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AMMI Model based Stability of Little millet [*Panicum sumatrense* Roth. Ex. Roem. & Schult.] Advanced Lines Evaluated across Eighteen Environments in India

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Abstract: Identification of superior and stable genotype for commercial cultivation is constrained majorly by the existence of genotype × environment interaction (GEI). Nine little millet advanced lines with checks, were employed over nine Indian locations throughout two rainy seasons during 2017 and 2018 to access the patterns of GEI governing traits *viz*., days to 50% flowering, early flowering and yield (seed & fodder). Statistical analysis (AMMI model and best linear unbiased predictors (BLUP) was performed. The variance due to genotype, environment and GEI was highly significant for all three traits. Environment attributed to a higher proportion of the variation (28.68%-73.44%), while genotypes contributed 1.41-47.30% of the total variation. The GEI contributed 24.00-27.79% of the total variation for all three traits. The testing environments were partitioned into four, three and two mega-environments for seed, fodder yield and days to 50% flowering, respectively. The environments E9, E13 and E6 were representative and discriminative for days to 50% flowering, seed and fodder yield, respectively and can be used to recognize superior early flowering genotypes with high seed and fodder yield adapted to specific agro-ecology. Check (OLM203) performed better than all the genotypes except the advanced line DHLT28-4 for seed and fodder yield, but it was late flowering. DHLT28-4 which is early flowering and most stable with high seed and fodder yielding cultivar can be commercialized in India as a better substitute for the existing varieties.

Keywords: Genotype × environment interaction, Multi-environment trial, Yield stability, GGE biplot, AMMI

Globally, 7000 crop species are grown (Khoshbakht and Hammer 2008), yet the majority of research and breeding is focused on a few crops (Hammer et al 2001), resulting in ignorance about many crops, particularly Little millet. Little millet (*Panicum sumatrense* Roth. Ex. Roem. & Schult.) is a tetraploid (2n = 4x = 36) minor cereal grown in the tropics and sub-tropics is nutritionally comparable to rice and wheat (Saha et al 2016). A 100 grams of little millet seeds include 4.70 g of fat, 7.70 g of crude fibre, 9.30 mg of iron, and 220.00 mg of phosphorus, which is equivalent to cereals and other millets (Gopalan et al 2010). Quite apart from being nutritionally dense, it is a short-duration crop with low water requirements and is also used as livestock fodder, making it more appealing to be cultivated in crop-pasture-based farming in areas with little to no rainfall. It is critical to identify stable and high seed and fodder yielding little millet genotypes for farmer direct use that can replace current cultivars. Before recommending any cultivar for commercial cultivation, it is essential that they be evaluated in varying environments to identify consistent and high seed and fodder-yielding cultivars. Consequently, quantification of the interaction of these cultivars with the target environment under which they are evaluated is essential, this aids in determining the breeding objectives, identifying ideal test environments and recommending regional cultivars with better adaptation (Yan et al 2000). To quantify the impact of GEI and recognize stable and adaptable cultivars across different environments, various statistical tools such as joint regression (Finlay and Wilkinson 1963), stability models (Eberhart and Russell 1966), additive main effects and multiplicative interaction (AMMI; Gauch 1992) and genotype main effects in addition to genotype by environment interaction (GGE) biplots (Yan et al 2000) are employed. The two most popular and highly effective multivariate models to analyze the stability, adaptability, rank genotypes and mega environments (ME) are the AMMI and GGE biplots (Gauch 1992). The farmer interprets the effects of genotypes and environments as an additive and the interaction between them as multiplicative by principal component analysis (PCA). The latter group the additive genotypic effects in the AMMI analysis, together with the multiplicative effects of GEI and analyzes these effects by principal components (PC).

