

Research Article

Genetic Variability and Cluster Analysis of Faba Bean (*Vicia faba* L.) Genotypes in Debre Tabor, Northwestern Ethiopia

Solomon Sharie Shferaw^{1,*}, Wossen Tarekegne²

¹Ethiopian Institute of Agricultural Research (EIAR), Fogera National Rice Research and Training Center, Bahir Dar, Ethiopia

²Department of Plant Sciences, College of Agriculture and Environmental Sciences, Bahir Dar University, Bahir Dar, Ethiopia

Abstract

Faba bean, a globally important pulse, offers genetic variation for plant breeders, although information on this variability is scarce in Ethiopia. Therefore, the study was conducted to assess the genetic variability of genotypes using 49 genotypes with 7 × 7 simple lattice designs. The experiment was conducted at in Fogera National Rice Research and Training Center at Debre Tabor research site in north western Ethiopia. Analysis of variance revealed that there were highly significant differences among forty-nine genotypes for all studied traits (days to flowering, days to maturity, grain filling period, number of branch, plant height, pod per plant, biomass yield, harvest index, hundred seed weight, chocolate spot and seed yield). High GCV and PCV was observed in pod per plant and chocolate spot both at genotypic and phenotypic level including number of branch at phenotypic level. Moderate to high heritability estimates were observed in all studied traits. A high genetic advance in percent of mean was observed in the number of branches per plant, the number of pods per plant, grain yield, seed weight, and chocolate spot. In conclusion, the study found that the ET 07013-1 and ET 07005-1 genotypes are potential for future breeding programs, but further experimentation across locations and seasons is needed. It is recommended to give much attention to traits with high heritability and GAM, which include the number of branches per plant, the number of pods per plant, grain yield, hundred seed weight, and chocolate spot. The best genotypes should be included in future breeding programs to maximize yield even further. It is recommended to closely monitor traits with high heritability and high GAM.

Keywords

Faba Bean, GAM, Heritability, Traits

1. Introduction

Faba bean (*Vicia faba* L., 2n = 12) is one of the oldest domesticated food legumes with a controversial origin (the Near East is considered a center of origin for faba bean [6]. It

is an ancient legume with high seed protein content, is a significant cool-season grain legume globally farmed for animal feed and human consumption. The faba bean, a significant

*Corresponding author: solomonsharie21@gmail.com (Solomon Sharie Shferaw)

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cool-season food legume, is cultivated in Ethiopia's highlands, primarily in high and mid-altitude regions. It grows between 1800-3000 meters above sea level, receiving 700-1000 millimeters of rainfall annually [18]. Faba bean production is concentrated in nine agro-ecological regions, with China leading in cultivated area and production, followed by Ethiopia [12].

The study of genetic variability on different germplasm of a crop help the breeders in identification the most potential genotypes by using various genetic parameters like heritability, genetic advance and genetic coefficient of variation. The genetic variability study has paramount role in breeding for wide adaptation. If in any crop, sufficient genetic variability is present, help in further improvement as well as development of superior cultivars. It helps in selection of desirable parents for an efficient hybridization program. It is the primary consideration of many investigators.

Despite Ethiopia's efforts to start breeding faba beans in the 1950s, biotic and abiotic stresses have prevented the crop's production from reaching its full potential, resulting in significant yield losses. Lack of improved varieties, chocolate spot (*Botrytis fabae*); waterlogging; drought and cold weather conditions and at the moment, faba bean leaf gall (*Olpidi-umviciae* (Kusano), which is locally known as Qormid in Ethiopia, are some of the major obstacles to increased faba bean production [7]. Therefore, developing tolerant varieties is one option to address this challenge. Thus, the study was done to evaluate the genetic variability, heritability and genetic advancement in faba bean genotypes.

2. Material and Methods

2.1. Description of the Study Area

The field experiment was conducted in 2022 main cropping season, under rain-fed condition at Fogera National Rice Research and Training Center in Debre Tabor research site, northwestern Ethiopia. The experimental location represent the highland areas of major faba bean growing area of south Gondar and located about 660 km Northwest of Addis Ababa, about 103 km from Bahir Dar town. The latitude and longitude of the experimental site is 11°88'N and 37°98' E, respectively, and an elevation of 2706masl. The experimental site receives high amount of rainfall and an average annual rainfall of 1500.9 mm with maximum and minimum temperatures of 25.5 and 6.1 °C, respectively.

2.2. Treatments, Experimental Design and Procedure

49 faba bean genotypes were used for the study (Table 1). The genotypes were arranged in simple lattice design with two replications. The experimental areas was 780 m² (30 m * 26 m) with experimental plot area 3.6 m² (3 m * 1.2 m) having

three rows and thirty plants per row. Spacing between replication, incomplete block, plots, rows, and plants was 2m, 1.5m, 0.6m, 0.4m, and 0.1m, respectively. Fertilizer were applied at the rate of 121kg/ha in the form of NPS. Weeding practice was applied uniformly for all treatments.

2.3. Data to Be Collected

Data was collected for phenology and growth, yield and yield components on plant basis and plot basis.

I. Phenology and growth traits

Days to 50% first flowering (DF): this parameter was recorded by counting the number of days from planting to the time when 50% first flowering by visual observation.

Days to 90% physiological maturity (DM): The number of days from planting to the stage when 90% of the plants in a plot have reached physiological maturity.

Grain filling period: The number of days between 50% flowering and days to 90% physiological maturity.

Plant height (cm): The plant heights of five randomly taken plants from each of the two middle rows will measured from the ground level to the tip of the plant at physiological maturity and expressed as an average of heights of five plants per plot.

II. Yield and yield components

Number of pods per plant: The number of pods per plant was counted from five randomly taken plants from the middle two rows and expressed as an average for each plot.

