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RESEARCH ARTICLE

Determining the potential and adaptability of multi-cut forage sorghum (*Sorghum bicolor* L. Moench) genotypes through AMMI, genotype by environment interaction and GGE biplot analysis

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Abstract

Forage sorghum **(***Sorghum bicolor* L. Moench**)** is a vital crop in the global fodder supply chain, especially in arid and semi-arid regions, due to its high biomass yield, efficient water utilization and adaptability to diverse climates. The challenge in optimizing forage sorghum productivity lies in the intricate interaction between genotype and environment **(**G × E interactions). Seventeen multi-cut forage sorghum genotypes were evaluated under field conditions for their green fodder yield (GFY) and dry fodder yield (DFY) during the *kharif* season (Wet season) at three locations, namely, Pantnagar, Ludhiana and Hisar employing biplot models such as genotype + genotype × environment (GGE), and additive main effects and multiplicative interaction (AMMI). Statistical analysis revealed significant effects of genotype, environment, and their interactions on the target traits, with AMMI and GGE biplot models capturing over 87.9% of the total variance, thus demonstrating their applicability. The environment accounted for the majority of the variability in GFY and DFY, highlighting its influence on sorghum production. The genotypes CSH 43MF and SPH 2018 emerged as superior hybrids across all environments, while CSV 33MF (variety)**,** SPH 2024 and SPH 2043 showed specific adaptability to the Pantnagar, Ludhiana and Hisar environments, respectively. The findings also underscore the potential of multicut forage sorghum varieties/hybrids, CSH 43MF and SPH 2018, for enhancing green and dry fodder production under three different mega-environments in northern India, thereby contributing to the region's agricultural sustainability and fodder security.

Keywords: *Sorghum bicolor* L., multicut, environment, AMMI, GGE

Introduction

Sorghum bicolor (L.) Moench, a 5F crop (food, feed, fodder, fuel and fibre), is cultivated across the arid and semi-arid tropics of the world (Laxmi et al., 2019). It is a diploid species (2n = 2x=20) primarily self-pollinated with 5 to 30% out-crossing. It contains high levels of micronutrients like zinc, iron and phosphorus. After wheat, rice, maize and soybeans, it is the world's fifth-largest multipurpose cereal crop (Taylor and Duodu 2018). In 2023-24, 47.3 million metric tons of sorghum were produced in the world (Department of Agriculture and Farmers Welfare 2024). Cultivated on 4.48 mha of fertile land, it had a production of 4.38 mt in 2019-20 with a productivity level of 1051 kg/ha (Anonymous 2020). Yield is a complex quantitative trait greatly influenced by genotype-environment interaction, and the selection of superior genotypes based on evaluation trials in a single environment within a year may not be suitable. To enhance the production and productivity of forage sorghum, it is crucial to investigate the genotype-by-environment interaction for the development of high-yielding and stable varieties/hybrids. Additionally, to increase the efficiency of detecting genotypes particular to each season, the use of the additive main effects and multiplicative interaction (AMMI) model and Genotype and Genotype × Environment (GGE) biplot is helpful in identifying stable and acceptable forage sorghum genotypes under various seasonal situations, specifically for cultivation in northern India. The way that genotypes interact with various environments determines whether selection in a breeding effort is successful. (Kumar et al. 2009) stated that the observed yield of each cultivar in each test environment is a measure of the genotype × environment (GE) interaction, the environment main impact (E) and the genotype main effect (G). Generally, E accounts for 80% or more of the overall yield variation;

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however, Heidari et al. (2016) stated that G and GE are more important for cultivar evaluation. The relationship between genotype and phenotype, as well as the advancement of selection, is weakened by the GE interaction. Plant breeders understand the value of looking at the whole spectrum of genetic diversity instead of just GEI. Numerous scholars have examined the GE interaction in great detail, and several analytical techniques have been proposed to do so. These include univariate techniques like the coefficient of variability of Francis and Kannenberg, the mean-variance component of Plaisted and Peterson for pair-wise GE interactions, the ecovalence of Wricke, the stability variance of Shukla, the regression coefficients of Finlay and Wilkinson, Perkins and Jinks, and the sum of squared deviations from regression of Eberhart and Russell model.

Modified models, such as the AMMI model and the GGE biplot, are useful for successfully describing, analyzing, comprehending and predicting the GEI component from overall genetic variation. AMMI analysis can help determine the performance of various genotypes (crop types) under different environmental variables (e.g., varying soil types or climate conditions). This information is invaluable in creating resilient and flexible cultivars. Many sites, seasons and years are typically used to test a large number of genotypes, and without the aid of a graphical display of the data, it is frequently challenging to ascertain the pattern of genotypic response across locations or seasons. Principal component analysis (PCA) produces biplots that help us comprehend the link between GEI, environment, and genotypes, aiding in the identification of stable and highly productive genotypes for specific environments (Kumar et al., 2016). Genotype × environment interaction has been visualized using two forms of biplots that are commonly used in conjunction with the GGE biplot and the AMMI biplot.

In contrast to AMMI analysis, which uses double-centred principal component analysis (PCA), GGE biplot analysis is based on environment-centred PCA. However, AMMI might be deceptive if the goal is to determine which-won-where (Rakshit et al. 2014). Furthermore, when it comes to explaining the PC1 score—which indicates a genotypic influence rather than an additive main effect—the GGE biplot is more biological and logical for practice than AMMI (Akinwale et al. 2014). Numerous studies (Enyew et al. 2021; Singh et al. 2019; Khandelwal et al. 2024) have demonstrated the usefulness of the AMMI and GGE techniques in their research to identify genotypes that potentially produce consistent performance across a range of environmental conditions. A which-won-where pattern, environment ranking, mean vs. stability, genotype rankings, discriminativeness and representativeness of the environments and the application of singular value decomposition (SVD) are all included in the GGE biplot. In order to determine the potential and adaptability of multi-cut forage sorghum varieties/hybrids for northern India, multilocation evaluation trials were conducted to estimate the genotype-environment interaction pattern for green fodder yield (GFY) and dry fodder yield (DFY) across three environments/locations, namely, Hisar (E1), Ludhiana (E2) and Pantnagar (E3).

