications, respectively. Then, the table of the probability distribution of F_{max} consulted.

Analysis of variance: The data were subjected to the analyses of variance (ANOVA) and combined analysis of variance over environment for Randomized Complete Block Design RCBD was performed using the SAS program (SAS, 1996).

The total variability for the traits was quantified using pooled analyses of variance over three years and locations using the following model:

$$P_{imkt} = \mu + y_m + l_t + r_{i(m)(t)} + g_k + (gy)_{km} + (yl)_{mt} + (gl)_{kt} + (ylg)_{mtk} + e_{imkt}$$

Where:

P_{imkt} = Phenotypic value of kth genotype under ith replication during mth year at tth location with replication i, location t and year m

y_m = mth year

l_t = tth location

$r_{i(m)(t)}$ = The effect of replication i with in year m and location t

g_k = The effect of kth genotypes

μ = Grand mean and $(gy)_{km}$, $(yl)_{mt}$, $(gl)_{kt}$ and $(ylg)_{kmt}$ = the interaction effects and

e_{imkt} = Random error

Partitioning of the total variation into components due to genotype $((\sigma_g^2)$, environment (σ_e^2) and genotype by environment interaction (σ_{ge}^2) deviations was performed from the analyses of variance by calculating expected mean squares and similarly, the components from pooled analysis of variance over years and locations were calculated.

Variance component: The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson *et al.* (1955). Broad-sense heritability (h^2) was estimated for pooled analyses over three years and locations using the formula adopted by Allard (1960). Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, was estimated in accordance with the methods illustrated by Johnson *et al.* (1955).

Distance analysis: Grouping the germplasm in to different groups based on multiple traits including the seed yield was conducted in this investigation by following the average linkage. Thus the analysis was computed based on multivariate analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936). Squared distance (D^2) for each pair of genotype combinations was computed using the formula suggested by Singh and Chaudhary (1999).

RESULTS AND DISCUSSION

It can be seen from Table 1 that the mean squares due to year were highly significant $(p<0.01)$ for the traits seed yield (28763.58), number of seeds and pods per plant which was 16889.97 and 1390.26, respectively. However, non significant was observed for number of seeds per

Table 1: Analysis of variance for four traits of faba bean germplasms tested over three cropping seasons (2006-2008) and three locations (Haramaya, Boreda and Hima)

Traits	MSY (2)	MSL (2)	MSR (2)	MSG (24)	MSYL (4)	MSYG (48)	MSLG (48)	MSYLG (96)	MSE	CV (%)
SPP	0.63^{ns}	39.01^{**}	2.63^{**}	0.31^{ns}	2.66^{**}	0.37^{ns}	0.25^{ns}	0.35^{ns}	0.62	21.57
PPL	1390.26^{**}	36.14^{*}	164.48^{**}	15.32^{ns}	1383.50^{**}	8.14^{ns}	3.97^{ns}	6.49^{ns}	3.28	27.58
SPPL	16889.97^{**}	926.00^{**}	326.33^{**}	16.28^{ns}	1623.81^{**}	11.30^{ns}	9.95^{ns}	8.18^{ns}	12.04	34.53
SYLD	28763.58^{**}	76070.50^{**}	9084.06^{**}	2262.98^{**}	40821.22^{**}	1451.32^{ns}	1614.27^{*}	1004.55^{ns}	334.74	45.17

*,**Significant at 0.05 and 0.01 probability level, respectively, ^{ns}Non significant, MSY: Mean square due to year, MSL: Mean square due to location, MSR: Mean square due to replication, MSG: Mean square due to genotypes, MSYL: Mean square due to the interaction between year and location, MSYG: Mean square due to the interaction between year and genotypes, MSLG: Mean square due to the interaction between location and genotypes, MSYLG: Mean square due to the interaction between year and location and genotypes, MSE: Mean square due to error, CV%: Coefficient of variation in percentage. $^{\beta}$Values in parenthesis indicate degrees of freedom, SPP: No. of seeds per pod, PPL: No. of pods per plant, SPPL: No. of seeds per plant, SYLD: Seed yield in g per plot

Table 2: Estimates of minimum, mean and maximum value, variance and coefficient of variation at phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) level, heritability in broad sense ($h^2\%$), genetic advance in absolute (GA) and percent of mean (GAM) for four traits of *Vicia faba*

