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Stability analysis under diverse environments of fenugreek (*Trigonella foenum-graecum)* genotypes by AMMI model

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ABSTRACT

Fenugreek (*Trigonella foenum-graecum* L.) is one of the most important seed spices crop in the world. India being one of the largest fenugreek producing country, has released many varieties, but within few years of release, many of these are no longer under cultivation owing to inconsistent performance in diverse environments, however, some of the varieties which depicted stable performance are under cultivation. This study aimed to evaluate the adaptability and yield stability of different fenugreek genotypes using AMMI model. Total 60 elite fenugreek genotypes were evaluated under six environments during *rabi* 2015–16 and 2016–17 seasons at Vegetable Research Farm, CCS HAU, Hisar. AMMI model was employed to assess the magnitude of genotype × environment (GE) interaction and stability of genotypes across environments. Analysis of variance for seed yield clearly indicates that the mean sum of square for genotypes is significant, suggesting broad range of diversity among the genotypes. The environmental variances are highly significant for most of the characters. G × E mean sum of square was significant for seed yield (q/ha) which indicates that the performance of genotypes that was differential over the environments. The proportion of sum of square for G × E interaction for seed yield was 80.94%. The genotype, viz. JFg 240, HM 346, HM 258, NDM 20, NDM 13 and RM 28 exhibited stable performance over all environments for seed yield. The environments E4 (4 Nov 2016), E3 (28 Nov, 2015) and E2 (15 Nov, 2015) were the main contributors to the phenotypic stability of the genotypes and E2 and E5 are the favourable environments for obtaining higher seed yield.

Key words: AMMI, Biplot, Environment, Fenugreek

Fenugreek (*Trigonella foenum-graecum* L.) commonly known as '*methi*' is one of the most important seed spice crops of India. It is also used as leafy vegetable, for medicinal purposes and fodder as well. Fenugreek is a cool season crop, requiring frequent light irrigations during the cropping season. There is an increasing trend in cultivation in the non-traditional areas of the country owing to its multipurpose use but inconsistent performance of cultivars is alarming in terms of yield which vary from region to region and diverse environments. In view of this the analysis of performance of fenugreek germplasm in different environments is of vital importance in screening them for their stability, sustainability as well as for possibility of cultivation in non-conventional areas including unfavorable environments. Considering the genotype × environment interaction (GEI), genotypes should be planted in multi-environment trials to ascertain the high performing genotype and their stability.

The reaction of different genotypes is often resulted from the varied response of genes or their different expression ability in different environments (Brandiej and Meverty 1994). Several statistical models such as linear regression analysis, non-regression analysis, multivariate analysis, etc. are available to estimate the effects of G × E interaction for selection of varieties and prediction of phenotypic response to environmental changes. Among these the additive main effects and multiplicative interaction effects (AMMI) model, which integrates analysis of variance to study the main effect of genotypes and environment and principal component analysis for residual multiplicative interaction among genotypes and environments is considered an efficient model. The utilization of AMMI and GGE biplot models can be powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programs (Yan *et al.* 2000, Ebdon and Gauch 2002, Samonte *et al.* 2005). Many researchers have already utilized both AMMI and GGE biplot methods simultaneously in confirmation of stable genotypes with high yield. Since AMMI is a powerful, effective and efficient tool, this study aimed to evaluate the adaptability and yield stability of fenugreek genotypes using AMMI analysis to select genotypes that have both high performance and phenotypic stability in reducing the G × E interaction effects and make selection of genotypes more refined and precise.

MATERIALS AND METHODS

The experimental material comprised of 60 diverse genotypes (Table 1) from various origin and these genotypes

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were evaluated in randomized block design with three replications. The experiment was laid out at Vegetable Research Farm of CCS HAU, Hisar in *rabi* 2015–16 and 2016–17 in row length of each genotype was of 3 m with spacing 50 cm. Sowing was done at different date of sowing, i.e. 4 November 2015 (E1), 15 November 2015 (E2), 28 November 2015 (E3), 4 November 2016 (E4), 15 November 2016 (E5) and 28 November 2016 (E6). Recommended agronomical practices and plant protection measures were followed timely for successful cultivation of the crop. Following harvest, grain yield was determined for each genotype in each test environment. Seed yield was recorded on the plot basis and further calculated in q/ha.