Material and methods

Plant material, site and layout

The material for the study included 17 multi-cut forage sorghum genotypes, including 3 checks, 2 varieties and 12 hybrids (Table 1) that were obtained from All India Coordinated Research Projects (AICRP) on Indian Institute of Millets Research (IIMR), Hyderabad. The experiment was conducted at three experimental sites: Chaudhary Charan Singh Haryana Agricultural University (CCSHAU, Hisar), G. B. Pant University of Agriculture and Technology, Pantnagar, and Punjab Agricultural University, Ludhiana. HAU is situated at 29.10°N, 75.46°E, 215.2 m above mean sea level has sandy loam soil type with pH value of 7.8 whereas G.B Pant University, situated at 29.0°N, 79.30°E, 243.84 m above mean sea level and PAU situated at 30°N, 75.52°E, 247 m above mean sea level has sandy clay loam (pH 7.2) and sandy loam (pH 7.6) kind of soil type, respectively. The mean temperature, rainfall and humidity of the three test

locations over the experimental period are depicted in Fig. 1.

The experiment was laid out in randomized complete block design (RCBD) with three replications across the three test environments during *kharif* 2023 (Monsoon cropping season). The crop was sown before monsoon and harvested in the fall. The seeds of various genotypes (treatment) were planted in 5 x 4.5 m (plot size) using plant-to-plant spacing of 15 cm and row-to-row spacing of 25 cm. Data for morphological parameters was recorded by an average of 5 randomly selected plants from each plot 70 days after sowing, 2nd cut was taken after 50 days of 1st cut and 3rd cut was taken 40 days after 2nd cut. Green Fodder Yield (GFY) was recorded on a plot basis and for dry fodder yield (DFY) estimation, 500 g sample of green fodder was taken at the time of harvest of each cut per plot. In addition, data on plant height (PH, measured from base to flag leaf), leaf length (LL, 4-5 leaves from bottom) and leaf width (LW, measured on 4 to 5 leaves from bottom) were also recorded. Recommended agronomic packages of practice were adopted.

Statistical analysis

With genotypes and locations fixed and all interactions, including replications and errors, random, the combined analysis of variance across locations was performed using R studios. If random error is excluded, the fundamental effects model for a multi-environment experiment can be expressed as $Y_{ij} = \mu + \alpha_i + ß_j + \gamma_{ij}$, where Y_{ij} is the measured mean of i^{th} genotype in j^{th} environment, μ is the grand mean, α_i is the main effect of i^{th} genotype, $ß_j$ is the main effect of j^{th} environment, j_{ij} is interaction between i^{th} genotype and j^{th} environment. Genotype plus genotype × environment (G+GE) interaction is examined in GGE biplots. To do this, the G+GE effect is isolated from the observed mean, and the model ultimately becomes as $Y_{ij} - (\mu + ß_j) = \alpha_i$. But in the case of AMMI, the genotype impact is likewise isolated, and only the genotype-environment (GE) interaction is examined for the biplot; ultimately, the model becomes as $Y_{ij} - (\mu + ß_j + \gamma_{ij}) = \alpha_i$.

In this research article, we have discussed about the mathematical expressions for the G+GE model partitioning since the mathematical partitioning of GE is similar with the exception of the model difference. The effect of G+GE (for GGE and GE for AMMI) is divided into multiplicative parts using SVD as $Y_{ij} - \mu - ßj = l_1 x_{i1} h_{j1} + l_2 x_{i2} h_{j2} + e_{ij,}$ Where l_1 and l_2 are the singular values (SV) for the first and second principal

Table 1. A list of genotypes under study

S. No.	Genotype no.	Accession	Hybrid/Variety
1	G1	CSH 24MF	Check (ICSA 467 x PC 6)
2	G2	CSH 43MF	Check (11A2 x PC 6)
3	G3	CSV 33MF (C)	EMS mutant of Co (FS) 29
4	G4	SPH 1998	*Private entry*
5	G5	SPH 2018	*Private*
6	G6	SPH 2019	*Private*
7	G7	SPH 2039	*Private*
8	G8	SPH 2040	*Private*
9	G9	SPH 2041	*Private*
10	G10	SPH 2042	*Private*
11	G11	SPH 2043	*Private*
12	G12	SPH 2044	*Private* MJ-10A x MJ-233-3-6R
13	G13	SPH 2045	CMSA9 x Pant Chari 6
14	G14	SPH 2046	CMSA5 x Pant Chari 6
15	G15	SPH 2047	*Private*
16	G16	SPV 3045	Composite of 6 lines
17	G17	SPV 3046	Sel from SSG59-3x HJ 541

