Stability Analysis of Faba bean (*Vicia faba* L.) Yield trials by AMMI Model Across seven Environments in Ethiopia

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Abstract: **Twelve faba bean genotypes were evaluated in 2018/2019 cropping season across seven environments in Ethiopia using randomized complete block design with four replications. The objectives were identifying stable faba bean genotypes for seed yield across the target environments using Additive Main effects and Multiplication (AMMI) model. Highly significant difference (P<0.01) among genotype, environment and genotype by environment interaction were observed for seed yield. The AMMI analysis of variance for seed yield indicated that environment accounted 88.4% followed by G x E interaction 2.7% and genotype accounted 1.1% of the total treatment variation. This indicated that the large effects that influence the faba bean production are accounted by environment. The significance of mean square of environment indicated the test environments are very diverse and causing most of the variations in seed yield. The genotype by environment interactions was decomposed into IPCA. The first and the second interaction principal component axis explained 34.0% and 23.8% of the total G x E interaction and the two IPCAs together explained 57.8 % of the total treatment variation. Genotypes or environments found on the right side of the midpoint of the axis in AMMI-1 biplot have higher yields than those on the left hand side. Accordingly, G7, G9 and G10 had lower yield than those genotypes found on the right side of the axis. The genotypes or environments has small interactions appears close to the center of the axis; genotypes G6, G8, and G2, revealed small interaction and they were considered as relatively stable genotypes. Conversely, G11, G3, G9 and G1 are relatively far apart from the origin and thus showed strong interaction effects. Based on the ASV the genotype G6, G2, and G12 (Tumsa) and G8 had the lowest AVS score thus, which were widely adapted across environments. However, the genotypes such as the standard check G1 (Gora), G3, G5 and G11, which had the highest ASVs, were unstable genotypes over the testing environments. AMMI model selected best genotypes that suit for a specific environment. Accordingly, G11, G8, G4 and G3 were selected as best for Assasa; G11, G3, G8 and G12 for Kulumsa; G12, G5, G1 and G8 for Bekoji; G12, G3, G8 and G5 for Adet and G12, G1, G4 and G5 for Debark.**

Keywords: **AMMI, ASV, Environment, Genotypes.**

1. INTRODUCTION

Stability usually refers to a genotype's ability to perform consistently whether at high or low yield levels across a wide range of environments (Tewodros and Zelalem, 2017). In plant breeding program yield stability is an important feature to measure consistence relative performance of genotypes across a wide range of environments. The relative performances of genotypes for quantitative traits i.e. yield and other characters were influence from one environment to another (Fasahat P. *et al.,* 2015). Multi-environment trials (MET) also helps to identify locations that best represent the target environments (Yan *et al.,* 2000 and Gurmu *et al.,* 2012). Moreover, to select a cultivar with high yielding ability and stability, high attention should be given to the importance of stability in performance for genotypes under different environments and their interaction (Ghazy *et al.,* 2012).

Yield is a complex quantitative character and is greatly influenced by environmental variation therefore, selections based on yield *per se* at a single location in a year may not be effective (Eyeberu Abere, 2017). Yield trial, typically testing a number of varieties in a number of environments, is one of the most common activities in agricultural research evaluating of genotypes across different range of environments and years helps to select either consistently yielding genotypes across environment and year (wide adaptation) or specifically best performing cultivars at few environments (specific adaptation).

Statistical analysis of yield trials can help agronomists, breeders, and other agricultural researchers to make faster progress (Gauch, 2006). Hence stability analysis provides a general summary of the response patterns of genotypes to change environments or the interaction of genotypes with locations and other agro-ecological conditions that help in getting information on adaptability and stability of performance of genotypes (Abuali *et al.,* 2014).

The stability of genotype performance can be evaluated using numerous statistical methods therefore; AMMI model important to visual comparison and identification of superior genotypes for supporting decision on variety selection and recommendation in different environments. The AMMI model first applies the additive analysis of variance (ANOVA) model to two-way data, and then applies the multiplicative principal components analysis (PCA) model to the residual from the additive model that is to the interaction (Gauch, 2013).

2. MATERIALS AND METHODS

Descriptions of Experimental Area and planting Materials

The experiment was conducted at seven different locations from June to December, 2018 in the main cropping season under rain fed condition. These locations represent the varying agro ecologies of the major central faba bean growing areas of Ethiopia. The description of the test locations in terms of geographical position, altitude and climatic conditions and soil properties is given in Table1.

