
Genetic Diversity of Elite Faba Bean (*Vicia faba* L.) Genotypes Based on Agronomic Traits and Soil Acidity Stress Indices

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Abstract: Faba bean plays an important role in human food, animal feed and soil fertility restoration. However, its productivity is low due to soil acidity problem in the central highlands of Ethiopia. Hence, this study was designed to know the genetic diversity existing among 50 elite faba bean genotypes tested at three locations (Holetta, Watebecha Minjaro and Jeldu) in 2017 using randomized complete block design with three replications. The genetic distances estimated by Euclidean distances ranged from 1.55 to 15.60. The 50 genotypes were grouped in to 10 distinct clusters by Unweighted Pair group Method with Arithmetic Means clustering method based on Euclidian distances matrix estimated from overall mean of genotypes for 19 traits over locations and soil managements. Among the 10 clusters 5 were solitary (III, VI, VIII, IX and X) including the best and least performing genotypes CS20DK (IX) and Wayu (X), respectively. Cluster II consisted of soil acidity stress tolerance genotypes. The results of the first three principal components (PC) analysis accounted 84.32% of the total variations observed among genotypes of which PC1 and PC2 contributed 45.8 and 25.36%, respectively. In each PC single or few traits were not identified as having much contribution than others traits. In conclusion, cluster IX was found as best of all the other clusters in most of traits performance and genotypes grouped under cluster II, VI and VIII needs further evaluation to obtain genotypes with lowest relative yield reduction and stress susceptible index and resistant to chocolate spot disease with other desirable agronomic traits.

Keywords: Cluster, Euclidean Distance, Principal Component Analysis

1. Introduction

Faba bean (*Vicia faba* L.) is produced worldwide in different agro-ecological regions. The world leading producers were China followed by Ethiopia [1]. It's the leading among pulse crops in Ethiopia, sharing 30% of area coverage and 34% of the total production of pulses [2]. To boost the productivity of this crop more than 30 varieties have been released nationally [3]. However, there are different newly emerged biotic and abiotic factors that limit its productivity in Ethiopia [4].

In breeding programs, existence of wide genetic diversity is a key factor for successful crop improvement for different traits [5]. Hence, assessment of existing genetic diversity in

faba bean is very important to characterize available germplasms to determine the presence of valuable trait variation to use in the future breeding programs [6]. As plant genetic resources play a major role in providing sources of resistance to different biotic and abiotic stresses; understanding genetic diversity among faba bean genotypes is crucial to use in the future breeding programs.

Awareness of genetic diversity is vital for germplasms conservation because the development of ideal crop varieties depends on screening and selection of desirable genotype available in the breeding program [7]. Genetic resource is a base for crop improvement through selection to ensure the needs of food security. However, the genetic difference among genotypes of several pulse crops is being eroded

vastly hence modern cultivars are replacing the locally adapted cultivars over large areas across the world [8]. The presence of genetic diversity in Ethiopian faba bean is proved from morphological characterization of accessions collected from different regions [9]. Thus, this experiment was initiated with the objective to assess the genetic divergence in different Ethiopian faba bean genotypes.

2. Materials and Methods

2.1. Experimental Locations and Test Materials

The experiment was conducted at Holetta, Watebecha

Minjaro and Jeldu with soil of pH 4.66, 4.96 and 4.49, respectively, in central highlands of Ethiopia under rain fed during the main cropping season (June to December) of 2017. The soil type of at each location was nitisol. Fifty faba bean genotypes were used for this study (Table 1).

The genotypes were arranged in a randomized complete block design with three replications. Each experimental plot consisted of one row of 4m long with inter-row spacing of 40cm continuously and intra-row spacing of 10cm. Fertilizer were applied at the rate of 121 kg/ha in the form of NPS. Weeds were controlled by hand uniformly to all experimental units.

Table 1. Description of 50 faba bean genotypes used in this study.

Code	Genotypes	Year of release	Code	Genotypes	Year of release
G1	Cool-0030	---	G26	EKLS/CSR02017-3-4	---
G2	Wolki [¥]	2008	G27	Kasa	1980
G3	EKLS/CSR02012-2-3	---	G28	Cool-0025	---
G4	Obse	2007	G29	EH06070-3	---
G5	NC58	1978	G30	EKLS/CSR02010-4-3	---
G6	Ashebeke [¥]	2015	G31	Cool-0031	---
G7	Hachalu [¥]	2010	G32	Cool-0018	---
G8	Degaga	2002	G33	EKLS/CSR02028-1-1	---
G9	EH09031-4	---	G34	EK 05037-4	---
G10	Holetta-2	2001	G35	Cool-0035	---
G11	EH09007-4	---	G36	KUSE2-27-33	1979
G12	EH07023-3	---	G37	EH07015-7	---
G13	EK05006-3	---	G38	Cool-0024	---
G14	EKLS/CSR02014-2-4	---	G39	Selale [¥]	2002
G15	Numan	2016	G40	Moti	2006
G16	Bulga 70	1994	G41	EH06027-2	---
G17	EK05001-1	---	G42	EKLS/CSR02019-2-4	---
G18	Dosha	2008	G43	EH09002-1	---
G19	Gora	2012	G44	Tumsa	2010
G20	EH08035-1	---	G45	Gebelcho	2006
G21	Wayu	2002	G46	EK05037-5	---
G22	EKLS/CSR02023-2-1	---	G47	Didi'a [¥]	2014
G23	Mesay	1995	G48	Cool-0034	---
G24	EH09004-2	---	G49	CS20DK	1977
G25	EH06088-6	---	G50	Tesfa	1995

“---” = pipeline genotypes, ¥ = Varieties released for areas with waterlogging problems.

2.2. Data Collection and Analysis

The agronomic data were recorded on the entire plot or on five randomly selected faba bean plants in each row. Accordingly, data for days to 50% flowering, days to 90% physiological maturity, gain filling period, hundred seeds weight (g) and chocolate spot disease severity were recorded on the entire plot. On the other hand, plant height, number of podding node per plant, number of pods per podding node, number of pods per plant, number of seeds per pods and grain yield (g/5 plants) were recorded on five randomly pre-tagged plants from each experimental plot. The average of the five plants in each experimental plot was used for statistical analysis. Chocolate spot disease was recorded using 1-9 scale [10].

