

GGE biplot analysis of genotype × environment interaction in *rabi* grain sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

Nature and complexity of genotype × environment interaction (GEI) was studied among eight *rabi* grain sorghum cultivars across 11 locations during *rabi* 2011-12 and 2012-13 using GGE biplot analysis. Location (L) contributed for 89.9% of variation for grain yield, while genotypes (G) and G × L interactions accounted for 1% and 9% of variation only. The first two principal components (PCs) of GGE biplot accounted for 50% of variation in data for grain yield, which not ideally explained overall variation in the data. However, the biplot clearly demonstrated that across environments, SPH 1721 was the highest yielding stable genotype followed by CSH 15R. High crossover GEI was recorded among the testing locations and close correlation among these locations was not detected. 'Which-won-where' analysis detected three mega-environments (ME) among the testing locations, with ME1 represented by 5 locations, ME2 with 4 locations and ME3 with 2 locations. The study indicated the possibility to reduce the number of testing locations.

Key words : GGE biplot, G×E interaction, sorghum, mega-environment

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most important cereal grown extensively in the arid and semi-arid tropics under low fertile soil conditions. India ranks first in area and second to the USA in production across the world [1]. Sorghum of two adaptive types, viz., *kharif* and *rabi* sorghum, are cultivated in India, of which *rabi*

sorghum is predominantly consumed as food grain [2, 3]. Productivity of *rabi* sorghum is much lower than the *kharif* sorghum [4]. Concentrated breeding efforts are being made under All India Coordinated Sorghum Improvement Project (AICSIP) to release better yielding *rabi* cultivars. Multi-location trials (MLT) play a crucial role in the process of identification and release of improved and stable cultivars. However, often during the analysis of MLT data genotype evaluation is limited on genotype main effects (G), while genotype × environment interactions (GEI) are ignored as noise, which is otherwise equally important [5]. Various statistical models like analysis of variance (ANOVA), principal component analysis (PCA), and linear regression (LR) have been suggested over time to understand the complex GEI [6, 7]. Each procedure has its own advantages and disadvantages [6, 8-10]. Genotype (G) main effect plus GE interaction (GGE) biplot analysis [7] is a robust method to visualize and interpret MLT data graphically. Utility of GGE biplot in understanding GEI has been demonstrated in many crops including sorghum [10, 11]. To have an insight into the nature and complexity of GEI in the *rabi* grain sorghum MLT data, performances of eight *rabi* sorghum cultivars across 11 locations for two years (*rabi* seasons of 2011-12 and 2012-13) were studied using GGE biplot analysis. Efforts were also made to identify mega-environments within the testing locations.

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Materials and methods

Plant materials and testing locations

In the current study a sub-set of eight genotypes from the AICSIP *rabi* grain sorghum database was used, in which two hybrids and 6 varieties were grown over 11 locations (environments) during the *rabi* seasons of 2011-12 and 2012-13. Details about the test locations and the cultivars are given in Table 1. All four major *rabi* sorghum growing states of India, viz., Maharashtra, Karnataka, Gujarat and Telangana were represented in the study. Experimental materials were sown during September-October in randomized block design with three replications. Each entry was sown in a plot with 6 rows of 6 m length with 45 cm × 15 cm crop geometry. Internal four rows were considered for estimation of grain yield. Standard crop management practices were followed across all locations. Yield data were recorded at physiological maturity. Plot yield data were converted to kg ha⁻¹ using the plot size as factor.

Data analysis

Statistical theory of GGE methodology as described by Yan and Kang [7] was followed in the present study. Data was evaluated as described by Rakshit et al [10]. GGE biplot software ver. 6.3 was used in the analysis [13]. Data were analyzed by scaling the data with standard deviation and weighing with heritability (*h*) ('Scaling 2' option) and tester centered GGE biplot (centering 2) was generated as suggested by Yan [14]. 'Mean vs. stability' option of GGE biplot software was used to evaluate genotype using genotype-focused singular value partitioning (SVP = 1). Environment-

focused singular value partitioning (SVP = 2) was used to evaluate locations using 'Relation among testers' option of GGE biplot software. 'Which-won-where' option was used to identify the mega-environments and to find out winning genotype in a given set of environments.

