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Abstract: A field experiment was conducted on fourteen faba bean genotypes at Haro Sabu Agricultural Research Center sub-sites during 2015-2017 main cropping season with the objective to evaluate and select high yielding and stable genotype over test environments that are tolerant to major faba bean diseases. Randomized complete block design with three replications with net plot size of 1.6m x3m was used. Pooled ANOVA declared significant difference among evaluated genotypes for plant height, number of pods per plant, hundreds seed weight and grain yield. All observed agronomic traits excluding days to flowering and days to maturity showed significant differences across the testing environments. On the other hand, genotype by environment interaction had significant effect on number of pods per plant and grain yield. Stability parameters were estimated by employing AMMI stability Value, Genotype selection Index and explained by GGE biplot. The total variation of 45.55%, 6% and 22.51% were contributed by environment, genotypes and genotype by environment interaction for grain yield, respectively. G10 (16.740t/ha) and G12 (16.320t/ha) were identified for their better yield performance with yield advantage of 5.42 and 2.77%, respectively over the best standard check (Shalo=15.88Qt/ha). G10 and G12 had better mean value of thousand seed weight viz. 76.78 gram (G10) and 73.90 gm (G12) over Shalo (62.87 gram). AMMI biplot, ASV, GSI and GGE Biplot further confirmed that G10 and G12 were most stable and widely adapted genotypes. Therefore, the identified genotypes (G10 and G12) were suggested to be released as new varieties for West and Kelem Wollega Zones and areas with similar agro-ecology.

Keywords: Faba bean, Stability, Yield

1. INTRODUCTION

Faba bean (*Vicia faba* L.) is an important pulse crop grown in highlands of Ethiopia, where the soil and weather are considered to be congenial for better growth and development of the crop. The crop shares the largest area under pulses production in Ethiopia [1]. Faba bean is a crop of manifold merits in the economy of the farming communities in the highlands of Ethiopia and serves as income and source of food to farmers, earns foreign exchange to country, and plays a significant role in soil fertility restoration in crop rotation through fixation of atmospheric nitrogen.

The crop is mainly produced in Tigray, Gondar, Gojjam, Wollo, Wollega, Shoa and Gamo-Gofa regions of Ethiopia [5]. Nevertheless, faba bean production in Ethiopia is constrained by stress like water logging, low yielding indigenous cultivars [1] and other stresses like diseases [2]. Correspondingly, the yield potential of faba bean has not been exploited in West and Kelem Wollega Zones of Western Oromia which might be attributed due to low yielding local cultivar usage by farmers and disease stresses prevalence in the locality. In order to uplift the production and productivity of the crop; screening of faba bean genotypes that withstands major production constraints in the area is crucial. Therefore, the study was conducted to identify and develop stable and high yielding varieties that are tolerant to major faba bean diseases in the study areas of West and Kelem Wollega Zones and other areas having similar agro-ecologies

2. MATERIALS AND METHODS

2.1. Description of the Study Area

A field experiment was conducted at Haro Sabu Agricultural Research Center sub-sites (Badesso and Mata) for three (2015-2017) consecutive main cropping seasons and one extra site (Lalo Asabi). The

study sites were recognized with an elevation of 2016 m.a.s.l (Mata) and 2054 m.a.s.l (Badeso) with unimodal rain fall distribution pattern. Besides, these sites had sandy loam type soil textural class with PH of 4.59 and 5.65 and exchangeable acidity of 0.07 and 0.14 dS/m for Mata and Badesso, respectively.

2.2. Testing Genotypes

Fourteen (14) faba bean genotypes including local check and two standard checks (Shallo and Moti) were evaluated for their performance on grain yield and yield related agronomic traits (Table 1).

