

AMMI AND GGE BILOT ANALYSIS OF YIELD PERFORMANCES IN FENUGREEK (*TRIGONELLA FOENUM-GRÆCUM* L.) GENOTYPES.

Abukiya Getu*¹, Tewodros Leulseged² and Wassu Mohammed³

¹Ethiopia Institute of Agricultural Research Tepi National Spice Research Center P.O.Box 34, Tepi, Ethiopia.

²Ethiopia Institute of Agricultural Research Debrezeit Agricultural Research Center P.O.Box 32, Debrezeit, Ethiopia.

³Haramaya University, School of Plant Sciences, P. O. Box 138, Dire Dawa, Ethiopia.

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*Corresponding Author

Abukiya Getu

Ethiopia Institute of
Agricultural Research Tepi
National Spice Research
Center P.O.Box 34, Tepi,
Ethiopia.

ABSTRACT

The multi-location trial and stability analysis are important to identify wider adapted and specific adapted genotypes which is cultivated in different agro ecology of the country. AMMI and GGE biplot stability model used to identify stable and specific adapted genotypes of fenugreek across different locations. Eleven pipe line genotypes and two standard checks (Chala and Burka) grown in seven different locations to identify wider and specific adapted genotypes. Genotypes FG-12 and FG-4 identified as stable or wider adapted genotypes which are suitable to cultivated across the test locations where as genotypes FG-10 and FG-1 identified as specific adapted and suitable for unfavorable and favorable environments, respectively. Thus the four genotypes could be evaluated further to develop as varieties for the environment(s) the genotypes best suited. In addition, FG-12 had yield advantages of 10.39 and 35.69% over the grand mean and standard check (Burka/FG-13), respectively, while FG-4 had 4.53 and 28.49% yield advantages over the grand mean and standard check, respectively.

KEYWORDS: Wider adaptation, specific adaptation, Stability.

INTRODUCTION

Fenugreek is widely cultivated in different part of the world mainly in India, Egypt, Ethiopia and Morocco and occasionally in England (Davoud *et al.*, 2010). In Ethiopia fenugreek seed is used as food crop, natural herbal medicine in the treatment of diabetes, Milk producing agent to nurse mother, Seasoning traditional sauce and one of the potential export crops for generating foreign currency. Therefore, it is considered as one of the strategic spice crops to increase spice production in the country (SHAPPM, 2014). However, the national total yield of fenugreek is in a fluctuation trend. The total yield of fenugreek was 42012 and 36293.9 tons in 2007 and 2012, respectively (SHAPPM, 2014), 35633.76 tons in 2015 (CSA, 2016) and 454,807.61 tons in 2016 (CSA, 2017).

Among many factors that contributed to the fluctuation of fenugreek yield were competition of major food crops for the cultivated land, crop management practices, insufficient quality seed multiplication and distribution of limited number of improved varieties which is produced in different agro ecology of the country (Girma *et al.*, 2016).

Genotype by environment interaction refers the inconsistency performance of genotypes across different locations. Therefore, an ideal variety should have a high

mean yield combined with a low degree of fluctuations when grown over diverse environments (Arshad *et al.*, 2003). Therefore, cultivar evaluation needs to be conducted over a large range of test sites to include varying regional climatic characteristics that make cost effective cultivar testing in the face of limited resources (Yang *et al.*, 2005). Therefore, development of varieties encompasses multi-location trials and yield data are need subjected to appropriate stability analysis methods. Differences in genotype stability and adaptability to environment can be quantitatively assed by stability parameters of Additive Main Effects and Multiplicative Interaction (AMMI) (Zobel *et al.*, 1988; Guach, 1988). The data also qualitatively assessed using the genotype, genotype by environment (GGE) biplot (Yan, 2001) which is graphical representation that scatters the genotypes according to their principal component values.

MATERIAL AND METHODS

Eleven genotypes (FG-1, FG-2, FG-3, FG-4, FG-5, FG-6, FG-7, FG-8, FG-10, FG-11 and FG-12) and two standard checks (FG-9/chala and FG-13/Burka) were included in this stability study of fenugreek genotypes across seven different locations (Debrezeit, Chefe-Donsa, Akaki, Kulumsa, Haramaya, Hirena and Girawa). Interaction principal component axes (IPCA) scores of genotypes and environments were computed as stability parameters of AMMI model (Guach, 1988; Zobel *et al.*,

1988) as per the established standard procedures for the model. GenStat statistical software (16th edition) was used to compute stability parameters of AMMI model. Since AMMI model does not make provision for a quantitative stability measure, AMMI stability value (ASV) (Purchase, 1997) measure was computed in order to quantify and rank genotypes according to their yield stability by using Microsoft office excel 2007.

$$ASV = \sqrt{\left[\frac{IPCA1SS}{IPCA2SS} (IPCA1score) \right]^2 + [IPCA2score]^2}$$

The ASV is the distance from zero in a two-dimensional scatter graph of IPCA1 (Interaction Principal Component Analysis Axis 1) scores against IPCA2 (Interaction Principal Components Analysis Axis 2) scores. Since the IPCA1 score contributes more to GEI sum of squares; it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to total GEI sum of squares and AMMI Stability Value (Purchase, 1997).