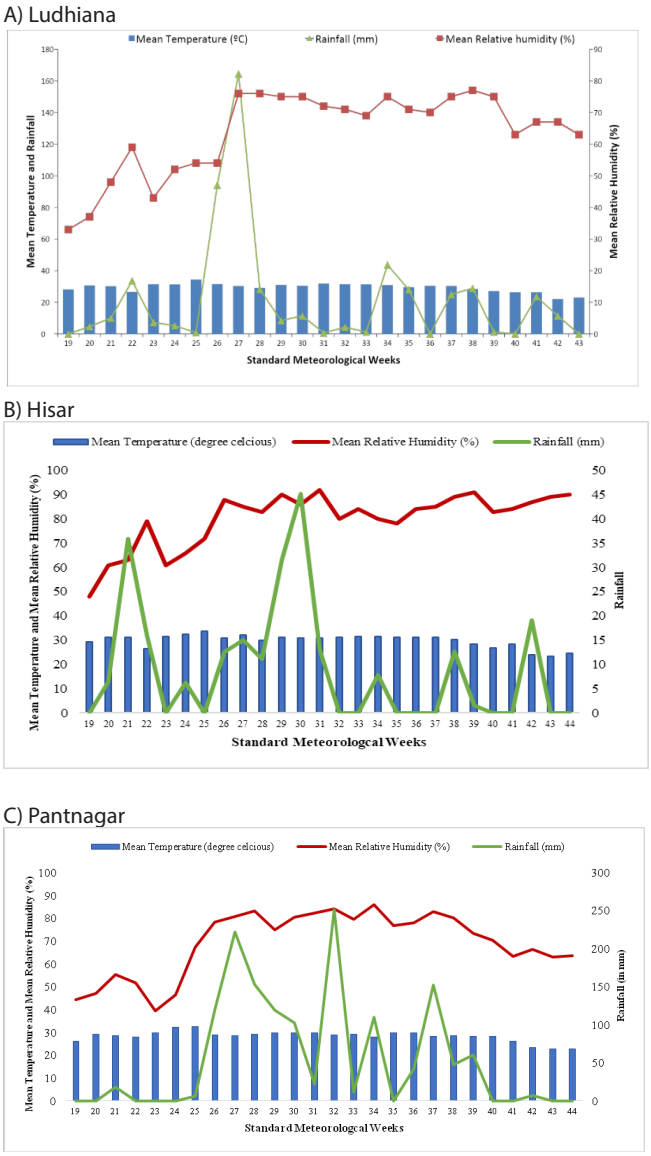

Fig. 1. Graphs showing the mean temperature, mean relative humidity and rainfall across the test locations during the experimental period. A) Ludhiana, B) Hisar and C) Pantnagar

component (PC1 and PC2), x_{i1} and x_{i2} are eigenvectors of genotype i for PC1 and PC2, h_{1j} and h_{2j} are eigenvectors of environment j for PC1 and PC2 and e_{ij} is the residual not explained by PC1 and PC2 for genotype i in environment j. It is not possible to plot the PC1 and PC2 eigenvectors directly to create a meaningful biplot prior to the singular values being divided into the genotype and environment eigenvectors. Implementing singular-value partitioning is done by $g_{il} = l_l^f x_{il}$ and $e_{lj} = l_l^{1-f} h_{lj,}$ where f is the partition factor, which has a possible value of any number between 0 and 1. In this study, we assigned equal weight to surroundings and genotypes using a value of 0.5. Hence, $Y_{ij} - \mu - ß_j = l_1 x_{i1} h_{j1} + l_2 x_{i2} h_{j2} + e_{ij} = g_{i1} e_{1j} + g_{i2} e_{2j} + e_{ij}$ is used to create biplots utilizing scores from the first two PCs, which are referred to as the primary (g_{i1} and e_{1j}) and secondary (g_{i2} and e_{2j}) scores for environment j and genotype i, respectively.

For a mixed model with fixed genotype's random locations, the required F-test was carried out. The combined studies are predicated on the idea that the total effect of random interactions at every fixed factor level equals zero. In short, the genotypes, genotypes × locations mean squares were compared to the pooled error mean square, and the genotypes mean square was compared to the replications mean square within the locations. In order to determine if the genetic impacts on the phenotypic expression vary depending on the environmental conditions. Bartlett's test (Arsham and Lovric, 2011) was used to assess the homogeneous variance assumption and determine the relevance of genotype-by-environment interactions. The components of variation influencing genotype by environment interactions and the consistency of forage sorghum biomass production across trials were analyzed using the AMMI model. AMMI combines univariate analysis of variance (ANOVA) and multivariate principal component analysis (PCA). The standardized residuals from the ANOVA model were then used to integrate the trait data using principal component analysis (PCA), allowing the trait data to be examined with and without the interaction between the main effects of environment and genotype. The GEI effect and experimental error make up these residuals. The biplot graph of the AMMI1 (IPCA1 scores vs. additive main effects from genotypes and environments) and AMMI2 (IPCA1 vs. IPCA2) were constructed. While genotypes far from the origin are assumed to be especially adapted, the GGE biplot shows the stability of genotypes near the biplot origin, which are thought to be broadly adapted. The biplots, which compare environments and genotypes to a hypothetical ideal environment, visually depict genotypic performance in various contexts based on main components. Relationships between test environments, genotypes, and genotype-environment interactions can be visually explored using the GGE biplot. Thus, to graph the GxE and determine the rank of test genotypes and environments, the first two primary components (PC1 and PC2) were employed (Thakur et al. 2023).

Result and discussion

The analysis of variance (ANOVA) calculated on the combined data from different locations is presented in Table 2. The combined ANOVA revealed highly significant ($p < 0.001$) differences between test environments, G×E effects and genotypes of forage sorghum. Furthermore, the largest sum of squares for the location indicated that environmental variation contributed much more to the overall variability than genotype and GxE effects for GFY and DFY.