Table 1: Summary of Experimental Locations

| Locations | Geographical position | | Altitude | Average | Temperature | | agro- | Soil |
	Latitude	Longitude	m.a.s.l	Rainfall	Min.	Max.	ecology	type
Asassa	07°06′12″N	39°11′32E	2300	620	5.8	23.6	THMH	Clay
Kulumsa	08°01′00″N	39°09′32E	2200	820	10.5	22.8	TSMMH	Clay
Bekoji	07°31′22″N	39°14′46E	2780	1010	7.9	16.6	CHMH	Clay
Holeta	09°04′12″N	38°29′45E	2400	1044	6.05	22.4	TMMH	Nitosol
Kofele	07°04′27″N	38°46′45E	2660	1211	7.1	18.0	CHMH	Nitosol
Debark	130 7' N	37053'E	2900	1044	8.6	19.8	CHMH	Nitosol
Adet	110 16' N	372 29'E	2240	1119.1	11.8	25.8	THMH	Nitosol

THMH: Tepid Humid Mid-Highland; TSMMH: Tepid Sub Moist Mid-Highland; CHMH: Cool Humid Mid-Highland; TMMH: Tepid Moist Mid-Highland.

A total of twelve faba bean genotypes that comprise ten advanced breeding lines and two recently released varieties (standard checks) were used for field experiment. The list of genotypes, pedigree information and their code were described in Table 2

Table 2: Descriptions of Experimental Materials

Codes	Genotype	Pedigree
G1	Gora (standard check)	EH91020-8-2 X BPL44-1
G2	EH 010002-1-1	EH00126-1 X ILB938
G3	EH 010008-5	EKLS/CSR02017-1-4 X ILB938
G4	EH 010051-1	EKLS/CSR02018-1-1 X ATOM

G5	EH 010058-1	EKCSR/01004-2-1 X ATOM
G6	EH 010058-2	EKCSR/01004-2-1 X ATOM
G7	EH 09012-1	EH95132-1 X ILB938
G8	EH 09017-5	EH00014-1 X ILB4726
G9	EH 09021-1	EH01012-1 X ILB4726
G10	EH 09028-3	Wolki X ILB4726
G11	EH 09046-3	Wolki X ILB1563
G12	Tumsa (standard check)	Tesfa X ILB4726

Experimental Procedure and Data collected

The experiment was laid using a randomized complete block design (RCBD) with four replications. For each experimental unit a plot size of 4m by 1.6m (6.4m^2) was used with inter row spacing of 40cm and between plant spacing of 10cm.The spacing of 0.6m and 1.5 m was used between each experimental units and replications, respectively. All the agronomic practices were applied uniformly to the experimental units according to the recommendation. Fertilizer was applied to each plot at the rate of 121 kg NPS ha^{-1} at planting. The yield data was recorded on the two middle rows of each experimental unit (net plot size 3.2m^2).

Grain Yield (g): yield was measured from the harvestable plot area (two central rows) and adjusted to 10% moisture level using the following formula;

$$\text{Adjusted grain yield } (\frac{g}{plot}) = \frac{(100 - MC) \text{ x unadjusted grain yield}}{100 - standard \; mositure \; (10)}$$

3. DATA ANALYSIS

Additive Main effect and Multiplicative Interaction (AMMI) model

The AMMI analysis was performed using the following model suggested by Crossa *et al*., (1990).

:$\qquad Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{n} \lambda_n \alpha_{in} \, y_{jn} + e_{ijk}$

Where, Y_{ij} is the yield of the ith genotype in the jth environment, μ is the grand mean, G_i is the mean of the ith genotype minus the grand mean, E_j is the mean of the jth environment minus the grand mean, λ_n is the square root of the Eigen value of the principal component analysis (PCA) axis α_{in} and y_{jn} are the principal component scores for PCA axis n of the ith genotype and j^{th} environment and e_{ijk} is the error term.

To estimate the unknown model parameters usually first uses row/column means for the main effects and then performs a singular value decomposition of the residual matrix for the interaction parameters. This classical approach corresponds essentially to a least square fit of the full model. That is, estimates of the overall mean (μ) and the main effects (G$_i$ and E$_j$) are obtained in the context of a simple two-way ANOVA of the array of means Y$_{(gxe)}$. The residuals from this array then constitute the array of interactions $Z_{gxe} = z_{ij}$, Where, z$_{ij}$ = y$_{ij}$ − y$_{i.}$ − y$_{.j}$ + y$_{..}$ and the multiplicative interaction terms are estimated from the singular value decomposition (SVD) of this array. Thus, λk is estimated by the kth singular value of Z, αik is estimated by ith element of the left singular vector αk (g x1) and γ jk is estimated by jth element of the right singular vector γ k' (1x k) associated with λk (Zelalem Tazu, 2011).