Code	genotype	Hosting Center
G1	Ek02016-1-4	Holeta Agricultural Research Center
G2	EK02018-1	Holeta Agricultural Research Center
G3	Eh06005-1	Holeta Agricultural Research Center
G4	Ek 01019-7-1	Holeta Agricultural Research Center
G5	Local check	Local
G6	Eh00126-2	Holeta Agricultural Research Center
G7	EKLS01022-1	Holeta Agricultural Research Center
G8	Eh00009-3	Holeta Agricultural Research Center
G9	EKIsr01009-2-2	Holeta Agricultural Research Center
G10	Eh00016-2	Holeta Agricultural Research Center
G11	Moti	Standard Check
G12	Eh06079-7	Holeta Agricultural Research Center
G13	Eh000012-4	Holeta Agricultural Research Center
G14	Shalo	Standard Check

Table1. Designation of genotypes

Key: *G*=*genotype*

2.3. Experimental Design

Randomized Complete Block Design (RCBD) with three replications, having a net plot size of 1.6mx3m each consisting of four harvestable rows was used. Six rows with 40 cm between rows and 10cm between plants were used for the experiment with the seed rate of 135 kg/ha. Inorganic fertilizer DAP was applied at the rate of 100 kg/ha at sowing time. All agronomic practiceswere done as uniformly as required.

2.4. Data Collection

Agronomic data were collected on plot and plant basis. Some of the data taken were number of pods per plant, number of seeds per pod, plant height in centimeter, days to 50% flowering, days to physiological maturity, thousand seed weight, grain yield and major faba bean disease (Chocolate leaf spot)

3. RESULTS AND DISCUSSIONS

3.1. Analysis of Variance

Analysis of variance (ANOVA) was done for grain yield and seven yield related traits. The collected data were organized and analyzed using SAS statistical package [6]. Homogeneity of variance was tested and combined analysis was done using general linear model (Proc GLM) procedure to estimate contribution of genotype, environment and their interaction towards total variation. Mean separation was done using least significant difference (LSD) employing the procedure developed by Gomez and Gomez [4], whereas GGE biplot and AMMI stability analysis was done using GenStat computer software (2012). Combined analysis of variance showed significant (($P \le 0.01$) yield difference among genotypes, environments and their interaction for grain yield (Table 2). The significant interaction effect of genotype × environment showed that the evaluated genotypes responded differently to the variation in environmental conditions. The same finding was reported so far [5].

Table2. Combined Mean square of yield and related agronomic traits of Faba bean genotype

Source of	DF		Mean Square									
Variation		DF	DM	PH	PPP	SPP	HSW	GY				
Geno	13	10.99	6.98	1054.6*	28.28**	0.14	523.58**	35.67**				
Rep	2	39.47	27.12	136.30	6.90	0.13	38.28	49.23				
Env	6	31.99	298.6**	10779**	70.00**	2.32**	1983.26**	262.18**				

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G*E	52	12.22	5.49	302.34	7.16*	0.33	79.60	22.69**
Error		14.13	4.85	390.64	3.80	0.29	117.61	10.02

Key: - DF = days to flowering, DM = days to maturity, PH = plant height, PPP = number of pods per plant, SPP = number of seeds per pod, HSW = hundred seed weight, GY = grain yield

3.2. Mean Performance of Grain Yield And Yield

Plant height ranged from 142cm (G6) to 165.43cm (G9) with over all mean value of 156.35 cm. On the other hand, G10, G11 and G14 had higher number of pods per plant than the rest. Higher mean value of thousand seed weight was recorded from all faba bean genotypes over Shallo which had a mean value of 62.87gram (Table 3). The minimum (10.14 Qt/ha) and maximum (21.08 Qt/ha) mean value of grain yield was obtained at environment 2 and environment 4, respectively with mean value of 14.72 Qt/ha (Table 4). On the other hand, the pooled analysis detected the lowest (12.44 Qt/ha) and highest (16.74 Qt/ha) mean value of grain yield from G8 and G10, respectively with over all mean value of 14.72 Qt/ha. The highest mean of grain yield was exhibited by G10, and followed by G12 and G13. Yield advantage of 5.42 and 2.77% was estimated for G10 and G12, respectively over the best standard check Shalo (Table 3).

