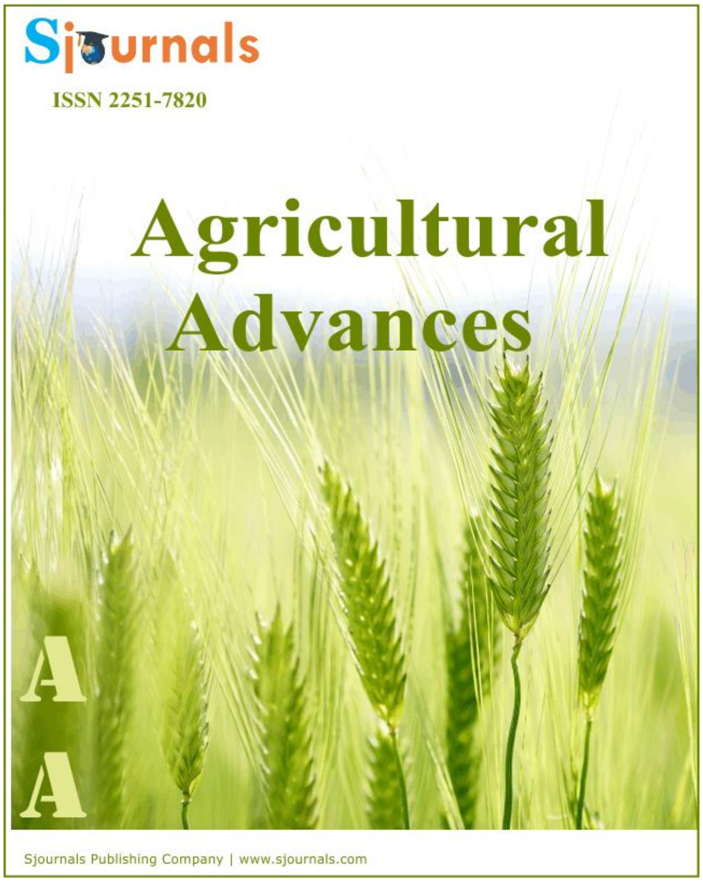
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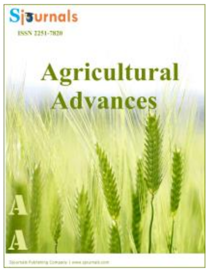

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Original article

Genotype-environment interaction and stability analysis for seed yield of Fenugreek (*Trigonella foenum-graecum* L.) genotypes

Mohammed Beriso* **and Getachaw Asefa**
Sinana Agricultural Research Center, Oromia Agricultural Research Institute, Ethiopia.

*Corresponding author: mbariis2008@gmail.com

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Yield data of 12 Fenugreek (*Trigonella foenum-graecum* L.) genotypes tested across 9 rain-fed environments during the 2015-2017 growing season using RCBD in 3 replications were analyzed using the AMMI model. The AMMI analysis tested in nine environments (years) were showed that the yield was significantly affected (P<0.001) by environment main effects. However, it was not significantly affected by genotypes main effect as well as GxE interaction. The model revealed that differences between the environments accounted for about 91.28% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 0.92 % and 7.79% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 48.61% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 24 % of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at P=0.01 and cumulatively contributed to 72.61% of the GxE interaction SS, leaving 27.44% of the variation in the GxE interaction in the residual. The AMMI and AMMI stability value (ASV) identified G7 and G5 as the stable and high yielding genotypes.

1. Introduction

Plant breeders invariably encounter genotype x environment interactions (GEIs) when testing varieties across a number of environments. Depending on the interactions or the differential genotypic responses to environments, the varietal ranking can differ greatly across environments. In field crop trials, this interaction is often analysed with the aim of determining the stability of the genotypes especially when there is a reasonable genotype by environment interaction (GEI). A combined analysis of variance (ANOVA) can quantify the interactions, and describe the main effects. However, analysis of variance is uninformative for explaining GEI. Various statistical methods (parametric and non-parametric) have been proposed to study Genotype × environment interactions (Mohammadi and Amri, 2008; Mohammadi et al., 2010). The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (Hohls, 1995). The reason is that a genotype's response to varying environments is multivariate (Lin et al., 1988) whereas the stability indices are usually univariate (Gauch, 1988; Crossa, 1990).