The current study aimed to evaluate the stability and adaptability of nine little millet advanced lines including checks across eighteen environments for days to 50% flowering, seed yield and fodder yield using the AMMI methodology and GGE biplot. For simultaneous identification of high seed fodder-yielding genotypes that were also early flowering with good stability and adaptability, the best linear unbiased prediction (BLUP)-based simultaneous selections, such as the harmonic mean of genotypic values (HMGV), the relative performance of genotypic values (RPGV) and harmonic mean of the relative performance of genotypic values (HMRPGV) are used (de Resende 2004).

MATERIAL AND METHODS

Data of little millet initial and advanced varietal trials (LIAVT) from All India Coordinated Research Project (AICRP) on Small Millets, in which nine little millet advanced lines including three checks (Table 1) evaluated across nine locations (Table 2) in the rainy seasons of 2017 and 2018 is used in this study. The testing locations represented seven states of India. Depending on the onset of monsoon across the test locations of this study, the crop was sown during June-July. The experiment was conducted in a randomized complete block design with three replications. The plot size of each replicate was 6.75 square meters with 10 rows of 3-meter length. A spacing of 22.50 cm × 10 cm was followed. Crop management was followed as recommended in the package of practices. Observations on days to 50% flowering, seed and fodder yield were recorded from each plot. At physiological maturity, seed yield was recorded, further plot size was used as a factor to convert plot yield data to kg ha^{-1}.

Statistical analysis: A combination of a single year and a single location made up eighteen test environments in this study (Table 3). The phenotypic data of days to 50% flowering, seed and fodder yield collected from the nine little millet genotypes evaluated across eighteen environments was confirmed for the homogeneity of variance by Bartlett's test (Bartlett 1937). To determine the significance level of genotypes (G), environments (E) and GEI, combined analysis of variance using a mixed linear model (R Core Team 2020) was used. To determine the GEI effects to assess the adaptability and stability of the little millet genotypes across the eighteen test environments, the AMMI model was used. The genotypes were treated as fixed variables, while the environments as random. The AMMI amalgamates ANOVA for genotype and environment main effects with PCA of the GEI with the axes of the principal components of interactions (Gauch 1988; Yan et al 2007). The AMMI model used is as follows:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k a_{ik} \gamma_{jk} + e$$

Y_{ij}	=	Trait mean of the i^{th} genotype in the j^{th} environment
μ	=	Experimental genotype mean
g_i and e_j	=	Genotype and environment deviations from the grand mean
k	=	Eigen value of the PCA analysis axis k
α_{ik} and γ_{jk}	=	Genotype and environment principal component scores for axis k
n	=	Number of principal components retained in the model
e_{ij}	=	Error term

Genotype + Genotype × environment (GGE) bi-plot is a subjective/qualitative means to characterize patterns of GEI and assess the relative stability of test genotypes. The first two principal components (PC1 and PC2) derived using adjusted trait mean value from ANOVA are used to construct the GGE biplot (Yan 2001, Yan 2002).

The GGE bi-plot is suggestive of visual interpretation of the GEI patterns, representativeness and discriminating ability of the environments and relative stability of test genotypes. In the current study, the biplots were based on singular-value partitioning = 2, transformed (transform = 0), environment-centered (centering = 2) and standard deviation-standardized (scaling = 0).

The BLUP-based stability parameters such as HMGV (to infer both yield and stability), RPGV (to investigate the mean yield and genotypic adaptability) and HMRPGV (to evaluate stability, adaptability and yield simultaneously; de Resende (2004) and (2016) were estimated. The analysis was computed using the metan package in R software version 4.2.1 (Olivoto et al 2020).

RESULTS AND DISCUSSION

Analysis of variance: The combined analysis of variance emphasized that the sources of variations were significant for days to 50 % flowering, seed yield and fodder yield and supported the existence of environmental heterogeneity and stipulated significant differences between the genotypes since their responses were not coincident in the test environments (Table 3). A significant GEI is suggestive of the need to further analyze the data for AMMI analysis of variance.