4. RESULTS AND DISCUSSION

The grain yield data were subjected to AMMI analysis of variance by combining ANOVA with additive main effects and multiplicative effects into single model for 12 faba bean genotypes over seven locations (Table 3). The results showed that highly significant difference (p<0.01) for genotypes, environments and genotype and environment interactions. According to the AMMI ANOVA result environment, genotype and interaction contributed 88.4 %, 1.1 % and 2.7% from the total treatment variations, respectively. From the treatment component environment contributed the largest source of variation this finding is similar with Agegnehu Mekonen (2017) report on bread wheat, who found large portion of variations was accounted by environment followed by interaction.

The significance of MS of environment indicated the test environments are very diverse and causing most of the variations in seed yield. The genotype by environment interactions was decomposed into IPCA. The first and the second interaction principal component axis explained 34.0% and 23.8% of the total G x E interaction (Table 3). The two IPCAs explained about the 57.8 % of the total genotype x environment interaction sum of square. AMMI Stability Value (ASV), IPCA1 and IPCA2 scores for each genotype were also computed and presented in Table 4

Table 3: AMMI analysis of Variance for mean grain yield across seven environments

Source	DF	SS	MS	Explained (%)
Total	335	555808844	1659131	
Treatments	83	512481097	6174471**	92.2
Genotypes	11	6319688	574517**	1.1
Env.t	6	491153462	81858910**	88.4
Rep/Env.t	21	8672059	412955	1.6
Interactions	66	15007947	227393*	2.7
IPCA 1	16	5100778	318799**	34
IPCA 2	14	3568960	254926*	23.8
IPCA 3	12	2644506	220375^{ns}	17.6
Residuals	36	6338210	176061	1.14
Error	231	34655688	150025	6.2

DF = degree of freedom, SS = sum square, MS = mean square, ** and * significant difference at 1% and 5%

AMMI Stability Value

ASV is the distance from the coordinate point to the origin in a two-dimensional scatter diagram of IPCA1 scores against IPCA2 scores. The larger the IPCA scores, either positive or negative the more specifically adapted genotype to a certain environments, whereas, the smaller the IPCA scores, the more stable the genotype in all environments. Therefore, based on ASV the genotype G6, G2, G12 (Tumsa) and G8 had the lowest AVS score thus, which were widely adapted across environments. However, the genotypes such as the standard check G1 (Gora), G3, G5 and G11, which had the highest ASVs, were unstable genotypes over the testing environments (Table 2). According to AMMI analysis the genotype and environmental scores of AMMI-2 (interaction IPCA one and IPCA two) are presented in (Table 3 and 4), respectively. The IPCA score indicated the stability or general adaptability of genotype/s across environments. The larger the IPCA score, either positive or negative, as its order of importance, the more specifically adapted a genotype to certain environments.

Table 4: Mean grain yield (GY) (kg ha^{-1}), AMMI stability value (ASV) and genotypic IPCA1 and IPCA 2 score for tested genotypes

Genotypes	GY	Rank	IPCAg[1]	IPCAg[2]	ASV	Rank
G1	2986	7	17.0	1.5	24.3	11
G2	2960	8	1.9	-4.8	5.5	3
G3	3081	3	-8.3	14.1	18.4	9
G4	3053	5	-0.4	-11.3	11.3	6
G5	3030	6	12.2	7.2	18.8	10
G6	3081	3	-2.0	1.2	3.1	1
G7	2644	12	4.8	7.4	10.1	5
G8	3125	2	-2.6	3.3	4.5	2
G9	2866	10	-0.9	-16.0	16.1	8
G10	2895	9	-4.0	-12.8	14	7
G11	3078	4	-23.2	4.8	33.5	12
G12	3172	1	5.5	5.4	9.6	4

Where, IPCAg1 and IPCAg2 = Interaction principal component axis one and two for each genotype

The closer the IPCA scores near zero, the more stable or adapted genotype in overall test environments. Similarly environment scores from AMMI analysis regarding to interaction also interpreted as environments with large IPCA scores are more discriminating of genotypes, while environments with low IPCA scores or near to zero revealed small interaction across genotypes and low discrimination power among genotypes (Gauch and Zoble, 1996). The combination of environment and genotype IPCA scores of the same signs indicated positive specific interaction effect, whereas, combination of opposite signs have negative specific interactions. Accordingly, G1, G2, G5, G7 and G8 with E3 (Bekoji), E5 (Adet) has positive specific interaction effect with E7 (Holetta) whereas, genotypes G1, G2, G5, G7 and G8 have negative specific interaction effect with E1 (Assasa). Environment/s which has same signs of interaction IPCA scores discriminate genotypes similarly and environments having opposite sign of interaction discriminating genotypes differently for example Assasa and Bekoji or Kulumsa and Kofele these are main contributors for rank change of genotypes performance Table 5.