Since the genotype response to environmental variations is usually multivariate, therefore, a multivariate method of analysing genotype stability across environments will be the best option. One of the multivariate techniques is the AMMI (additive main effects and multiplicative interaction) model. AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two way data structure. The AMMI analysis is a combination of analysis of variance (ANOVA) and principal component analysis (PCA) in which the sources of variability in genotype by environment interaction are partitioned by PCA. The AMMI is, therefore, also known as interaction PCA (Gauch and Zobel, 1990), and can have several models: AMMI0, which estimates the additive main effect of genotypes and environments, and does not include any principal component axis (IPCA); AMMI1, which combines the additive main effects from AMMI0 with the genotype by environment interaction effects estimated from the first principal component axis (IPCA 1); AMMI2, and so forth, until the full model with all IPCA axis (Gauch, 1988). It has both linear and bilinear component of GEI and hence very useful in visualizing multi-environment data (understanding complex GEI and determining which genotype won which environment) and gaining accuracy (improving cultivar recommendation and accelerating progress) (Gauch, 2006). The additive main effects and multiplicative interactions (AMMI) is defined powerful tool for effective analysis and interpretation of multi-environment data structure in breeding programs (Ebdon and Gauch, 2002a; Samonte et al., 2005; Yan et al., 2000; Zobel et al., 1988). The objectives of the study are: to evaluate, select and verify promising genotypes with desirable traits.

2. Materials and methods

Twelve fenugreek genotypes were evaluated at three locations (Sinana on station, Goro and Ginniir) for three consecutive years (2015-2017) during *bona* production season following selection method. The trial was laid out in RCB design with three replications. Data was collected from central two rows. Data was subjected to analyses of variance using GENSTAT software program. Duncan's multiple range test was done for grain yield. The genotype by environment interaction analyses (GxE) and stability analyses were conducted using the AMMI model.

3. Results and discussion

The AMMI analysis tested in nine environments (years) were showed that the yield was significantly affected (P<0.001) by environment main effects. However, it was not significantly affected by genotypes main effect as well as GxE interaction. The model revealed that differences between the environments accounted for about 91.28% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 0.92 % and 7.79% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 48.61% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 24 % of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at P=0.01 and cumulatively contributed to 72.61% of the GxE interaction SS, leaving 27.44% of the variation in the GxE interaction in the residual (Table 1).

The AMMI model 1 biplot of the varietal trials was demonstrated in Figure 1. The abscissa shows the main effects while the ordinate shows the first PCA axis. The environments showed much variability in both main effects and interactions. However, the high potential environments were sparsely distributed in quadrant II and III, while the lower potential environments were also sparsely distributed in quadrants I and IV with high IPCA1 values (Figure 1).

Table 1
Combined analysis of variance of yield data of Fenugreek genotypes tested across 9 environments.

Source	df	SS	MS	F	F_prob	% Explained
Total	323	31295	96.9	*	*	
Treatments	107	27271	254.9	13.47	0	
Genotypes	11	252	22.9	1.21	0.2827	0.92
Environments	8	24894	3111.8	202.66	0	91.28
Block	18	276	15.4	0.81	0.68579	
Interactions	88	2125	24.2	1.28	0.08287	7.79
IPCA(1)	18	1033	57.4	3.03	0.00007	48.61
IPCA(2)	16	510	31.8	1.68	0.05239	24.00
Residuals	54	583	10.8	0.57	0.99173	27.44
Error	198	3748	18.9	*	*	

Table 2
Environment means and scores.

NE	Environment	Mean	IPCAe[1]	IPCAe[2]
E1	Ginir 2015	18.47	0.26035	1.25811
E2	Ginir 2016	14.34	0.99451	0.83702
E3	Ginir 2017	13.89	0.94106	0.22657
E4	Goro 2015	12.57	0.67011	1.17174
E5	Goro 2016	12.84	-0.57399	-0.16977
E6	Goro 2017	16.66	-0.80555	0.42601
E7	Sinana 2015	42.51	-3.4496	-0.94318
E8	Sinana 2016	16.11	1.80515	-2.86727
E9	Sinana 2017	18.97	0.15797	0.06077