The biplot of AMMI model (Guach, 1988; Zobel *et al.*, 1988) was constructed if residual mean square for grain yield was non-significant in ANOVA of this model to identify genotypes best performed in which environment and stable/unstable genotype(s) across environments. However, if the residual mean square for grain yield was significant, GGE biplot was constructed for visual observation to understand which genotypes best performed in which environment “Which-Won- Where” Patterns (Yan *et al.*, 2001; Yan and Tinker, 2006). The GGE biplot was constructed to visualize the discriminating ability and representativeness of the environment(s) and also used to cluster mega environments. GenStat statistical software (16th edition) and GEA-R (Genotype x Environment Analysis with R for Windows) Version 2.0 was used to construct GGE biplot graph.

RESULTS AND DISCUSSIONS

The IPCA's scores for each genotype was considered as stability parameters of AMMI model. The larger the IPCA's scores either negative or positive direction the more specifically adapted genotypes for a certain environments; the smaller the IPCA's scores (approaching to zero) the more stable or wider adapted genotypes across environments. However, AMMI stability value (ASV) for each genotype was calculated to identify more stable genotypes easily since it considered both IPCA1 and IPCA2 scores according to Purchase (2000). The mean grain yields per hectare of the genotypes and ASV used to rank the genotypes and to identify genotypes with high mean yield and stable across the test environments, the results presented in the table.

Stability parameters from AMMI

AMMI model				
Genotypes	Mean	IPCA 1	IPCA 2	ASV
FG-1	1264(2)	-1.209	-16.676	16.84(7)
FG-2	1198(4)	10.70	8.51174	22.71(10)
FG-3	1178(5)	-21.52	1.66306	42.38(13)
FG-4	1178(5)	-2.293	-0.0904	4.51(1)
FG-5	1162(7)	11.797	1.50001	23.26(11)
FG-6	913(13)	3.6476	5.7317	9.18(3)
FG-7	1069(9)	0.3395	15.489	15.50(6)
FG-8	1126(8)	-8.801	2.94588	17.57(8)
FG-9	1054(10)	-14.13	1.97766	27.88(12)
FG-10	1293(1)	10.227	2.15717	20.24(9)
FG-11	1039(11)	2.6923	-7.1537	8.90(2)
FG-12	1243(3)	4.1947	-9.2295	12.38(5)
FG-13	916(12)	4.3549	-6.8262	10.95(4)
Grand mean	1126			

Numbers in parenthesis represented the rank for mean and ASV in descending and ascending, respectively.

The 13 fenugreek genotypes could be categorized based on IPCA scores, ASV and mean performance of the grain yields. Based on the two IPCA's scores genotype FG-4 and FG-6 had low scores for IPCA1 and IPCA2, which indicated as stable or wider adapted genotypes and genotypes FG-1, FG-7 and FG-11 had lower IPCA1 scores but higher IPCA2 score these indicated that even if the IPCA1 considered as stable or wider adapted genotypes, but the IPCA2 score considered as specific adapted genotypes. Genotypes FG-5, FG-3 and FG-9 scores higher IPCA1 but lower IPCA2 scores. Accordingly, genotypes FG-10, FG-11, FG-12, FG-13, FG-2, FG-5, FG-6 and FG-7 had positive IPCA1 scores, among these genotypes FG-10, FG-12, FG-2 and FG-5 scores higher mean yield above the grand mean yield but based on ASV ranked 9th, 5th, 10th and 11th respectively and the higher ASV rank except FG-12 indicated that the specific adaptation of the genotypes.

The second group genotypes FG-1, FG-3, FG-4, FG-8 and FG-9 had negative IPCA1 scores, from these genotypes FG-1, FG-3 and FG-4 scores higher mean yield above the grand mean yield, except genotype FG-4 the remaining genotypes had higher ASV rank which indicated the specific adaptation of the genotypes. The genotypes FG-8 score the mean yield similar with the grand mean and FG-9 scores lower mean yield below the grand mean and ASV ranked 8th and 10th among the genotypes across the test locations these indicated that both genotypes were unstable and also low performance of mean grain yield across the test locations.