Means performance

The forage sorghum genotypes' characteristic means clearly differ from one another, and wide range of variability was reported among GFY and DFY evaluated within the genotypes across locations (Fig. 2). The results on G×E interaction and the environment effects were highly significant ($p \leq 0.001$) influencing green and dry fodder yield (Table 2). Further analysis is necessary to identify the size of G×E and break it down into multiplicative component terms, and estimate the yield stability of the genotypes. The genotype SPH 2040 (274.00 and 59.37, respectively for GFY and DFY recorded the highest yield of green fodder and dry fodder in E3, whereas the lowest-yielding green fodder and dry fodder genotypes were SPH 2041 (89.10 in E1) and SPH 2039 (19.97 in E1), respectively (Table 3). The genotype with the highest plant height (PH) was SPH 2043 (245.70 cm

Table 2. Analysis of variance for various traits under study

Source of variation	Degree of freedom	Mean square				
		GFY	DFY	PH	LL	LB
Location (L)	2	158276.30*	4534.91*	2176.20*	569.40*	3.035*
Replication (R)	6	1637.53*	59.21*	880.47*	38.69	0.37*
Genotype (G)	16	707.52*	42.83*	2206.36*	127.13*	3.71*
GxL	32	703.11*	41.78*	634.17*	50.313*	2.26*
Residuals	96	232.41	13.00	305.16	31.15	0.62

*All values are significant at 1% ($p < 0.001$)

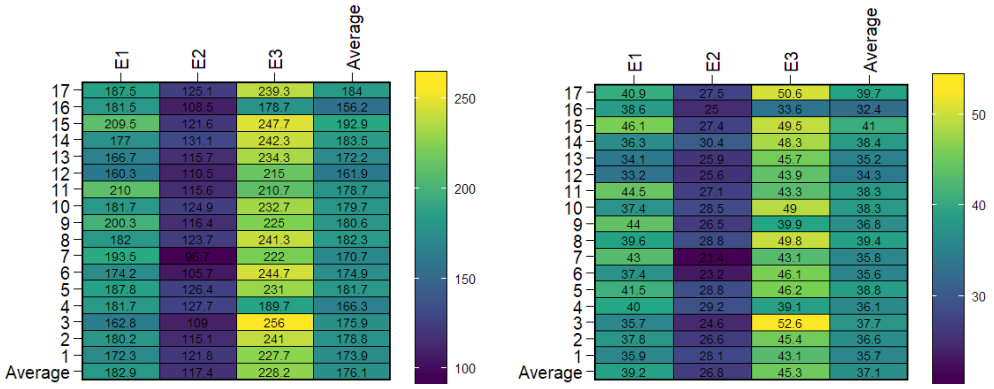

Fig. 2. Heat map for A) GFY (left) and B) DFY (Right)

Table 3: The details of statistical parameters for studied traits analyzed

Parameters	GFY	DFY	PH	LL	LB
Mean	176.14	37.06	172.62	87.1	6.54
SE	4.06	0.74	2.02	0.59	0.09
Min	89.1 (SPH 2041 in E1)	19.97 (SPH 2039 in E1)	90 (SPV 3045 in E2)	65 (SPV 3045 in E2)	2.8 (CSV 33MF in E3)
Max	274 (SPH 2040 in E3)	59.37 (SPH 2040 in E3)	245.7 (SPH 2043 in E2)	109 (SPH 2046 in E3)	9 (CSH 24MF in E2)
Min ENV	E1 (117.37)	E1 (26.75)	E1 (168.53)	E1 (83.93)	E3 (6.33)
Max ENV	E3 (228.18)	E3 (45.25)	E3 (180.16)	E3 (90.59)	E1 (6.81)
Min GEN	SPV 3045 (156.23)	SPV 3045 (32.39)	SPV 3045 (130.8)	SPH 1998 (80.3)	CSV 33MF (5.06)
Max GEN	SPH 2047 (192.91)	SPH 2047 (41.03)	SPV 3046 (193.74)	SPH 2039 (91.96)	CSH 24MF (7.6)

in E2) while SPV 3045 (90.00 cm in E2) had the lowest. SPH 2046 (109.00 cm in E3) and CSH 24MF (9.00 cm in E2) had maximum leaf length (LL) and leaf breath (LB), respectively, whereas SPV 3045 (65.00 cm in E2) and CSV33MF (2.8 cm in E3) had least LL and LB, respectively.

Table 4 presents the grand mean of various genotypes and environments for the recorded parameters. It is observed that SPH 2047 followed by SPV 3046 had the maximum GFY and DFY, respectively, whereas SPV 3045 had the minimum GFY and DFY. In terms of plant height, SPV 3046, followed by SPH 2043, had the maximum plant height, whereas SPV 3045 showed the least plant height. SPH 2039 had longer leaves and SPH 1998 had the smallest leaf length as compared to the other genotypes. CSH 24MF and CSV33MF had the maximum and minimum leaf breadth, respectively. In comparison to the grand mean values of the three environments, the sorghum green and dry fodder yield in E3 (Pant Nagar) was the highest (228.18 and 45.25, respectively). The environment that yielded minimum green and dry fodder (117.37 and 26.75, respectively) was found to be E1 (Hisar).