Traits	Min.	Max.	Mean	$\beta^2 p$	$\sigma^2 g$	GCV (%)	PCV (%)	h^2 (%)	GA	GAM
SPP	1.00	12.80	2.89	0.60	0.17	5.74	20.61	27.84	0.36	12.32
PPL	1.20	34.20	11.87	30.43	17.41	146.66	256.28	57.23	3.87	32.62
SPPL	1.68	112.00	34.86	383.62	113.46	325.45	1100.36	29.58	7.35	21.07
SYLD	136.60	7031.00	741.01	196564.64	74793.99	10093.53	26526.61	38.05	262.77	35.46

SPP: No. of seeds per pod, PPL: No. of pods per plant, SPPL: No. of seeds per plant, SYLD: Seed yield in g per plot

pod. Similarly, except for number of pods per plant, the mean squares due to location were highly significant for all traits (seed yield, (76070.50) number of seeds per pant and per pod with 926.00 and 39.01, respectively, indicating that there are differences between the nine environments which are significant enough to see the genetic performance of faba bean germplasm. It is evident from the results that mean squares due to genotypes (2262.98) were highly significant for seed yield, indicating the existence of sufficient genetic variability for seed yield.

Mean squares due to the interaction between year and location were highly significant for all the traits studied. Mean squares due to the interaction between location and genotype were non-significant for all traits, except for seed yield.

The elite faba bean evaluated under Eastern Ethiopia in this study showed significant phenotypic variability in terms of seed yield and yield attributes. Therefore, future breeding program should take the finding as to improve for the benefit the welfare of the community. These results are similar with the findings of other scholars like Asfaw *et al.* (1994) and Yohannes (2000) with faba bean and also with other crops (Fahmi *et al.*, 2012).

Range of parameters: The maximum seed yield (7031 g/plot) and the minimum (136.60 g/plot) with the over all mean seed yield per plant of 741.01 g/plot (Table 2). The result from this investigation is in agreement with the previous reports from Ethiopia (Asfaw *et al.*, 1994; Dawit *et al.*, 1994; Getahun, 1998) who reported the existence of considerable variation for the morpho-agronomic traits in faba bean landraces.

High genotypic coefficient of variation (10093.53%) This is not the CV used to measure the validity of the

experiment. It is the value the observed genotypic or phenotypic variability among the genotypes under study expressed in percentage and the value indicated that there was variability (diversity) among the genotypes and no need to transform the data was observed for seed yield followed by number of seeds per plant (325.45%). The estimated values of phenotypic variances were in the range of 0.60 for number of seeds per pods to 196564.64 for seed yield (Table 2). The lowest and highest genotypic variances were found for number of seed per pods (0.17) and seed yield per plot (74793.99), respectively. There fore, the result indicated the existence of variability in the tested faba bean genotypes.

The results depicted in Table 2 showed that estimates of heritability in broad sense were medium for number of pods per plant (57.23%), indicated it may respond moderately to phenotypic selection (Singh and Ceccarelli, 1996). Moreover, the value is low for the rest of the traits including seed yield, indicating limited possibility of improvement for this character through selection. In earlier studies (Banziger and Edmeades, 1997), the findings are thus only partially in agreement with the results obtained in the present investigation. The probable cause of the disparity could be due to the fact that the heritability of a given trait refers to a particular population under a particular condition or environment. The effectiveness of selection for a trait depends on the relative importance of the genetic and environmental factors in the expression of phenotypic differences among genotypes in a population.

Estimation of expected genetic advance: Genetic gains that expected from selecting the top 5% of the genotypes, as a percent of the mean, varied from 12.32% for number of seeds per plant to 35.46% for seed yield, indicating an

Table 3: Mean and range of genetic divergence in seed yield and related traits of the five clusters of *Vicia faba*

	Cluster														
	I			II			III			IV			V		
Character	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean
SPP	2.86	3.14	2.96	2.77	3.07	2.89	2.78	2.90	2.83	2.68	2.90	2.81	-	-	2.88
PPL	10.77	12.79	11.99	11.50	11.83	11.68	10.70	11.50	11.03	11.89	13.64	12.82	-	-	12.37
SPPL	31.97	35.89	39.42	31.96	37.86	34.44	31.11	33.57	31.96	33.81	39.50	36.71	-	-	35.35
SYLD	739.70	785.20	758.10	677.90	726.80	702.60	603.40	633.40	618.20	835.70	881.80	853.30	-	-	982.50

SPP: No. of seeds per pod, PPL: No. of pods per plant, SPPL: No. of seeds per plant, SYLD: Seed yield in g per plot