For multivariate analysis like cluster, distance and principal component analysis, records on all traits were standardized to means zero and variances of unity

(subtracting the mean value and dividing it by the standard deviation) to avoid bias due to differences in measurement scales [11].

2.2.1. Genetic Distance and Clustering of Genotypes

The genetic distances of genotypes were estimated using Euclidean distance (ED) based on pooled mean data after standardization as established by Sneath and Sokal [12] as follows:

$$ED_{jk} = \sqrt{\sum_{i=1}^n (X_{ij} - X_{ik})^2}$$

Where, ED_{jk} = distance between genotypes j and k; X_{ij} and X_{ik} = phenotype traits values of the i^{th} character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance.

The distance matrix from 19 traits (12 agronomic and 7 stress tolerance indices) was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrogram. The numbers of clusters were determined using a formula (cutting point = mean ED – SD). In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other genotypes. The calculated average distance (ED) was used to estimate which genotype is closest or distant to others.

2.2.2. Principal Component Analysis

The principal component analysis was computed to explore traits that accounted most to the total observed variation. It was calculated based on correlation matrix using SAS software according to Gutten’s lower bound principle, eigenvalues <1 should be ignored [13].

3. Results and Discussion

3.1. Genetic Distances Among Evaluated Genotypes

Assessment of genetic distances measured by Euclidean Distances (ED) using cluster analysis from 19 traits for all possible pairs of 50 faba bean genotypes resulted in 1225 pairs (Figure 1A-C). The ED showed wider differences among genotypes in the range between 1.55 and 15.60 with the mean ED, SD and CV of 5.79, 2.21 and 33.44%, respectively, over locations and managements (Table 2). The three highest ED over 6 environments (three locations with lime and without lime applications) were calculated between G21 and G49 (15.60) followed by G21 and G40 (15.26), G4 and G21 (14.58). The three lowest ED was registered between G12 and G42 (1.55) followed by G28 and G31 (1.60) and G38 and G48 (1.62) (Figure 1A-C).

A

Geno	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25
G1	0.00	6.04	3.35	6.17	5.30	3.75	5.06	4.34	4.32	7.40	4.69	4.38	3.41	3.16	5.33	3.67	3.35	4.92	4.13	4.24	9.89	3.30	4.92	4.39	3.35
G2		0.00	7.18	5.16	5.75	4.36	3.46	5.55	8.01	9.97	9.19	7.35	5.09	7.13	6.24	6.72	6.08	4.04	5.56	8.21	12.74	8.66	7.06	6.86	7.43
G3			0.00	5.54	7.65	4.41	6.17	6.52	3.07	8.64	4.06	2.17	3.60	3.13	4.85	5.98	3.64	5.57	4.03	4.57	12.35	2.95	6.95	4.34	2.81
G4				0.00	7.39	4.40	4.05	7.37	6.23	10.13	8.08	4.58	3.44	5.23	3.31	8.00	4.90	2.60	2.87	7.14	14.58	7.54	8.28	6.55	6.23
G5					0.00	6.67	5.49	3.18	7.96	6.76	8.33	8.24	6.61	6.61	7.74	3.58	5.07	5.81	7.04	7.20	9.31	7.33	2.78	6.72	7.23
G6						0.00	2.98	6.20	5.78	9.45	7.17	4.34	2.93	4.45	4.48	6.53	4.58	3.38	3.06	6.67	12.32	6.06	7.12	6.23	5.58
G7							0.00	5.73	6.48	8.37	8.06	6.21	3.96	5.12	4.04	6.67	4.57	3.23	4.05	7.76	11.74	7.38	6.43	7.09	6.69
G8								0.00	6.65	6.66	6.36	7.56	6.04	5.84	7.22	2.47	4.30	5.89	6.51	5.34	8.79	5.97	2.50	4.51	5.40
G9									0.00	6.82	2.68	4.33	4.39	2.55	4.09	6.46	3.50	6.58	4.95	5.16	11.28	3.28	6.75	5.14	2.69
G10										0.00	6.94	9.93	8.71	6.69	8.28	6.64	6.14	9.63	9.52	9.01	6.96	7.27	5.00	8.92	7.80
G11											0.00	5.72	6.11	4.07	6.29	5.98	4.46	8.01	6.49	4.28	10.36	2.57	6.47	4.48	2.63
G12												0.00	3.20	3.64	4.69	7.14	4.41	4.81	3.15	5.14	13.87	4.45	8.12	5.33	3.99
G13													0.00	3.14	3.43	6.12	3.68	2.87	1.92	5.45	12.50	5.31	6.96	5.36	4.10
G14														0.00	3.68	5.68	2.32	4.92	3.62	4.86	10.95	3.29	5.91	5.32	3.19
G15															0.00	7.83	4.03	4.46	3.29	6.90	12.96	6.32	7.74	6.53	5.17
G16																0.00	4.60	6.56	6.74	4.93	8.42	5.00	2.58	4.63	5.13
G17																	0.00	4.44	4.14	4.75	10.67	3.85	4.40	4.41	3.49
G18																		0.00	2.65	6.40	13.28	7.07	7.02	6.07	5.95
G19																			0.00	5.28	13.12	5.63	7.47	5.38	4.50
G20																				0.00	11.60	3.75	6.30	2.52	2.70
G21																					0.00	10.36	7.58	11.77	11.29
G22																						0.00	5.82	4.45	2.67
G23																							0.00	5.87	6.14
G24																								0.00	2.91
G25																									0.00

