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Research Article

Graphical analysis of genotype by environment interaction of Finger millet grain yield in India

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Abstract
Finger millet (*Eleusine coracana* (L.) Gaertn. subsp. *coracana*) is an important food-grain in semi-arid, hilly tribal areas of India and Africa for subsistence farming. GGE biplot techniques were applied for the assessment of stability and patterns of Genotype by Environment Interaction (GEI) in elite finger millet genotypes grown in four different locations. The combined ANOVA for grain yield of thirteen finger millet cultivars at four environments showed that Environments (E), Genotypes (G) and GEI were highly significant. The partitioning of GEI sum of squares showed that first and second IPCA axis accounted for 64.1% and 28.1% of the interaction sum of squares for GGE analysis. The biplot analysis grouped the four environments into two mega environments with VL 368 and VR 988 as winning genotypes. The genotype VL 368 was found to be an ideal genotype in terms of high yield and stability followed by KOPN 942, PPR 2773, TNAU 1214, VR 988 and VL 369 as desirable genotype. Among environments, E1 and E3 were the most interactive environments while, E2 and E4 showed little variation in genotypes relative ranking.

Key words
Eleusine coracana, Elite genotypes, GGE biplot, Stability

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn. subsp. *coracana*) is an important food-grain for subsistence farming in semi-arid, hilly tribal areas of India and Africa under rainfed ecology. The crop occupies special niche areas where the major food crops are difficult to grow. It has exceptional growth characteristics like resilience to climate change, drought tolerance and ability to perform better under adverse soil and weather conditions compared to major cereals. Besides, the crop also has excellent nutritional properties and has the potential to cope up with malnutrition. Its seeds are consumed in variety of forms, such as unleavened bread (roti), thin or thick porridge, and fermented porridge, and also used in brewing. Finger millet food has high biological value. Seed protein content is about 7.4 per cent, which is comparable to that of rice. However, some lines with 14.2 per cent protein are reported (Iyengar *et al.* 1945). Finger millet seeds are particularly rich in tryptophan, cystine, methionine, and total aromatic amino acids compared to other cereals (Kurien *et al.* 1959). The seeds are exceptionally rich in calcium containing about 0.34 per cent in whole seed compared with 0.01–0.06 per cent in most cereals (Kurien *et al.* 1959). The seeds are also rich in iron (46 mg kg-1) (Serna-Saldivar and Rooney 1995), which is much higher compared to wheat and rice. Despite of so many merits, finger millet has remained grossly a neglected crop in terms of research on genetic improvement as compared to other cereals. The crop national productivity is 1661 kg/ha, while few states like Tamil Nadu has recorded highest productivity of 3053 kg/ha (Directorate of Economics and Statistics 2014). This indicates that the crop grain yield potential has not been realized yet due to several factors including identification of widely adaptable stable varieties and regional deployment of high yielding cultivars.

Identification of wide adaptable stable cultivars with low GE interaction is the major aim of all crop breeders. There are two possible strategies for developing genotypes with low GE interactions. The first is sub-division or stratification of heterogeneous area into smaller, more homogeneous sub-regions, with breeding programs aimed at developing genotypes for specific sub-regions. However, even with this refinement, the level of interaction can remain high, because breeding area does not reduce the interaction of genotypes with location on years (Eberhart and Russell 1966, Tai 1979). The second strategy for reducing GE interaction involves selecting genotypes with a better stability across a wide

range of environments in order to better predict behaviour (Yaghotipoor and Farshadfar 2007).
Regional deployment of genotypes is more suitable for finger millet in comparison to wide adapted genotypes because of crop cultivation in varying ecologies right from hills at an altitude of 2400 m amsl to 400m amsl in Southern hemisphere of India. Early maturing genotypes are preferred in hills because of short growing season while medium to long duration genotypes are grown in plains.