Hundred Seed weight (HSW): The weight in gram of one hundred randomly taken seed from each plot was measured.

Above ground biomass yield (BY): This parameter was measured after the plant was dried.

Seed yield (Kg): Seed yield was measured by taking the weight of the grains threshed from the net plot area of each plot and was converting into ton per hectare.

Harvest index (HI): It was calculated as $\frac{\text{Grain yield}}{\text{Biomass yield}} \times 100$.

Chocolate spot disease: The severity of the chocolate spot disease was recorded using 1-9 scale. 1=no disease symptom (Highly resistant), 3=small few small disease lesions (resistant), 5=some defoliation (moderately resistant), 7=50% defoliation some dead plants (susceptible) and 9=extensive, heavy sporulation, stem girdling, blackening and death of more than 80% of plants (heavily susceptible).

PSI (%) calculated as $\frac{\sum(NPC*CR)*100}{NIP*MSC}$, where NPC=number of plants in each class rate, CR=class rate, NIP=number of infected plants and MSC=maximum severity class rate.

The response of tested genotypes were classified into six reaction groups according to [1] where 0 to 2% is highly resistant (HR), > 2 to 15% is resistant (R), > 15 to 40% is moderately resistant (MR), > 40 to 60% is moderately susceptible (MS) and > 60 to 80% is susceptible (S) >80 to 100% is highly susceptible (HS) based on percent disease severity values.

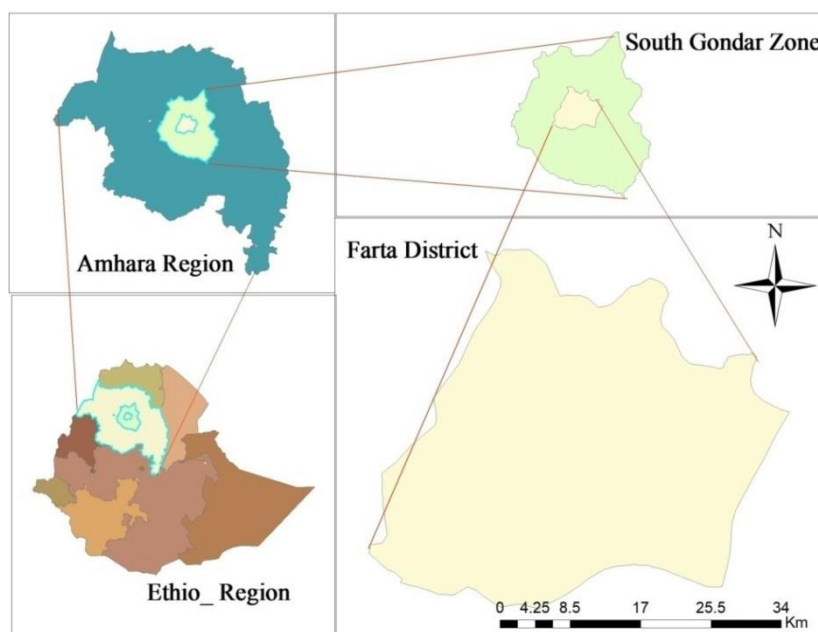


Figure 1. Map of the study area.

2.4. Data Analyses

Analysis of variance (ANOVA) was computed to test the presence of significant differences among genotypes for different traits. Normality of data and homogeneity of variance was tested using Shapiro wilks and Bartlett Test in SAS program, respectively. After test of data normality and homogeneity of variance, the data collected for each quantitative trait were subjected to analysis using Proc lattice and Proc GLM procedures of SAS version 9.0. Duncan's Multiple Range Test (DMRT) at 5% level of significance was used for genotypes mean comparisons, whenever genotypes difference was significant. The model for lattice design is: $Y_{ijk} = \mu + g_i + b_k(j) + r_j + e_{ijk}$, Where; Y_{ijk} the observations of the i th genotype grown in the k th block of the replication j , μ is the grand mean; g_i is the effect of the i th genotype; $b_k(j)$ is the effect of the k th block in the j th replication; r_j is the effect of replication and e_{ijk} is the residual effect.

2.4.1. Estimation of Variance Components

The variance components were estimated according to the method suggested by [15] as follows: -

Environmental variance (σ_e^2) = MSe

Genotypic variance (σ_g^2) = $\frac{MSg - MSe}{r}$

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2$

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$

Where, \bar{x} = grand mean of a character, r = number repli-

cation, MSg = mean square due to genotype and MSe = mean square of error.

According to [8], PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%).

2.4.2. Estimation of Heritability in Broad Sense

Broad sense heritability (h^2) will estimate as the percentage of the ratio of the genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2) as suggested by [2] as:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability was estimated or calculated by [15] as follows 0 - 30% = low, >30 - 60% = medium, >60 = high.

2.4.3. Estimation of Genetic Advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM) was estimated according to the method suggested by [15] as:

$$GA = k(\sigma_p) h^2 = k(\sqrt{\sigma_p^2}) h^2$$

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where k = selection differential ($k = 2.06$ at 5% selection intensity), σ_p = phenotypic standard deviation on mean basis and h^2 = Heritability in broad sense and \bar{x} = mean of the trait.

Genetic advance as percent of mean is categorized as low (0-10%), moderate (>10-20%) and high (>20% and above) as given by [15].

Table 1. List of faba bean genotypes used in the study.