Stability analysis

The estimates of stability coefficients were computed using three environments (Table 5). SPH 1998 had the least coefficient of variation and POLAR (Power Law Residuals) value, followed by CSH24MF, suggesting that the genotypes are highly stable in their performance across test environments. In contrast, CSV33MF had the maximum coefficient of variation and POLAR value, indicating a high influence of environmental factors. According to Shukla's stability coefficient and Wricke's ecovalence value, SPH 2018 has the lowest value and is, therefore, more stable, followed by CSH43MF. SPV 3045 had the highest value, indicating that this genotype is the least stable among those considered for the study. Based on the deviation from joint regression analysis followed by the Eberhart and Russel model, CSH24MF, followed by SPV 3046, was found to be the most stable compared to other genotypes. SPH2041 was the least stable-performing genotype, as indicated by deviation from joint regression analysis. However, according to the superiority index, SPH2047 and SPV3046 were the superior-performing genotypes. Using mean absolute differences of pairs of ranks (MADPR), the genotypes CSH43MF and SPH2045 were found to be the most stable, whereas SPV3045 and SPH1998 were found to be the least. The two genotypes that were most stable, according to variances of

Table 4. Grand mean across genotypes and environment

Genotypes	DFY (Kg/plot)	GFY (kg/plot)	PH (cm)	LL (cm)	LB (cm)
CSH 24MF	35.69	173.93	169.07	85.78	7.60
CSH 43MF	36.62	178.75	173.21	88.11	6.72
CSV 33MF	37.66	175.94	152.49	87.88	5.06
SPH 1998	36.12	166.34	186.08	80.30	6.64
SPH 2018	38.82	181.74	171.27	90.41	6.46
SPH 2019	35.56	174.85	173.16	89.63	6.98
SPH 2039	35.81	170.72	155.36	91.96	6.86
SPH 2040	39.38	182.33	178.61	87.04	6.00
SPH 2041	36.81	180.59	175.34	86.23	7.53
SPH 2042	38.30	179.73	169.42	89.18	6.16
SPH 2043	38.31	178.74	192.43	89.89	6.62
SPH 2044	34.25	161.93	177.87	82.00	6.39
SPH 2045	35.23	172.22	170.62	88.72	6.78
SPH 2046	38.37	183.46	173.82	90.37	6.71
SPH 2047	41.03	192.91	191.30	90.77	6.37
SPV 3045	32.39	156.23	130.80	80.82	6.92
SPV 3046	39.66	183.98	193.74	81.59	5.43
Mean of Environments					
ENV	*DFY*	*GFY*	*PH*	*LL*	*LB*
E1	26.75	117.37	168.53	83.93	6.81
E2	39.17	182.88	169.18	86.78	6.49
E3	45.25	228.18	180.16	90.59	6.36

ranks, were CSH43MF, followed by SPH2018, while the two least stable genotypes were SPV3045 and CSV33MF.

SPH2018 was ranked 1st by Shukla's stability coefficient, 2nd in terms of variance among the ranks over the k environments, 3rd according to POLAR, 4th in terms of coefficient of variance and superiority index, 5th in MADPR, and ranked 6th in deviation from joint regression analysis. CSH43MF was ranked 1st according to MADPR and variance among the ranks across the k environments, 2nd based on Shukla's stability coefficient, Wricke's ecovalence of ranks, and 4th based on deviation from joint regression analysis. Hence, SPH 2018 and CSH43MF were found to be the most stable genotypes. On the other hand, SPH 2039 and SPV3045 were the most unstable genotypes as per stability coefficient scores.

AMMI model

The genotypes (G), environments (E) and their interactions effect (G×E) had a substantial impact on the AMMI analysis of variance (p <0.01). Table 6 depicts significant G×E interactions and stability assessments of GFY and DFY among all the forage sorghum genotypes under study. According to the AMMI model's findings, environmental factors significantly influenced changes in green and dry fodder yield, as evidenced by the fact that 78.16 and 64.63%, respectively of the entire sum of squares could be attributed to them. Furthermore, environmental factors were the largest contributor to the overall fluctuation in yields. According to the partition of GEI mean squares, the two IPCAs (76.1 and 23.9% for GFY and 73.3 and 26.7% for DFY) among genotypes contribute to 100% of the total GEI [Figure 3(b) and 4(b)]. This finding aligns with the findings of Shimray et al. (2022), who also reported that the first 2 IPCAs accounted for 100% of the GEI.

A genotype's specific adaptation to a given environment is indicated by its greater IPCA1 score, which can be either positive or negative (Funga et al. 2017). The IPCA scores of each genotype (both GFY and DFY) are shown in Table 7. The AMMI1 biplot (Figure 3(a) and 4(a)) for GFY and DFY showed that the genotypes SPH2047 and SPV3046 are stable and produced high green and dry fodder yield than the other genotypes, whereas SPV3045 was found to be least stable and had minimum average green and dry fodder yield across test locations. The levels of G x E were elevated in SPV 3045, SPH 1998, SPH 2043 and CSV33MF for GFY and in CSV 33MF, SPH 2043, SPH 1998, SPH 2041 and SPV 3045 for DFY, whereas the G×E in SPH 2042, SPH 2047 and SPH 2018 were low for GFY and in CSH24MF, SPH 2018, CSH 43MF and SPH 2047 were low for DFY. The G×E of the remaining genotypes was moderate. The highest GFY and DFY were recorded in E3. E2 and E1 had above-average GFY and DFY, respectively, whereas E1 and E2 had below-average GFY and DFY, respectively (Figure 3(a) and 4(a)). E3 followed by E2 and E1 in that order, made greater contributions to the interaction in the case of GFY. In the case of DFY, E3 made the greatest contribution, and E1 made the least contribution to the interaction.

When G and E are shown against PC1 and PC2, the length of the environmental vectors from the origin in the AMMI2 biplot (Figure 3(b) & 4(b)) indicates the degree of interaction between the environments and genotypes. The genotypes' distance from the origin also indicates their susceptibility to different environmental influences (Thakur et al. 2023). The AMMI2 biplot is segmented into four quadrants, wherein genotypes close to the ordinate axis exhibit greater overall adaptability (Nagesh et al. 2021). In the AMMI2 biplot, stronger interactions were seen in the E3 for both GFY and DFY, indicating a greater ability of E3 environments for genotype discrimination. E2 and E1 had moderate interaction for GFY and DFY, respectively. Conversely, E1 and E2 exerted the least G×E for GFY and DFY, respectively, indicating that they are more representative and least discriminating environments.