AMMI analysis of variance: The most important source of variation for yield was environment, accounting for 73.44% and 60.50% of the total variance (G+E+GE) for seed and fodder yield respectively, contrastingly 28.68% for days to 50% flowering (Table 4). The selection of AMMI as the appropriate model for analyzing the multi-environment trials (METs) data is justified by a large variation due to the environment that is impertinent to evaluate cultivars. The variation due to the GEI accounted 24.00, 25.13 and 27.79%

Table 1. Pedigree information of the little millet genotypes used in the study

Genotype	Developing center	Pedigree
WV 126	Waghai (Gujarat)	Local Collection from Dangs Taluka, Dangs District
DHLT 28-4	Hanumanamatti (Karnataka)	CO 2 x TNAU 26
OLM 217	Berhampur (Orissa)	OLM 217 Selection from Udayagiri Local Bhubaneswear
IIMR LM 7162	Indian Institute of Millets Research (Hyderabad)	Selection from GPMR 1153
TNPSu 186	Athiyandal (Tamil Nadu)	MS 507 x MS 1211
WV 125	Waghai (Gujarat)	Local Collection from Waghai Taluka, Dangs District
JK 8 (Check)	Rewa (Madhya Pradesh)	Selection from local germplasm
OLM 203 (Check)	Berhampur (Orissa)	Pureline selection from Lakshmipur local
BL 6 (Check)	Jagdalpur (Chhattisgarh)	Paiyur 1 x OLM 29

Table 2. Geographical identity and climate variables of the locations during the crop growth period

Location	2017			2018			Latitude	Longitude	Altitude (ft)
	T Max.	T Min.	Rainfall (mm)	T Max.	T Min.	Rainfall (mm)			
Athiyandal	35.52	26.63	18.94	34.57	26.58	18.30	12.07° N	78.99° E	561
Berhampur	35.55	24.35	69.72	35.26	24.37	86.70	19.31° N	84.79° E	78
Dindori	34.52	25.69	49.63	32.59	26.98	54.23	22.94 º N	81.06° E	2099
Jagdalpur	30.78	22.88	74.91	28.13	20.85	62.09	19.08 º N	82.02 º E	1811
Nandyal	33.66	25.77	40.30	34.90	24.98	16.80	15.47 º N	78.48 º E	666
Perumallapalle	34.72	25.75	44.88	35.33	25.96	28.07	13.60° N	79.35° E	1000
Ranchi	28.61	19.83	75.00	29.53	19.60	54.23	23.34° N	85.30 º E	2135
Vizianagaram	30.55	27.83	39.88	30.78	28.75	60.10	18.10° N	83.39° E	242
Waghai	31.42	24.28	126.80	27.59	23.29	55.00	20.77° N	73.49° E	830

T Max.: Maximum temperature during crop period; T Min.: Minimum temperature during crop period

Table 3. Description of combination of a single year and a single location making up eighteen test environments

Code	Description
E1	Rainy season-2017, Athiyandal
E2	Rainy season-2017, Berhampur
E3	Rainy season-2017, Dindori
E4	Rainy season-2017, Jagdalpur
E5	Rainy season-2017, Nandyal
E6	Rainy season-2017, Perumallapalle
E7	Rainy season-2017, Ranchi
E8	Rainy season-2017, Vizianagaram
E9	Rainy season-2017, Waghai
E10	Rainy season-2018, Athiyandal
E11	Rainy season-2018, Berhampur
E12	Rainy season-2018, Dindori
E13	Rainy season-2018, Jagdalpur
E14	Rainy season-2018, Nandyal
E15	Rainy season-2018, Perumallapalle
E16	Rainy season-2018, Ranchi
E17	Rainy season-2018, Vizianagaram
E18	Rainy season-2018, Waghai

