Genetic Variability and Character Associations of Faba bean (*Vicia faba*L.) Genotypes, Southeastern Ethiopia

ABSTRACT

Faba bean is an important legume crop because of its high□yield potential and nutrition-dense grains. This study was conducted to determine variability, heritability, and correlation between yield and yieldcomponents in 22 faba bean germplasm accession.The trial was conducted with RCBD design across two locations in the 2015/16 main cropping season. The ANOVA result showed ~~that highly~~ significant variation among genotypes with $p<0.05$. The genotype by environmental interaction result showed ~~that non-~~significant difference$p<0.05$ on chocolate spot among genotypes ~~for all traits except chocolate spot~~in the trial. The minimum grain yield was recorded at 2380.8kgha-1 from genotype 17 and the maximum grain yield was recorded from genotype 5(5598.1kgha-1). The genotypic and phenotypic coefficient of variation ranged from 2.91 to 15.64 and 3.23 to 23.42 respectively.Moderate phenotypic and genotypic coefficients of variation were recorded from grain yield and thousand seed weight, while days to maturity, plant height, and the number of seeds per pod recorded lower phenotypic and genotypic coefficients of variation.Days to 50% flowering, days to maturity, and thousand seed weights were recorded as higher estimates of heritability. Thousand seed weights showed higher estimate of heritability along with high genetic advance.For the future breeding strategies, this information helps the researcher to improve faba bean genotypes.

Key words: Correlation, heritability, variability, genetic advance

Include the p value for the yield

1. INTRODUCTION

Faba bean (*Vicia faba* L.) is named alsobroad beans or horse bean) is the fourth most widely grown cool-season legume after pea (*Pisum sativum*), chickpea (*Cicer arietinum*), and lentil (*Lens culinaris*)[1].Its protein content is higher than othercommon food legumes [2].Faba bean was originated in different geographical areas. Evidence showed that it originated in European and North Africa [3].The crop grows at an altitude ranging from 1800 to 3000 m above sea level and receives an annual rainfall of 700 to 1100 mm [4].

Faba bean is one of the most variable species, possessing a wide range of variation in plant architecture, seed size, seed color, seed shape, and leaf size and shape; this is due to a long history of cultivation, wide distribution across a different environment and mating system [5]. In the recent faba bean breeding program in Ethiopia special focus has been given to developing varieties with improved grain yield, large seed size, and resistance to major diseases [16]. Ethiopia is considered the secondary center of diversity; some zones such as West Shoa, North Shoa, South Wello, andEast Gojjam are identified as major production areas of faba bean (6).

Genetic variability is important for the development and release of improved cultivars. Genotypic and phenotypic variations in a trait occurred due to genetic differences between individuals and variations due to environments. Characterization of the genetic variability between faba bean germplasm could be a good tool for selecting this germplasm in faba bean breeding program.So to improve the trait of interest we should understand the heritability and related genetic parameters of the base population.

In Ethiopia, faba bean productivity is still far belowits potential as compared to the national average productivity in the world due to many challenges including abiotic and biotic factors. Among these are diseasesand lack of genotypes that consistently perform well across different chickpea growing environments is the most important factor causing faba bean yield reduction[7]. The present study aimed to estimate genetic variability in faba bean genotypes for yield and yield-related traits and to assess associations among yield and yield-related traits of 22 faba bean genotypes.

2. MATERIALS AND METHODS

2.1. Description of trial sites and experimental materials

The field experiments were carried out at two locations; Kulumsa and Kofele during the 2015/16 main cropping season. The materials used for this experiment consist of twenty-two advanced faba bean genotypes including two standard checks Gora and Tumsa ~~which is~~ released recently were used for the experiment. Descriptions of the study experimental sites were presented in Table 1 below.

Table 1. Description of the experimental sites

Location	Latitude	Longitude	Altitude	Mean annual rainfall	T^0		Soil type	Agroecology
					Min	Max		
Kulumsa	0801'10"N	3909'11"E	2,200	820	10.5	22.8	clay	Mid altitude
Kofele	0704'28"N	3847'11"E	2,660	1,211	7.1	18	Heavy clay	Highland