The third group genotypes FG-11, FG-13, FG-6 and FG-7 scores lower mean yield below the grand mean and ASV ranked 2nd, 4th, 3rd and 6th among the genotypes across the test locations these indicated that even if these genotypes were identified as wider adapted genotypes relative to other genotype across the test locations but due to low performance of grain yield these genotypes cannot

be cultivated at any test locations (Table 9). This result was in agreement with the finding of Muluken (2009) stability studies in malt barley from 20 genotypes only two genotypes were identified as stable based on low score of ASV.

In general from AMMI stability model parameters and mean yield performance of the genotypes across the test locations FG-4 was the first more stable or wider adapted genotype and had 4.53% yield advantage over the grand mean and FG-12 was the 5th more stable or wider adapted genotype with grain yield advantage 10.39% over the grand mean these two genotypes were recommended for

cultivation across the test locations among the tested genotypes. This result was in agreement with the finding of Solomon *et al.* (2008) in maize and Farshadfar (2008) in Bread wheat stability studies.

GGE biplot “Which-Won-Where” Patterns Stability model.

The GGE biplot is important in order to understand which genotypes were stable and unstable and also the GGE biplot used to visualize the discriminating and representative ability of the test environments. GGE biplot was best fits for “which-won-where” pattern analysis (Yan *et al.*, 2007).

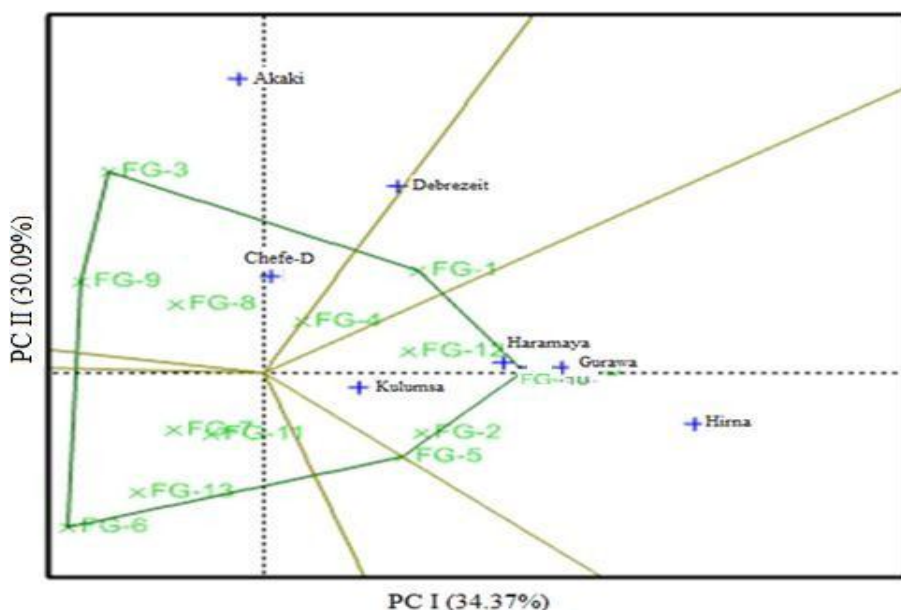


Figure 1: GGE biplot in “which-won-where” pattern.

In GGE biplot graph the genotypes located at vertex of the polygon in each sectors were the winner genotype at those environments whose markers fall into the respective sector. Environments within the same sector share the same winning genotypes and environments in different sectors have different winning genotypes and the genotypes within the polygon and nearer to origin were less responsive than vertex genotypes (Yan *et al.*, 2001; Yan and Tinker, 2006). Yan *et al.* (2000) and Yan and kang (2003) reported as the polygon view of GGE biplot is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. The GGE biplot has therefore, been used in crop genotypes trials to effectively identify the best-performing genotype(s) across environments, identify the best genotypes for specific environments delineation, whereby specific genotypes can be recommended to specific environments and evaluate the yield and stability of genotypes (Yan and Kang, 2003; Yan and Tinker, 2006).

Accordingly, the vertex genotypes were FG-1, FG-10, FG-3, FG-5, FG-9 and FG-6 (Fig1), genotypes FG-3 and

FG-6 having the largest vertex distance from the origin which were more responsive to environmental change these indicated that these two genotypes were highly specific adapted genotypes and FG-6 gave the least yielder genotypes among the tested genotypes. Genotypes FG-12, FG-4, FG-8, FG-7 and FG-11 were located within polygon which were less responsive or less vulnerable to environmental changes across the test environments according to (Kaya *et al.*, 2006).