for days to 50% flowering, seed yield and fodder yield, respectively. The variance due to genotypes was relatively meager in comparison to the other two sources of variation, 1.41 and 11.70% for seed and fodder yield, respectively (Table 4). On contrary, 47.30% of the genotypic variance was observed for days to 50% flowering. Considerable differences in the response of genotypes across environments are indicated by a higher magnitude of GEI sum of squares than genotypes alone for seed and fodder yield (Tonk et al 2011, Alam et al 2015, Vaezi et al 2017). These pieces of evidence are suggestive for the possible existence of different mega-environments in our study (Yan and Hunt 2002, Mohammadi et al 2009). The multiplicative variance of the treatment sum of squares due to interaction was partitioned into eight significant interaction principal components for days to 50% flowering and seed yield, whereas, six for fodder yield (Table 4). The first two PCs explained 73.70, 75.30 and 76.90% of the total variation for days to 50% flowering, seed yield and fodder yield, respectively. The contribution of PC1 and PC2 was 42.00 and 31.70% for days to 50% flowering, 53.00 and 22.30% for seed yield and 59.10 and 17.80% for fodder yield.

GGE Biplot: the GGE biplot has not been implemented to analyze the MET data of little millet yield trials. Approximately, 73% of the variability of the three traits studied was captured by the first two principal components. Consequently, the number of PCs used in this study is reasonable, especially when coupled with Gollob's F-test which also suggested the usage of two PCs (Zobel et al 1988, Yan 2000).

Mean performance and stability of the genotypes across environments: The mean days to 50% flowering of the nine genotypes across the eighteen environments varied from 49.10 (JK8) to 88.40 days (OLM 217), while the seed yield varied from 1311 (JK8) to 1742 kg/ha (DHLT28-4), and the fodder yield varied from 3940 (JK8) to 8355 kg/ha (OLM 203) (Fig. 1). The range of days to 50% flowering varied from 47 (E1) to 91 (E18) days (Fig. 2). The mean seed yield per environment varied from 346 (kg/ha) in E4 to 3737 (kg/ha) in E13 (Fig. 2). The mean fodder yield per environment varied from 988 (kg/ha) in E13 to 11790 (kg/ha) in E7. The "mean *vs.* stability" biplot enables visualization of the mean performance of genotypes in addition to their stability, this is aided by the average environment coordination (AEC) abscissa that bears a single arrowhead. It also serves as a marker for the average environment and points towards a higher mean. The perpendicular lines on the AEC are referred to as AEC ordinates. The stability of a genotype is inversely proportional to the length of the AEC ordinate. The genotypes are arranged along the average environment axis based on their average seed or fodder performance across all the environments with the arrow pointing to the highest value of yield. The genotypes JK8, TNPSu186 and DHLT28-4 took least time to flower while, the genotypes OLM217, OLM203 and WV125 were late flowerings (Fig. 1 and Fig. 3). The genotypes TNPSu186, WV125 and IIMRLM7162 were highly stable for flowering. The genotypes DHLT28-4, BL6 and OLM203 produced higher seed yields, while the genotypes JK8 and TNPSu186 were the poorest seed yielders. The genotypes IIMRLM7162, OLM203 and DHLT28-4 were stable for seed yield, whereas, the genotypes WV126, WV125 and OLM217 were highly unstable. The genotypes OLM203, OLM217 and IIMRLM7162 produced higher fodder yield, while the genotypes JK8, TNPSu186 and WV125 were poor fodder yielders (Fig. 1 and Fig. 3). Most stable for fodder yield were OLM203, JK8 and WV126, while the genotypes WV125, OLM217 and BL6 were highly unstable. The genotype OLM203 produced higher seed and fodder yield, besides being stable across all the environments, it took maximum duration to flower. While the genotype DHLT28-4 was early flowering and high seed yielding with good stability across all the environments. On the contrary, the genotype

Table 4. Combined analysis of variance for days to 50% flowering, seed yield and fodder yield of little millet genotypes across eighteen environments