No.	Genotypes code	No.	Genotypes code	No.	Genotypes code
1	Cool-0030	18	EH96009-1	35	Coll 155/00-3
2	EK 01002-1-1	19	EH95078-6	36	EK05005-4
3	Cool-0025	20	EK 01007-2-6	37	EH01048-1
4	EH011070-1	21	CSR02010-4-3	38	Gora (S.C)
5	EH011040-1	22	CSR02012-2-3	39	EH99051-3
6	EH011001-1	23	EH011089-3	40	EK 01004-2-1
7	EH011093-2	24	EK 01019-2-1	41	EH 06028-1
8	Cool-0031	25	Numan (S.C)	42	EH95073-1-
9	EK 01001-5-1	26	EH011029-2	43	EK 01019-7-5
10	Cool-0018	27	EK05024-2	44	EH00102-4-1
11	Cool-0035	28	EH011049-2	45	R-878-3
12	Cool-0024	29	ET 07013-1	46	EK 01024-1-1
13	EK 01001-8-1	30	EK 01006-7-1	47	EH96049-2
14	EK 05014-3	31	EK 01015-1-1	48	EK 01021-4-1
15	EK05027-5	32	EH011037-2	49	ET 07005-1
16	EK 01001-9-2	33	EK 05023-1		
17	EK 01001-10-5	34	EH 06007-2		

3. Results and Discussion

All of the traits that were studied days to flowering, days to maturity, number of branches, grain filling period, plant height, pod per plant, biomass yield, harvest index, hundred seed weight, chocolate spot, and grain yield showed highly significant differences ($p < 0.01$) among genotypes, according to analysis of variance (Table 2). This suggested that variability existed among the genotypes under study for future faba bean improvement. According to this outcome, [16] found

comparable results for the following parameters: plant height, pod per plant, plant height, days to flowering, days to maturity, chocolate spot, and faba bean grain yield. Similar findings were reported by [11] in their previous study regarding grain yield, plant height, pod per plant, seed per pod, and thousand seed weight, all of which showed significant differences between twelve genotypes in seven different environments. According [24], there was a highly significant difference in the number of branches, plant height, pods per plant, seed weight per pod, and hundred seed weight between genotypes.

Table 2. Mean squares from analysis of variance for 12 traits of 49 faba bean genotypes.

Traits	Mean squares					
	Replication (df=1)	Genotypes (df=48)	Entra-block error (df=36)	CV (%)	R ² (%)	RE to RCBD (%)
Days to flowering	4.08	24.98**	2.64	2.92	91	83.33
Days to maturity	3.68	15.18**	2.19	1.07	88	94.95
Grain filling period	1.46	16.9**	1.73	1.54	82	83.73
Plant height	58.93	198.66**	26.35	4.01	89	93.85

Traits	Mean squares					
	Replication (df=1)	Genotypes (df=48)	Entra-block error (df=36)	CV (%)	R ² (%)	RE to RCBD (%)
Number of branch per plant	0.01	0.44**	0.01	4.29	97	102.04
Pod per plant	0.26	90.22**	1.92	6.34	93	115.28
Grain yield	2.4	48.88**	1.27	3.63	80	87.7
Biomass yield	0.05	174.5**	28.22	5.20	97	91.17
Harvest index	2.05	25.35**	3.93	6.46	87	92.95
Hundred seed weight	0.045	402.53**	5.27	2.97	87	109.94
Chocolate spot	65.30	576.29**	47.53	15.56	98	93.30

**=Highly significant at 1%.

3.1. Performance of Genotypes for Yield and Yield Related Traits

The study analyzed genotypes for twelve traits, with a mean performance range of 55.73 days to flowering. The shortest days to flowering were recommended for moisture stress areas. The maximum days to maturity were recorded for genotypes G-1, G-13, G-21, G-10, G-17, G-19, and G-36, while the minimum was for genotype G-7. The shortest maturity genotypes are suitable for late rainfall regions and drought-resistant faba bean genotypes, while genotypes with maximum days to maturity are suitable for highland areas.

The grain filling period ranged from 78 to 92 days, with G-31 having the longest (92 days), followed by G-8 (90 days), and G-49 having the shortest (79 days). Plant height varied from 97cm to 146cm, with G-38 having the highest height and G-1 having the lowest. The study found that the number of pods per plant ranged from 8 to 38, with G-49 having the highest number (37.5), followed by G-29 (37) and G-25 (human) and G-38 (Gora).

The study found that the highest above ground biomass yield was achieved by genotype G-38 (11.757 ton per hectare), followed by genotypes G-29 and G-39 (11.612 and 11.513 ton per hectare), respectively. The harvest index varied from 16.6 to

40.1 with a mean value of 30.67, with G-49 having the highest value (38.15) followed by G-4 and G-29. The study found that the highest seed weight was recorded for genotype G-5 (108.7 gram), followed by G-34 (101.4 gram) and G-26 (104.8 gram), and the lowest was G-45 (46.75 gram).

Disease scores for chocolate spot were ranged from 6% to 69 based on percentage severity index (PSI) conversion. EK 05014-3, ET 07013-1, EK 05023-1 and EH 06007-2 were disease resistant genotypes. The highest disease chocolate disease score was recorded from the genotype G-31 and G-40. The least disease score was scored from genotypes ET 07013-1, EH 06007-2, EK 05014-3, EK 05023-1, ET 07005-1, Cool-0035 and Cool-0024. Birhanu. [4] was reported similar result for ET 07013-1, EH 06007-2, EK 05014-3, EK 05023-1, ET 07005-1. This indicates that these genotypes are resistant to chocolate spot disease.

The study found a wide range of grain yields, with G-49 showing the highest yield at 4.385 ton per hectare, followed by G-29 at 4.285, indicating significant variability among genotypes.

Generally, from the result of the study, G-49 and G-29 genotypes are promising genotypes for improving faba bean grain yield. Birhanu [4] reported similar yields at Hashenge and Aiba locations, with G-49 and G-29 yielding highest at Aiba.