FG-4 and FG-12 were located near to the origin which indicated that these genotypes were stable or wider adapted across the test locations. Genotype FG-10 located at the vertex and the winner genotype at Girawa, Haramaya, Kulumsa and Hirna (Figure 1). Genotype FG-1 was located at the vertex and the winner genotype at Debrezeit. Genotype FG-3 was the winner genotypes at Akaki and Chefe-Donsa. FG-5 and FG-6 were located at vertex but cannot win at any test locations. These result was in agreement with the finding of (Ukalski and Klisz, 2016) studies on application of GGE biplot graphs in multi environment trial.

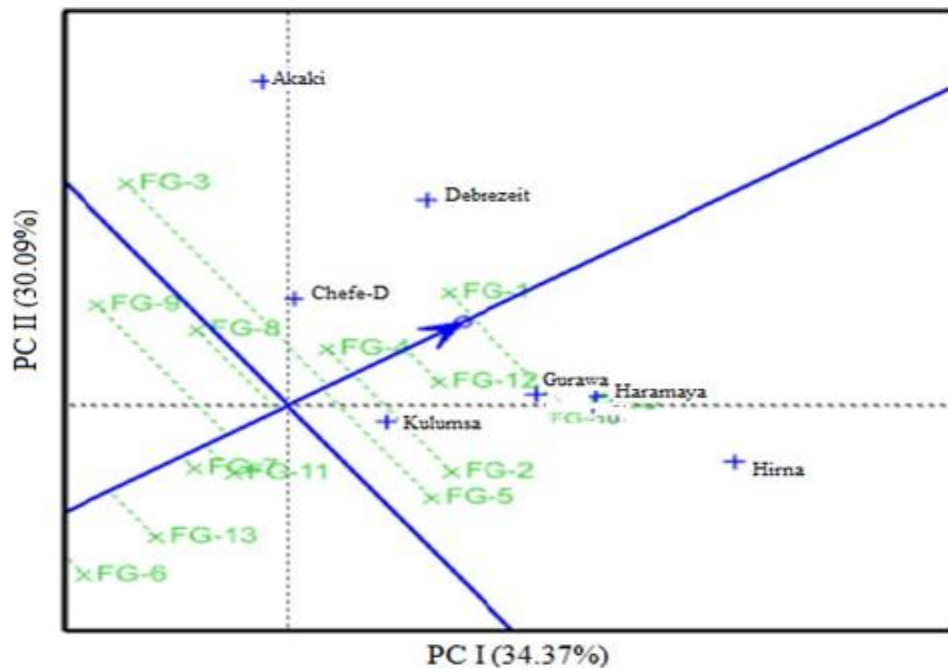


Figure 2: GGE biplot graph mean values and stability ability of the genotypes.

GGE biplot graph ranked the genotype based on the mean yield performance across the test environments and also indicated their level of stability on the vector length from average genotype axis (Figure 2). Genotypes FG-1 and FG-10 were the leading genotypes among the tested genotypes. Genotype FG-1 was wider adapted genotype than FG-10 because of short vector length from average genotype axis. Genotypes FG-12, FG-4, FG-2, FG-3 and FG-5 had higher mean yield above the grand mean. Genotype FG-3 was highly vulnerable to environmental fluctuation or specific adapted genotype because the genotype had large vector length from the average genotype axis. Genotypes FG-9, FG-7, FG-11, FG-13 and FG-6 had lower mean yield than the grand mean, except FG-9 the rest genotypes had short vector length and identified as wider adapted genotypes. Genotype FG-8 was score almost similar mean yield with the grand mean and moderately stable genotype among the tested genotypes. This result was in agreement with the finding of Blanche *et al.* (2007) studies on AMMI, Stability and GGE biplot Analysis for cotton.

CONCLUSION

The presence of significant effect of GEI on yield and yield related traits makes difficult to select genotypes cultivated across different locations depending on the pooled mean generated from Multi locations trial, therefore conducting stability analysis is very important to select the genotypes either to cultivated across different locations or specific locations. From this study different genotypes were selected for cultivation at specific locations and across the test locations, accordingly, genotypes FG-1 and FG-10 were identified as specific adapted genotypes from AMMI and GGE biplot stability models and scoring high mean value above the grand mean among the tested genotypes. Genotype FG-1 had

higher yield advantage of 12.16% and 37.88% over the grand mean and standard check (Burka or FG-13) and genotype FG-10 had yield advantage 14.83% and 41.15% over the grand mean and standard check (Burka or FG-13), respectively. Genotype FG-12 and FG-4 were selected as stable or wider adapted genotype based on the two stability model which had a yield advantage of 10.39% and 35.69% over the grand mean and standard check (Burka or FG13) and 4.53% and 28.49% over the grand mean and standard check (Burka or FG13), respectively.

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