Source of variation	df	Days to 50% flowering				Seed yield				Fodder yield			
		SS	MSS	'F' value	Probability	SS	MSS	'F' value	Probability	SS	MSS	'F' value	Probability
Environment (E)	17	5.87×10^4	3.45×10^3	2.32×10^3	<0.001	3.63×10^8	2.13×10^7	562.45	<0.001	3.19×10^9	1.88×10^8	351.22	<0.001
Replication (Environment)	36	130.14	3.61	2.42	<0.001	3.10×10^6	8.62×10^4	2.27	<0.001	2.32×10^7	6.46×10^5	1.20	<0.001
Genotype (G)	9	9.68×10^4	1.07×10^4	7.23×10^3	<0.001	1.10×10^7	1.23×10^6	32.41	<0.001	7.01×10^8	7.79×10^7	145.47	<0.001
G × E Interaction (GEI)	135	4.91×10^4	3.63×10^2	2.44×10^2	<0.001	1.21×10^8	8.96×10^5	23.59	<0.001	1.49×10^9	1.10×10^7	20.63	<0.001
Residuals	288	428.51	1.48			1.09×10^7	3.80×10^4			1.54×10^8	5.35×10^5		

df: Degrees of freedom; SS: Sum of squares; MSS: Mean sum of squares

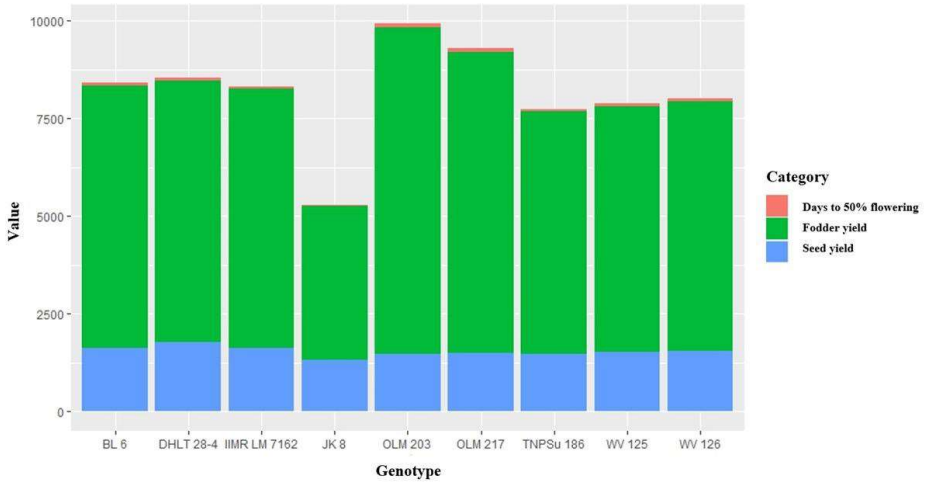

Fig. 1. Grand mean of days to 50% flowering, seed yield and fodder yield of nine little millet genotypes evaluated across eighteen environments