Results and discussion

Combined analysis of variance for grain yield of the eight sorghum cultivars tested in 11 environments over two years showed that location (L) explained highest proportion of variation for grain yield, accounting for 89.9% of it, followed by G × L interactions (GLI) effects (9%) and genotype (1%). The GLI effects were much higher than the genotypic effects. Observed contribution of location is higher than as reported by Rakshit et al. [10] in sorghum and other crops [15-17]. Observed effects of G and GLI were close to as reported in pea [18]. Higher proportion of GLI in explaining variation as against contribution of G alone indicated possible existence of different mega-environments among the testing locations [10, 19, 20].

Identification of stable genotypes with highest mean performance

In GGE biplot the complex GEIs are partitioned in different principal components (PCs) and the data are presented graphically against various PCs [5]. Fig. 1 depicts the GGE biplot summarizing mean performance and stability of genotypes using average environment coordination (AEC) method. Projection of a genotype over AEC abscissa (line with single arrow head in Fig. 1) indicates its average yield, while dispersion of the genotype along the AEC ordinate (double arrowed line

Table 1. Codes and details of the genotypes and environments used in the study

Location code	Centre	State	Genotype code	Genotype name	Pedigree	Developing center
E1	Annegiri	Karnataka	G1	CSH 15R	104A × RS 585	Solapur
E2	Aurangabad	Maharashtra	G2	CSV 22	SPV 1359 × RSP 2	Rahuri
E3	Bagalkot	Karnataka	G3	SPH 1721	104A × SLR 75	Solapur
E4	Bijapur	Karnataka	G4	SPV 2139	SPV 1502 × RSFR 9509-14-1-1-1-1	Rahuri
E5	Dharwad	Karnataka	G5	SPV 2140	RSV 491 × RSV 273-44-1-1-1-1	Rahuri
E6	Ekarjuna	Maharashtra	G6	SPV 2143	Sel from cross PVR 453 × Gidda Maldandi	Parbhani
E7	Parbhani	Maharashtra	G7	SPV 2144	Sel from cross Phule Yashoda × PVR 655	Parbhani
E8	Rahuri	Maharashtra	G8	SPV 2152	M35-1 × CSV216R	Bijapur
E9	Solapur	Maharashtra				
E10	Tancha	Gujarat				
E11	Tandur	Telangana				

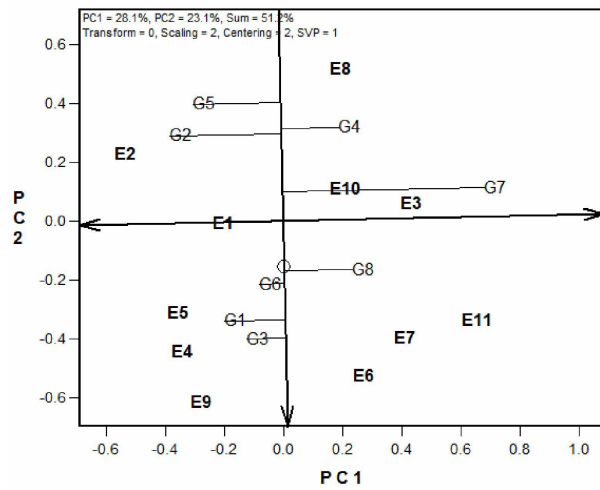


Fig. 1. GGE Biplots of the combined analysis for grain yield: Mean vs. stability of the genotypes (genotype and environment codes are in Table 1)

in Fig. 1) is indicative of its stability. The greater the absolute length of the projection of a cultivar, the less stable it is [12]. Thus, G3 is the best performing cultivar followed by G1, G6 and others. G7 is the most unstable cultivar followed by G2 and G8. Yan *et al.* [21] suggested that if the first two PCs explain more than 60% of the variability in the data and G together with GE explains over 10% of the variation the overall variability in G × E data can be adequately summarized in the biplot. However, in the present study the first two PCs in the biplot explained about 51.2% of variation in data for grain yield and G + GE explained 10% of the variation. Thus, it may be pointed out that unlike as reported in sorghum earlier [10] the biplot failed to summarize the complexity in the data effectively. Still it was observed that very effectively it could identify the best performing cultivar (G3) in the biplot (Table 2). The same genotype, G3 was closest to the 'ideal genotype', which is denoted by small circle at the center of broken concentric rings in Fig. 2. An 'ideal genotype' is high performer with high