As shown in Table 3 environments were variable for both interaction and main effects. Among the testing environments, Assasa (E1) recorded the largest negative IPCA-1 scores and ranked second in environmental average mean grain yield (3820 kg/ha) relative to the rest of the environments. Following Assasa; Bekoji (E3) had largest positive IPCA-1 scores with above average mean grain yield. These two environments were highly interactive environments, which contributed the largest interaction effects.

Table 5: Environment mean grain yield, IPCAe1 and IPCAe2 score

Environments	Environment mean	IPCAe[1]	IPCAe[2]
Assasa	3820	-19.6	-7.4
Kulumsa	3245	-17.5	12.2
Bekoji	3730	17.7	11.7
Kofele	3177	5.2	-22.0
Adet	950	3.8	7.1
Debark	1493	9.0	-6.5
Holetta	4569	1.4	4.9

Where, IPCAe1 and IPCAe2 = interaction principal component axis one and two for each environment

On the other hand Holetta (E7), Kofele (E4) and Adet (E5) scored the least positive IPCA-1 score associated with highest average mean grain yield except Adet indicating their minimal contribution to the GEI and less discriminating power of the genotypes. The other environments were found in between of the highest and the lowest interactive environments. The tested genotypes relatively explained their genetic potential at five environments namely; Kofele (E4), Bekoji (E3), Assasa (E1), Kulumsa (E2) and Holetta (E7), providing above average grain yield. These environments are classified as high yielding (high potential) environments, whereas, Adet (E5) and Debark (E6) recorded below average grain yield, and hence clustered under low yielding (poor) environments (Table 5).

According to AMMI-2 biplot graph the first two axis accounted 57.78% of the interaction SS (fig.1). Since the interaction component of the AMMI model is based on the product of interaction PCA scores, the genotypes or environments has small interactions appears close to the center of the axes. Therefore, from the present study genotypes G6, G8, and G2, revealed small interaction and they were considered as relatively stable genotypes. Conversely, genotypes such as G11, G3, G9 and G1 are relatively far apart from the origin and thus showed strong interaction effects (fig.1). A high absolute IPCA1 score of the genotype far from the origin shows variable performance of the genotype across the environment and reflects instability across environments. In this study the genotype G11 and G3 specifically adapted to E2 and E1 Genotypes G11, G3, G8, and G12 and environments E1, E2 and E7 on fig.1 have large magnitude of IPCA1 score that showed high interaction. There are no genotypes suitable or adaptable for E5 and E6 fig.1 among the tested genotypes this indicates the environments were not favorable for the evaluated genotypes.
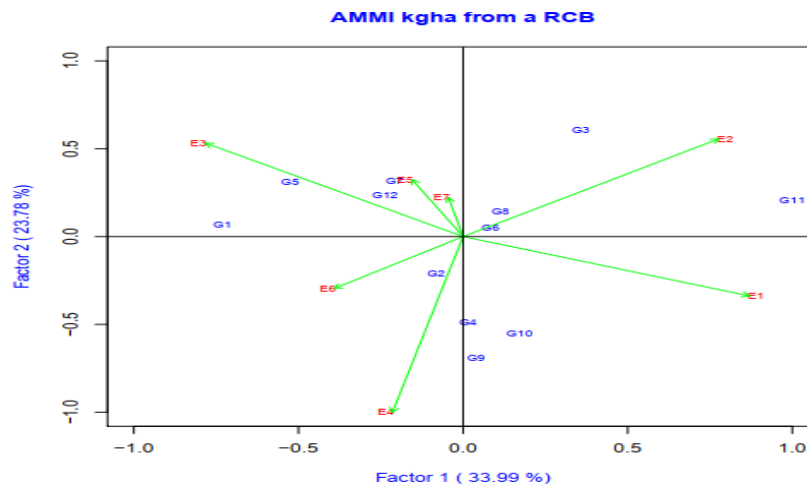
Figure 1: AMMI-2 biplot for grain yield (kg/ha) showing the interaction of IPCA2 against IPCA1 score of 12 faba bean genotypes (G) grown at seven environments (E)