Cod	genotype	DF	DM	PH	PPP	SPP	HSW	GY(Qt/h	YAD	DR (Chocolate
e							(gm)	a)	(%)	spot)
G1	Ek02016-1-4	46.95ab	132.52b	148.36de	7.04g	3.09a	75.46ab	13.13ef	-17.32	2.67
G2	EK02018-1	47ab	132.86b	154.43b-e	7.07g	3.12a	75.36ab	14.26c-f	-10.2	2.46
G3	Eh06005-1	47.29ab	133.81ab	148.59de	8.11e-g	3.15a	74.07а-с	14.31c-f	-9.89	2.71
G4	Ek 01019-7-1	47.57ab	132.95b	157.13a-d	8.5c-f	3.12a	78.76ab	14.9а-е	-6.17	2.29
G5	Local check	47.48ab	133.33ab	161.23а-с	9.18b-e	3.14a	68.53с-е	13.71ef	-13.66	2.4
G6	Eh00126-2	47.05ab	132.57b	142.74e	8.32ef	3.08a	72.65b-d	13.5ef	-14.99	2.63
G7	EKLS01022-1	47.24ab	132.81b	159.75a-d	8.7с-е	3.18a	79.42a	14.73b-е	-7.24	2.50
G8	Eh00009-3	45.62b	133.29ab	157.28a-d	7.4fg	3.24a	79.65a	12.44f	-21.66	3.04
G9	EKIsr01009-2-2	47.38ab	133.05ab	165.43ab	8.47d-f	3.33a	76.42ab	14.06d-f	-11.46	2.42
G10	Eh00016-2	48.14a	133.86ab	158.44a-d	10.07ab	3.18a	76.78ab	16.74a	5.42	2.21
G11	Moti	47.05ab	133.62ab	151.2с-е	9.96ab	3.2a	66.53de	15.87a-d	-0.06	2.38
G12	Eh06079-7	45.76b	133.29ab	166.57a	9.6a-d	3.22a	73.91a-c	16.32ab	2.77	1.92
G13	Eh000012-4	47.19ab	133.86ab	159.03a-d	9.67a-c	3.33a	74.01a-c	16.18a-c	1.89	2.25
G14	Shalo	47.43ab	134.38a	158.66a-d	10.44a	3.21a	62.87e	15.88a-d	0	2.58
	Mean	47.08	133.3	156.35	8.75	3.18	73.89	14.72		2.46
	CV	7.99	1.65	12.64172	22.27	17.03	14.63	21.5		26.08
	Lsd	2.29	1.34	12.03	1.19	0.33	6.58	1.93		0.52

Table3. Combined mean performance of grain yield and yield related traits of genotype

Key: Whereas, DF= days to flowering, DM= Days to maturity, PH= Plant height, PP= Pod/plant, SPP= Seed/pod, HSW=Hundred seed weight, YAD (%) = Percent of yield advantage, DR= Disease reaction, CV= Coefficient of variation, Lsd= least significant difference, GXE= Interaction of genotype by environment

The mean grain yield of the tested genotype at the testing sites showed significant variation. From the pooled data, two genotypes, EH00016-2 (16.74Qt/ha) and EH 06079-7 (16.32Qt/ha) gave relatively higher yield than the standard check, Shallo (15.88Qt/ha). Tolessa (2015) reported that the varieties responded differentially in southeastern and central Oromia [9], while (Tadesse and Abay, 2011) noted the same trend on sesame in northern Ethiopia [7].

