Research Article

Finger millet (*Eleusine coracana* (L.) Gaertn.) varietal adaptability in North-Western Himalayan region of India using AMMI and GGE biplot techniques

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Abstract

Finger millet (*Eleusine coracana* (L.) Gaertn. subsp. *coracana*) production has become stagnant over the years and one of the possible ways to increase the production can be spread of widely adaptable high yielding cultivars. Five national finger millet cultivars were grown in randomized complete block design at ICAR-Vivekananda Institute of Hill Agriculture for six consecutive years to evaluate the grain yield stability. The grain yield data were subjected to AMMI and GGE biplot techniques for assessing the stability and patterns of GE interaction in finger millet National cultivars. The combined ANOVA showed that finger millet grain yield was significantly affected by environment, which explained 54.67% of the total treatment (G+E+GE) variation, whereas the G and GEI accounted for 10.38% and 34.96%, respectively. The partitioning of GEI sum of squares using AMMI analysis indicated that the first two PCAs were highly significant. The first IPCA axis (IPCA1) accounted for 50.3% of the G×E interaction sum of squares. The second IPCA axis accounted for 38.2% of the interaction sum of squares. Both represented a total of 88.5% variation. AMMI 1 biplot indicated the general adaptation of genotype HR 374 across the environments, whereas the other genotypes showed specific adaptation to one or other environments. GGE-biplot graphical analysis further confirmed the results and revealed that HR 374 as an ideal genotype in terms of high yield and stability followed by RAU 8 as desirable genotype. In our research, both of AMMI and biplot models were successful in assessing the performance of genotypes and the selection of best genotype was identical in both of them.

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn. subsp. *coracana*) is one of the important cereals in India and East Africa (Hilu and DeWet 1976). It is originally native to the Ethiopian highlands and was introduced into India approximately 3000 years ago (Dida *et al*. 2008). It is a short-day plant, and requires an optimum photoperiod of 12 hours. It is mainly produced within 20° N and 20° S latitude. It is a tropical, rainfed crop, best suited for dry farming. However, its annual precipitation tolerance ranges from 300 to 4000 mm. Well distributed moderate rainfall (500 to1000 mm) during the growing season without prolonged droughts are the most favourable conditions for its cultivation. Dry weather is required for drying of the grains at harvest. The crop also tolerates a cooler climate than other millets. It is highly adaptable crop and grown up to 2400 m above mean sea level in higher elevations in the Himalayas.

Finger millet contains a large proportion of carbohydrates and thus provides bulk of energy in diets. It is also rich in proteins, sulphur containing amino acids and because of its low glycemic index with high fibre, it is recommended for diabetic patients. Apart from the major nutrients, it also contains iron and calcium, which are deficient in most Indian and African women. High calcium, high soluble fibre, low fat, high diastatic power of malted grains renders finger millet unique place in food (Goron and Raizada 2015). It has proved to be very effective in controlling blood glucose level of diabetics. Besides, consumption of finger mill*et al*so prevents constipation and cholesterol.

In spite of all these advantages, the productivity of finger millet continues to be low which can be ascribed to diverse poor growing conditions and/or lack of well adapted suitable varieties for these growing conditions. The diverse agro-ecology of the region can also impose significant genotype by environment interaction (GEI) and hamper crop improvement (Yan and Kang 2003). Knowledge on the nature and magnitude of GEI is helpful to determine whether there is a need to develop a widely adapted cultivar for all environments of interest, or specifically adapted cultivars for specific target environments (Yan and Kang 2003). Breeders generally want to minimize GEI and generate varieties that are adapted to wider areas as it is easier and cost effective both in terms of variety evaluation and seed multiplication.

However, the success to develop a widely adapted variety is dependent upon the kind of interaction prevailing (Yan and Kang 2003). The GEI can be either quantitative *i.e,* there is no change in genotypes ranking; or qualitative when change in ranking happens. Qualitative (crossover) interaction is the type of interaction that poses a challenge to breeders. If crossover (qualitative) interaction happens consistently, then the breeding environments may be classified in to mega environments and specifically adapted varieties can be developed for each sub environment separately. The selection of widely adapted genotypes that perform well across many locations is more economical despite the fact that it is at the cost of some yield gains from specifically adapted genotypes (Yan and Kang 2003). Multi environment evaluation of genotypes across diverse locations/environments before release of a new variety is a common practice.