Table 1 List of genotypes and source of origin

S No.	Genotypes & Source	S No.	Genotypes & Source
1.	HM 258 CCS, HAU, Hisar	31.	NDM 72 NDUAT, Faizabad
2.	HM 259 CCS, HAU, Hisar	32.	NDM 74 NDUAT, Faizabad
3.	HM 267 CCS, HAU, Hisar	33.	RM 13 RAU, Dholi, Bihar
4.	HM 271 CCS, HAU, Hisar	34.	RM 16 RAU, Dholi, Bihar
5.	HM 273 CCS, HAU, Hisar	35.	RM 18 RAU, Dholi, Bihar
6.	HM 277 CCS, HAU, Hisar	36.	RM 27 RAU, Dholi, Bihar
7.	HM 278 CCS, HAU, Hisar	37.	RM 28 RAU, Dholi, Bihar
8.	HM 280 CCS, HAU, Hisar	38.	RM 70 RAU, Dholi, Bihar
9.	HM 281 CCS, HAU, Hisar	39.	RM 190 RAU, Dholi, Bihar
10.	HM 282 CCS, HAU, Hisar	40.	RM 191 RAU, Dholi, Bihar
11.	HM 297 CCS, HAU, Hisar	41.	RM 194 RAU, Dholi, Bihar
12.	HM 57 (Hisar Sonali) CCS, HAU, Hisar	42.	RM 196 RAU, Dholi, Bihar
13.	HM 103 (Hisar Suvarna) CCS, HAU, Hisar	43.	RM 203 RAU, Dholi, Bihar
14.	HM 346-1 CCS, HAU, Hisar	44.	JFg 13 SRS, Jagudan, Gujarat
15.	HM 444 CCS, HAU, Hisar	45.	JFg 15 SRS, Jagudan, Gujarat
16.	HM 355 CCS, HAU, Hisar	46.	JFg 196 SRS, Jagudan, Gujarat
17.	HM 346 (Hisar Mukta) CCS, HAU, Hisar	47.	JFg 201 SRS, Jagudan, Gujarat
18.	NDM 7 NDUAT, Faizabad	48.	JFg 211 SRS, Jagudan, Gujarat
19.	NDM 8 NDUAT, Faizabad	49.	JFg 219 SRS, Jagudan, Gujarat
20.	NDM 10 NDUAT, Faizabad	50.	JFg 240 SRS, Jagudan, Gujarat
21.	NDM 13 NDUAT, Faizabad	51.	GM 1 SRS, Jagudan, Gujarat
22.	NDM 20 NDUAT, Faizabad	52.	GM 2 SRS, Jagudan, Gujarat
23.	NDM 25 NDUAT, Faizabad	53.	AM 292 NRCSS, Ajmer
24.	NDM 37 NDUAT, Faizabad	54.	AM 293 NRCSS, Ajmer
25.	NDM 43 NDUAT, Faizabad	55.	AM 298 NRCSS, Ajmer
26.	NDM 45 NDUAT, Faizabad	56.	AM 300 NRCSS, Ajmer
27.	NDM 48 NDUAT, Faizabad	57.	AM 301 NRCSS, Ajmer
28.	NDM 61 NDUAT, Faizabad	58.	AM 302 NRCSS, Ajmer
29.	NDM 67 NDUAT, Faizabad	59.	AM 304 NRCSS, Ajmer
30.	NDM 69 NDUAT, Faizabad	60.	AM 305 NRCSS, Ajmer

The following mathematical model was used for AMMI analysis:

$$Yij=\mu + gi + ej + \Sigma\lambda k + \alpha ikyjk + Rij$$

where, Yij is the the yield of i^{th} genotypes in j^{th} environment; μ the overall mean, gi is the effect of the ith genotype; ej is the effect of the j^{th} enviroment; λk is the square root of the given value of the PCA axis k. Then αik and yjk are the principal components scores for PCA axis k of the i^{th} genotype and j^{th} environment, respectively, and Rij is the residual. The GE interaction sum of squares was subdivided into PCA axis SS, where axis k is regarded as having t + s-1-2k degrees of freedom and t and s are the number of the genotypes and environments; respectively. The data was analyzed by using WINDOSTAT software.

RESULTS AND DISCUSSION

The linear regression model of Eberhart and Russell (1966) is most frequently used for G × E interaction study but in this model a stable genotype should have low deviation from regression (S^2di). Therefore, many genotypes having very high potential often get rejected in this model due to high S^2di over the range of environments. The Eberhart and Russell model does not provide critical analysis of interaction of genotypes in specific environments. AMMI analysis gives estimate of total G × E interaction effect of each genotype and also further categorise it into interaction effects due to individual environments. Presence of low G × E interaction of a genotype indicates stability of the genotype over the range of environments. A genotype showing high positive interaction in an environment has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and it will be therefore best suited to that environment. AMMI analysis enablesevaluation of interaction effect of a genotype in eachenvironmental condition.