Table 3. Mean, minimum and maximum values of 12 traits of 49 fababeen genotypes.

Traits	Mean	Std. Dev.	Min	Max	Range
Days to flowering	55.73	3.67	43	63	43-63
Days to maturity	138.52	2.93	127	146	127-146
Grain filling period	85.45	3.02	78	92	78-92
Plant height	128	10.54	97	146	97-146

Traits	Mean	Std. Dev.	Min	Max	Range
Number of branch per plant	2.34	0.48	2	3	2-3
Pod per plant	21.86	6.76	8	38	8-38
Biomass yield	10.11	9.96	54.94	117.57	54.94-117.57
Grain yield	3.105	4.98	1.6	4.4	1.6-4.4
Harvest index	30.58	3.79	16.6	38.14	16.6-38.14
Hundred seed weight	77.17	14.21	43.9	108.7	43.9-108.7
Chocolate spot	44.29	17.54	6	69	6-69

3.2. Estimation of Variance Components

The study was supported by [5] who revealed that genotypic and phenotypic coefficients of variation (GCV) are crucial for predicting genotype variability. The results show that phenotypic coefficients of variation (PCV) are slightly greater than genotypic coefficients of variation (GCV) for most studied traits, suggesting less environmental influence. High GCV and PCV values suggest substantial variability, suggesting selection for promising genotypes. PCV was higher than GCV for all quantitative traits, suggesting environmental interaction.

3.2.1. Estimation of Genotypic and Phenotypic Coefficients of Variation

The traits such as, chocolate spot (36.72) and pod per plant (30.76) had high estimates of GCV, which indicated that there was the minimum environmental influence on these traits and further selection could be done since the variation of these traits is due to under the control of genetic factor. This is in agreement with the results obtained in the previous studies of [21, 24] for pod per plant and [3] for both chocolate spot and pod per plant.

The study found moderate GCV in branch per plant, seed per pod, harvest index, hundred seed weight, and grain yield, which is partially in line with previous results from [5, 10, 20]. The study found that traits like days to flowering, maturity, grain filling period, plant height, and biomass yield have limited selection scope due to environmental effects, confirming previous research. [14, 16, 20] all found similar results regarding days to flowering, maturity, grain filling period, and plant height.

Phenotypic coefficient of variation (PCV) ranged from 2.13 for days to maturity to 39.88 for chocolate spot. High estimates of phenotypic coefficient of variation were observed in chocolate spot (39.88), pod per plant (31.42) and number of branch (20.13). In line to this result, [3, 14] had shown that chocolate spot, pod per plant and number of branch per plant have high PCV values. The traits which recorded moderate

PCV values were seed per pod (13.78), harvest index (12.48), hundred seed weight (18.5) and grain yield (16.13). Consistently, moderate PCV value was reported in the previous study for seed per pod, hundred seed weight and harvest index traits [20].

Low PCV values were observed in traits such as days to flowering, days to maturity, grain filling period, plant height, and biomass yield. Studies was supported by [16] who found similar results regarding days to flowering, maturity, grain filling period, and plant height. High GCV and PCV values in traits indicate high variability, suggesting effective selection for trait improvement, while low values indicate low genetic variability.

3.2.2. Estimation of Heritability and Genetic Advance as Percent of the Mean

Heritability is a crucial factor in plant breeding, aiding in the selection of genotypes from diverse genetic populations. It ranges from 60 for seed per pod to 97.41% for hundred seed weight and 3.28 for days to maturity to 69.62 for chocolate spot. [3, 20, 16, 22] reported high heritability in various plant parameters.

High heritability values suggest genetic control over trait variation, allowing direct selection for crop improvement. However, high broad-sense heritability doesn't guarantee accurate genetic gain predictions for effective selection. High heritability estimates and genetic advances are more effective in predicting gain under selection than heritability alone, as high heritability doesn't always indicate high genetic gain [15].

In this study high GAM were recorded for chocolate spot (69.62%), pod per plant (61.3%), number of branch (39.58%), hundred seed weight (37.13%) and grain yield (31.54%). High genetic advance (GAM) is a powerful selection tool, controlled by genes and influenced less by the environment [19].

The study found high heritability and genetic advance in plant traits such as branch number, pod number, seed weight, chocolate spot, and grain yield, consistent with previous findings [3]. The author [10] found high heritability and genetic advance in pod per plant and seed weight, but low ge-

netic advance in days to maturity and grain filling period. High heritability values in days to maturity and grain filling

period suggest that selection based on these traits may not be effective.

Table 4. Estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advance for 12 traits of 49 faba bean genotypes based on the analysis of variance.

Traits	Mean	σ^2_e	σ^2_g	σ^2_p	GCV	PCV	H ²	GA	GAM
DF	55.73	2.64	11.17	13.81	5.99	6.67	80.88	6.19	11.11
DM	138.52	2.19	6.49	8.68	1.84	2.13	74.77	4.54	3.28
GFP	84.44	1.73	7.58	9.31	3.26	3.61	81.42	5.12	6.06
PH	128	26.35	86.15	112.5	7.25	8.28	76.58	16.73	13.07
NB	2.33	0.01	0.21	0.22	19.66	20.13	95.45	0.92	39.58
PPP	21.86	1.92	44.15	46.07	30.76	31.42	95.83	13.4	61.3
BY	101.15	28.22	73.14	101.36	8.45	9.95	72.16	14.97	14.8
GY	31.04	1.27	23.80	25.07	15.72	16.13	94.93	9.79	31.54
HI	30.66	3.93	10.71	14.64	10.67	12.48	73.16	5.77	18.81
HSW	77.17	5.27	198.63	203.9	18.26	18.50	97.41	28.65	37.13
CS	44.28	47.53	264.38	311.95	36.72	39.88	84.75	30.83	69.62

σ^2_e = Environmental variance, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, H² = Broad sense heritability, GA = Genetic Advance, GAM = Genetic advance as percent of mean, DF = days to flowering, DM = days to maturity, NB=number of branch GFP= grain filling period, PH = plant height, PPP=pod per plant, SPP=Seed per pod, BY =Above ground biomass yield, HI=Harvest index, HSW=Hundred seed weight, CS=chocolate spot.