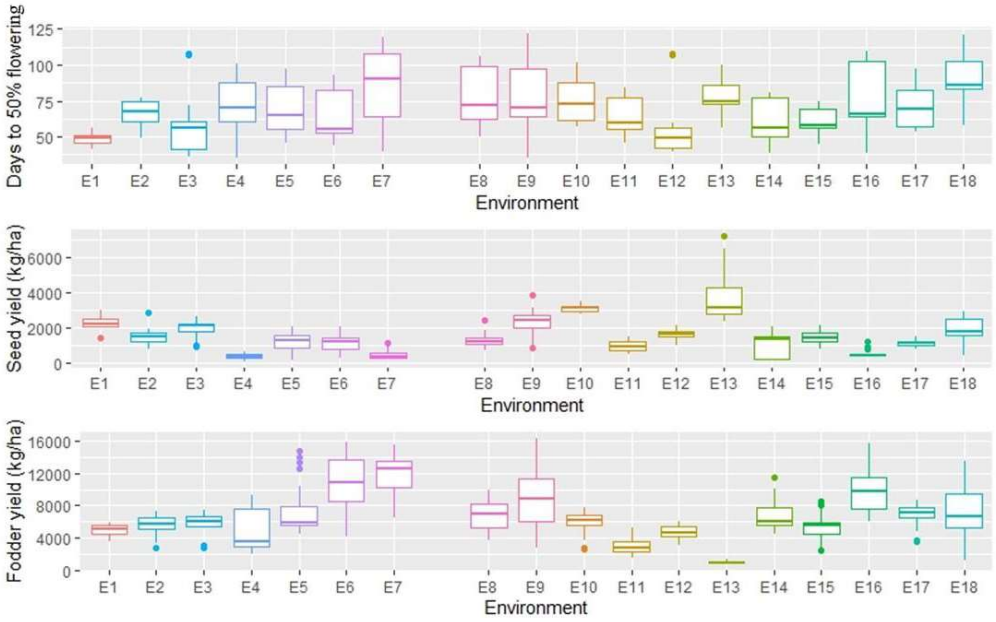

Fig. 2. Mean of days to 50% flowering, seed yield and fodder yield of nine little millet genotypes in each of the eighteen environments

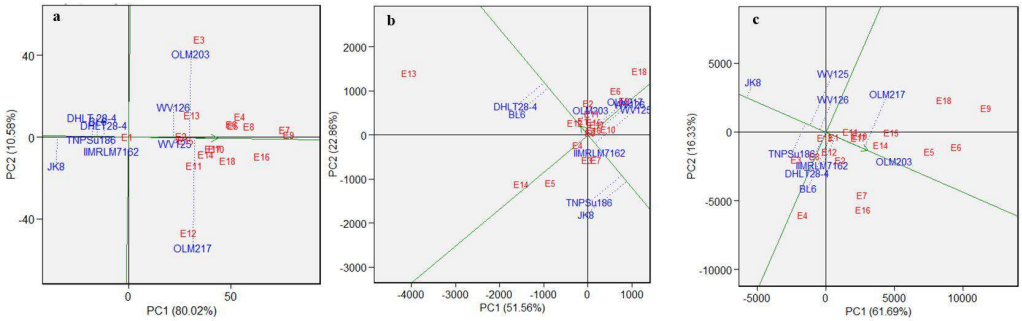

Fig. 3. Average environment coordination view of GGE-biplot based on environment-focused scaling for the mean performance *vs.* stability of nine little millet genotypes for (a) days to 50% flowering (b) seed yield and (c) fodder yield

IIMRLM7162 and JK8 were highly stable but poor seed and fodder yielders, respectively. For days to 50% flowering, wide variability was observed, thus indicating that a genotype stable for one trait may not necessarily be stable for the other. Perhaps, each trait is governed by different genes and the influence of the environment on the expression of different genes varies substantially, this is visualized by way of varying levels of stability of genotypes for seed yield, fodder yield and flowering time.

Ideal genotype: An ideal genotype is the one with a high mean yield and good stability within a mega-environment. It is present at the center of concentric circles with AEC passing through it in the positive direction and has a vector length equal to the longest vector of the genotype on the positive side of AEC (Yan and Tinker 2006). Genotypes located closer to the 'ideal genotype' are more desirable than others. The genotypes WV125 and WV126 were positioned towards the ideal genotype for flowering, although their mean days to 50% flowering across all the environment were as high, making them late flowering types and not desirable by farmers (Fig. 4a). DHLT28-4, BL6 followed by OLM203 were close to ideal genotypes for seed yield (Fig. 4b). The first two genotypes (DHLT28-4, BL6) had highest grand mean for seed yield performance. The genotypes OLM203 and OLM217 were ideal for fodder-yielding, also evident by higher grand mean for fodder-yield (Fig. 4c). The genotype OLM203 was ideal for seed and fodder yield.