Materials and Methods

Thirteen finger millet genotypes including three check varieties *viz*., VR 708, VL 352 and GPU 45 were grown at four diverse locations in India. The details of genotypes along with codes and mean grain yield at each location are given in Table 1. The experimental sites and their details are shown in Figure 1 and Table 2, respectively. The crop was raised in the rainy season of 2013 from June to October. Five rows (ten rows at Kolhapur location) of each genotype were planted in randomized complete block design with three replications. The row length was 3 m with row to row spacing of 22.5 cm. Initially the plots were over-planted and later thinned to maintain plant to plant spacing of 10 cm within the rows.
Fertilizers were applied at the rate of 50:40:25 (N: P: K) kg/ha, where the entire amount of phosphorous, potash and half of the nitrogen was applied as basal dose during field preparation. The remaining half of the nitrogen was applied as top dressing after 45 days of sowing. Manual weeding was done twice during the crop season, 20 and 40 days after sowing.
Data on grain yield were recorded on plot basis and converted into quintals per hectare~~s~~ for statistical analyses.

Statistical analysis

The data were subjected to combined analyses of variance followed by GGE biplot analyses using R software version 3.1.2 (R Core Team 2014) and PBtools (2014).

Results and Discussion

Analysis of Variance

The analysis of variance of grain yield (q ha^{-1}), fodder yield and days to maturity of 13 genotypes evaluated in four diverse locations showed significant genotype × environment interactions ($P<0.001$) exhibiting the influence of changes in environment on traits under study. Similarly, the environmental factor i.e. years and the genotype main effect was also significant ($P<0.001$). Even though the genotypes showed significant differences, the major part of the variation was explained by environments. This indicated that the environments were diverse and all the three traits were affected due to change in the environment. Similar results in finger millet have been reported by earlier workers also (Adugna et al. 2011, Lule et al. 2014, Sood et al. 2015).

Genotype+Genotype × Environment Interaction Biplot analysis (GGE)

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 (Yan et al. 2007). Visualization of the "which-won-where" pattern of MET data is important for studying the possible existence of different mega-environments in a region (Yan et al. 2000) (Figure 2). 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). The genotypes G13 (VR 988), G10 (VL 368), G8 (VL 348), G5 (PR 10-30) and G12 (VR 708) were vertex genotypes. The vertex genotype for each sector is the one that give the highest yield for the environments that fall within that sector. The four environments of our study were falling in three sectors, E1 and E4 in one sector and E2 in second and E3 in third sector. The environments E1 and E4 comprise one mega environment while E3 and E4 represent two different mega environments individually. The vertex genotypes G13 (VR 988), G10 (VL 368) and G5 (PR 10-30) were the winning genotypes for mega-environment 1, mega-environment 2 and mega-environment 3, respectively. The genotypes G8 (VL 348) and G12 (VR 708) although vertex genotypes, but were not corresponding to any environment. Mean performance and stability of genotypes view of GGE biplot showed that the genotypes G10 (VL 368), G2 (KOPN 942), G6 (TNAU 1214), G4 (PPR 2773), G11 (VL 369) and G13 (VR 988) had the highest mean yield, greater than the check varieties G1 (GPU 45) and G9 (VL 352) whereas the early duration national check G12 (VR 708) had the poorest mean yield. Among top three genotypes for grain yield G10 (VL 368) was the most stable, followed by G2 (KOPN 942), G6 (TNAU 1214) and G4 (PPR 2773), and the performance of all other genotypes was variable (Figure 3). However, G2 (KOPN 942), G6 (TNAU 1214) and G4 (PPR 2773) were the consistent genotypes across the environments although they had lower yield than G10 (VL 368).
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 (Yan and Kang 2003, Yan et al. 2007). Concentric circles rippling around the average environmental coordinate (AEC) of a genotype focussed GGE biplots (Figure 4) encompass genotypes that are relatively similar in their overall desirability (Yan et al. 2007, Kaya et al. 2006). Therefore, genotypes G2 (KOPN 942), G6 (TNAU 1214) and G4 (PPR 2773) which fell into the centre of concentric circles were ideal genotypes in terms of higher yield ability and stability, compared with the rest of the genotypes. In addition G11 (VL 369) and G10 (VL 368) 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. 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 test environments. Although none of the test environments was ideal however, E1 and E3 were the most discriminating environments for the genotypes under study (Figure 5). The superior genotypes for E1 and E3 were G11 (VL 369) and G10 (VL 368), respectively.