3.3. Genetic Divergence Analysis

The studied 49 faba bean genotypes were grouped into six clusters with a variable number of genotypes ranged from 1 to 20 genotypes.

3.3.1. Clustering of Genotypes

Cluster analysis using the whole genotypes was grouped into six distinct groups. The numbers of genotypes per clusters were varied from 1 to 20 to each cluster. Each of six clusters ranged from one to twenty in the smallest and largest, respectively, as presented in Table 5 & Figure 2.

Cluster II was the largest cluster comprising 20 genotypes,

followed by cluster I (16) and cluster III (7) whereas the remaining cluster were contained the least number of genotype (genotypes) which were cluster IV (3), V (2) and VI (1). The two standard checks were grouped under cluster III. Different authors reported the presence of diversity among faba bean genotypes classified into different number of distinct clusters. Likewise, [9] classified eighty faba bean genotypes into seven clusters by using ten characters. Forty six faba bean genotypes into eight clusters by using nine characters, 22 genotypes into three clusters on the basis of nine traits, respectively. These indicated that the existence of genetic diversity in evaluated faba bean genotypes.

Table 5. Distribution of 49 genotypes into six clusters based on square distance analysis for 49 faba bean genotypes.

Cluster	Number of genotypes	Percent distribution	Name of genotypes
Cluster I	16	32.65	EH011001-1, EH96009-1, Coll 155/00-3, EH95073-1, EK 01019-2-1, EK05024-2, EK 01001-8-1, EK 01024-1-1, EH95078-6, Cool-0035, Cool-0024, EK05027-5, EK 01001-10-5, EK 05023-1, EK 05014-3, EH96049-2
Cluster II	20	40.82	EK 01002-1-1, EK 01007-2-6, EH01048-1, EH00102-4-1, EK 01006-7-1, EK

Cluster	Number of genotypes	Percent distribution	Name of genotypes
			01021-4-1, CSR02010-4-3, EK 01015-1-1, Cool-0018, CSR02012-2-3, EK05005-4, EK 01019-7-5, EH011093-2, EH011049-2, EK 01004-2-1, EH99051-3-1, EK 01001-9-2, Cool-0031, EK 01001-5-1, EH 06028-1
Cluster III	7	14.27	EH011089-3, Numan (Standard Check), EH 06007-2, ET 07013-1, ET 07005-1, EH011070-1, Gora (S. Check)
Cluster IV	3	6.12	EH011040-1, EH011037-2, EH011029-2
Cluster V	2	4.08	Cool-0025, R-878-3
Cluster VI	1	2.04	Cool-0030

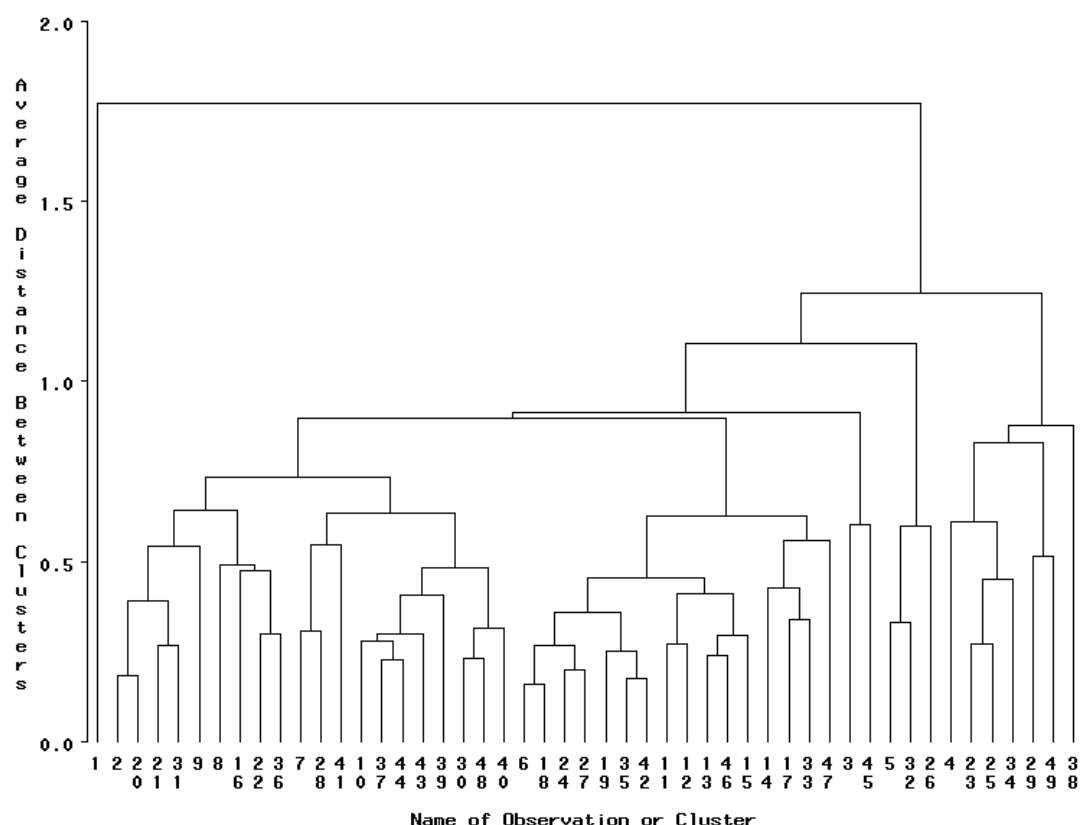


Figure 2. Dendrogram depicting relationship among 49 faba bean genotypes based on 12 traits. Numbers in the clusters indicates genotype code.