With higher G x E (far from the origin), CSV33MF, SPH2043, SPV3045 and SPH1998 for GFY and SPV 3045,

Table 5. Estimates of stability coefficients analysed under various methods

Code	Genotype	Coefficient of variance		Power law residual		Shukla's stability coefficient		Wricke's ecovalence		Deviation from joint regression analysis		Superiority index		MADPR (S1)		S2	
		Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank
G1	CSH 24MF	20.89	2.00	-0.17	2.00	5.83	6.00	35.78	6.00	-1.08	1.00	33.67	13.00	3.00	12.00	24.33	5.00
G2	CSH 43MF	25.83	8.00	-0.01	9.00	-0.23	2.00	3.69	2.00	-3.10	4.00	22.61	8.00	0.00	1.00	0.33	1.00
G3	CSV 33MF	37.45	17.00	0.30	17.00	38.79	16.00	210.25	16.00	34.14	15.00	23.72	9.00	4.67	15.00	70.33	16.50
G4	SPH 1998	16.61	1.00	-0.38	1.00	22.85	13.00	125.88	13.00	6.90	8.00	36.97	15.00	5.00	16.50	58.33	14.00
G5	SPH 2018	23.13	4.00	-0.14	3.00	-0.35	1.00	3.07	1.00	-3.74	6.00	11.00	4.00	1.00	5.00	4.33	2.00
G6	SPH 2019	32.58	15.00	0.21	15.00	4.78	4.00	30.20	4.00	-3.38	5.00	28.62	10.00	3.33	13.00	25.33	6.50
G7	SPH 2039	34.86	16.00	0.27	16.00	23.50	14.00	129.33	14.00	27.20	14.00	30.56	12.00	1.33	7.50	60.33	15.00
G8	SPH 2040	26.67	9.00	-0.02	8.00	3.99	3.00	26.04	3.00	2.71	3.00	8.97	3.00	1.67	9.50	10.33	3.00
G9	SPH 2041	24.81	6.00	-0.04	7.00	27.99	15.00	153.09	15.00	41.29	17.00	30.20	11.00	1.67	9.50	50.33	13.00
G10	SPH 2042	26.93	10.00	0.00	10.00	8.06	8.00	47.57	8.00	11.02	10.00	15.56	5.00	1.33	7.50	25.33	6.50
G11	SPH 2043	25.34	7.00	-0.05	6.00	14.62	12.00	82.30	12.00	22.70	13.00	16.73	6.00	0.67	3.00	28.00	8.00
G12	SPH 2044	26.94	11.00	0.07	13.00	7.34	7.00	43.75	7.00	9.56	9.00	44.22	16.00	1.00	5.00	21.00	4.00
G13	SPH 2045	28.14	12.00	0.09	14.00	8.61	9.00	50.49	9.00	12.49	11.00	35.69	14.00	0.33	2.00	30.33	9.50
G14	SPH 2046	23.78	5.00	-0.11	4.00	13.79	11.00	77.90	11.00	19.68	12.00	19.07	7.00	1.00	5.00	46.33	12.00
G15	SPH 2047	29.00	13.00	0.03	11.00	10.31	10.00	59.50	10.00	5.21	7.00	3.11	1.00	2.00	11.00	30.33	9.50
G16	SPV 3045	21.18	3.00	-0.10	5.00	41.30	17.00	223.59	17.00	34.97	16.00	75.08	17.00	5.00	16.50	70.33	16.50
G17	SPV 3046	29.20	14.00	0.05	12.00	5.59	5.00	34.49	5.00	-1.59	2.00	6.66	2.00	3.67	14.00	31.00	11.00

S1 (mean of the absolute rank differences of a genotype over the n environments),
S2 (variance among the ranks over the k environments)

Table 6: ANOVA of AMMI Model for GFY and DFY

S. No.	Source of variation	GFY					DFY				
		Df	Sum Sq	Mean Sq	F value	Pr(>F)	Df	Sum Sq	Mean Sq	F value	Pr (>F)
1	ENV	2	316552.56	158276.28	96.65	0.000027	2.00	9069.82	4534.91	76.59	0.000054
2	REP (ENV)	6	9825.21	1637.53	7.05	0.000003	6.00	355.24	59.21	4.55	0.000418
3	GEN	16	11320.31	707.51	3.04	0.000378	16.00	685.37	42.84	3.29	0.000143
4	GEN: ENV	32	22499.48	703.10	3.03	0.000016	32.00	1336.90	41.78	3.21	0.000006
5	PC1	17	17133.00	1007.82	4.34	0.000000	17.00	979.69	57.63	4.43	0.000000
6	PC2	15	5366.48	357.76	1.54	0.010600	15.00	357.21	23.81	1.83	0.041100
7	Residuals	96	22311.85	232.41	NA	NA	96.00	1248.33	13.00	NA	NA
8	Total	184	405008.89	2201.13	NA	NA	184.00	14032.55	76.26	NA	NA

All values are highly significant at 1% except PC2 of GFY and DFY (Significant at 5%)

