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Genotypes×Environment Interaction of Faba bean (*Vicia faba* L.) Genotypes Using AMMI Model in Arsi Zone, Southeastern Ethiopia

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ABSTRACT

The experiment was conducted during 2016 and 2017 main cropping season (August–December) at Kulumsa, Bekoji and Kofele in southeastern Ethiopia to select the most promising faba bean genotypes across different environmental conditions in the southeastern Ethiopia. Thirteen faba bean genotype were evaluated by RCBD using four replications. From the combined mean performance none of the candidate genotypes showed better yield performance than the standard check Gora and Tumsa. The AMMI analysis of variance for grain yield showed a significant difference among environments and genotype by environment ($p \leq 0.05$). Non-significant variation were observed among genotypes. The environmental effect accounted for 50% of the total variation, whereas the genotype by environment and genotype effect accounted about 4 and 6% respectively. Higher mean grain yield was recorded from environment 6 (4,754.6 kg ha^{-1}) followed by environment 2 (4,563 kg ha^{-1}) and 1 (4,236.2 kg ha^{-1}). The first IPCA1 captured about 30.9% of genotype×environmental interactions sum square, while the second IPCA1 explained about 26.4%. The two IPC cumulatively explained 57.3%. G_6, G_8, G_9, G_{11} and G_5 have the lower ASV value and these were the most stable genotypes. Using AMMI bi-plot analysis E_3, E_4 and E_5 are unfavorable environments while E_1, E_2 and E_6 were favorable environments. The results showed the promising genotypes for future release of well adapted faba bean varieties in the growing areas of Ethiopia.

KEYWORDS: Genotypes, AMMI, IPCA, interaction, environment, bi-plot

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1. INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most important pulse crops cultivated in Ethiopia ranging from 1,800–3,000 meters above sea level. Ethiopia is the second most faba bean producer in the world next to China and also the second center of diversity for faba bean (Mussa and Gemechu (2006). Faba bean is a major source of protein and stable food consumed as in different forms by small scale farmers and generates foreign currency to the country.

In Ethiopia, faba bean is mostly produced in the Amhara, Oromia, Tigray and SNNRP regions, and cultivation covers about 0.5 million hectares of land with an annual national production of 1 million tons and its productivity was 2.1 tons hectare^{-1} (Anonymous, 2019). Despite its multipurpose important faba bean production and productivity is very low as compared to other cereal crops. The productivity is unstable across different growing environments and production is highly affected by biotic, abiotic stresses and the scarcity of widely adapted and productive cultivars in the country. These researchers address those constraints by developing stable and wide adaptable varieties for improving faba bean production and productivity. In recent year faba bean breeding in Ethiopia, special focus has been placed on development of varieties with improved grain yield, large seed size and resistance to major diseases (Temesgen et al. (2015).

Genotypes×environment interaction (GEI) is a great challenge for faba bean breeders for variety recommendations because of inconsistence performance of genotypes across different environments and seasons. Tekalign et al. (2017), Takele et al. (2024) and Sheikh et al. (2021) reported highly significant effects of genotype×environment interaction on the yield performances of faba bean. Zewdu et al. (2024) also reported significant genotypic differences for bread wheat, Anand et al., 2024), and Assen et al. (2024) for field pea genotypes. Genotype performance highly depend on their genetic potential, environment and their interaction. Hence, Achenef and Alemu (2021), Temesgen et al. (2015), Mesfin et al. (2020), Gela et al. (2022) and Haile et al. (2022), reported higher effects of environments on yield performances of faba bean.

The additive main effects and multiplicative interaction (AMMI) and genotype main effects are among the most frequently used models for statistical analysis (Gauch and Zoble (1996). The AMMI stability value (ASV) explained based on the first and second interaction principal component axis (IPCA) scores of the AMMI model for each genotypes. Dereje et al. (2019) and Achenef and Alemu (2021) reported that 67.2% and 57.8% of the total sum square of genotype×environment interaction variation were explained by the first two IPCA. A genotype is stable if it possesses a constant performance across diverse environments and its contribution to G×E interaction is small (Becker and Leon, 1988, Fasahat et al., 2015). AMMI stability value (ASV) measures the distance from the genotype coordinate points to the origin in a two dimensional scatter diagram of IPC2 against IPCA1 scores.