The Additive Main Effects and Multiplicative Interaction (AMMI) analysis has been reliably used for better decision making with regard to selection of genotypes. However, there is need to perfectly incorporate genotype (G) and genotype by environment interaction (GEI) in cultivar evaluation and plant breeding programme in multi-environment trials (MET). The objective of this research was to examine the relative discriminatory abilities of AMMI and GGE stability models in selection for grain yield and stability among finger millet genotypes.

Materials and Methods
Five finger millet national check varieties *viz.*, VL *Mandua* 149, PES 400, VR 708, RAU 8 and PR 202 were grown from 2002 to 2007 at experimental farm, Hawalbagh, ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora (79°39'E latitude and 25°35'N longitude, 1250 m above msl). The crop was raised in the rainy season from June to November every year. Five rows of each variety were planted in randomized complete block design with 3 replications. The row length was 3 m with row to row spacing of 22.5 cm. Plots were initially over-planted and thinned later during first weeding (within 20-25 days of sowing) to maintain plant to plant spacing of 10 cm within the rows.

The crop received recommended dose of fertilizers at the rate of 40:20:0 (N: P: K) Kg/ha. The entire amount of phosphorous and half of the nitrogen were applied as basal dose during field preparation. The remainder half of the nitrogen was applied as top dressing after 45 days of sowing after second weeding. Manual weeding was done twice during the crop season, 20 and 40 days after sowing to keep the crop free from weed competition. No chemical was sprayed as the prevalent diseases finger and neck blast did not appear.

Data on grain yield were recorded on plot basis and converted into quintals per hectares (q ha^{-1}) for statistical analyses. Years were taken as environments for working out genotype environment interaction. The data were subjected to combined analyses of variance. The Additive Main Effect and Multiplicative Interaction (AMMI) analysis was performed in R using Agricolae package.

The AMMI model is stated below:
$$Y_{ge} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n Y_{gn}\pi_{en} + \theta_{ge}$$
Where
Y_{ge} = the yield of genotype;
g, in environment e;
μ = the grand mean;
α_g = the genotype mean deviation;
β_e = the environment mean deviation;
λ_n = the eigen value of the PCA axis n;
Y_{gn} and π_{en} = the genotype and environment PCA scores for the PCA axis n;
N = the number of PCA axes retained in the model; and θ_{ge} = the residual error.

The GGE biplot methodology, which is composed of two concepts, the genotype (G) concept and the genotype plus genotype by environment interaction (GGE) concept, was applied for visual examination of the genotype by environment interaction (GEI). The GGE biplot was constructed using first two principal components (PC1 and PC2) derived from subjecting environment centered yield data.

All the statistical analyses were performed using R software version 3.1.2 (R Core Team 2014). The GGE biplot analysis in R was performed using GGEBiplotGUI package. The AMMI analysis was performed using agricolae package in R software.

Result and Discussion
Analysis of Variance: The analysis of variance of grain yield (q ha^{-1}) of 5 varieties tested for 6 years is presented in table 1. Combined analysis of variance showed significant genotype × environment interactions exhibiting the influence of changes in environment on grain yield performance of genotypes. Similarly, the environmental factor *i.e.*, years and the genotype main effect was also significant. The relative magnitudes of G, E and G×E variances accounted for 10.38, 54.67 and 34.96 per cent, respectively. A large yield variation, explained by environments, indicated that the environments were diverse and a major part of variation in grain yield could be resulted from environmental changes (Table 1). The GEI significantly explained 34.96% of the treatments' variation in grain yield. Environment grain yield ranged from 17.28 q ha-1 in 2003 to 27.05 q ha-1 in 2004 (Table 2).

Genotype grain yield ranged from 22.65 (VR 708) to 27.84 q ha-1 (HR 374) (Table 2). Only a small portion (10.38 %) of the total sum of squares was attributed to genotypic effects. High percentage of E and G×E interaction out of total variations of finger millet grain yield implies the low efficiency of indirect selection to improve potential yield, ignoring the G×E interaction effect. The large yield variation due to environment justified the selection of GGE biplot as an appropriate method for analyzing the multi-year data. Large variation due to environment among all sources of variation was regarded as irrelevant to genotype evaluations (Yan and Kang 2003). Similar results for higher magnitude of environmental variance were reported earlier by Ullah *et al*. (2012). However, our focus should be on G and G × E, which is more relevant for genotypes evaluation in multi-year testing. The significance of G × E interaction might be attributed to differential influence of stress factors, sowing time, soil fertility and rainfall distribution encountered by genotypes in different years. The environmental factor in this study was different years at the same location. Environment is a combination of different factors *i.e.,* soil, weather and year. The soil element regarded as fixed, whereas the weather element was more complex because it has a persistent part represented by the general climatic zone, and an unpredictable part represented by year to year variation (Ullah *et al*. 2012).