Min = Minimum, Max = Maximum, T^0 = temperature

Table 2. List of faba bean experimental materials

Genotype	Variety name	Origin	Genotype	Variety name	Origin
Geno-1	Gora	Hybridization	Geno-12	EH 09019-4	Hybridization
Geno-2	EH 010010-1	Hybridization	Geno-13	EH 09026-2	Hybridization
Geno-3	EH 010013-1	Hybridization	Geno-14	EH 06007-4	Hybridization
Geno-4	EH 010012-2	Hybridization	Geno-15	EH 09028-8	Hybridization
Geno-5	EK 05037-4	Hybridization	Geno-16	EH 09031-4	Hybridization
Geno-6	EH 07023-3	Hybridization	Geno-17	HBP/SAT/20022	Hybridization
Geno-7	EH 09001-4	Hybridization	Geno-18	EH 08031-2	Hybridization
Geno-8	EH 09002-1	Hybridization	Geno-19	EH 08035-1	Hybridization
Geno-9	EH 09004-2	Hybridization	Geno-20	EH 08035-3	Hybridization
Geno-10	EH 09007-4	Hybridization	Geno-21	EH 08038-2	Hybridization
Geno-11	EH 09012-2	Hybridization	Geno-22	TUMSA	Hybridization

Geno = Genotypes 1, 2, 3… 22

2.2. Experimental design

The experiment was carried out using a randomized complete block design intwo replications. Each genotype was planted in two rows with a length of 4m and 0.8m in width, i.e. 3.2m^2 areas with a spacing of 40cm and 10cm between rows and plants respectively. Each plot had a spacing of 1m between treatments to separate two genotypes. 100 kgha^{-1} of DAP fertilizer was applied and ~~all~~ other agronomic practices were done throughout the growing season. The grain yield harvested from a 3.2m^2 plot size was finally converted into hectare and the moisture contents were adjusted to the standard units of field pea 10%.

Your spacing give 3 rows of beans, at 0, 40 and 80cm

2.3.Data collected

Data collected from the plot base were days to 50% flowering, days to maturity, thousand seed weight (g), grain yield (kgha^{-1}), chocolate spot (1-9) scale, and rust (1-9) scale, where 1 for nil:

No visible disease symptom (Immune), 3 for a slight (resistant), 5 for medium (moderately resistant), 7 for severe (susceptible), 9 for very severe (highly susceptible). Plant height (cm), number of pods per plant, and number of seeds per pod were recorded from randomly selected five plants. The ANOVA results for the combined result were done by R software.

3. Result and Discussion

The combined analysis of variance showed that highly significant variations (0.01%) were observed among the tested genotypes for all traits (Table 3). This revealed the presence of variability among the faba bean genotypes evaluated. Highly significant (0.01) variation were reported for all traits except plant height, chocolate spot, and rust [8]. The genotype by environment interaction over two locations showed non-significant variation for all evaluated traits except chocolate spot. In contrast to this finding highly significant genotype by environment interaction was recorded for grain yield, plant height, number of pods per plant, and number of seeds per plant [9].Non-significant genotype by environment interaction effect implied that the genotypes did not perform differently across tested environments.Traits that have significant genotype by environment interactions means good performing genotypes in one location may not have better yield components in another environment.

Table3. Mean square of yield and yield-related traits of 22faba bean genotypes.

Geno	DF	MTD	FLD	PH	PPL	SPP	TSW	GYH	CHS	Rust
Entry	21	73**	114**	203**	38.1**	0.2	42840**	1890559**	1.1**	1.5**
Location	1	36614**	3014**	3757**	72.4**	0.7*	84382**	46649720**	48.0**	69.1**
Loc: Rep	2	27*	1	139	96.3**	0.2	2498	3154982**	0.1	0.3
Entry: Loc	21	8	16	77	14.6	0.2	1823	485288	0.5*	0.6
Residuals	42	6	16	78	9.3	0.2	2264	354018	0.3	0.4
CV (%)		3.1	3.6	9.0	22.3	13.9	7.3	24.8		13.1

Geno = genotypes, Df = degree of freedom, MTD = Days to maturity, FLD = Days to 50% flowering, PH = Plant height, PPL = Number of pods per plant, SPP = Number of seed per pod, TSW = Thousand seed weight, GYH = Grain yield in kgha-1, CHS = Checolate spot.