3.3.2. Cluster Mean Analysis for Different Characters

In the finding, cluster I was characterized by the shortest days to flowering (54.31) and third highest days to maturity (38.81) next to cluster II and VI (Table 6). This cluster had the second highest in number of branch (2.38), grain filling period (85.97) plant highest (128.97), pod per plant (20.78) and grain yield (30.61) next to cluster III. Genotypes under this cluster had better in yield performance and yield related traits suggested that the breeder needs to evaluate the members of this cluster to improve yield and other yield contributing traits.

Cluster II consists of twenty genotypes and it had the maximum distance D^2 from cluster VI (182.03) and minimum distance was from cluster V (26.44). This cluster had the second highest cluster mean performance in days to maturity (139.03) and chocolate spot (59.35) next to cluster VI. Highest inter cluster mean performance of chocolate spot indicates that the selection of the genotype should be against this traits. This cluster also had the third best performance in number of branch (2.28) and pod per plant (19.7).

Cluster III had the maximum distance value D^2 from cluster VI (365.76) and it had minimum distance value D^2 from cluster IV (34.75) and this cluster was consists of seven gen-

otypes including two standard checks (Numan and Gora). It revealed the highest mean performance for number of branch (2.86), plant height (140.64), above ground biomass (111.60), harvest index (35.82) and grain yield (39.99). It also share with clusters V and VI in the highest cluster mean performance of seed per pod (3.00). The cluster mean performance of hundred seed weight under this cluster was (94.29) which recorded second most important mean performance next to cluster IV (105.48). On the other hand, this cluster had the shortest days to flowering (54.50) shared with cluster V next to cluster I.

Cluster IV consisted by three genotypes and it had maximum and minimum distance value D^2 from cluster VI and V which was (341.71) and (106.38), respectively. This cluster was revealed the highest cluster mean performance for days to flowering and hundred seed weight which was 61.67 and 105.48, respectively plant height was the second lowest mean performance next to cluster VI.

The fifth cluster was consisted from two genotypes maximum and minimum distance was from cluster VI and II that was (151.39) and (26.44), respectively. It was characterized by shortest days to maturity (136) lowest hundred seed weight (47.63gram) followed by cluster VI (48.30gram). Similarly it had the lowest number of branch per plant compared to cluster I, II, and III. On the other hand it highest cluster mean performance was observed in number of seed per pod compared to cluster I, II and IV. Chocolate spot was the third highest cluster means value next to cluster VI and II. Grain yield in this cluster had relatively similar mean performance (29.53 ton per hectare) compared to cluster I (30.61), II (29.47 and IV (28.00) ton per hectare.

The last cluster (cluster VI) consists of one genotype. It had maximum distance D^2 value from cluster III (365.76) and also its minimum distance value D^2 was (151.39) from cluster VI. This cluster was characterized by the highest mean performance of days to maturity (140.5), grain filling period (89.5), seed per pod (3.00) and chocolate spot (65.00). In this cluster, days to flowering recorded the second highest mean perfor-

mance (59.00) next to cluster IV (61.67). Contrary, number of branch per plant, plant height, pod per plant, above ground biomass and grain yield recorded the minimum cluster mean performance in this cluster which was 2.00, 102.5, 9.5, 5.842 and 1.91 ton per hectare, in respective orders. This cluster also characterized by lowest mean performance of hundred seed weight (48.30gram) next to cluster V (47.63gram).

The result indicates sufficient scope for genetic improvement through hybridization between the genotypes from divergent clusters. The genotype in cluster VI not be selected for further evaluation due to undesirable characters of lowest grain yield and greatly affected by the disease. Genotypes which had lower inter cluster mean performance for grain yield and chocolate spot could be selected for traits with greater mean values based on the breeding objectives. The lowest mean performance of yield and other important yield related traits of this cluster suggested that the chance of getting segregants with high yield is limited between cross of cluster VI with other clusters.

Generally, comparative study of cluster mean performance suggested that cluster III had the highest cluster means for grain yield and its contributing traits, therefore, genotypes under this cluster may be considered superior for selecting the promising parents in hybridization program. Therefore, cluster III could be used as a parent for crossing to develop high yielding faba bean varieties. It also revealed the minimum performance for chocolate spot which indicated that the genotypes grouped under this cluster have the potential to resist chocolate spot disease. Therefore, this is a good opportunity to select potential parents across the cluster for specific traits to improve in future faba bean breeding program even though the selection of parents depending on the special advantage of each cluster and each genotype depending on the specific objectives of hybridization.

Thus, in the present result cross involving cluster III with cluster are suggested to exhibit high heterosis and could result in segregates with higher grain yield.

Table 6. Cluster mean values for twelve traits in forty-nine (49) faba bean genotypes.