Table 2. Year-wise grain yield (kg ha⁻¹) of *rabi* sorghum cultivars under testing over two years

Location/ year	Cultivars							
	G1	G2	G3	G4	G5	G6	G7	G8
2012								
E1	3035	2274	2459	2737	2407	3012	2695	2119
E2	2153	3610	2724	2895	3592	3261	1970	2853
E3	3906	3290	4362	4714	4473	4625	4598	3765
E4	2271	2197	2532	1792	2019	1935	2181	2486
E5	3436	4064	4501	3897	3868	4194	4081	3590
E6	2874	2360	2410	3201	2192	2622	2922	3249
E7	3219	3330	3816	3433	3067	3259	3881	3763
E8	2417	2727	2450	2976	2649	2357	2769	2802
E9	1651	1176	1796	1357	1210	1308	1298	1368
E10	913	1333	1417	1706	559	811	1039	1105
E11	1990	2082	2228	1790	1972	2155	2629	2593
Mean	2533	2586	2791	2772	2546	2685	2733	2699
2013								
E1	4018	3676	2985	3162	3354	2817	3042	2339
E2	2492	3423	2733	2252	1802	1622	1532	1712
E3	3281	3271	3347	3333	2788	2573	3465	2889
E4	1866	1735	1770	1428	1608	1463	903	1665
E5	3425	2751	3737	2891	3302	3354	2110	2673
E6	2764	2195	2764	2358	1951	3008	2057	2439
E7	3607	3438	3640	2826	3565	3712	3844	3691
E8	2632	2733	2850	2904	3027	2240	2703	2781
E9	1571	1148	1524	960	1123	1180	676	1190
E10	793	1252	1402	1081	1162	766	1267	1186
E11	2652	2354	2526	2898	2225	2438	2414	2246
Mean	2646	2543	2662	2372	2355	2288	2183	2255
Grand mean	2589	2565	2726	2572	2451	2487	2458	2477

stability across environments [5]. In 16 occasions G3 ranked among top three best performing genotypes among 22 environments. The ease with which such genotypes could be identified using GGE biplot cannot be exercised from mean table alone (Table 2). In seven locations (E1, E4, E5, E6, E7, E9 and E11) G3 recorded above average performance with best performance at E4 and E9, while at E8, E3 and E10 it recorded below average performance (Fig. 3). This as well as higher contribution of GLI over G to total variation in the MLT data suggested existence of high crossover GEI. Similar observation was reported in sorghum and other crops [10, 15, 16, 22, 23].

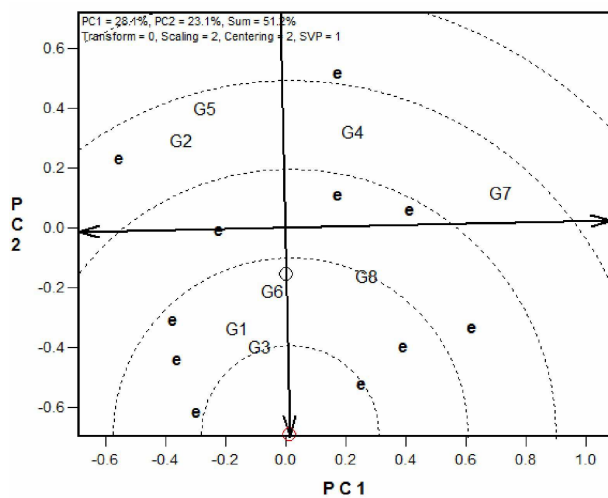


Fig. 2. Ranking of genotypes relative to an ideal genotype (the small circle at the center of the concentric circles on average-environment coordinate, AEC) (genotype codes are in Table 1)