B

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G1	3.25	6.00	2.99	4.12	3.99	2.96	3.30	2.87	3.55	4.22	4.46	3.62	4.63	5.58	6.15	2.90	3.58	4.05	4.41	4.82	4.24	4.76	3.47	8.72	5.68
G2	7.59	8.44	5.32	8.33	7.47	6.24	4.57	6.63	5.15	3.76	6.89	6.20	3.68	8.97	5.31	6.05	6.39	6.87	3.60	5.33	8.44	3.34	3.76	4.47	8.03
G3	2.08	8.34	5.33	3.93	2.82	5.56	5.16	2.87	2.71	5.97	6.63	1.80	5.78	7.90	5.96	3.37	2.38	3.95	5.06	6.27	5.12	4.76	4.86	9.44	7.84
G4	6.12	9.80	5.99	7.42	5.94	6.96	6.37	4.98	4.27	4.96	8.70	4.60	5.50	10.06	5.06	5.48	4.00	6.18	5.13	6.89	8.23	2.93	4.97	7.72	9.75
G5	7.70	3.68	4.34	7.66	8.31	4.93	4.12	7.11	6.53	3.92	4.59	7.80	5.13	5.17	8.26	5.75	7.23	6.17	7.21	6.55	6.16	6.88	4.72	9.10	5.18
G6	5.13	8.52	4.45	6.03	4.86	4.85	4.88	4.12	3.51	4.43	7.02	3.58	4.59	8.50	5.10	3.93	3.27	5.87	2.51	4.25	7.07	2.43	3.96	7.24	8.18
G7	6.79	7.82	5.11	6.64	7.01	5.84	5.30	5.44	5.06	4.29	7.55	5.43	5.21	8.05	6.52	4.20	4.94	5.93	3.66	3.73	7.28	3.09	4.48	7.35	7.65
G8	6.04	3.65	3.94	6.25	6.97	4.80	2.66	6.15	5.68	3.76	3.21	6.52	4.88	4.63	7.34	4.92	6.63	4.54	6.29	5.95	4.44	6.38	4.31	8.73	3.33
G9	3.42	7.99	6.63	2.00	5.14	6.95	6.30	3.33	4.73	7.05	7.64	3.48	7.49	7.02	8.00	2.92	3.97	2.64	6.02	5.99	4.04	5.91	6.19	10.72	7.03
G10	8.85	5.30	8.78	5.71	10.59	8.85	8.21	8.27	9.19	9.02	8.47	9.21	10.06	4.00	12.47	6.10	8.97	5.72	9.66	7.41	4.97	9.86	8.88	13.55	4.93
G11	3.36	7.40	6.93	2.53	5.42	7.21	6.35	4.75	5.88	7.72	6.96	4.82	8.21	6.45	8.76	4.24	5.55	3.09	7.37	7.11	2.83	7.54	7.05	11.79	6.16
G12	3.10	9.52	5.55	5.53	2.74	5.86	6.07	2.93	2.80	5.97	7.68	2.21	5.85	9.27	5.31	4.59	1.55	5.35	5.51	7.28	6.74	4.51	5.13	9.41	9.38
G13	4.07	8.32	4.26	5.30	4.20	4.75	4.83	1.96	2.66	4.15	6.85	2.63	4.51	7.98	4.93	3.70	2.21	4.70	3.58	5.41	6.41	2.63	3.38	7.62	8.00
G14	3.49	7.19	5.13	2.95	4.79	5.38	5.57	2.41	4.02	5.63	6.95	3.34	6.45	6.53	7.29	2.39	2.64	3.27	5.53	5.57	4.28	5.09	5.20	10.31	6.85
G15	5.44	9.18	6.65	5.14	6.13	7.41	6.76	4.16	4.90	6.22	8.94	4.10	7.02	8.84	7.04	3.79	3.86	4.66	4.97	5.35	6.69	3.94	5.90	9.26	8.59
G16	5.57	3.20	3.46	6.02	6.42	3.67	2.70	5.78	5.61	4.35	1.96	6.50	4.94	3.79	7.64	4.94	6.48	4.86	6.76	6.47	4.08	6.93	4.21	9.32	3.78
G17	3.96	6.04	4.62	3.70	5.24	5.29	4.33	3.66	3.61	4.58	5.89	3.85	5.47	6.00	6.86	2.29	3.40	2.32	5.47	5.46	3.75	4.82	4.45	9.62	5.79
G18	5.84	8.43	4.11	7.31	5.58	5.08	4.95	4.50	3.74	2.93	7.08	4.64	3.91	8.85	4.44	5.16	3.80	6.08	4.52	6.29	7.66	2.76	3.52	7.07	8.60
G19	4.14	8.76	4.38	5.96	3.91	5.14	5.35	2.89	3.45	4.32	7.37	3.12	5.07	8.75	4.62	4.23	2.40	5.38	4.28	5.90	6.83	2.90	4.15	8.03	8.64
G20	2.75	7.08	4.62	5.71	3.69	5.29	4.82	4.37	5.00	5.49	5.11	4.85	6.20	7.18	6.31	5.47	5.11	4.68	7.27	8.13	4.63	6.86	5.44	10.28	6.84
G21	12.01	6.32	10.74	9.68	13.38	10.38	10.38	11.91	12.93	11.69	9.43	12.92	12.66	5.34	15.26	9.98	12.93	10.27	12.31	9.58	8.20	13.37	11.71	15.60	5.98
G22	2.58	6.78	5.50	3.09	4.21	5.49	5.48	3.91	4.83	6.70	5.92	4.22	7.06	6.13	7.92	3.66	4.31	3.75	6.87	6.82	3.14	6.91	6.00	11.28	6.40
G23	6.81	1.94	5.01	6.01	7.98	5.42	4.22	6.84	6.65	5.27	4.13	7.44	6.32	3.20	9.09	4.90	7.19	4.79	7.55	6.30	3.89	7.60	5.59	10.47	2.94
G24	3.13	7.00	4.72	5.73	3.97	5.70	3.68	4.87	4.24	4.95	4.64	4.41	5.22	7.34	5.45	5.07	5.25	3.96	6.27	7.38	4.64	5.92	4.66	8.85	6.32
G25	1.63	7.28	5.10	3.55	3.51	5.61	4.77	2.79	3.84	5.69	5.81	3.06	6.10	6.76	6.43	3.66	3.81	2.79	5.84	6.59	3.76	5.67	4.98	9.76	6.45