Analysis of variance: The joint analysis of variance showed differences for environments (E), genotypes (G) and the G × E interaction (Table 2). Mean squares differences were also significant for genotypes showing that the differences among the genotypes were persistent over the environment. The significant effect of G × E interaction showed that genotypes had high variable performance in the tested environment. Therefore, this change in the average seed yield of fenugreek genotypes as a consequence of the environment justifies the need for a more refined analysis to increase selection efficiency and varietal recommendations. The AMMI analysis of fenugreek seed yield in six environments showed that 80.94% of the sum of squares was explained by environment, and 5.12% and

Table 2 Combined ANOVA and through AMMI model for fenugreek

Source	Df	SS	MS	AMMI	
				% Explained	% Accumulated
Environment (E)	5	5161.4507	1032.2902	80.94	
Genotypes (G)	59	327.0650	5.5435	5.12	
G × E	295	524.3638	1.7775	8.22	
IPCA 1	63	232.8941	3.6967	44.41	44.41
IPCA 2	61	137.3784	2.2521	26.2	70.61
IPCA 3	59	81.2740	1.3775	15.50	86.11
IPCA 4	57	50.5108	0.8862	9.63	95.75
Residual	55	22.3066	0.4056	4.20	100.00
Error	720	363.3464	0.5046		

8.22% were attributable to the genotype effects and G × E interaction, respectively. The large percentage contributed by environment sum of squares indicates the significant differences between the averages of some environments, which caused most of the variation in seed yield. This response to environmental and genotypic effects coincides with those found by Shadi Heidari *et al.* (2016) and they also found that in durum wheat the genetic variation for seed yield is largely attributed by genotypic and environmental effects.

The G × E interaction variance (8.22%) was further partitioned into interaction between principal component axes (IPCAs). Four IPCA axes were found to be adequate to explain the entire G × E variance. The IPCA-1 has accounted for 44.41% and IPCA-2 for 26.20%, both together accounted for 70.61% for the total variance. The value explained by these first two IPCAs presents the same magnitude as those found by Balapure *et al.* (2016). In view of this, the IPCA I and IPCA II axes of AMMI-I model were selected for drawing AMMI I biplot. Similarly, biplot of AMMI models for yield variable was generated using genotypic and environmental scores of the first two AMMI components. In the above analysis, however seems to suggest the presence of complex and multidirectional variation in genotype-environment data. According to Crossa *et al.* (1990) AMMI model with many IPCA axes are expected to involve rather more noise than the highly complex interaction among genotype and environments. As the first IPCA contributes more in G × E interaction as compared to other IPCA, in present study, were pooled into residual. Thus AMMI, model with first IPCA axis was accepted for further study. The mean performance along with IPCA 1 score for both genotypes and environment were used to construct biplot and are represented in Table 3.

Mean yield, ASV and Sustainability index: The pooled mean of seed yield of all the environments are presented in Table 3. AMMI analysis variance for seed yield indicated that significant differences were observed in genotype, environment and Genotype environment interaction. Out

Table 3 Mean, ASV (Stability value), Sustainability index, stability index of fenugreek genotypes

Genotype	Variety mean	ASV	Sustainability Index Si	Stability Index I
NDM 7	13.83	1.23	61.33	0.82
NDM 8	14.02	1.48	58.66	0.80
NDM 10	14.21	0.56	53.33	0.23
NDM 13	15.44	0.12	46.86	0.01
NDM 20	15.49	0.32	51.09	0.04
NDM 25	15.18	0.55	53.36	0.16
NDM 37	14.09	0.65	50.46	0.15
NDM 43	15.02	1.02	60.82	0.47
NDM 45	14.26	0.70	59.32	0.17
NDM 48	13.63	1.37	49.28	1.10
NDM 61	14.67	1.59	52.24	1.04
NDM 67	15.60	0.84	58.96	0.67
NDM 69	14.63	0.46	51.70	0.13
NDM 72	15.38	0.67	48.77	0.38
NDM 74	15.94	0.67	50.92	0.45
RM 13	14.02	0.63	56.48	0.14
RM 16	14.36	0.92	56.24	0.29
RM 18	14.67	0.39	48.64	0.08
RM 27	14.35	0.56	51.51	0.27
RM 28	14.53	0.22	54.55	0.02
RM 70	15.63	0.63	50.14	0.15
RM 190	15.48	0.93	45.50	0.52
RM 191	14.39	0.49	58.69	0.23
RM 194	15.59	1.01	48.75	0.37
RM 196	14.78	1.01	43.59	0.90
RM 203	15.93	1.15	47.06	0.51
JFg 13	14.23	0.25	51.98	0.06
JFg 15	13.47	1.16	55.17	0.64
JFg 196	14.92	0.54	46.34	0.10
JFg 201	14.76	1.53	53.15	2.33
JFg 211	16.96	2.13	65.42	1.73
JFg219	15.94	1.19	45.17	0.63
JFg 240	15.84	0.17	57.92	0.03
AM 292	15.60	1.73	62.18	1.06
AM 293	16.08	1.43	63.77	0.71
AM 298	14.18	0.61	53.23	0.17
AM 300	15.72	0.86	51.62	0.26
AM 301	15.81	0.60	50.27	0.20
AM 302	15.57	0.61	49.29	0.16
AM 304	16.56	0.37	53.30	0.10
AM 305	13.55	1.99	61.11	1.39
HM 258	14.36	0.14	49.84	0.01
HM 259	16.80	1.34	45.53	0.78