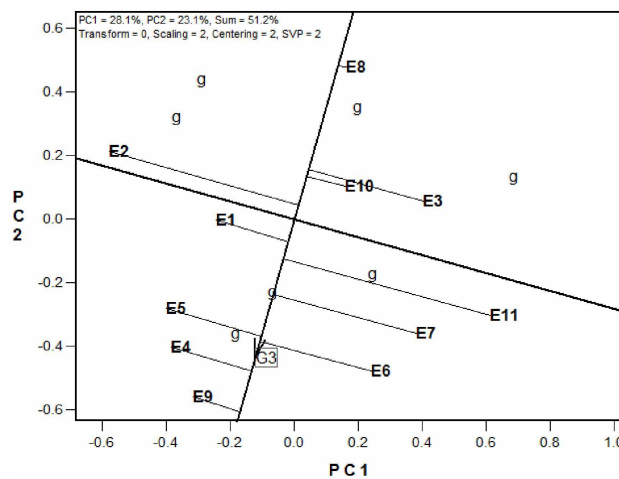


Fig. 3. Ranking of environments based on the performance of highest yielding genotype, G3 (genotype and environment codes are in Table 1)

Environment evaluation

Relations among the test environments is presented in Fig. 4, which was produced by environment centered preserving of data (SPV = 2). Angles between the environment vectors in such biplots indicate their relationships as the cosine of the vector angles is indicative of their correlation [5]. An acute angle between two environment vectors is indicative of positive correlation, while an obtuse angle indicates negative correlation and right angle suggests no relation ($r = \sim 0$). Unlike earlier report in sorghum [10] the environments indicated very complex relationships among themselves. The ‘Ideal environment’ is denoted by a small circle at the center of the broken concentric rings in Fig. 4. ‘Ideal environment’ has maximum representativeness as well as discrimination ability with highest vector length. E4, E15, E6, E7, E9 and E11 with acute vector angles with ideal environment are highly correlated. Closer relationships between the test environments suggested that same information could be obtained from fewer environments. Similar environments may be removed from multi-location testing of *rabi* sorghum cultivars as they will generate similar information. This will help in optimal allocation of the scarce resources during multi-location trial allocations [10]. On the contrary, several location vectors showed obtuse angles among themselves. For example E2 with E11, E8 with E9 or E5 with E10 showed near opposite relationships. Observed mixture of crossover and non-crossover types of GEI in MET data is of very common occurrence [10, 11, 16, 22] and is indicative of existence of mega-environments within the testing locations. Discrimination ability of the locations is measured by the length of the environment vectors and

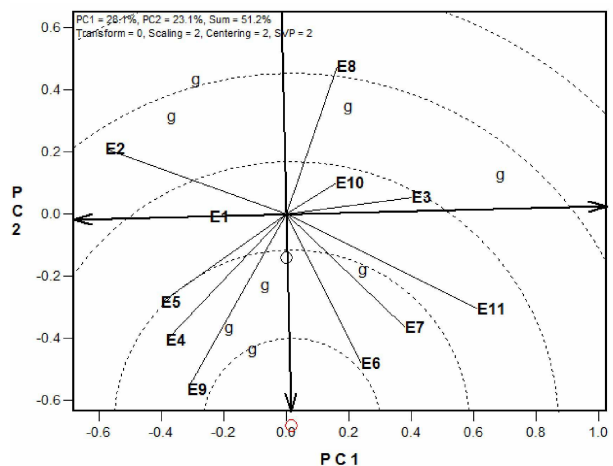


Fig. 4. Ranking of environments based on discriminating ability and representativeness (environment codes are in Table 1)