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G26	0.00	7.96	4.91	4.21	2.11	5.32	4.90	2.86	3.51	5.77	6.01	2.57	5.95	7.62	5.79	4.03	3.28	3.93	5.70	6.84	4.63	5.47	5.03	9.70	7.36
G27		0.00	5.84	7.12	9.11	6.02	5.40	8.01	8.23	6.44	4.52	8.91	7.57	2.56	10.38	6.30	8.65	6.24	8.90	7.32	4.69	9.10	6.82	11.54	2.97
G28			0.00	6.76	4.79	1.60	2.60	4.52	4.32	2.21	3.62	5.28	3.17	6.42	5.17	4.94	4.86	5.80	5.23	6.13	5.96	4.92	2.54	7.67	6.44
G29				0.00	6.04	6.88	6.32	4.28	5.58	7.42	7.35	4.53	7.97	5.90	8.99	2.72	4.90	2.84	6.34	5.42	3.11	6.70	6.68	11.38	5.93
G30					0.00	5.17	5.21	3.54	3.41	5.67	6.42	2.89	5.45	9.03	4.46	5.26	3.39	5.70	5.58	7.50	6.47	5.14	4.88	8.92	8.82
G31						0.00	3.49	4.74	4.88	3.53	3.86	5.74	3.95	6.24	6.09	5.32	5.23	6.43	5.67	6.39	6.26	5.69	3.31	8.34	6.74
G32							0.00	5.09	4.00	2.73	2.63	5.14	2.78	6.02	5.28	4.60	5.44	4.79	4.78	5.66	5.26	4.88	2.31	6.97	5.25
G33								0.00	3.18	5.08	6.57	2.49	5.46	7.35	5.84	3.53	2.35	4.15	4.72	5.95	5.45	4.34	4.19	8.92	7.60
G34									0.00	4.13	5.95	2.14	3.58	8.23	4.13	4.05	2.38	4.48	4.06	6.27	6.19	3.20	3.06	7.44	7.91
G35										0.00	4.51	5.47	2.30	7.26	4.57	5.31	5.11	5.82	4.94	6.26	6.73	4.13	2.10	6.54	6.84
G36											0.00	7.01	4.61	5.36	7.15	6.23	7.20	6.09	7.09	7.42	5.47	7.38	4.38	8.80	4.91
G37												0.00	5.32	8.52	4.98	3.64	1.97	4.20	4.02	5.96	5.90	3.59	4.46	8.41	8.17
G38													0.00	8.20	3.75	5.92	5.33	6.44	4.58	6.75	7.57	4.02	1.62	5.34	7.77
G39														0.00	10.88	5.81	8.41	5.73	8.65	6.85	4.04	9.16	7.12	11.97	2.77
G40															0.00	7.27	5.37	7.65	5.15	8.27	9.13	4.09	4.26	5.59	10.17
G41																0.00	3.61	2.78	4.50	3.72	3.74	4.59	4.66	9.36	5.71
G42																	0.00	4.68	4.71	6.21	6.13	3.73	4.48	9.03	8.47
G43																		0.00	5.94	5.73	2.84	5.78	5.29	9.98	5.14
G44																			0.00	3.75	7.43	2.32	3.89	5.74	8.00
G45																				0.00	6.33	5.04	5.68	8.39	6.36
G46																					0.00	7.64	6.44	11.55	3.77
G47																						0.00	3.45	5.84	8.65
G48																							0.00	5.89	6.89
G49																								0.00	11.10
G50																									0.00

Geno= genotype, G1-G50 genotypes list given in Table 1.

Figure 1. Euclidean distances based on 12 agronomic traits and 7 stress tolerance indices of 50 faba bean genotypes evaluated over locations and soil managements in 2017 main cropping season.

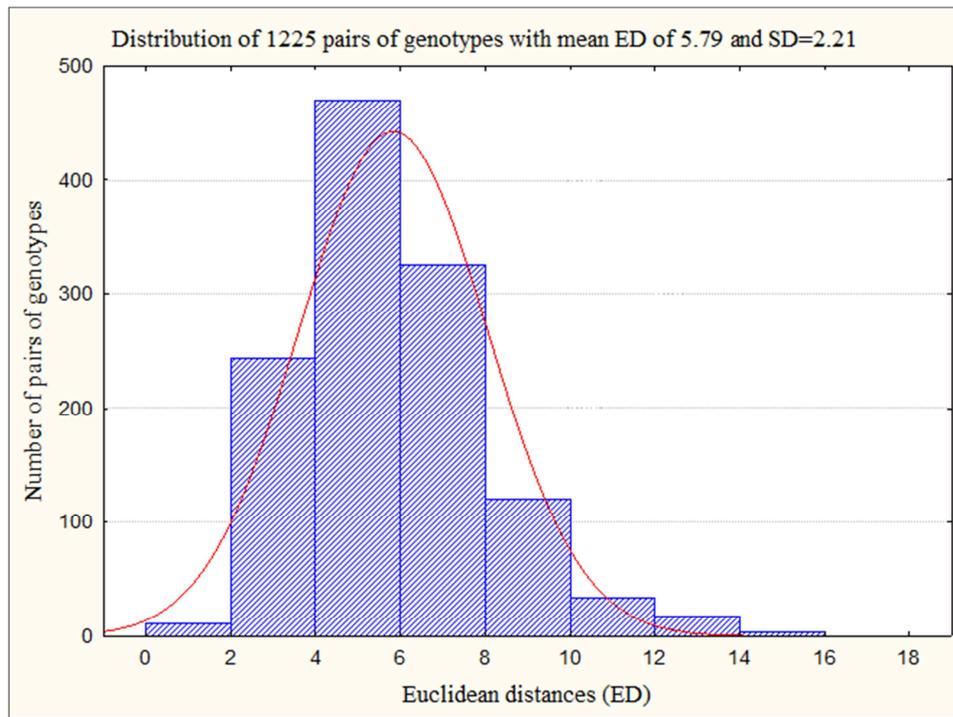


Figure 2. Distribution of 1225 pairs of 50 faba bean genotypes into 8 different categories of Euclidean distances with mean Euclidean distance of 5.79 and standard deviation 2.21 in the central highlands of Ethiopia in 2017.