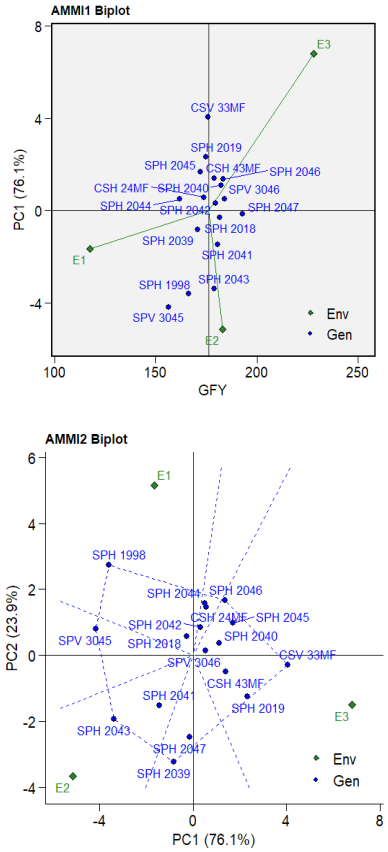

Fig. 3. (a). AMMI 1 (left) and (b). AMMI 2 (right) for GFY

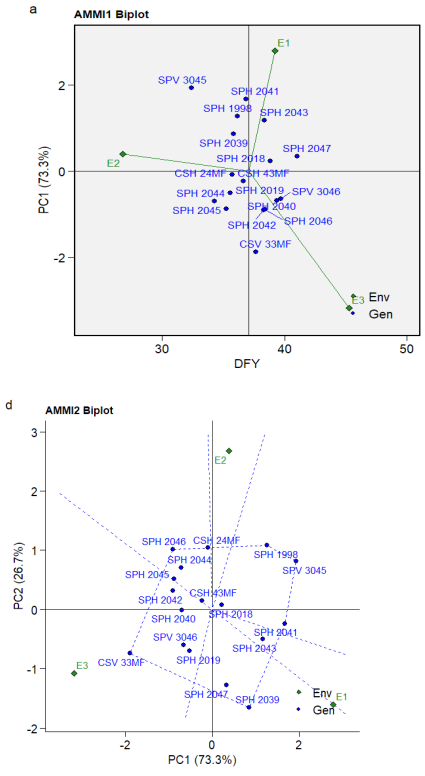

Fig. 4. (a). AMMI 1 (left) and (b). AMMI 2 (right) for DFY

Table 7. IPCA scores of each genotype (both DFY and GFY)

S. No.	Type	Genotype	GFY			DFY		
			Yield	PC1	PC2	Yield	PC1	PC2
1	GEN	CSH 24MF	173.90	-0.58	-1.47	35.69	-0.09	1.04
2	GEN	CSH 43MF	178.80	-1.39	0.50	36.62	-0.24	0.14
3	GEN	CSV 33MF	175.90	-4.06	0.28	37.66	-1.88	-0.74
4	GEN	SPH 1998	166.30	3.61	-2.74	36.12	1.27	1.08
5	GEN	SPH 2018	181.70	0.28	-0.57	38.82	0.23	0.08
6	GEN	SPH 2019	174.90	-2.33	1.26	35.56	-0.51	-0.70
7	GEN	SPH 2039	170.70	0.82	3.23	35.81	0.85	-1.66
8	GEN	SPH 2040	182.30	-1.11	-0.38	39.38	-0.69	-0.01
9	GEN	SPH 2041	180.60	1.45	1.51	36.81	1.67	-0.24
10	GEN	SPH 2042	179.70	-0.32	-0.86	38.30	-0.90	0.31
11	GEN	SPH 2043	178.70	3.38	1.94	38.32	1.17	-0.50
12	GEN	SPH 2044	161.90	-0.50	-1.58	34.25	-0.71	0.71
13	GEN	SPH 2045	172.20	-1.70	-0.97	35.23	-0.88	0.51
14	GEN	SPH 2046	183.50	-1.38	-1.68	38.37	-0.90	1.02
15	GEN	SPH 2047	192.90	0.15	2.48	41.03	0.33	-1.28
16	GEN	SPV 3045	156.20	4.17	-0.80	32.39	1.93	0.81
17	GEN	SPV 3046	184.00	-0.52	-0.15	39.67	-0.65	-0.60
18	ENV	E1	182.90	5.15	3.66	39.17	2.79	-1.60
19	ENV	E2	117.40	1.66	-5.16	26.75	0.39	2.68
20	ENV	E3	228.20	-6.81	1.51	45.25	-3.18	-1.08

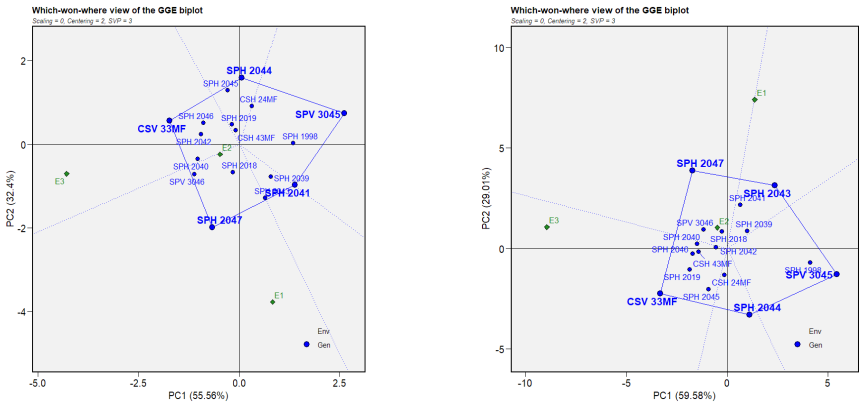

Fig. 5. GGE biplots for (a) GFY (left), (b) DFY (Right)

SPH 2041, SPH2043 and CSV33MF, for DFY are more sensitive to environmental changes. On the other hand, because the wide-adapted genotypes SPH2042, SPH2047, SPH2018, SPH2044, CSH24MF and SPV3046 in case of GFY and CSH43MF, SPH2018, SPH2040 and SPH 2042 in case of DFY were closer to the origin, so they had shown fewer interactions and are more stable across environments. The six rays in the AMMI2 graphs are widely dispersed. In the case of GFY, SPH1998 and SPH2043 were found to be best for E1 and E2, respectively. In E3, CSV33MF followed by SPH2019 were best performing (Figure 3(b)). For DFY, at E1 (Hisar), SPH2039 and SPH2047 were found to be the best, whereas CSV33MF was found to be the best for E3 (Pant Nagar). No genotype was found to be good for E2 (PAU) (Figure 4(b)).