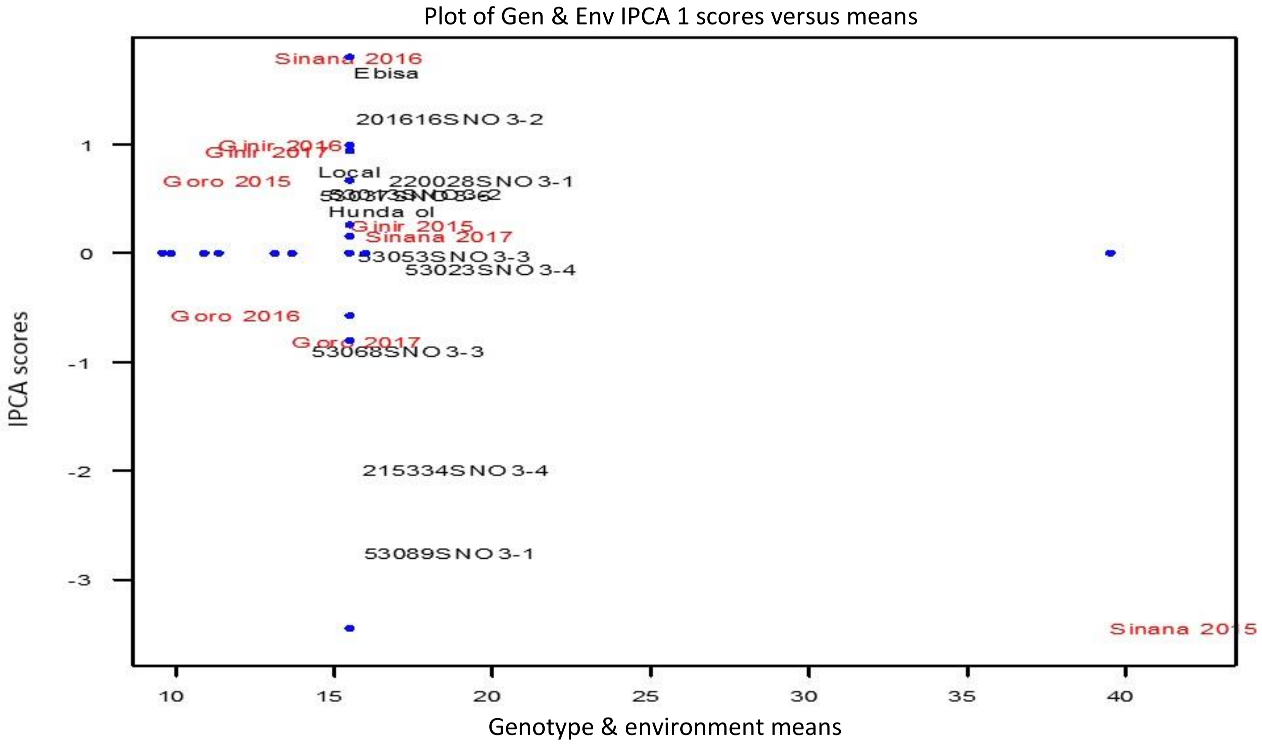

Fig. 1. AMMI model I biplot of the seed yield of Fenugreek genotypes evaluated in 9 environments.

Table 3
AMMI yield mean, AMMI stability values (ASV), and ranking orders of the 12 genotypes tested across 9 environments.

G	Genotype	Yield(Qt/h)	IPCAg[1]	IPCAg[2]	ASV
G1	201616SNO3-2	18.7	1.24771	-1.62107	3.002454
G2	215334SNO3-4	18.9	-1.99516	1.14587	4.200492
G3	220028SNO3-1	19.73	0.67177	-0.54236	1.464773
G4	53013SNO3-2	17.84	0.55189	1.95316	2.250426
G5	53023SNO3-4	20.23	-0.14302	0.67797	0.737266
G6	53037SNO3-6	17.51	0.53211	-1.35106	1.728288
G7	53053SNO3-3	18.76	-0.01704	0.15815	0.161872
G8	53068SNO3-3	17.28	-0.90284	-0.84161	2.013064
G9	53089SNO3-1	18.92	-2.76117	-0.98638	5.67904
G10	Ebisa	18.63	1.67095	0.23297	3.392502
G11	Hunda ol	17.82	0.38613	0.93902	1.222065
G12	Local	17.5	0.75866	0.23534	1.554575

In ASV method, a genotype with least ASV score is the most stable, accordingly genotype G7, followed by G5 were the most stable. In addition G5 is high yielder Genotype. Therefore, release of this genotype for production in the mid and lowlands of Bale will result in increased production and productivity of Fenugreek in the country.

4. Conclusion

AMMI analyses revealed the stable and high yielding genotypes over ranges of environments. That is genotypes G5. Therefore, the release of this genotypes for production in the mid and lowlands of Bale will result in increased production and productivity of Fenugreek in the country. It can be concluded and recommended from this study that genotypes should be selected for wider adaptations.

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