In this study, the mean genetic distance of each faba bean genotype as compared to other 50 genotypes were calculated to generate information about the most distant and closest genotypes (Table 2). Accordingly, the estimated mean genetic distances of genotypes Wayu (G21), CS20DK (G49), Holetta-2 (G10) and Kasa (G27) were the highest in descending order, while Cool-0030 (G1), EK05001-1 (G17), EH06027-2 (G41)

and EK05006-3 (G13) had the lowest ED in ascending order. A total of 16 faba bean genotypes (32%) had mean genetic distances higher than the overall mean 5.79 while 34 genotypes (68%) including all advanced lines had mean genetic distance below 5.79 (Table 2). The result showed considerable dissimilarities among the genotypes that could be used as parents in the faba bean breeding program in Ethiopia.

Similar findings were also reported among faba bean genotypes by different scholars [14, 15].

Further, the Euclidean distance values were higher among released varieties than advanced lines. This indicated that there is a chance of improving grain yield, and soil acidity stress tolerance traits through selection and hybridization of faba bean genotypes due to a higher distance in released varieties. Genotypes with minimum distance were not genetically diverse. A cross between two distantly related parents results a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F₂ and F₃ generation that leads to greater opportunities for effective selection for yield factors [16].

The result suggested that, maximum genetic recombination is expected from the hybridization of the parents selected

from divergent genotypes. Conversely, crossing of parents selected from similar genotypes could not give higher heterotic value in F₁ and will result in narrow range of variability in the segregating F₂ generation. However, the breeder should specify objectives for best use of the traits where the traits are divergent. This finding is parallel with the reports of Million [14]; Million and Habtamu [15].

Generally, among 1225 pairs of genotypes four ranges of Euclidean distances had the largest number of pairs. The 243 genotype pairs (19.8%), had genetic distances between 2.00 and 3.99; 469 genotype pairs (38.3%) had genetic distances between 4.00 and 5.99; 324 genotype pairs (26.4%) had genetic distance between 6.00 to 7.99 and 124 genotype pairs (10.1%) had genetic distances between 8.00 and 9.99 while the genetic distance between 14.00 to 15.99 had 3 genotype pairs (Figure 2).

Table 2. Minimum, maximum, mean ED, SD and CV of 50 faba bean genotypes in each pair over locations and managements.

Genotype	Min	Max	ED	SD	CV	Genotype	Min	Max	ED	SD	CV
Cool-0030	2.87	9.89	4.52	1.43	31.59	EKLS/CSR02017-3-4	1.63	12.01	5.11	2.12	41.54
Wolki	3.34	12.74	6.42	1.91	29.70	Kasa	1.94	11.54	7.03	2.09	29.74
EKLS/CSR02012-2-3	1.80	12.35	5.09	2.15	42.14	Cool-0025	1.60	10.74	5.09	1.60	31.49
Obse	2.60	14.58	6.28	2.25	35.76	EH06070-3	2.00	11.38	5.75	1.93	33.49
NC58	2.78	9.31	6.33	1.57	24.87	EKLS/CSR02010-4-3	2.11	13.38	5.70	2.19	38.50
Ashebeka	2.43	12.32	5.33	1.95	36.66	Cool-0031	1.60	10.38	5.56	1.50	26.96
Hachalu	2.98	11.74	5.82	1.72	29.58	Cool-0018	2.31	10.38	4.95	1.49	30.15
Degaga	2.47	8.79	5.49	1.51	27.50	EKLS/CSR02028-1-1	1.96	11.91	4.89	1.97	40.30
EH09031-4	2.00	11.28	5.55	2.07	37.33	EK 05037-4	2.14	12.93	4.88	2.00	41.08
Holetta-2	4.00	13.55	8.14	1.92	23.63	Cool-0035	2.10	11.69	5.26	1.75	33.18
EH09007-4	2.53	11.79	6.10	2.07	33.95	KUSE2-27-33	1.96	9.43	6.13	1.68	27.34
EH07023-3	1.55	13.87	5.64	2.40	42.54	EH07015-7	1.80	12.92	5.01	2.24	44.59
EK05006-3	1.92	12.50	4.84	2.05	42.38	Cool-0024	1.62	12.66	5.66	1.94	34.23
EKLS/CSR02014-2-4	2.32	10.95	4.95	1.87	37.79	Selale	2.56	11.97	6.99	2.03	29.03
Numan	3.29	12.96	6.00	1.98	33.03	Moti	3.75	15.26	6.77	2.32	34.24
Bulga 70	1.96	9.32	5.46	1.66	30.32	EH06027-2	2.29	9.98	4.72	1.52	32.26
EK05001-1	2.29	10.67	4.70	1.52	32.32	EKLS/CSR02019-2-4	1.55	12.93	5.04	2.25	44.65
Dosha	2.60	13.28	5.57	2.08	37.29	EH09002-1	2.32	10.27	5.11	1.63	31.82
Gora	1.92	13.12	5.21	2.17	41.68	Tumsa	2.32	12.31	5.70	1.85	32.39
EH08035-1	2.52	11.60	5.78	1.78	30.84	Gebelcho	3.72	9.58	6.27	1.17	18.70
Wayu	5.34	15.60	11.10	2.3	20.73	EK05037-5	2.83	11.55	5.72	1.82	31.89
EKLS/CSR02023-2-1	2.57	11.28	5.49	1.96	35.59	Didi'a	2.32	13.37	5.44	2.21	40.59
Mesay	1.94	10.47	5.99	1.80	30.09	Cool-0034	1.62	11.71	4.91	1.73	35.23
EH09004-2	2.52	11.77	5.49	1.62	29.44	CS20DK	4.47	15.60	8.98	2.17	24.17
EH06088-6	1.63	11.29	4.99	1.96	39.22	Tesfa	5.68	11.10	6.78	1.91	28.22
Overall mean							1.55	15.60	5.79	2.21	33.44

Min= minimum, Max= maximum, ED= Euclidean distance, SD= standard deviation, CV= coefficient of variation in percent.