GGE biplot analysis

A total 88.59 and 87.96% of the variation in GGE was explained by the first two PCs for GFY and DFY, respectively.

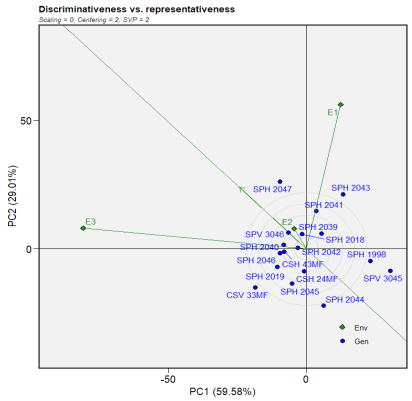

Fig. 6. Discriminativeness vs representativeness plot for GFY

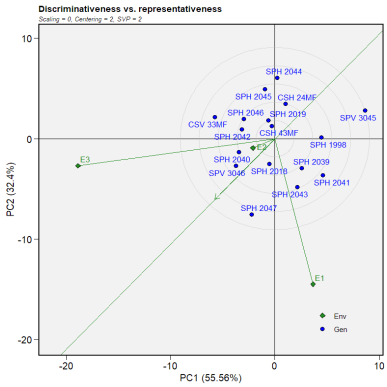

Fig. 7. Discriminativeness vs representativeness plot for DFY

The optimal genotype(s) for each environment is shown in the polygon view of the GGE biplot for GFY (Figure 5(a)) and DFY (Figure 5(b)). In order to include all other genotypes, the polygon is created by joining the markers of the genotypes that are located furthest from the biplot origin. According to Yan (2007), the rays or equality lines are lines that run perpendicular to the polygon's sides, making it easier to visually compare the genotypes. The biplots are divided into five portions by these five rays, with three environments falling into three and two of those areas in case of GFY and DFY, respectively. The vertex families in each quadrant correspond to the seasons that produced the highest yield within that quadrant. According to Figure 5, the environments and genotypes inside the polygon were less receptive to environmental fluctuations. The environments studied were unsuitable for genotypes from polygon vertices that did not cluster in any environment. Due to the lack of comparable environments, genotypes SPV3045 and SPH2044 were the poorest performers for GFY and DFY located outside the limits across all environments. For a given trait of interest, the genotype that is found closest to the origin is thought to be the ideal genotype; it must have a high suggestive overall mean performance with large PC1 value but a small absolute PC2 value (i.e., high environmental stability) (Reddy et al. 2022). For GFY, SPH2042, SPH2018 and CSH24MF (Fig. 6) and for DFY, CSH43MF, SPH2018, SPH2019, SPH 2044 and SPH2045 (Fig. 7) are found to be more stable as compared to other genotypes. Hence, for each of the three environments, these genotypes might be deemed appropriate.

The vector view of the GGE biplot is shown in Figure 8, where environments are connected to the biplot origin *via* lines. It measures the environment's capacity for discrimination and is proportionate to the standard deviation within each environment. This biplot view facilitates comprehension of the relationships between the environments. Compared to other environments, a test environment with a smaller angle relative to the average-environment axis (AEA) is more representative. The correlation coefficient between two environments can be roughly calculated using the cosine of the angle formed by their vectors. Seasons that had tiny angles between them showed a strong positive correlation and comparable genotype information. Hence, E1 is strongly correlated with E2 as compared to the correlation between E2 and E3. E1 and E3 show the least degree of correlation. According to the plots obtained, E1 was a non-representative and more discriminating (informative) environment that may be helpful for selecting genotypes specifically tailored for high GFY and DFY (Fig. 8). E2 is more representative than the

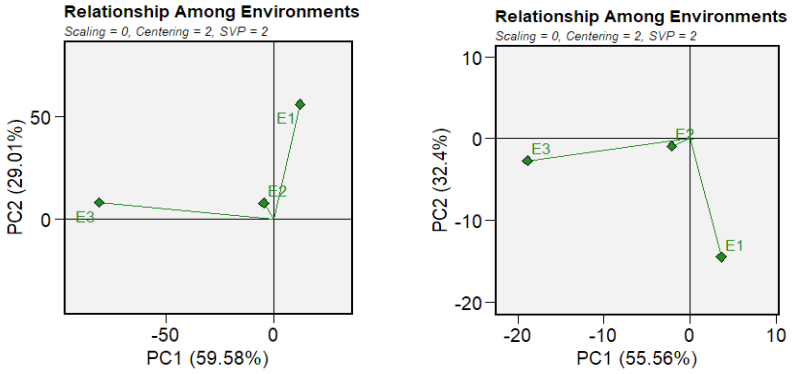

Fig. 8. Relationship among Environment (a) GFY (left), (b) DFY (Right)

other environments for both GFY and DFY. However, E3 is the least informative among the three. Hence, E2 asserts that test environment(s) for selecting widely adapted genotypes are best for MLTs (multilocation location testing).

Authors' contribution

Conceptualization of research (PK, BVB, PKP, RSS); Designing of the experiments (BVB); Contribution of experimental materials (BVB); Execution of field/lab experiments and data collection (PK, PKP, RSS); Analysis of data and interpretation (PK, SKP, DS, AVU); Preparation of the manuscript (PK, RSS, PKP, DSRM, AVU).

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