Where is the p value in the table and the meaning of * and **

3.1.Range and mean performance of genotypes

Range, mean, and variance components for the combined data were described in Table 3 below. Days to 50% flowering were recorded as a maximum from genotype 13 (65 days) and a minimum number of days from genotype 19 (48.3 days). Genotypes differ significantly by days to maturity and range from 130.3 (genotype 19) to 143 (genotype 14) days. Ten candidate genotypes have a higher number of days for physiological maturity than standard check Tumsa. Plant height also showed a significant mean performance variation, maximum and minimum plant height was observed from genotype 5 (140.3cm) and genotype 3 (110.8cm) respectively. Genotypes 5, 7, 9and 16 have a greater number of pods per plant than the standard check Tumsa. Thousand seed weight differed significantly among the genotypes and all advanced genotypes have better thousand seed weight than the standard check Tumsa. Fourteencandidate genotypes have better thousand seed weights as compared to the standard check Tumsa and Gora. Like other traits, grain yield revealed highly significant differences among the genotypes, the minimum grain yield was recorded at 2380.8kgha-1 from genotype 17 and the maximum grain yield was recorded from genotype 5(5598.1kgha-1). Higher grain yields were recorded from 68% of the candidate genotypes as compared to the standard checks Gora and Tumsa.

There should be a p value to show significance

Table 4.Mean comparison of 22faba bean genotypes for 9 traits

Geno	FLD	MTD	GYH	TSW	SPP	PPL	PH	CHS	Rust
1	55def	140.8abc	4708.9bcdef	787.5gh	3.25ab	14.5defg	110.8f	2.75de	3.5bcd
2	57.8cde	142.3a	5082.2abcde	739.75hijk	3ab	14.5defg	116.6ef	2f	2.25f
3	61.5abc	143a	4499.8def	986.5ab	3.25ab	16.6bcde	116.7ef	2f	2.75def
4	63.5ab	142.3a	4782.3abcde	748.75hij	2.75b	16.7bcde	117.3def	2.5ef	2.75def
5	52.3efg	140.8abc	5598.1a	704ijk	2.75b	22.7a	120.4cdef	3cde	3.5bcd
6	48.5g	140.5abc	5223.1abcd	966.25bc	3.25ab	14.6defg	120.6cdef	3cde	3.5bcd
7	63.3abc	142.5a	3898.5f	857.75def	3ab	19.9ab	120.8cdef	2.5ef	3cdef
8	57.8cde	141.3ab	5110.1abcde	830.75efg	3.25ab	14.8defg	121.2cdef	2.75de	3.75bc
9	50.3fg	132.5de	5328.5abcd	746.5hij	3ab	19.5abc	125.1bcde	3.25bcd	3.75bc
10	51.5fg	140.5abc	5545.7ab	917.5cd	3.5a	12.6efgh	125.8bcde	2.75de	3cdef
11	54.8def	139.8abcd	4604.4cdef	771.5ghi	3ab	10.9gh	126.8bcde	2.5ef	3cdef
12	62.5abc	142a	4354.5ef	988.5ab	2.75b	13.6defg	126.9bcde	2f	3.25cde
13	65a	141.8ab	4920.3abcde	949.75bc	3ab	11.6fgh	127.2bcde	2.5ef	2.75def
14	61.5abc	143a	5304.7abcd	880.25de	3.25ab	15.1defg	127.3bcde	2.5ef	3.75bc
15	59.3bcd	142.3a	5049.9abcde	782.25gh	3.25ab	16.9bcde	128.3abcde	2.5ef	2.5ef
16	54.3def	142.5a	5214.8abcd	1035.25a	3ab	17.7bcd	128.7abcde	2.75de	2.75def
17	54.8def	134.5bcde	2380.8g	871.25de	3ab	8.9h	129.4abcd	4a	4.75a
18	50fg	133.8cde	4909.9abcde	857.25def	2.75b	15.3cdef	130.7abc	3.5abc	4.25ab
19	48.3g	130.3e	5449.9abc	831.5efg	3ab	16.8bcde	131.7abc	3.75ab	3.75bc
20	49.8fg	133de	5228.1abcd	798.25fgh	3.25ab	16.7bcde	134ab	3.25bcd	3.75bc
21	51fg	131.3e	4730.3bcdef	692.75jk	3.25ab	14.3defg	137.2ab	3cde	3.75bc
22	55def	139abcd	4672.7cdef	678k	3.5a	17.4bcd	140.3a	3cde	3cdef

Geno = genotypes, MTD = Days to maturity, FLD = Days to 50% flowering, PH = Plant height, PPL = Number of pods per plant, SPP = Number of seed per pod, TSW = Thousand seed weight, GYH = Grain yield in kgha-1, CHS = Chocolate spot.