Table 3. Distribution of 50 faba bean genotypes in to ten clusters using mean of 19 traits of agronomic and stress indices over locations and managements (six environments) in 2017.

Cluster	Number of genotypes	List of genotypes
I	7	Cool-0030 (1), Cool-0025 (28), Cool-0031 (31), Cool-0018 (32), Cool-0035 (35), Cool-0024 (38) and Cool-0034 (48)
II	8	Wolki (2), Ashebeka (6), Tumsa (44), Didi'a (47), Hachalu (7), Obse (4), Dosha (18) and Numan (15)
III	1	Moti (40)
IV	20	EK LS/CSR02012-2-3 (3), EH07015-7 (37), EH07023-3 (12), EK LS/CSR02019-2-4 (42), EK 05037-4 (34), K05006-3 (13), EK LS/CSR02028-1-1 (33), EK LS/CSR02010-4-3 (30), EH09031-4 (9), EH06070-3 (29), EH09002-1 (43), EK LS/CSR02014-2-4 (14), EK05001-1 (17), EH06027-2 (41), EH09007-4 (11), EK LS/CSR02023-2-1 (22), EH06088-6 (25), EK LS/CSR02017-3-4 (26), EK05037-5 (46) and Gora (19)
V	2	EH08035-1 (20) and EH09004-2 (24)
VI	1	Gebelcho (45)
VII	8	NC58 (5), Degaga (8), Bulga 70 (16), KUSE2-27-33 (36), Mesay (23), Kasa (27), Selale (39) and Tesfa (50)
VIII	1	Holetta-2 (10)
IX	1	CS20DK (49)
X	1	Wayu (21)

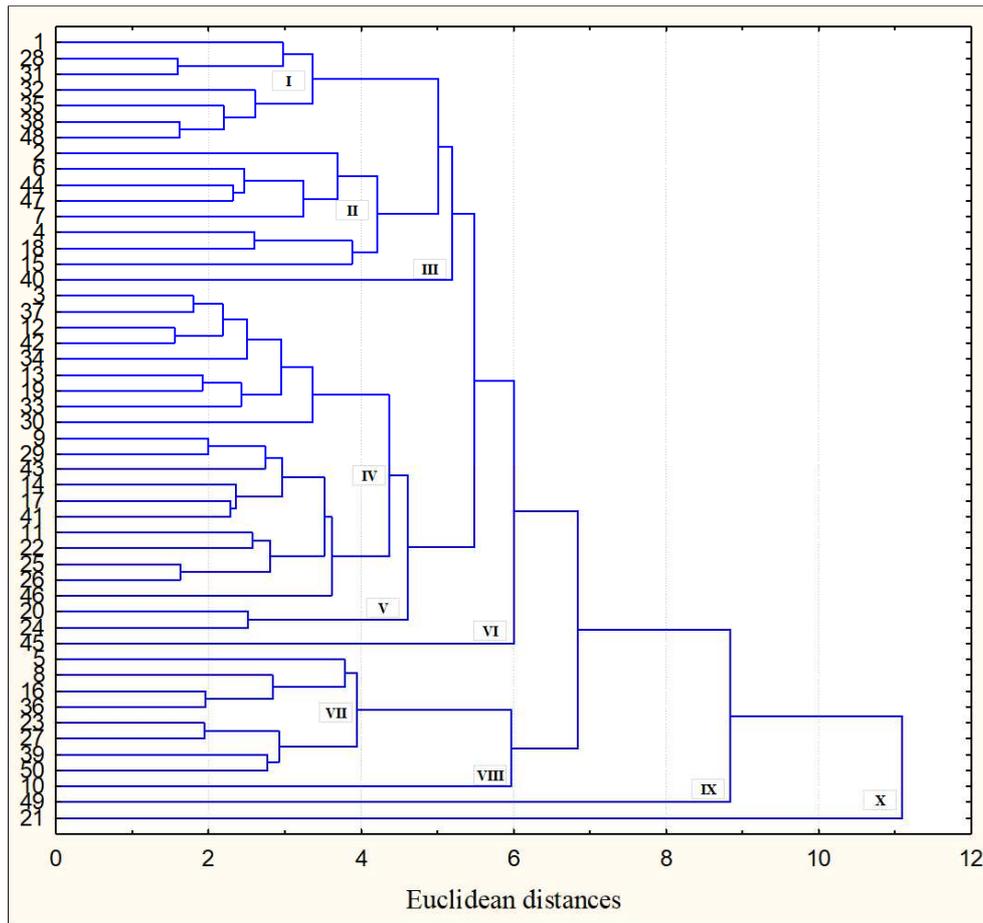


Figure 3. Dendrogram of 50 faba bean genotypes developed by UPGMA clustering method based on Euclidian distance matrix estimated from overall mean of genotypes for 19 traits over locations and managements (six environments).

3.2. Clustering of Genotypes

The Euclidean Distance matrix of the 1225-genotype pairs estimated for grain yield and soil acidity stress tolerance indices were used to construct dendrograms based on the Unweighted paired group method with arithmetic means (UPGMA). Based on ED matrix, the 50 faba bean genotypes were grouped into 10 clusters over locations and management levels using 3.58 as cutting point (mean ED - SD) to determine number of clusters (Figure 3). This implied the presence of wide diversity or variability among the tested genotypes. Likewise, previously different results were reported that 8 released faba bean varieties were grouped into 3 clusters and their differences were largely attributed to the variation on thousand seeds weight (Million, 2012) and also 36 faba bean genotypes were constructed 7 clusters based on 8 yield traits [17]. The disparities in the number of clusters were due to the variation in tested genotypes the number of parameters considered for evaluation.