Traits	Cluster					
	I	II	III	IV	V	VI
DF	54.31	56.38	54.50	61.67	54.50	59.00
DM	138.81	139.03	137.43	137.17	136.00	140.50
NB	2.38	2.28	2.86	2.00	2.00	2.00
GFP	85.97	85.55	83.64	85.33	84.75	89.50
PH	128.97	125.75	140.64	116.50	128.25	102.50
PPP	20.78	19.70	34.86	18.33	18.25	9.50
SPP	2.84	2.73	3.00	2.67	3.00	3.00

Traits	Cluster					
	I	II	III	IV	V	VI
BY	102.37	98.68	111.60	99.51	103.48	58.42
HI	29.96	29.71	35.82	28.13	28.55	32.80
HSW	74.15	73.74	94.29	105.48	47.63	48.30
CS	32.34	59.35	25.64	39.83	50.25	65.00
GY	30.61	29.47	39.99	28.00	29.53	19.10

DF =days to flowering, DM = days to maturity, NB=number of branch GFP= grain filling period, PH = plant height, PPP=pod per plant, SPP=Seed per pod, BY = above ground biomass yield, HI=Harvest index, HSW=Hundred seed weight, CS=chocolate spot

3.3.3. Inter Cluster Distance Analysis

Inter-cluster distance is the main criterion for selection of genotypes implying that the genotypes belonging to the cluster with maximum inter cluster distance are genetically more divergent suggesting that selection of genotypes should be based on large inter cluster distance, which may lead to broad spectrum of favorable genetic variability. The averages inter cluster distance D^2 values are presented in Table 7. The range of inter-cluster distance was 9.93 to 365.76.

According to the χ^2 -test, there were highly significant differences among the clusters except cluster I with II which were non-significant. The maximum inter-cluster was observed between cluster III and VI ($D^2=365.76^{**}$) followed by cluster V and VI ($D^2=341.71^{**}$). This indicated that the presence of genetically distant genotypes in this clusters, which indicates that genotypes of these clusters could be used in hybridization program which is expected to release better segregants for respective traits of clusters in segregation generations through recombination of the most desirable traits to develop varieties. Increasing parental distance a greater number of constraining alleles at desired loci and then to the extent that these loci recombine in the F2 and F3 generation following a cross of distantly related parents, the greater will be the opportunity for successful selection for any character of yield interest [13].

For crossing of parents, selection should be taken from

cluster with highest genetic distance to obtain the highest genetic recombination and transgressive segregates in subsequent generation. Increasing parental distance mean great number of contrasting alleles at the desired loci therefore, the extent of these loci recombine in the F2 and F3 generation following a cross of distantly related parents has a high potential. [23, 17] suggested, for the chance of obtaining good recombinants in segregating generations crossing should be attempted between genotypes belonging to the clusters separated by large inter-cluster distance. According to the present finding, crossing of genotypes from cluster III and VI followed by cluster V and VI would give maximum recombination and segregation of the progenies.

The lowest inter-cluster distance was observed between cluster I and II ($D^2=9.93$), which showed the presence of less genetic variability or diversity between these clusters. The cross between genotypes belonging to cluster pairs separated by low inter-cluster distances are unlikely to generate promising recombinants in segregating generations [25].

Apart from selecting genotypes from the clusters which have higher inter cluster distance for hybridization one can also think selecting genotypes based on the extent of genetic divergence in respect to a particular character of interest. This is to mean that, if the intention of the breeder is to improve grain yield, he/she can select genotypes which are highly divergent with respect to this character.

Table 7. Inter-cluster distance between five clusters of 49 faba bean genotypes.

Cluster	I	II	III	IV	V	VI
I	0					
II	9.93 ^{ns}	0				
III	36.23 ^{**}	48.95 ^{**}	0			
IV	35.71 ^{**}	45.47 ^{**}	34.75 ^{**}	0		
V	30.68 ^{**}	26.44 ^{**}	114.1 ^{**}	106.38 ^{**}	0	

Cluster	I	II	III	IV	V	VI
VI	214.075**	182.03**	365.76**	341.71**	151.39**	0

$\chi^2=19.67$ and 24.72 at 0.05 and 0.01 probability level, respectively. ** indicate highly significant at 0.01 probability level. ns indicate non-significant.

3.3.4. Principal Component Analysis

Principal component analysis (PCA) was performed to estimate the relative contribution traits towards the variation in 49 faba bean genotypes. Eigen values, percent of total variance, percent of cumulative variance and Eigen vectors for twelve traits of 49 faba bean genotypes are presented in (Table 8).

Table 8. The first four principal components of 49 fababeen genotypes evaluated for twelve traits.

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Days to flowering	-0.18	0.37	-0.51	0.24
Days to maturity	-0.14	0.56	-0.29	0.17
Number of branch	0.21	0.22	-0.39	0.03
Grain filling period	-0.17	0.49	-0.23	0.1
Plant height	0.35	-0.13	-0.21	0.1
Pod per plant	0.43	0.15	0.02	0.05
Seed per pod	0.16	0.13	0.3	-0.65
Biomass yield	0.36	-0.18	-0.17	0.32
Harvest index	0.3	0.36	0.14	-0.26
Hundred seed weight	0.21	0.01	0.51	0.53
Chocolate spot	-0.29	-0.1	-0.03	0.07
Seed yield	0.43	0.16	0.03	-0.01
Eigen value	4.72	1.63	1.31	1.04
% Of total variance explained	39.32	13.57	10.95	8.68
Cumulative % of total variance explained	39.32	52.90	63.85	72.53

In the present study, the first four principal components exhibit more than one Eigen values and explained about accounted for about 72.52% of the total variation for twelve studied traits that showed the presence of genetic variability among the studied genotypes.

In the experiment the data revealed that traits with high contribution in the first component had the maximum variability (39.32) indicate they contributing maximum variability towards divergence. Pod per plant (0.43) and grain yield (0.43) had the highest variation for the first principal component analysis followed by biomass yield biomass yield (0.36) (Table 8 and Figure 3). On the other hand other traits are less important to PC1. The second prin-

cipal component (PC2) contributed about 13.57% of total variation and this variation was contributed by the traits such as days to flowering (0.37), days to maturity (0.56), grain filling period (0.49) and harvest index (0.36).