There is need for lsd value to separate the means

3.2.Estimation of genetic parameters

3.2.1. Estimation of genotypic and phenotypic coefficient of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was classified as high for values greater than 20%, moderate for values between 10 and 20%, whereas values less than 10% are considered as low [12]. Accordingly to this classification, the number of pods per plant, chocolate spot, and rust recorded a higher phenotypic coefficient of variation.The high phenotypic coefficient of variation (PCV) reported for number of pods per plant [10].Grain yield and thousand seed weight showed a moderate phenotypic and genotypic coefficient of variation; while days to maturity, plant height, and number of seeds per pod recorded lowerphenotypic and genotypic coefficient of variation. The lower estimate of the genotypic and phenotypic coefficient of variation was reported for days to maturity [11]. Medium estimates of genotypic coefficient of variation were reported for days to 50% flowering and number of pods per plant [8]. This indicates that the presence of narrow genotypic variation of these traits and improvement of the traits through simple selection may not be possible.

The high genotypic coefficient of variation traits suggested the possibility of improvement through selection. Moderate genotypic coefficient of variation was reported for plant height and thousand seed weight [10]. The phenotypic coefficient of variation is greater than the genotypic coefficient of variation for all studied traits, this implied the influence of environments on the expression of genotypes. A higher difference between the genotypic coefficient of variation and the phenotypic coefficient of variation indicates the greater environmental influence on the traits and vice versa. Hence relatively moderate environmental effects on the expression of genotypes for chocolate spot, rust, and number of pods per plant

3.2.2. Estimation of broad sense heritability and genetic advance

Broad sense heritability was classified as high greater than 60%, a medium between 30 – 60%, and low for values less than 30% [12]. Accordingly, the highest estimates of heritability were found fordays to 50% flowering, days to maturity, and thousand seed weight. This implies that direct selection of traits at the phenotypic level can improve the traits to get a better yield. High heritable traits are mainly expressed by additive gene effect and more gain of selection in the next selection. The highest estimate of heritability reported for a hundred seed weights [11]. Higher estimate of heritability also reported for grain yield [8].High estimates of heritability also reported for grain yield, thousand seed weight, days to 50% flowering, days to maturity, and plant height [10].Plant height, number of pods per plant, grain yield, chocolate spot, and rustwere recorded as medium estimates of heritability, while the lowest estimate of heritability was observed from the number of seeds per pod. This low estimate of heritability traits is influenced by the environments and improvement of such low heritable traits with simple selection is difficult. In agreement with this result, Mesfin et al. reported a lower estimate of heritability for the chocolate spot.

Genetic advances as a percentage of the mean (GAM) are classified as high (>20%), moderate (10-20%) and low (<10%) [12]. Based on this benchmark, higher genetic advances as a percent of mean were observed from number of pods per plant and thousand seed weights. But number of pods per plant, number of seeds per pod, and days to maturity exhibited a lower estimate of genetic advance. The low values of expected genetic advance for those traits were dueto low variability for the traits,while days to 50% flowering, grain yield, chocolate spot, and rust observed medium estimate of genetic advance as percent of the mean. In contradiction to this finding high genetic advance as percent of mean reported for number of pods per plant [13]. Heritability alone provides no indication of the amount of genetic improvement, thus high heritability along with high genetic advance as a percent of mean was very essential to improve traits of interest [12]. In this study highest estimate of heritability along with high genetic advance as percent of meanwas observed for thousand seed weight.The highest heritability along with high genetic advance was reported for hundred seed weight, grain yield, and number of pods per plant [14].

Table 5.Estimates of genetic parameters of 9 traits

Traits	GV	PV	H2	G.M	G.A	G.A.M	GCV	PCV	CV
FLD	24.6	32.5	0.76	55.78	8.91	15.98	8.90	10.22	6.99
MTD	16.4	20.2	0.81	139.06	7.51	5.40	2.91	3.23	1.82
PLH	31.4	70.1	0.45	125.63	7.73	6.15	4.46	6.67	7.01
PPL	5.9	13.2	0.45	15.50	3.34	21.56	15.64	23.42	19.69
SPP	0.0	0.1	0.13	3.09	0.08	2.64	3.53	9.70	12.77
TSW	10180.8	11239.0	0.91	837.35	198.11	23.66	12.05	12.66	5.49
GYH	351321	593965.9	0.59	4845.3	940.42	19.41	12.23	15.91	12.28
CHS	0.2	0.4	0.37	2.81	0.49	17.45	13.87	22.73	18.21
Rust	0.2	0.5	0.42	3.32	0.63	18.87	14.04	21.55	19.80

MTD = Days to maturity, FLD = Days to 50% flowering, PH = Plant height, PPL = Number of pods per plant, SPP = Number of seed per pod, TSW = Thousand seed weight, GYH = Grain yield in kgha-1, CHS = Chocolate spot.