Cluster I contained seven (14%) genotypes. Cluster IV was the largest cluster (40%) containing twenty genotypes. Clusters II, IV and VII together accounted 72% containing thirty-six genotypes having twenty, eight and eight genotypes each, respectively. Cluster IX and X constituted fourteen genotypes (28%) with six and eight genotypes, respectively.

Cluster III, VI, VIII, IX and X were solitary clusters that had 10% genotypes together. The four larger clusters (I, II, IV and VII) together accounted 86% containing forty-three genotypes (Figure 3; Table 3).

Five genotypes Moti, Gebelcho, Holetta-2, CS20DK and Wayu were clustered as solitary, which implied the performance of these five genotypes significantly, vary as compared to the other genotypes. In harmony with this result previously reported that Moti was clustered as solitary among 8 genotypes [15]. The numerous cluster groups in a small sample of genotypes used in this study reveal as in previous studies that faba bean has a wide genetic diversity [14, 15].

3.3. Cluster Mean Analysis

Cluster I consisted of 7 locally collected genotypes having the characteristic of susceptible to chocolate spot disease followed by cluster VII and moderate to the other traits. Eight released large seeded varieties of which four (Wolki, Hachalu, Ashebeka and Didi'a) released for areas with waterlogging problem made cluster II and this cluster considered the relatively most tolerant to soil acidity problems due to lower relative yield reduction similar to cluster VI next to cluster VIII. This cluster also characterized by tall plant height and high yield index. The rest traits were intermediate to this cluster (Table 4). This result implies that

genotypes released for water logging problem areas were better tolerate soil acidity problems too.

Cluster III consisted of one genotype having the characteristic of tall plant height, grain production efficiency and stress susceptible index. Twenty genotypes were included in cluster. Cluster IV characterized by long grain filling period and larger hundred seeds weight, low number of podding node per plant and pods per plant. Cluster V characterized by high relative yield reduction, late days to 50% flowering and 90% maturity, short plant height, low number of podding node per plant, pods per plant and pods per podding node. Cluster VI had genotype with a characteristic feature of late days to 50% flowering and 90% maturity, resistant to chocolate spot disease, low number of podding node per plant and relative yield reduction. Cluster VII characterized by susceptible to chocolate spot disease, early day to 90% maturity and smaller seed size (Table 4).

Cluster VIII had short plant height, lower grain yield, relative yield reduction and stress susceptible index. Cluster IX had high number of podding node per plant, pods per plant

and pods per podding node, high grain yield, economic growth rate, stress tolerance index, mean productivity, geometric mean productivity and harmonic mean and also characterized by short grain filling period and resistant to chocolate spot. The rest traits were intermediate to this cluster as compared to the other clusters and this cluster was found as best of all the other clusters in all traits performance. Cluster X had late days to 50% flowering and short grain filling period and plant height, less hundred seeds weight, grain yield, grain production efficiency, economic growth rate, yield index, stress tolerance index, mean productivity, geometric mean productivity and harmonic mean (Table 4).

According to the cluster mean analysis, Cluster III and V were constituted the most soil acidity susceptible genotypes due to high relative yield reduction and stress susceptible index whereas cluster VIII was the only cluster that had both lower relative yield reduction and stress susceptible index. Cluster IX was characterized by high performance of all traits in contradict to this, cluster X characterized by low performance of all traits.

Table 4. Mean performance of different clusters for 19 traits of agronomic and stress indices in faba bean genotypes evaluated over locations and managements levels (six environments) in 2017 main cropping season.

S.N	Traits	Cluster									
		I	II	III	IV	V	VI	VII	VIII	IX	X
1	Days to 50% flowering (days)	54.17	55.17	53.39	53.43	51.97	58.11	53.57	53.61	55.61	58.50
2	Days to 90% maturity (days)	145.48	146.56	144.50	146.93	143.28	147.50	143.56	146.33	144.44	145.94
3	Grain filling period (days)	91.31	91.39	91.11	93.50	91.31	89.39	89.98	92.72	88.83	87.44
4	Plant height (cm)	121.23	123.76	123.33	119.56	115.78	121.50	119.22	113.44	118.72	109.89
5	Number of podding node per plant	8.02	7.36	7.89	6.70	6.92	6.78	8.37	7.00	8.67	7.17
6	Number of pods per plant	11.63	10.12	10.50	8.51	8.75	10.06	12.11	9.67	14.33	11.22
7	Number of pods per podding node	1.46	1.37	1.34	1.27	1.26	1.50	1.45	1.37	1.66	1.57
8	Hundred seeds weight (g)	56.20	75.30	72.76	85.51	81.41	76.43	48.84	54.07	51.86	36.03
9	Grain yield (g/5plants)	81.24	85.15	93.92	78.31	79.09	76.07	72.54	58.63	96.40	51.16
10	Chocolate spot disease (%)	36.63	31.25	33.70	30.82	35.28	24.51	36.56	29.81	23.29	35.65
11	Grain production efficiency (g)	138.70	142.97	163.70	139.16	142.26	117.13	123.70	102.64	155.24	76.58
12	Economic growth rate (g/day)	89.35	93.47	103.35	84.01	87.16	85.60	80.89	63.48	109.20	58.85
13	Relative yield reduction	0.35	0.24	0.37	0.33	0.41	0.24	0.31	0.18	0.30	0.35
14	Yield index	0.91	1.05	1.04	0.89	0.84	0.93	0.84	0.76	1.14	0.58
15	Stress tolerance index	1.29	1.46	1.72	1.20	1.23	1.18	1.04	0.71	1.86	0.54
16	Stress susceptible index	1.54	1.03	1.86	1.42	1.78	0.96	1.20	0.48	1.48	0.92
17	Mean productivity (g)	81.23	85.14	93.92	78.31	79.09	76.06	72.54	58.62	96.40	51.15
18	Geometric mean productivity (g)	78.83	83.86	91.22	76.12	76.23	75.23	70.57	58.22	94.73	49.87
19	Harmonic mean (g)	76.56	82.63	88.63	74.05	73.51	74.41	68.77	57.84	93.11	48.64

3.4. Principal Component Analysis

Principal component analysis (PC) was carried out to understand sources of variance among the faba bean genotypes. The 12 agronomic traits and 7 stress indices were grouped into the first four axes. The PCs indicated that the first principal component accounted 45.80% of the total multi-trait standardized variations over locations and managements whereas the second principal component was accounted 25.36%. The first and second PCs together accounted 71.16% of the total variation. The first four PCs accounted 90.27% of the total variation among 50 faba bean genotypes of 19 considered traits over locations and managements (Table 5). This is because their eigenvalues were greater than 1, while factors having eigenvalue less

than one were ignored following Gutten's lower bound principle [13]. Similarly a previous report indicated that the first four PCs explained 83.7% of the total variation in which PC1 explained the most variability (36.1%), PC2 (22.3%) and PC3 (15.4%) [17].