Figure 6 shows the interaction of genotypes with different environments and genotypes G5 and G12 were the largest rank changers. The E1 and E3 were the dynamic environments whereas E2 and E4 were consistent environments in terms of performance of genotypes. In figure 7 the yield of each environment is plotted against the individual genotypes. Here, it shows which environments are similar in terms of genotype performance. The genotypes G12, G3 and G5 performed poorly in E1, and G8 performed poorly in E3. Moreover, it is clearly visible that E2 and E4 are low yielding environments crowding the lowest quarter of the graph in which there is little difference in the yield of the thirteen genotypes under consideration. The genotypes G13 and G10 were consistently high yielding in all the four test environments, whereas G5 and G12 were low performers over the environments (Figure 8).

The application of GGE biplot to finger millet multi-year grain yield data facilitated the identification of the winning genotype VL 368 and VR 988 for two mega-environments of four test environments, respectively. The results of AMMI were also similar and therefore not included in the results and discussion. The genotype VL 368 was found to be an ideal genotype in terms of high yield and stability followed by KOPN 942, PPR 2773, TNAU 1214, VR 988 and VL 369 as desirable genotype. The GGE biplot results were although conclusive, it seems difficult to draw valid conclusion on recommendation of genotypes for all or specific environments based on one year data. But, these results suggest the use of afore-mentioned high yielding wide adaptable genotypes in finger millet breeding programme for yield improvement.

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Table 1. Mean grain yield (q/ha^{-1}) of the thirteen finger millet genotypes in four different locations

Codes	Genotypes	Locations				Mean
		Almora	Jagdalpur	Vizianagram	Kolhapur	
		E1	E2	E3	E4	
G1	GPU 45*	36.46	20.24	29.19	20.26	26.54
G2	KOPN 942	37.65	19.01	35.40	13.23	26.32
G3	KRI 007-01	25.30	16.78	28.14	16.23	21.61
G4	PPR 2773	37.12	19.75	35.34	15.19	26.85
G5	PR 10-30	16.79	18.27	43.84	13.70	23.15
G6	TNAU 1214	37.91	19.25	35.74	12.28	26.30
G7	TNAU 1226	36.78	17.28	25.54	13.49	23.27
G8	VL 348	32.83	18.27	21.35	11.23	20.92
G9	VL 352*	26.49	19.75	33.10	13.22	23.14
G10	VL 368	37.14	18.76	43.00	16.22	28.78
G11	VL 369	42.25	15.55	32.86	11.38	25.51
G12	VR 708*	10.79	12.34	27.39	14.25	16.19
G13	VR 988	42.96	17.28	29.71	20.76	27.68
	Mean	32.35	18.20	32.16	14.99	
	SE (m)	1.90	0.96	2.66	1.08	
	CD at 5%	5.53	2.81	7.73	3.14	

Table 2. Finger millet trials evaluation sites along with geographical details

Trial sites	Soil type	Altitude (masl)	Annual Rainfall (mm)	Global position	
				Latitude	Longitude
Almora (E1)	Sandy Loam	1250	1000	79°39'E	25°35'N
Jagdalpur (E2)	Sandy Loam	554.42	1405	$19^0$05' N	$81^0$57' E
Vizianagram (E3)	Red Sandy Loam	63	1100	18°7'N	83°25'E
Kolhapur (E4)	Light textured shallow	574	1015.3	$16^0$43'N	$74^0$14'E

Table 3. Combined analysis of variance for grain yield (q ha^{-1}) of 13 finger millet genotypes evaluated in four locations

Source of variation	Degree of freedom	Mean Squares	F value	Pr (>F)	Per cent of total# sum of squares
Environment (E)	3	3473.1	839.89***	2.47e^{-10}	66.23
Replications (Environment)	8	4.1	0.47	0.873	
Genotypes (G)	12	139.4	15.92***	2.2e^{-10}	10.64
G x E	36	101.1	11.54***	2.2e^{-10}	23.13
Error	96	8.8			

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

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Fig. 1. Experimental locations in India.