3.3.Associations of character

Genotypic and phenotypic correlations of coefficient were presented in table 5 below. The result showed that grain yield was significantly and positively correlated with number of seeds per pod and number of pods per plant. Significant positive correlations were reported between the seed yield, number of pods per plant and plant height [10]. This significantpositivecorrelation of traits indicates that the improvement of one trait can result from a similar effect on the other trait. So to improve grain yield more emphasis should be given to these characters during selection.

Chocolate spot and rust were highly significant and negatively correlated with days to 50% flowering and days to maturity. Days to maturity and days to 50% flowering, number of pods per plant, and number of seeds per pod were highly significant and positively correlated with each other. A positive and significant correlation was reported between number of seeds per pod and plant length [15].Non-significant positive and negative correlations were observed for grain yield with days to 50% flowering, days to maturity, plant height, thousand seed weight, chocolate spot, and rust. This implies that this character is independent of other traits and they could be selected independently to improve grain yield.

Table 6.Estimates of correlation coefficients (r) at genotypic (above diagonal) and phenotypic level (below diagonal) among 9 traits

Traits	MTD	FLD	PLH	PPL	SPP	TSW	GYH	CHS	Rust
MTD	**1**	0.816**	0.241	0.040	0.168	0.383	0.004	-0.896**	-0.831**
FLD	0.72	**1**	0.218	-0.134	-0.413	0.252	-0.341	-0.897**	-0.602**
PLH	0.27	0.16	**1**	0.414	-0.081	-0.135	0.129	-0.018	0.064
PPL	0.04	-0.09	0.36	**1**	-0.58**	-0.321	0.521*	-0.001	-0.233
SPP	0.03	-0.17	-0.04	-0.16	**1**	-0.130	0.471*	-0.226	-0.236
TSW	0.34	0.23	-0.06	-0.28	-0.04	**1**	-0.155	-0.259	-0.021
GYH	0.04	-0.30	0.21	0.44	0.14	-0.10	**1**	-0.182	-0.386
CHS	-0.80	-0.71	-0.13	-0.02	-0.02	-0.20	-0.16	**1**	0.900**
Rust	-0.67	-0.50	-0.01	-0.17	-0.09	-0.06	-0.30	0.79	**1**

MTD = Days to maturity, FLD = Days to 50% flowering, PH = Plant height, PPL = Number of pods per plant, SPP = Number of seed per pod, TSW = Thousand seed weight, GYH = Grain yield in kgha-1, CHS = Chocolate spot.

Where is the G x E analysis?

4. CONCLUSIONS

Twenty-twofaba bean genotypes were conducted at two locations Kulumsa and Kofele in 2015/16 using randomized complete block design to estimate genetic variability and assess associations of yield and yield-related traits of faba bean genotypes.The analysis of variance showed that highly significant ($P \leq 0.01\%$) differences were observed for all evaluated traits.

This indicates the presence of high genetic variability among studied genotypes and has great opportunities to gate the genetic gain through selection or hybridization. From the tested genotypes maximum grain yield were recorded from genotypes-5(5,598.1 kgha^{-1}) followed by genotype-10(5,545.7 kgha^{-1}), genotype-19(5,449.9kgha^{-1}) and genotype-9 (5,328.5 kgha^{-1}), while minimum grain yield were recorded from genotype-17 (2,380.8 kgha^{-1}) and genotype-7 (3,898.5 kgha^{-1}).

Show the p value in the table and p value for the yields

Grain yield and thousand seed weight showed a moderate phenotypic and genotypic coefficient of variation,while days to maturity, plant height, and number of seeds per pod recorded lower phenotypic and genotypic coefficient of variation.The success of genetic improvement on a specific trait depends on the amount of genetic variability present in the populations. The highest estimates of heritability were found for days to 50% flowering, days to maturity, and thousand seed weight. Higher genetic advances as a percent of mean were observed from number of pods per plant and thousand seed weights.In this study highest estimate of heritability along with high genetic advance as percent of mean was observed for thousand seed weight. The presence of genetic variability and heritability would be helpful for the breeder to estimate genetic gain.

In this study highest estimate of heritability along with high genetic advance as percent of mean was observed for thousand seed weight.Grain yield was significantly and positively correlated with number of seeds per pod and number of pods per plant. This implies that the improvement of one trait can result in a similar effect on the improvement of the trait.

References should be done in a consistant manner and in alphabetical order

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