The top important traits responsible for genetic divergence in the major axis (PC1) include hundred seeds weight, grain filling period and yield, number of pods per plant and number of pods per podding node. The number of podding node per plant, days to 90% maturity, grain production efficiency, yield index, stress tolerance index, mean productivity, geometric mean productivity and harmonic mean were also important. The least contributors were relative yield reduction, stress susceptible index and economic growth rate. In PC2, the observed 25.36% variation was caused mainly by

plant height, number of podding node per plant, pods per plant and grain yield (Table 5). In line with this result, it was reported that the variance explained by PC1 was mostly due to traits related to days to 90% maturity and hundred seeds weight whereas PC2 was mostly related to grain yield, plant height and number of pods per plant [17]. Likewise, greater percentage of variation in PC1 accounted by number of pods per plant and PC2 by plant height [4].

The results of the PC indicated that more than two traits with small contribution accounted for each principal component load and the total contribution of the PC to the variation observed among genotypes. All the values under each principal component were in the absolute values due to

the fact that they represent the Eigenvector of PC. It is normally assumed that traits with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero [7]. Accordingly, many traits contributed to the total variation and for differentiation of the genotypes into different clusters was dictated by the cumulative effects of a number of traits. As the more variations explained by the PC1 its scores could effectively represent the genotype effect [17, 18]. In this experiment, the PC ultimately revealed the amount of variability for the traits that could be used for faba bean genotypes improvement.

Table 5. The first four PCs explained for 19 traits of 50 faba bean genotypes evaluated with and without lime application across three locations in 2017 main cropping season.

S.N	Traits	Eigenvectors			
		PC1	PC2	PC3	PC4
1	Days to 50% flowering	-0.17	0.04	0.64	0.33
2	Days to 90% maturity	0.30	-0.04	0.40	0.36
3	Grain filling period (days)	0.39	-0.06	-0.13	0.07
4	Plant height (cm)	0.15	0.40	0.00	0.37
5	Number of podding node per plant	-0.33	0.30	-0.13	-0.01
6	Number of pods per plant	-0.37	0.26	-0.01	0.04
7	Number of pods per podding node	-0.37	0.14	0.19	0.10
8	Hundred seed weight (g)	0.42	-0.04	0.08	-0.07
9	Grain yield (g/5plants)	0.19	0.48	0.04	-0.07
10	Chocolate spot disease (%)	-0.13	0.05	-0.51	0.38
11	Grain production efficiency (g)	0.27	0.40	-0.12	-0.12
12	Economic growth rate (g/day)	0.12	0.50	0.07	-0.10
13	Relative yield reduction	-0.03	-0.07	0.56	0.36
14	Yield index	0.31	0.10	-0.20	-0.09
15	Stress tolerance index	0.33	0.10	-0.01	0.06
16	Stress susceptible index	0.11	-0.07	0.53	0.31
17	Mean productivity (g)	0.33	0.07	0.05	0.05
18	Geometric mean productivity (g)	0.33	0.07	0.00	0.03
19	Harmonic mean (g)	0.33	0.08	-0.04	0.01
	Eigenvalue	8.70	4.82	2.50	1.13
	% variance explained	45.80	25.36	13.16	5.94
	Cumulative% of variance	45.80	71.16	84.32	90.27

PC= principal component.

4. Conclusion

Euclidean distances (ED) of genotypes estimated from 12 agro-morphological traits and 7 stress tolerance indices over locations and soil managements indicated the wide genetic distances among genotypes in the range between 1.55 and 15.60. The maximum segregation of progenies is expected from crosses involving parents selected from genotype G21 × G49, followed by genotype G21 × G40 and G4 × G21 across locations and soil managements. Conversely, crossing of genotypes with low ED such as G12 × G42, G28 × G31 and G38 × G48 could give to lower heterotic value in F₁ and leads to narrow range of variability in the segregating F₂ generation.

The 50 faba bean genotypes were grouped into 10 distinct clusters by UPGMA clustering method based on ED matrix estimated from overall mean of 19 traits. Cluster IV is the largest which constituted by 20 genotypes whereas five

clusters (III, VI, VIII, IX and X) were represented by single genotype. The overall mean trait performances clusters found IX and X as the best and least performing genotypes, respectively. Eight released large seeded varieties of which four (Wolki, Hachalu, Ashebeka and Didi'a) released for areas with waterlogging problem made cluster II and this cluster considered the relatively most tolerant to soil acidity problems due to lower relative yield reduction similar to cluster VI next to cluster VIII.

The first three principal components (PCs) accounted for 84.32% among 50 faba bean genotypes having more than 10% contribution in which PC1 and PC2 constituted 45.80% and 25.36% of the total variation, respectively. The genetic divergence of genotypes in PC1 was mainly contributed by hundred seeds weight, grain filling period, number of pods per plant and number of pods per podding node. Hence, it is difficult to identify one or few traits that had large contribution to each PC because each PC cumulative contribution was the results of small contribution of many

traits. Therefore, for future breeding program that employ hybridization, parental material selection should be carried out considering ED of genotypes and principal components that meets to breeders' interest.

Conflict of Interests

The authors declare that they have no conflict of interests.

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