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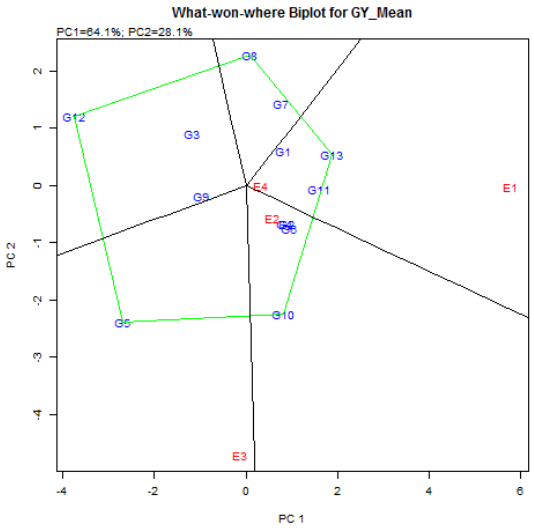

Fig. 2. GGE biplot exhibiting grain yield performance of finger millet genotypes across environments. Abbreviations of genotypes and environments are as given in Table 1. SVP-GH-(Column Metric Preserving); Centred by-2. Tester-Centered G+GE; Scaled by-0. No scaling.

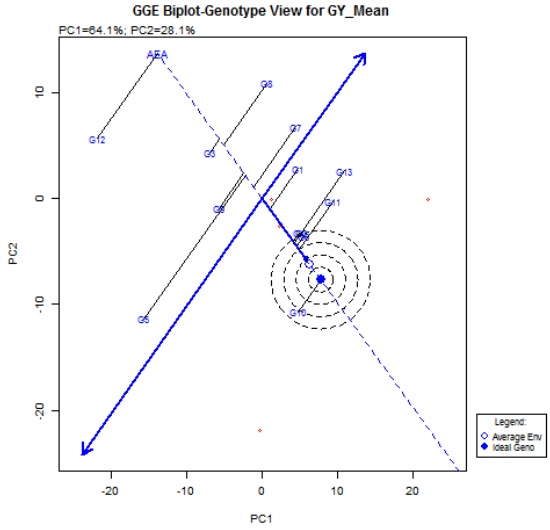

Fig. 3. Average environment coordination (AEC) view of the GGE biplot based on environment- focused scaling for the means performance and stability of genotypes.

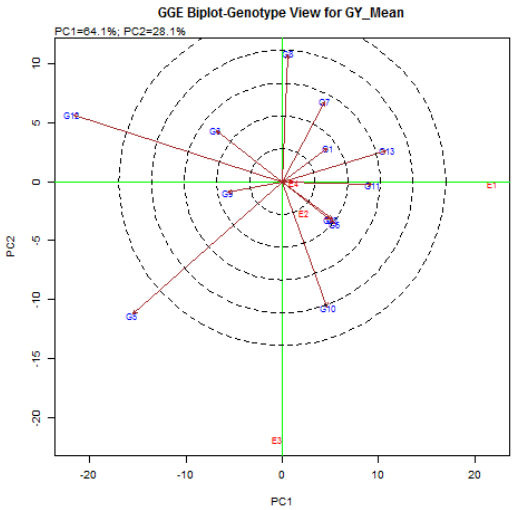

Fig. 4. Based on average grain yield the ideal and stable finger millet genotypes across environments. The genotypes with the ideal genotype.

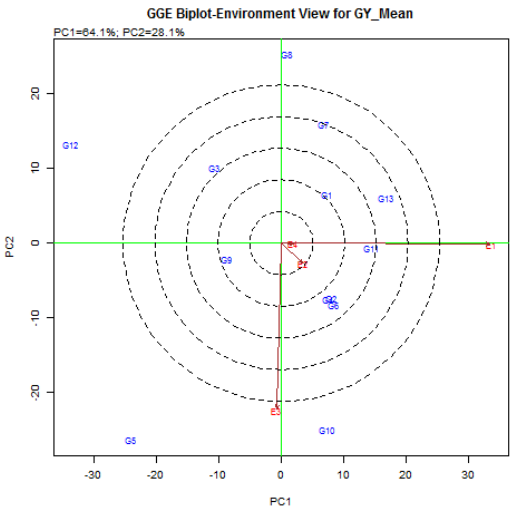

Fig. 5. Based on grain yield comparison of environments with the ideal environment for discriminating and representativeness for finger millet genotypes.