PC3 and PC4 contributed about 10.95% and 8.68% of total variations respectively. The traits which contributed the variation for the third principal component (PC3) were plant height (-0.21), days to flowering (-0.51), days to maturity (-0.29), number of branch (-0.39) and grain filling period (-0.23), seed per pod (0.30) and hundred seed weight (0.51). The traits which contribute the variation for the fourth principal component (PC4) were days to flowering (0.24), seed

per pod (-0.65), biomass yield (0.32), harvest index (-0.26) and hundred seed weight (0.53).

The first two PCs accounted for a commutative 52.9% of the total variation, which indicates much of variability that occurred from traits included in these principal components. Similar work had also been reported by [26] who were reported that the total variation was derived to 8 principal components. According to his finding, the first two principal components (PC1 and PC2) was contributed 54.40% and 14.30% total variation respectively on 22 studied genotypes.

The traits far from the PCA bi plot origin contributed more to the total variability (Figure 4). Accordingly, the primary traits contributing more total variability were pod per plant, grain yield, biomass yield, plant height, days to maturity, days to flowering and grain filling period. Traits close to the bi plot origin contributed less variability to total variability. In addition, traits nearest to the x-axis contributed more variation for first principal component, whereas those nearest to the y-axis contributed more variation for second principal component (Figure 4).

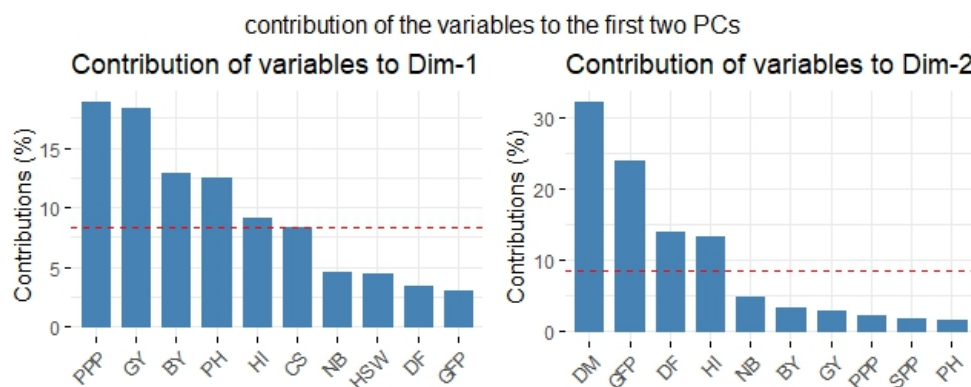


Figure 3. The contribution of variables for the first two PC1 and PC2.

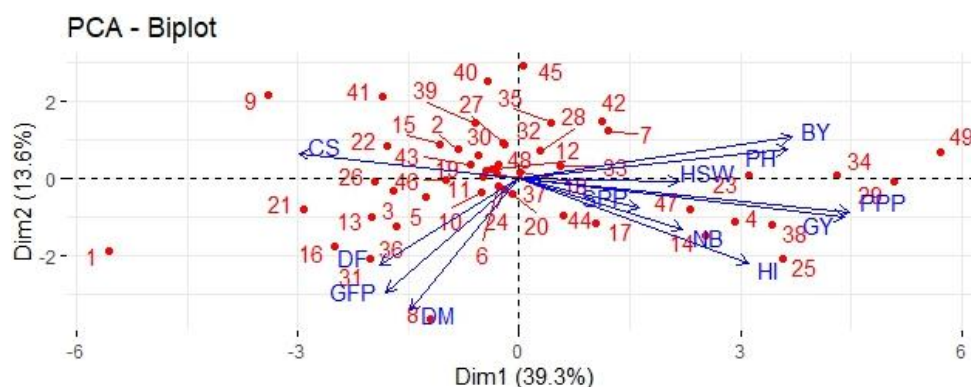


Figure 4. Principal Components of bi plots of faba bean genotypes based on twelve traits.

DF =days to flowering, DM = days to maturity, NB=number of branches GFP= grain filling period, PH = plant height, PPP=pod per plant, SPP=Seed per pod, BY =Above ground biomass yield, HI=Harvest index, HSW=Hundred seed weight, CS=chocolate spot and number=genotype for figure 4.

4. Conclusion and Recommendation

Genetic variability, trait interrelationships, and natural diversity are crucial for crop improvement strategies. The study found significant differences among genotypes, with ET 07013-1 and ET 07005-1 being the best for grain yield and related traits, with high variability in traits. High heritability and genetic advance in characters indicate high potential for trait transfer, while moderate heritability indicates low genetic advance and potential for direct selection. High H2 and GAM

values for branch number, pod per plant, seed weight, and grain yield suggest genotype selection for improved faba bean. High GCV, PCV, H2, and GAM traits suggest genetic control and a higher likelihood of improvement through selection. The study grouped 49 faba bean genotypes into six clusters, revealing genetic diversity. Cluster III had the highest grain yield per hectare, suggesting it could be used for hybridization in future breeding programs, particularly for genotypes ET 07013-1 and ET 07005-1. The inter cluster distance ranged from 9.93 to 365.76, with the highest distance between cluster III and VI and the lowest between cluster I and II, indicating

divergent genotypes among clusters. The analysis revealed that the first four principal components accounted for 72.53% of total variation among faba bean genotypes, with PC1 having the highest variability.

Abbreviations

PC Principal Component

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Author Contributions

Solomon Sharie Shferaw: Conceptualization, Data curation, Formal Analysis, Funding acquisition, Resources, Software, Supervision, Visualization, Writing – original draft, Writing – review & editing

Wossen Tarekegne: Conceptualization, Methodology, Supervision, Writing – review & editing

Conflicts of Interest

The author declares no conflicts of interest.

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