Different authors have reported high genotype×environment interaction effects on faba bean genotypes in Ethiopia. Several author also reported similar results on different crops, Tariku, 2018 and Gebeyaw et al. (2024) for cowpea, Delesa et al. (2023), Verma et al. (2024), Dabi et al. (2024) and Assefa et al. (2020) for bread wheat, Dela et al. (2023) for little millet. In view of this the current research was initiated with the objective to estimate the effects of genotype, environment and genotype by environment interaction on yield and yield related traits of faba bean genotypes.

2. MATERIALS AND METHODS

2.1. *Description of experimental area*

The experiment was conducted in two consecutive years of 2016 and 2017 main cropping season (August–December) at three locations Kulumsa, Bekoji and Kofele. The description of the testing environments is presented in Table 1. Those locations are representing from mid-land and highland agro ecologies of the potential Faba bean growing environments

Table 1: Summary of Experimental locations

Env	Year	Location	Geographical position		Altitude	Temperature		Rainfall (mm)
			Latitude	Longitude		Min	Max	
Env$_1$	2016	Kulumsa	08001’10”N	39009’11”E	2200	10.5	22.8	820
Env$_2$	2016	Bekoji	07032’37”N	39015’21”E	2780	7.9	16.6	1020
Env$_3$	2016	Kofele	07004’28”N	38047’11”E	2300	5.8	23.6	1211
Env$_4$	2017	Kulumsa	08001’10”N	39009’11”E	2200	10.5	22.8	820
Env$_5$	2017	Bekoji	07032’37”N	39015’21”E	2780	7.9	16.6	1020
Env$_6$	2017	Kofele	07004’28”N	38047’11”E	2300	5.8	23.6	1211

Env: Environment, Min: minimum, Max: maximum in the central highlands of Ethiopia.

2.2. Experimental materials

A total of thirteen faba bean genotypes was evaluated. Two standard check (Tumsa and Gora) and thirteen advanced lines were used for the experiment. The list of genotypes and their codes were described in Table 2 below.

2.3. Experimental design and procedure

The experiment was conducted using randomized complete block design (RCBD) with four replications. The experimental plot has 4 m length and has 4 rows with 1.6 m width. The spacing between plot and blocks was 0.6 m and 1 m respectively. All faba bean agronomic practices were applied uniformly to all experimental plots. Recommended rate of NPS fertilizer was applied at the time of sowing to each testing locations (25 kg NPS ha^{-1}).

2.4. Data collected

All agronomic data were collected either on whole plot or 5 random sample plant bases. Days to 50% flowering (DF) and days to 90% physiological maturity (DM), Disease (chocolate spot and rust) (1–9 scale). Plant height (PH), number of pods plant^{-1} (PPL) and number of seeds pod^{-1} (SPP) were recorded from the randomly selected 5 plants. Thousand seed weight (TSW) from randomly selected 100 seeds from each plot and then converted in to thousand seed weight. Grain yield was taken from the middle two rows and adjusted to standard grain moisture content of pulses (10%) and then converted into kg ha^{-1}.

Table 2: Lists of genotypes evaluated across 6 growing environments

Sl. No.	Code	G name	Source	Sl. No.	Code	G name	Source
1.	G_1	Gora	Released variety	8.	G_8	EH 06007-4	Breeding line
2.	G_2	EH 010010-1	Breeding line	9.	G_9	EH 09031-4	Breeding line
3.	G_3	EK 05037-4	Breeding line	10.	G_{10}	EH 08031-2	Breeding line
4.	G_4	EH 07023-3	Breeding line	11.	G_{11}	EH 08035-1	Breeding line
5.	G_5	EH 09002-1	Breeding line	12.	G_{12}	EH 08035-3	Breeding line
6.	G_6	EH 09004-2	Breeding line	13.	G_{13}	Tumsa	Released variety
7.	G_7	EH 09007-4	Breeding line				

G: Genotypes

3. RESULTS AND DISCUSSION

The analysis of variance for additive and multiplicative interaction effect on grain yield showed that significant variation among environments and genotypes×environment interactions, while a non-significant variation observed among the genotypes. Gela et al. (2022), Ertiro et al. (2023) and Dereje et al. (2019) reported highly significant genotype×environment interaction effects on faba bean grain yield. The analysis result indicated that there is different performance of genotypes over the testing environments. The effect of environment, genotype and genotype by environment interaction accounted for 35.5%, 23.1% and 33.4% of the total sum of squares respectively (Table 3).