AMMI analysis: In combined analysis of variance, environment had the greatest effect accounting for 83.81% of the total sum of squares (Table 3). The GEI sum of squares was about 3 times that of genotypes, indicating the importance of this source of variation (Table 3). Other researchers found this high percentage G×E and noted the importance of stability analysis and splitting of GEI to its parts (Najafian *et al.* 2010). Analysis of data shows the crossover type of GEI because the ranking of genotypes was not the same across environments. The GEI partitioning was done based on AMMI model, which is a valuable tool for identifying genotypes with either specific or wide adaptation. It is an important method as compared to joint regression based methods (Najafian *et al.* 2010). The partitioning of GEI sum of squares by using AMMI analysis indicated that the first two PCAs were highly significant. The first IPCA axis (IPCA1) accounted for 50.3% of the G×E interaction sum of squares. The second IPCA axis accounted for 38.2% of the interaction sum of squares. Both represent a total of 88.5% variation. The potential of AMMI analysis for describing G×E interactions in different crops has been proved (Misra *et al*. 2009; Lule *et al.* 2014 in finger millet, Farshadfar 2008 in wheat, Adugna 2008 in sorghum). The third IPCA was also significant in our study however; several researchers proposed using first two IPC axes and

believed these two to be enough for AMMI model. On the other hand, simpler AMMI 1 model also has merits because AMMI 1 often generates as many mega-environments as practical agricultural considerations (Mortazavian *et al.* 2014). Thus, the approximation of actual interaction pattern of the finger millet genotypes with 6 environments was best cross-validated with the first multiplicative terms of genotypes and environments that were easily visualized with the aid of a biplot (Figure 1). In AMMI 1 biplot, the abscissa showed the main effects and the ordinate the first multiplicative axis term (PC1). The genotypes close to ordinate expressed general adaptation, whereas the further genotypes depicted more specific adaptation to environments. The genotype HR 374 showed PC1 score close to zero and high mean yield indicating its general adaptation across the environments. The genotypes RAU 8 and VR 708 showed specific adaptation to environment 2. The genotypes PES 400 showed specific adaptation to environments 5 and 6. The PC 1 score of zero for environment 1 and 4 indicated stability in relative ranking of genotypes in these environments.

The AMMI 2 biplot revealed that the genotypes HR 374 and RAU 8 were observed to be similar in genetic performance based on small angle between these two genotypes and positive interaction was observed between HR 374, RAU 8 and PES 400 with environment 3. Environments 1 and 4 were close to biplot origin and thus were less interactive and considered to be good for selection of genotypes with average adaptation in the present study (Figure 2).

Genotype + Genotype × Environment Interaction Biplot analysis (GGE): The GGE biplot defines an ideal genotype, based on both mean performance and stability across environments (Aina *et al.* 2009). The GGE biplot is superior to the AMMI 1 graph in mega-environment analysis and genotype evaluation because it explains more G+GE than AMMI. Visualization of the "which-won-where" pattern of MET data is important for studying the possible existence of different mega-environments in a region (Figure 3). The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot (Yan and Kang 2003). Except PES 400 all other four genotypes *viz.*, VL *Mandua* 149, VR 708, RAU 8 and HR 374 were vertex genotypes in this investigation. The vertex genotype for each sector is the one that gives the highest yield for the environments that fall within that sector. Another important feature of Figure 3 is that it indicates environmental groupings, which suggests the possible existence of different mega-environments. Thus, based on biplot analysis of six environments of data, three mega-environments are suggested in Figure 3. The first mega environment contains environments E2,

with genotype VL *Mandua* 149 being the winner; the second mega environment contains environments E1, E3 and E4, with genotype HR 374 being the winner. The environments E5 and E6 make up another mega-environment, with RAU 8 the winner. Mean Performance and Stability of Genotypes view of GGE biplot showed that the genotypes HR 374 and RAU 8 had the highest mean yield and genotype VR 708 had the poorest mean yield. Mean yields of the genotypes were in the following order: HR 374> RAU 8> PES 400 > VL *Mandua* 149 > VR 708. Genotype HR 374 was the most stable and the performance of all other genotypes were variable (Figure 4).