Table4. Grain yield (Qt/ha) performance of faba bean genotypes over each seven environments

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Code	genotype	1 BD	1MT	2BD	2MT	3MT	3BD	1TA	Comb
G1	Ek02016-1-4	9.27а-с	7.12c	13.26b-d	18.51de	15.7b-d	8.29h	19.8a-c	13.13ef
G2	EK02018-1	14.26ab	9.74a-c	12.1cd	18.34de	14.35cd	11.62fg	19.37a-d	14.26c-f
G3	EH06005-1	14.66a	8.67bc	17.6a-d	19.09с-е	14.19cd	8.97gh	16.97а-е	14.31c-f
G4	Ek 01019-7-1	9.09a-c	10.33a-c	19.11a-c	22.61a-d	13.6de	16.07с-е	13.49e	14.9а-е
G5	Local check	6.38c	13.85a	15.63a-d	18de	13.8cd	13.3ef	15de	13.71ef
G6	Eh00126-2	8.45bc	11.98ab	12.51b-d	19.05с-е	13.23de	11.38f-h	17.91а-е	13.5ef
G7	EKLS01022-1	10.44a-c	9.61a-c	19.42ab	21.84b-d	10.93e	15.28с-е	15.62b-e	14.73b-e
G8	EH00009-3	11.9а-с	8.02bc	10.31d	14.95e	14.29cd	9.33gh	18.31a-d	12.44f
G9	EKIsr01009-2-2	8.76a-c	12.34ab	11.47d	20.45с-е	13.26de	13.94d-f	18.17a-d	14.06d-f
G10	EH00016-2	9.61a-c	12.01ab	20.92a	24.91a-c	17.8ab	16.6b-d	15.33с-е	16.74a

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G11	Moti	12.75ab	8.94bc	11d	27.87a	13de	17.3a-c	20.22a	15.87a-d
G12	EH06079-7	11.74a-c	9.84a-c	14.26a-d	19.5с-е	19a	19.95a	19.95ab	16.32ab
G13	EH000012-4	12.68ab	6.93c	16.07a-d	26.67ab	15.19b-d	19.33ab	16.39a-e	16.18a-c
G14	Shalo	9.96a-c	12.53ab	16.64a-d	23.3a-d	16.54a-c	14.82с-е	17.32а-е	15.88a-d
	Mean	10.71	10.14	15.02	21.08	14.63	14.01	17.42	14.72
	CV	12.60	26.86	29.02	16.57	11.62	13.30	15.62	21.50
	Lsd	6.13	4.57	7.32	5.86	2.85	3.13	4.57	1.93

Key: Whereas 1BD=Badesso 2015, 1MT=Mata 2015, 2BD=Badesso 2016, 2MT=Mata 2016, 3MT=Mata 2017, 3BD=Badesso 2017, 1LA= Lalo Asab 2017, CV= Coefficient of variation, Lsd= least significant difference.

3.3. Additive Main Effect and Multiplicative Interaction Effect (AMMI) Analysis

Combined analysis of variance declared significant variations of genotypes, environments and genotypes by environment interaction for grain yield and this sign posted unstable response of genotypes and fluctuation of grain yield with environmental change which clearly illustrated the presence of genotype by environment interactions.

Source	Df	SS	MS	Explained Variance (%)
Total	293	7872	26.87**	
Treatments	97	5830	60.11**	74.06
Genotypes	13	472	36.31**	6
Environments	6	3586	597.71**	45.55
Block	14	332	23.71**	4.22
Interactions	78	1772	22.72**	
IPCA	18	723	40.18**	40.8
IPCA	16	467	29.18**	26.4
Residuals	44	582	13.23	32.8
Error	182	1710	9.39	

Table5. Analysis of variance from AMMI model for grain yield

From the total variation obtained for grain yield 6%, 45.55% and 22.51% were contributed by genotypes; environment and genotype by environment inter action, respectively (Table 5). IPCA1 and IPCA2 attained 40.8% and 26.4% interaction sum square and contributed a total of 67.2% of total variation (Table 5). According to Kempton (1984) in AMMI model the first two interactions principal component axis was a best predictive model that explains the interaction sum of squares. The finding of the study supported Tamane *et al.* (2015) who reported highly significant ($p \le 0.01$) difference of genotype, environment and their interaction for grain yield in faba bean genotypes evaluated in multilocation of Ethiopia [8].