Cond.

Table 3 (*Concluded*)

Genotype	Variety mean	ASV	Sustainability Index Si	Stability Index I
HM 267	16.27	1.08	50.60	0.44
HM 271	14.98	1.28	35.94	1.49
HM 273	16.46	1.55	44.53	0.84
HM 277	16.63	1.26	47.35	0.55
HM 278	14.77	0.88	47.33	0.27
HM 280	16.86	0.87	50.23	0.29
HM 281	16.12	0.60	50.39	0.13
HM 282	14.26	0.99	49.76	0.49
HM 297	15.27	0.68	48.89	0.17
HM 57	16.34	0.98	53.13	0.33
HM 103	14.72	0.47	54.38	0.18
HM 346-1	17.81	0.67	53.43	0.16
HM 444	15.60	0.83	48.74	0.33
HM 355	15.42	0.62	55.26	0.37
HM 346	16.14	0.28	52.56	0.03
GM 1	14.45	0.35	48.72	0.09
GM 2	14.48	0.74	58.99	0.33

of 60 genotypes, 30 genotypes have produced seed yield above the grand mean yield.

The AMMI Stability Value (ASV) and AMMI stable index were calculated as suggested by Zobel *et al.* (1998) and Purchase *et al.* (2000) and their ranks are presented in Table 3. ASV was proposed to quantify and classify genotypes according to their yield stability in that ASV is the distance of the varieties from point zero of the scatter diagram (IPCA1 vs. IPCA2). Although the IPCA1 score contributes more to the sum of squares for G × E interaction, it must be weighted by the proportional difference between the scores of IPCA1 and IPCA2 in order to compensate for the relative contribution of IPCA1 and IPCA2 to the total sum of squares of the interaction. The genotypes which has low stability value (ASV) is said to be stable and the breeder chose the stable genotypes, having grain yield above the mean grand yield. The sustainability index of each variety is presented in Table 3. Most of the fenugreek genotypes were classified as having moderate sustainability index (40–60%) and genotype NDM 7, NDM 43, JFg 211, AM 292 and AM 305 showed high sustainability (61.33, 60.82, 65.42, 62.18, 61.11 respectively). The high sustainability index values coincided with high seed yield from genotype NDM 43, JFg 211 and AM 292. Similar results were observed for Darai *et al.* (2017).

IPCAs interaction: Principal components analysis (PCA) is a multivariate statistical method to identify data patterns along with similarities and dissimilarities among variables based on ordination techniques of multivariate methods. Biplot graphs of the AMMI 1 and AMMI 2 models (IPCA2 vs. IPCA1) are in Fig 1 and 2, respectively. Environment 5 and environment 3 produced the lowest seed yield of fenugreek. Moreover, the environmental effect scores were more scattered than the varietal effect scores, indicating that variability due to the environment is greater than variability caused by varietal effects. According to Duarte and Vencovsky (1999) stability is evaluated in the y-axis (IPCA1) by AMMI 1, so accordingly genotypes 33 (JFg 240), 15 (NDM 74), 58 (HM 346), 12 (NDM 67), 4 (NDM 13), 40 (AM 304), 50 (HM 281), 38 (AM 301) and 7 (NDM 37) were the most stable, as indicated by values near the origin of the IPCA 1 axis, which is indicative of a smaller contribution to the G × E interaction (Fig 1). However genotype 7 (NDM 37) had lower seed yield than overall mean and is therefore, not ideal. In contrast, genotypes 55 (HM 346-1), 43 (HM 259), 46 (HM 273) and 47 (HM 277) were found unstable with seed yield more than the overall mean. Similarly, genotypes 41 (AM 305), 2 (NDM 8), 11 (NDM 61), 10 (NDM 48) and 28 (JFg 15) were unstable with seed yield less than the overall mean.