The AMMI-1 biplot fig.2 is the most known and important component of AMMI analysis. The ordinate (y- axis) represent PCA1and abscissa (x-axis) represent the main effect (genotype and environment) scores. Therefore, it provides opportunity to visualize the mean performance of genotype and environment as well as stability using IPCA1 simultaneously. The IPCA1 score for 12 genotypes and seven environments were plotted against the mean yield of genotypes and environments fig. 2. Genotypes or environments on the right side of the midpoint of the axis have higher yields than those on the left hand side. Therefore, all genotypes found on the right side of the midpoint of the x-axis except G7, G9 and G10 are relatively better yielding genotypes (fig.2).

According to AMMI-1 biplot genotype G12 generally exhibited highest mean grain yield with highest additive main effect and plotted with E4 (Kofele), E3 (Bekoji) and E7 (Holetta). But G12 is specifically adapted to E4 and E3. Genotypes (G7) categorized under low yielding genotypes, which is shown at the lower left quadrant of the biplot. Generally G11 was the most unstable genotype identified by the AMMI model (fig. 2). Genotypes and environments close to each other or the same parallel line indicated having similar performance for given trait relative to coordinate. Hence, genotypes G1 and G5 were relatively adapted to environments E3; G12 best at E4. G2, G6, G8 and G10 more adapted to E4 and E7. Genotype G11 was more adapted to at environments E1 and E2 (fig. 2).
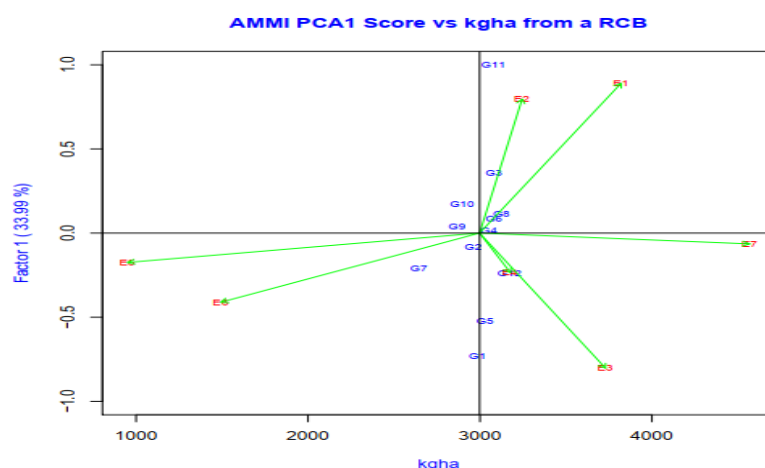

Figure 2: Mean grain yield of faba bean genotypes plotted against with IPCA1score across seven environments.

Best Genotype Selection using AMMI model

In the variety development processes, Multi-environment yield trial is crucial to select the best genotypes either for specific environment or general adaptable before recommending varieties for future production. In the present study the AMMI model selected four best adaptable genotypes for each testing environment. Accordingly, the standard check G12

(Tumsa) was best at E3, E6, E5 and E7 whereas, G11 was best at E1 and E2; G4 was best at E4. The next adaptable genotype at E5, E7 and E2 was G3 followed by G8 (Table 4). On the other hand, the mean grain yield at individual location ranged from 950 kg/ha to 4569 kg/ha at Adet and Holetta, respectively. This indicated the existence of high variation among environments that can be due to difference in temperature, soil variation pest and disease and amount of precipitation. Consequently the performance of genotypes varies from location to location.

Table 6: Selection of best faba bean genotypes per environment by AMMI model

| Environment | Mean Yield | Score | The first four AMMI genotype recommendation | | | |
			1st	2nd	3rd	4th
E1	3820	-19.6	G11	G8	G4	G3
E2	3245	-17.5	G11	G3	G8	G12
E3	3730	17.7	G12	G5	G1	G8
E4	3177	5.2	G4	G9	G10	G12
E5	950	3.8	G12	G3	G8	G5
E6	1493	9.1	G12	G1	G4	G5
E7	4569	1.4	G12	G3	G8	G6

Where, E1= Assasa, E2= Kulumsa, E3= Bekoji, E4= Kofele, E5=Adet, E6= Debark and E7=Holeta, number in the bracket is mean grain yield in kg ha^{-1}

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