3.4. AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

In AMMI model, the genotype with least AMMI stability value (ASV) score was considered as the most stable. According to ASV, EKISR01009-2-2, Shalo and EH06079-7 were showed a higher stability (Table 6). As stability per se is not a desirable selection criterion, because the most stable genotypes would not necessarily give the best yield performance, hence, simultaneous consideration of grain yield and ASV in single non-parametric index is needed. Accordingly, EH06079-7 (16.32 Qt/ha) and EH00016-2 (16.74Qt/ha) genotypes were found to be higher yielder genotypes and relatively stable.

Gen	Genotype	Mean	PC1	PC2	ASV	ASV Rank	Yd. Rank	GSI
G1	Ek02016-1-4	13.13	1.2417	0.2811	1.94289	8	13	21
G2	EK02018-1	14.26	1.4251	-0.2220	2.217584	9	9	18
G3	EH06005-1	14.31	0.7322	0.8668	1.42708	5	8	13
G4	Ek 01019-7-1	14.9	-1.552	0.5293	2.461124	13	6	19
G5	Local check	13.71	-0.407	1.3498	1.49024	6	11	17
G6	EH00126-2	13.5	0.5468	0.3888	0.93169	4	12	16
G7	EKLS01022-1	14.73	-1.151	0.3904	1.82429	7	7	14
G8	EH00009-3	12.44	1.7860	0.1113	2.76732	14	14	28
G9	EKIsr01009-2-2	14.06	0.3170	-0.2319	0.54289	1	10	11

Table6. AMMI stability value, genotype selection index, yield rank and principal component axis

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G10	EH00016-2	16.74	-1.460	0.7573	2.38832	11	1	12
G11	Moti	15.87	-0.152	-2.3739	2.38568	10	5	15
G12	EH06079-7	16.32	0.3168	-0.6193	0.79012	3	2	5
G13	EH000012-4	16.18	-1.218	-1.5561	2.44558	12	3	15
G14	Shalo	15.88	-0.420	0.32842	0.72892	2	4	6

3.5. Genotypes and Genotypes by Environment Interaction (GGE) Bi-Plot Analysis

GGE biplot is a pictorial representation which describes the stability of the genotypes and environment based on the IPCA scores. As the vertex cultivar is the highest-yielding cultivar in all environments that share the sector with it, G11 fell in two environments and was high yielding in respective environments for instance. Besides, no environments fell in the sectors with G8 as vertex cultivars showing that the vertex cultivar was not the best in any of the test environments. On the other terms, this indicates that the cultivar was the poorest in some or all of the environments. A cultivar located at the origin would rank the same in all environments and is not at all responsive to the environments.



PC1 - 46.26%



PC1 - 46.26% × Genotype scores
Environment scores
Vectors

Figure1. Scatter biplot 'Which won where'' analysis, where G indicates genotyppes, BD= Badesso, LA= Lalo Asab, MT= Mata

3.6. GGE Bi-Plot Analysis for Comparison of Genotype for Grain Yield Potential and Stability

In GGE biplot, the environments and genotypes obtained in the concentric (central circle) are considered as ideal environments and stable genotypes, respectively (Yan, 2002). Using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal variety. Therefore, ranking based on the genotypes-focused scaling, assumes that stability and mean yield are equally important (Farshadfar *et al.*, 2011). Genotype G13 followed by G10 and G12 were lied relatively near to the center of concentric circles were ideal genotypes in terms of yield and stability (Figure 2). Similarly, Tamane *et al.* (2016) identified the best genotypes which had superior grain yield and yield stability.



Figure2. GGE bi-plot for comparison of genotype and environment for grain yield potential and stability.

4. CONCLUSION

Combined ANOVA detected significant variation among genotypes, environments and their interaction. AMMI biplot, ASV, GSI and GGE Biplot further confirmed that G10 and G12 were most stable and widely adapted, whereas G13 had stable coupled with relative higher yield performance. Therefore, G10 and 12 was selected as the candidate genotypes and suggested for possible release as new variety of faba bean for West and Kellem Wollega zones of western Oromia and areas with similar agro-ecology.

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