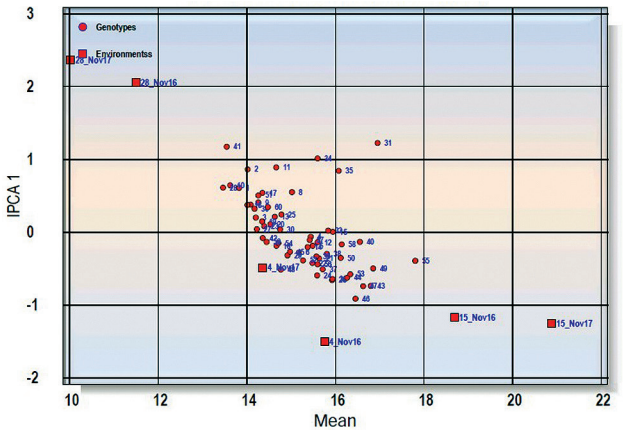

Fig 1 Biplot (AMMI 1) for seed yield (q/ha).

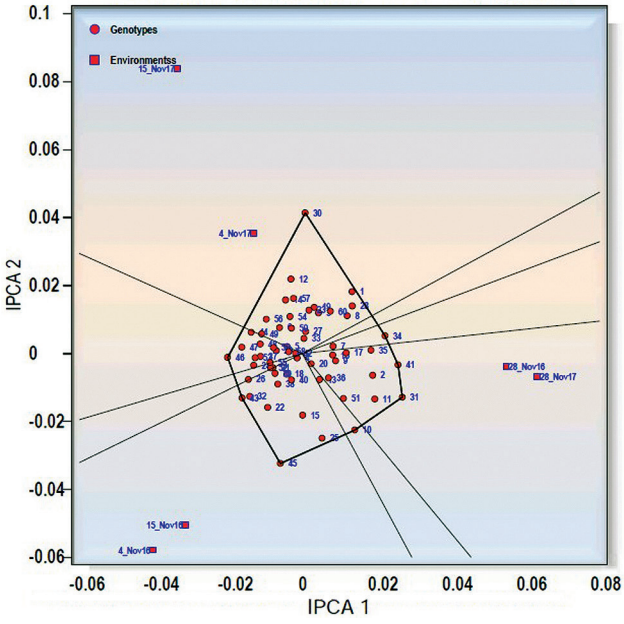

Fig 2 Interaction Biplot (AMMI 2).

To demonstrate the stability of genotypes as well as the relative magnitude of interaction effects of each genotype and environment, AMMI II biplot were drawn using IPCA 1 and IPCA 2 scores (Fig 2). Unlike AMMI I, in AMMI II biplot of IPCA 1 and IPCA 2 scores were regarded as more stable when they are positioned at close proximity of the origin of AMMI II than genotypes located far away from the centre. According to the principle, the genotypes JFg 240 (33), HM 346 (58), HM 258 (42), NDM 20 (5), NDM 13 (4) and RM 28 (20) confined closer to the origin point of AMMI II biplot have less interaction with environments. These genotypes may be regarded as stable one, similarly Meena *et al.* (2015, 2017) also identified stable genotypes through similar analysis. However, seed yield of HM 258 (14.36 q/ha) and RM 28 (14.53 q/ha) were lower than the average yield of tested genotypes and therefore, do not qualify as high yielding stable genotypes. Based on AMMI II analysis, E4, E3 and E2 environments were the main contributors to the phenotypic stability of the genotypes. Furthermore, the E4 and E3 environments showed no significant differences in seed yield between the genotypes studied. In contrast, E1, E5 and E6 made a significant contribution to the GXE interaction, since they were positioned away from the origin of the AMMI II biplot. Generally, genotypes and environments in close proximity on the biplot graph have positive correlation, which certainly facilitate the creation of more similar agronomic performances.

Yield is a quantitative trait that is strongly affected by environment. AMMI statistical model might be a great tool to select the most suitable and stable high yielding genotypes for specific as well as for diverse environments. In the present study, AMMI model has shown that the largest proportion of the total variation in seed yield was attributed to environments. The genotypes JFg 240, HM 346, HM 258, NDM 20, NDM 13 and RM 28 showed higher grain yield than all other genotypes across all the environments and performed well across a wide range of environments and are least affected by interaction.

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