The overall desirability of a genotype is a combination of high yield and stability in performance. An ideal genotype is one that has the highest yield and an absolute stability (Yan and Kang 2003). However, to get an ideal genotype is not easy. Genotypes closer to the ideal genotype are the most desired genotypes. Concentric circles rippling around the average environmental coordinate (AEC) of a genotype focussed GGE biplots (Figure 5) encompass genotypes that are relatively similar in their overall desirability (Kaya *et al*. 2006; Yan and Kang 2003). Therefore, genotype HR 374 which fell into the centre of concentric circles was ideal genotype in terms of higher yield ability and stability, compared with the rest of the genotypes. In addition RAU 8 located within the concentric circles, may be regarded as desirable genotype.

The GGE biplot way of measuring representativeness is to define an average environment and use it as a reference or benchmark. The average environment is indicated by small circle (Figures 6 and 7). The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments. Therefore, E3 was the most desirable test environment followed by E1 and E4.

Conclusion
The application of AMMI and GGE biplot to finger millet multi-year grain yield data facilitated the identification of the winning genotype in relation to the test environment. Based on the two analyses, AMMI and GGE-biplot models, the genotype HR 374 was characterized by high yield and stability, followed by the genotype RAU 8 which was close to the ideal genotype. Other 3 genotypes showed variable response in different environments. The interesting observation of the study was that although the genotype VL *Mandua* 149 showed consistent performance for all the years (Table 2), did not figure out as stable genotype in both the approaches.

Acknowledgements

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Table 1. Combined analysis of variance for grain yield (q ha^{-1}) of 5 finger millet genotypes evaluated for 6 environments.

Source of variation	Degree of freedom	Mean Squares	F value	Pr (>F)	Per cent of total[#] sum of squares
Environment (E)	5	344.20	32.69	1.37e^{-06}***	54.67
Replications (Environment)	12	10.53	1.52	0.15	
Genotypes (G)	4	81.66	11.75	9.83e^{-07}***	10.38
G x E	20	55.02	7.92	2.50e^{-09}***	34.96
Error	48	6.95			

***-Significant at the 0.1% probability level; [#]- Total is G+E+GXE

Table 2. Mean grain yield (q ha^{-1}) of the finger millet varieties in 6 environments.

Sl. No.	Years / Varieties	2002 (E1)	2003 (E2)	2004 (E3)	2005 (E4)	2006 (E5)	2007 (E6)	Mean
1	HR 374	25.38	17.28	33.74	28.96	32.34	27.85	**27.85**
2	RAU 8	25.38	13.83	31.49	23.92	34.11	30.62	**26.56**
3	PES 400	16.99	20.25	28.79	23.60	24.02	27.63	**23.55**
4	VR 708	18.37	10.37	17.96	24.14	33.07	32.00	**22.65**
5	VL 149	24.20	24.69	23.29	24.59	27.14	25.38	**24.88**
	Mean	**22.06**	**17.28**	**27.05**	**25.04**	**30.14**	**29.00**	**25.10**

Table 3. Additive Main effects and Multiplicative Interaction analysis of variance for grain yield (q ha^{-1}) of the genotypes across environments.

Source of variation	Degree of freedom	Sum of Squares	Mean Squares	F value	Percentage of total[#] sum of squares	Percentage of GxE sum of squares
Environments	5	7125.89	1425.18	204.47**	83.81	
Genotypes	4	293.44	73.36	10.53**	3.45	
Genotypes x Environments	20	1083.37	54.17	7.77**	12.74	
IPCA1	8	544.43	68.05	9.76**		50.3
IPCA2	6	414.18	69.03	9.90**		38.2
IPCA3	4	89.56	22.39	3.21*		8.3
Residuals	48	334.56	6.97			
CV (%)	12.71					

* and ** Significant difference at 0.05 and 0.01 probability level, respectively;
[#]- Total is G+E+GXE