Most of the total sum of squares of the model was contributed from the environment and the genotype×environments interaction. In agreement to this result Takele et al. (2024) and Sheikh et al. (2021) reported the larger contribution of genotype×environment interaction effects in faba bean for the observed grain yield difference. Temesgen et al. (2015) and Teklay et al. (2015) also reported that faba bean grain yield was significantly affected by the environment. Dela et al. (2023) reported a highly significantly affected by the environments on the rice genotypes. The presence of strong genotype×environment interaction indicated that

Table 3: AMMI analysis table

Sl. No.	Source	DF	SS	MS	Proportions
1.	ENV	5	1.38E+08	27621627.2**	35.5
2.	REP (ENV)	18	49284613	2738034.1**	17.2
3.	GEN	12	9001500	750125^{ns}	23.1
4.	GEN: ENV	60	42145101	702418.4*	33.4
5.	PC1	16	13009945	813121.5^{ns}	30.9
6.	PC2	14	11137860	795561.5^{ns}	26.4
7.	PC3	12	10041855	836821.3^{ns}	23.8
8.	Residuals	216	1.08E+08	500499.6^{ns}	
9.	Total	371	3.89E+08	1047957.9	

DF: Degree of freedom, SS: Sum of squares, MS: Mean squares, ENV: Environment, REP replication, GEN: genotypes, PC: Principal components, ** and * significant difference at (p=0.01) and (p=0.05) higher differences or unstable performance of faba bean genotype across different testing environments. In the presence of significant genotype×environmental interactions were observed, it is difficult to identify high grain yield genotypes by simple consideration of their mean grain yield performances across locations.

The significant genotype by environment interaction was decomposed in to the interaction principal component analysis (Gollob, 1968). The IPCA value closer to the center (origin), the more stable genotypes across testing environments (Purchase, 1997). The first principal component analysis explained about 30.6%, while the second interaction principal component additionally explained about 26.4%. The two principal component analysis explained about 81.1% of genotype by environment interactions. Dereje et al. (2019), Achenef and Alemu (2021) reported about 57% and 57.8% of the first two IPCA of the genotype by environment interaction of faba bean genotypes.

The combined mean performance of grain yield across environments showed that higher mean grain yield was recorded from environment 6 (4,754.6 kg ha^{-1}) followed by environment 2 (4,563 kg ha^{-1}) and 1 (4,236.2 kg ha^{-1}), while the smallest mean grain yield was obtained from environment 4 (2,958.6 kg ha^{-1}) (Table 4). This result showed the existence of great variation among testing environments the difference may be due to variation in rain fall, soil type, temperature e.t.c. From the candidate's genotypes, no any single genotypes perform better yield performance than the two standard checks Gora (4,029.8 kg ha^{-1}) and Tumsa (4,247.2 kg ha^{-1}) (Table 4).

Table 4: Mean performances of thirteen Faba bean genotypes evaluated across six testing environments

Genotypes	Env1	Env2	Env3	Env4	Env5	Env6	Mean
G_1	4348	4328	4036	3417	3579	4473	4030
G_2	3370	3846	4377	2515	3583	5004	3782
G_3	3615	4969	4010	2599	2979	3907	3680
G_4	3824	4278	3364	2530	3273	4235	3584
G_5	4710	4271	3912	2714	3339	4508	3909
G_6	4289	4295	3954	3377	3003	4365	3880
G_7	4172	4772	3766	3057	3660	4852	4047
G_8	4555	5315	3093	3130	3444	4458	3999
G_9	4516	4687	4032	2733	2117	5179	3877
G_{10}	3623	4687	3675	2999	3289	5136	3902
G_{11}	4769	4804	3522	2900	3146	5513	4109
G_{12}	4551	4321	3528	2864	3272	5404	3990
G_{13}	4731	4748	4655	3629	2944	4777	4247
Mean	4236	4563	3840	2959	3202	4755	3926

G: Genotypes; Env: Environment

AMMI stability value statistics (ASV) is developed to quantify and rank the genotypes on the basis of their yield stability. Lower ASV value indicates the more stable genotypes whereas genotypes with high ASV value are more unstable (Purchase et al., 2000). According to this definition G_6, G_8, G_9, G_{11}, G_5 were the most stable genotypes, while G_{12}, G_3, G_4, G_7, G_5 were the most unstable genotypes (Table 5).