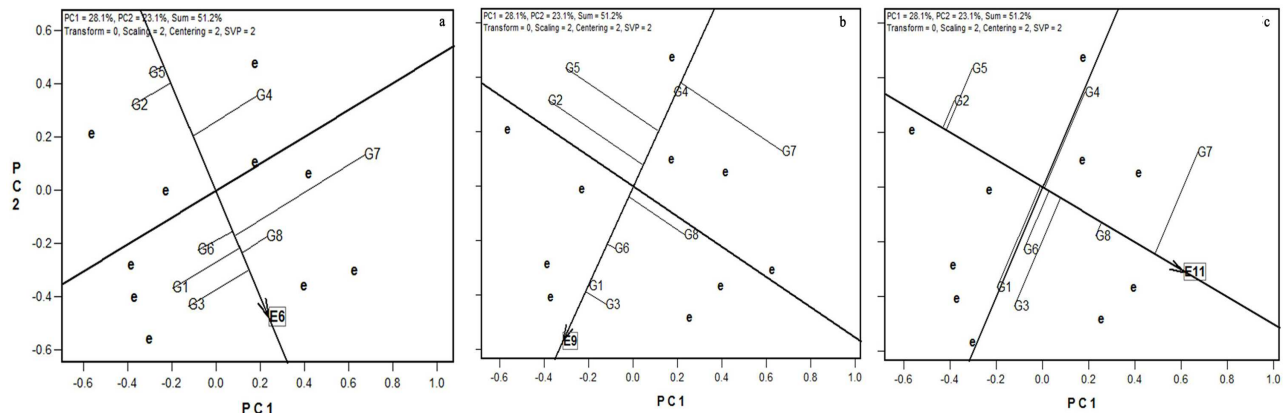


Fig. 5. Ranking of genotypes based on their performance in E6 (a), E9 (b) and E11 (c) (genotype codes are in Table 1)

the testing locations may be ranked from top to bottom as $E11 > E2 = E9 = E8 > E4 = E6 > E5 > E3 > E1 = E10$. E6 and E9 found to be closest to the ideal environment (Fig. 4). In both these locations G3 ranked best, while in E11 G7 top performed (Fig. 5).

Which-won-where and mega-environment identification

Most attractive feature of GGE biplot is 'Which-won-where' analysis, in which crossover GEI, mega-environment differentiation, specific adaptation of genotypes etc. are graphically addressed [5, 10-12, 24]. In the current study 'Which-won-where' biplots for grain yield gave rise to a hexagon with six genotypes, G1, G2, G5, G4, G7 and G3 at the vertices (Fig. 6). The equality lines divided the biplot into six sectors effectively. Eleven testing locations were spread in five sectors within the biplot, four in one, three in another, two locations in another sector, and one each in two separate sectors. This demonstrated that the testing locations could be partitioned into mega-environments (ME). Two sectors with sole location did not have any specific cultivar as winner, hence they effectively did not represent any distinctly separate ME and were merged with nearest MEs. First ME (ME1) was represented by E3, E7, E10, E11 and E8 with G7 followed by G4 as the winning genotypes. Second ME (ME2) was composed of E4, E6, E9 and with G3 and G1 as winners, and third ME (ME2) was represented by E1 and E2 with G2 as nominal genotype. No relation could be established among the locations within one ME and their geographical location (Table 1 and Fig. 6). Similar observation was made earlier [10]. The study showed that instead of conducting MLTs across closely related locations, near similar conclusion could be drawn from fewer locations clustered within a ME. However,

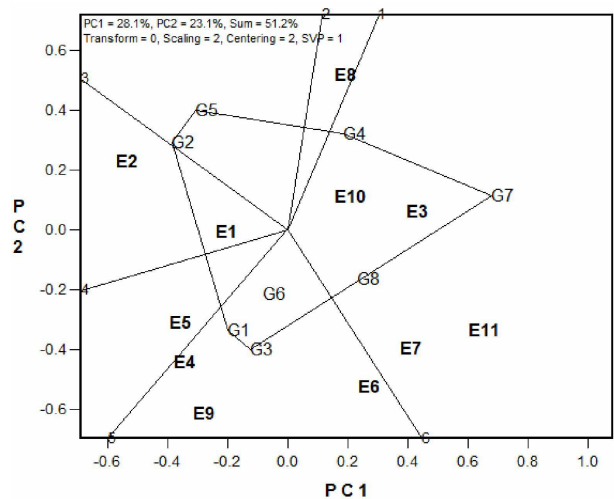


Fig. 6. GGE Biplots of the combined analysis for grain yield: 'Which-won-where' (genotype and environment codes are in Table 1)

reported groupings of environments need to be reconfirmed using MLT data over larger years of data as demonstrated by earlier authors [12, 24, 25].

The study demonstrated the utility of GGE biplot analysis in identifying stable and superior genotypes and visualization of mixed crossover effects (complex GEI) even if the first two PCs are not large enough. In view of detection of MEs within testing locations it is possible to reduce the number of testing locations without compromise with the final conclusion. However, the ME pattern needs to be reconfirmed over years before attempting to the exercise. In view of location specific adaptation of cultivars breeders need to focus on location-specific breeding efforts rather attempting breeding cultivars with wide adaptation.

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