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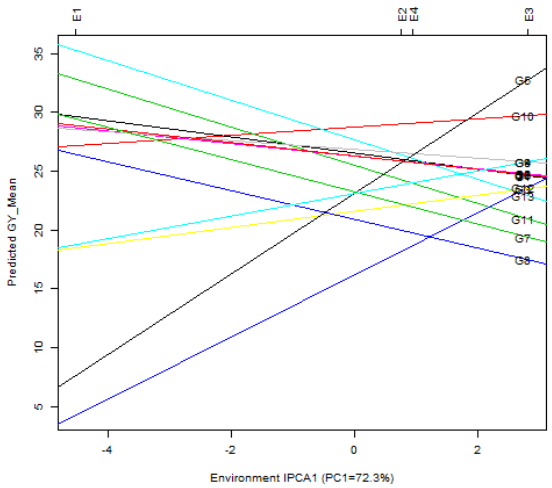

Fig. 6. Adapatation map of genotypes in different environments.

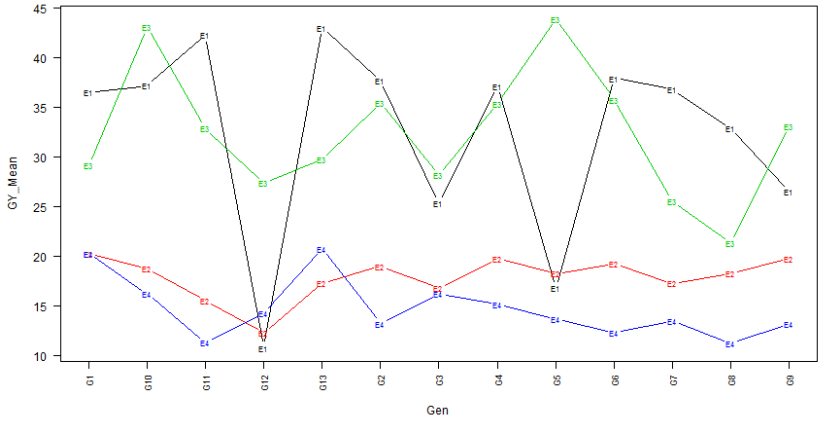

Fig. 7. Response plot of grain yield mean of environments corresponding to individual genotypes.

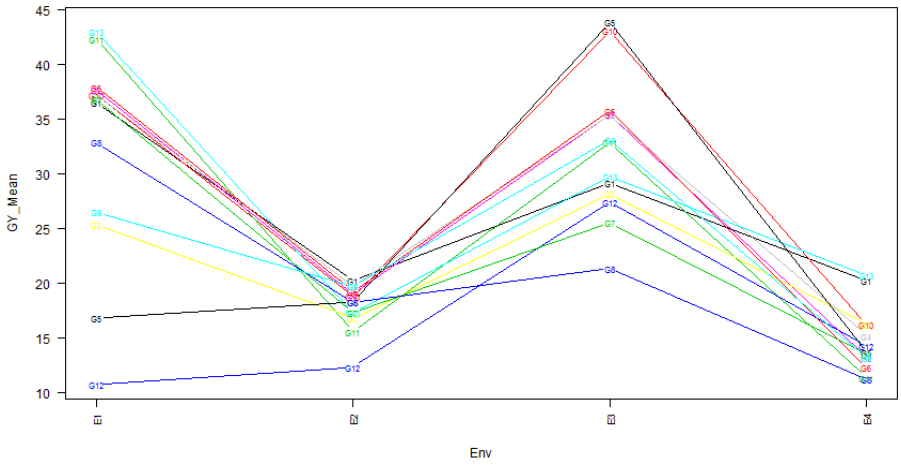

Fig. 8. Response plot of grain yield mean of genotypes in each environment.