Table 5: Mean grain yield (kg ha^{-1}), AMMI stability value (ASV) and Interaction principal component axis one IPCA1

Genotype code	ASV	YSI	IPCA1	rASV	rYSI	Mean
G_{13}	11.90	11	-1.3	7	4	4247
G_{11}	6.48	12	-17.25	4	8	4109
G_7	21.47	12	4.1	10	2	4047
G_1	15.06	14	8.98	8	6	4030
G_8	3.76	3	-13.06	2	1	3999
G_{12}	35.02	24	-8.95	13	11	3990
G_5	17.32	21	-0.81	9	12	3909
G_{10}	9.73	19	4.7	6	13	3902
G_6	1.07	8	2.18	1	7	3880
G_9	3.95	12	-18.73	3	9	3877
G_2	7.26	8	25.84	5	3	3782
G_3	28.21	17	9.12	12	5	3680
G_4	27.52	21	5.2	11	10	3584

By considering IPCA1 scores alone and regardless of the positive or negative signs, genotypes with large scores have high interactions (unstable), whereas varieties with small IPCA1 scores close to zero have small interactions and are stable (Zobel et al., 1988). Accordingly, G_5, G_{13}, G_6, G_7, G_4 scored the least positive and negative IPCA1 value as compared to the other genotypes, implies that the more stable genotypes across the testing environments (Table 5).

Environment 4 scored the least positive IPCA1 values with the least average mean grain yield indicating their minimum contribution to the genotype by environment interactions. While environment 1, environment 3 and environment 2 scored maximum positive and negative IPCA1 values (Table 6). Three environments namely E_6, E_2 and E_1 recorded greater grain yield than the average mean grain yield of overall six environments (Figure 1), it indicates that these environments is the best potential faba bean growing season and locations as compared to the rest environments.

Table 6: Environment mean grain yield, IPCAe1, IPCAe2 and IPCAe3 scores

Environment	Mean	IPCAe1	IPCAe2	IPCAe3
Env1	4236	-24.39	-1.937	6.864
Env2	4563	-11.65	-20	0.084
Env3	3840	21.01	14.6	23.65
Env4	2959	1.396	-8.179	10.75
Env5	3202	23.2	-13.03	-22.57
Env6	4755	-9.569	28.55	-18.79

IPCA1 and IPCA2: Interaction principal component axis one and two, Env: Environment

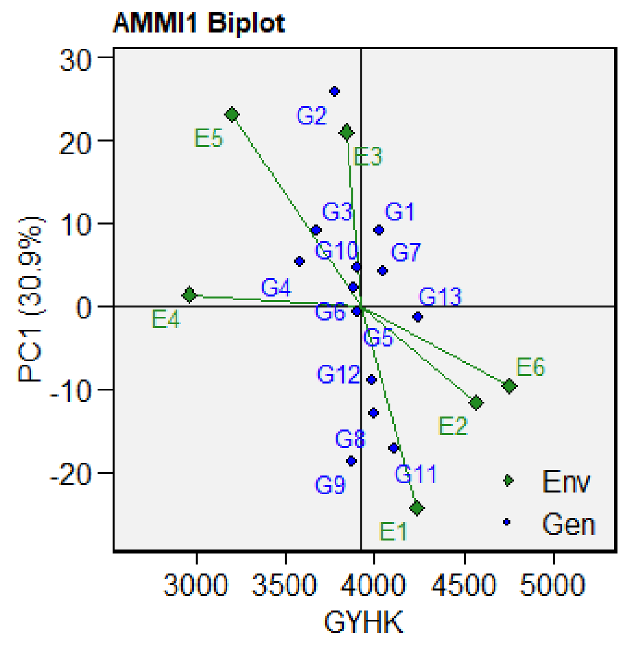

Figure 1: Mean grain yield of faba bean genotypes plotted against with IPCA1 score across six environments

3.1. *AMMI1 biplot*

From the AMMI1 bi-plot figure, the six genotypes namely G_7, G_1, G_{13}, G_{12}, G_8, and G_{11} were recorded as relatively higher grain yield than the other faba bean genotypes which are located on the right side of the grand mean (Figure 1). While the other remaining seven genotypes were located on the left side of the grand mean and scored the lowest grain yield. The testing environment showed a great variation on the performance of genotypes. Accordingly, E_3, E_4 and E_5 were categorized as unfavorable conditions for faba bean production, while E_1, E_2 and E_6 were categorized as high yielding potential environment (Figure 1).