Figure 1. AMMI biplot showing the main and interaction (PC1) effects of both genotypes and environments on grain yield. An estimate of the GE interaction effect for a specific genotype -environment combination is the product of their corresponding interaction PC1 scores.
AMMI, Additive main effects and multiplicative interaction; PC, Principal component analysis axis. Abbreviations of environments and genotypes are as given in Table 2.
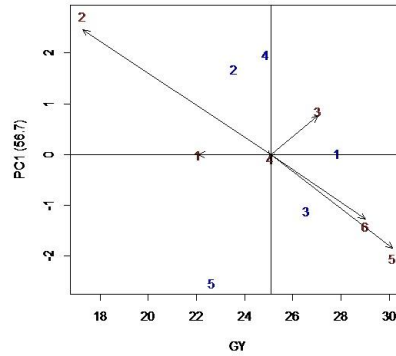

Figure 2. AMMI biplot analysis showing the mega-environments and their respective high yielding genotypes. Abbreviations of environments are as given in Table 2.
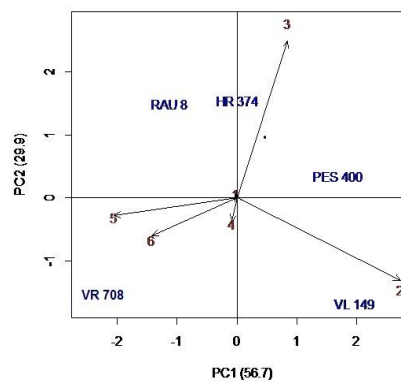

Figure 3. GGE biplot exhibiting grain yield performance of finger millet genotypes across environments. Abbreviations of environments are as given in Table 2.
**SVP-GH-(Column Metric Preserving); Centred by-2. Tester-Centered G+GE; Scaled by-0. No scaling.**


Which Won Where/What
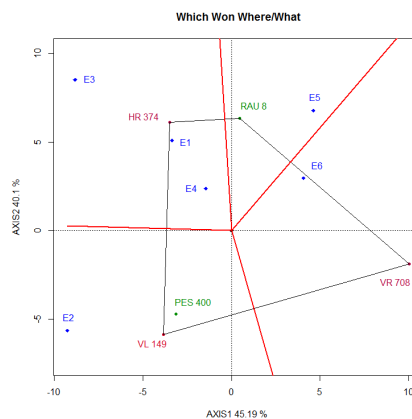
Figure 4. Average environment coordination (AEC) view of the GGE biplot based on environment- focused scaling for the means performance and stability of genotypes. Abbreviations of environments are as given in Table 2.
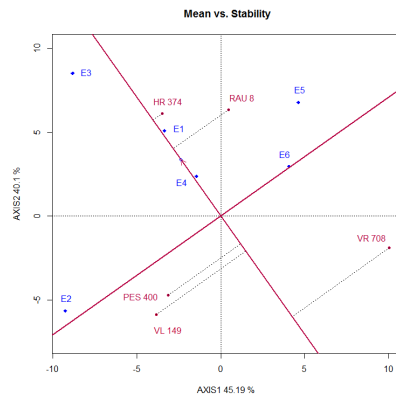
Figure 5. Based on average grain yield the ideal and stable finger millet genotypes across environments. The genotypes with the ideal genotype. Abbreviations of environments are as given in Table 2.
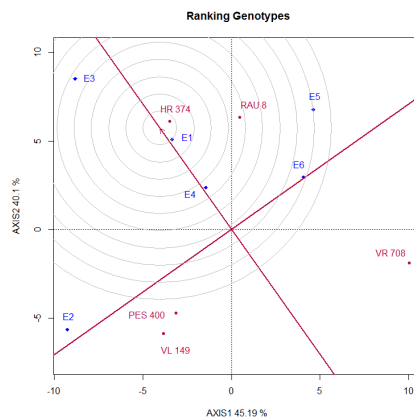
Figure 6. GGE biplot based on environment-focused scaling for comparison of the environments with the ideal environment. Abbreviations of environments are as given in Table 2.
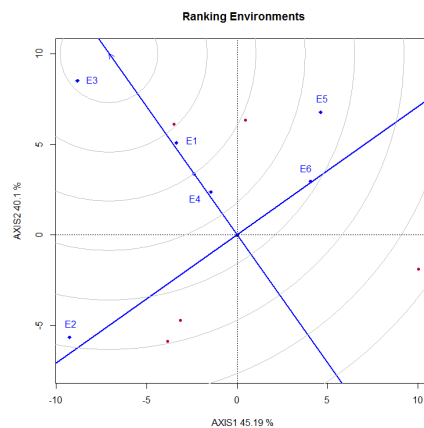
Figure 7. Based on grain yield comparison of environments with the ideal environment for discriminating and representativeness for finger millet genotypes. Abbreviations of environments are as given in Table 2.