Table 4: Pair wise generalized squared distance (D^2) among 5 clusters constructed from 25 elite faba bean genotypes

Cluster	C_1	C_2	C_3	C_4	C_5
C_1	0	15.65**	96.43**	49.30**	275.94**
C_2		0	34.52**	116.38**	420.55**
C_3			0	276.63**	691.47**
C_4				0	100.22**
C_5					0

*,**Significant at 5 and 1%, respectively

increase of 12.32 to 35.46% made by selection on these traits under similar conditions (Table 2). The low values of expected genetic advance for number of seeds per plant was due to low variability for the traits indicated by the low GCV and PCV values. The low expected genetic advance for number of seeds per pod in this study was due to low variability for the trait. Therefore, even if heritability estimates provide basis for selection on phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously, as high heritability is not always associated with high genetic advance (Johnson *et al.*, 1955).

Clustering of genotypes and divergence analysis: The average linkage technique of clustering produced a more understandable portrayal of the twenty five faba bean genotypes by grouping them into five clusters, whereby different members within a cluster being assumed to be more closely related in terms of the trait under consideration with each other than those members in different clusters. Table 3 indicates the range (minimum and maximum) and mean of genetic divergence in seed yield and related traits of the five clusters. From the analysis, there was range variability in different traits among clusters. The evaluated materials ranges for the trait seed yield 739.7-785.2 in cluster I, 677.9-726.8 in cluster II, 603.2-633.4 in cluster III and 835.7-881.8 in cluster IV. Therefore, from this finding, the tested faba bean materials exhibited difference in seed yield and other related traits. The detail account of the characteristics of each cluster is presented hereunder.

- **Cluster I:** It consisted of 9 genotypes which were laid on high in number of seeds per plant and intermediate value in the rest the traits under consideration
- **Cluster II:** It consisted of 6 genotypes which were intermediate for all the traits under studied
- **Cluster III:** It consisted of 5 genotypes characterized by intermediate in number of seeds per plant where as, the genotypes in this cluster exhibited inferior in the rest of the traits including seed yield
- **Cluster IV:** It had 4 genotypes which exhibited superior in number of seeds and pods per plant whereas inferior in number of seeds per plant. These genotypes exhibited intermediate for seed yielding potentials
- **Cluster V:** It consisted single genotypes which exhibited superior in seed yielding capacity where as intermediate in other seed contributing traits

From the estimated distance analysis, under this investigation, all the ten possible pairs of clusters, differences between thirteen pairs were highly significant ($p<0.01$) which ranged from 15.65 between cluster one and two to 691.47 between cluster three and five (Table 4). The details of each pair of cluster distances are discussed in the paragraphs below.

The maximum distance was found between cluster three and five ($D^2 = 691.47$). Cluster three constitutes five genotypes while cluster five constitutes a single genotype (Table 3). The second most divergent clusters were cluster five and two ($D^2 = 420.55$). Cluster two constitutes six genotypes.

The third most divergent clusters were cluster four and three ($D^2 = 276.63$). Cluster four constitutes 4 accessions including the checks (standard and local). Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate characters are measured. Generally, maximum genetic segregation and genetic recombination is expected from crosses that involve parents from the clusters characterized by significant distances. In the present investigation,

therefore, crossing of accessions from cluster three and five will give rise to maximum genetic segregation. This finding is inconsistent with Gemechu *et al.* (2005) who reported on evaluation 144 faba bean landraces.

CONCLUSION

The mean squares due to year were highly significant for all the three traits except number of seeds per pod. Similarly, except for number of pods per plant, the mean squares due to location were highly significant for all traits indicating that there are differences between the nine environments. The mean squares due to genotypes were highly significant for seed yield, indicating the existence of sufficient genetic variability for seed yield. High genotypic coefficient of variation was observed for seed yield followed by number of seeds per plant. Estimates of heritability in broad sense were medium for number of pods per plant and low for the rest of traits indicated it may respond moderately to phenotypic selection. From the result of genetic advance an increase of 12.32 to 35.46% magnitude made by selection.

The average linkage technique of clustering produced a more understandable portrayal of the twenty five faba bean genotypes by grouping them into five clusters. From the estimated distance analysis, under this investigation, all the ten possible pairs of clusters, differences between thirteen pairs were highly significant and the maximum distance was found between cluster three and five. This indicates, therefore, crossing of accessions between these clusters will give rise to maximum genetic segregation.

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