3.2. *AMMI 2 biplot*

The AMMI analysis for the first IPCA1 explained about 30.9% and the second IPCA2 explained about 26.4% of the total sum square of genotype by environment interaction and the two IPCAs cumulatively captured about 57.3% of faba bean genotypes environmental interaction. 67.2% and 57.8% of the total sum square of genotype × environment interaction were explained by the first two IPCA (Dereje et al., (2019) and Achenef and Alemu (2021)). In the IPCA1 and IPCA2 interactions, the closer the genotypes score to the center of the biplot, the more stable is the genotype and the reverse is true (Purchase, 1997). Environment E_2, E_1, E_5, E_3 and E_6 were the most discriminating environment by its long distance from the origin of the axis.

Genotype environment projection on the polygon reflects for the identification of best genotypes with respect to the environments. According to this assumption, G_2 and G_3 were identified as the highest yielding genotypes, while G_8 and G_9 were identified as the lowest yielding genotypes across the testing genotypes (Figure 2). G_2 was the highest mean grain yield genotypes at environment 3. Similarly, G_3 was the best yielder genotypes at environment 4 and environment 5.

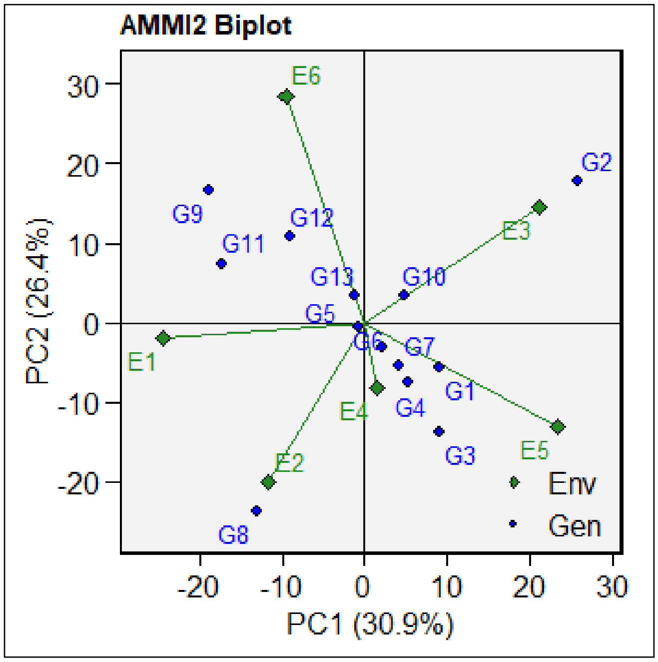

Figure 2: Polygon view of genotype by environment interaction for faba bean genotype

Genotypes within the polygon and nearest to the origin of the axes have wider adaptation to the environment and less response for the environmental variation (Yan and Tinker (2006) and Hugh et al. (2008). The distance from the center of the bi-plot is indicative of the amount of interactions that exhibited by the genotype over environments (Asfaw et al., 2009). Genotypes which located near to the origin of the bi-plot were less responsive to the environmental changes (Voltas et al., 1999). G_5, G_6, G_7, G_{10} were demonstrated low interactions or stable over the environments. This indicated that these genotypes demonstrated lower environmental response to the change in the growing environments. G_2, G_3, G8 and G_9 were unstable genotypes because they were located far apart from the origin of the biplot as compared to the other genotypes.

4. CONCLUSION

The highly significant GEI interaction was observed between environments and genotype×environment interaction. The presence of strong GEI indicated unstable performance of genotype across testing environments. The first IPCA1 and IPCA2 explained about 30.9% and 26.4% of the total sum square of genotype by environment interaction respectively. Four genotypes (G_5, G_6, G_7, and G_{10}) responded lower environmental response to the changes in the growing environment, while G_7, G_1, G_{13}, G_{12}, G_8, and G_{11} were relatively higher yielder genotypes.

6. ACKNOWLEDGEMENT

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