Discriminativeness vs. Representativeness: To reduce the cost of genotype evaluation, it is essential to better understand the environments and determine the most

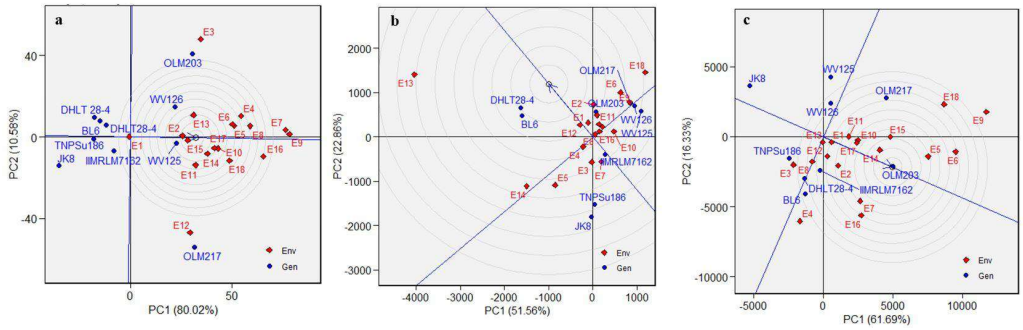

Fig. 4. GGE-biplot showing the ideal little millet genotypes based on mean (a) days to 50% flowering (b) seed yield and (c) fodder yield performance across eighteen environments

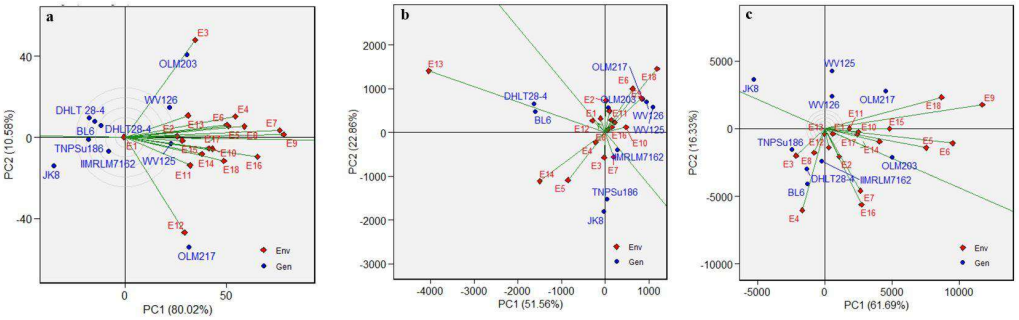

Fig. 5. Discriminative *vs.* representativeness view of GGE biplot for (a) days to 50% flowering (b) seed yield and (c) fodder yield of nine little millet genotypes evaluated across eighteen environments

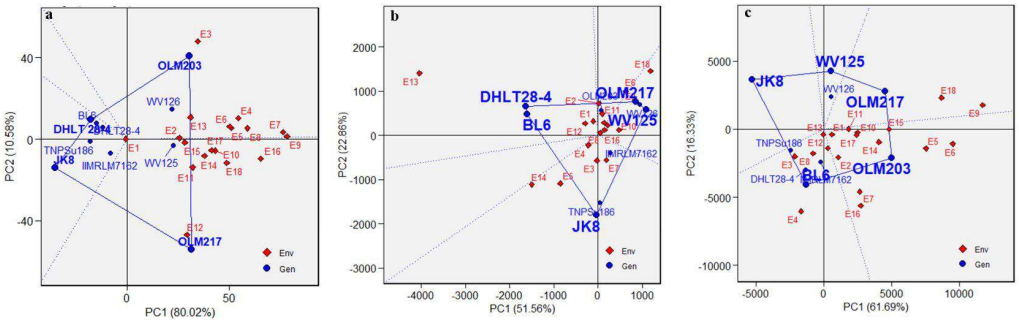

Fig. 6. Polygon view of GGE-biplot based on the symmetrical scaling for "which won-where" pattern of nine little millet genotypes and eighteen environments for (a) days to 50% flowering (b) seed yield and (c) fodder yield

Table 5. AMMI analysis of variance for days to 50% flowering, seed yield and fodder yield of little millet genotypes evaluated across eighteen environments

Source of variation	DF	Days to 50% flowering					Seed yield				
		SS	MSS	F value	Probability	Proportion (%)	SS	MSS	F value	Probability	Proportion(%)
Environment (E)	17	58724.74	3454.39	955.51	<0.0001		362211924	21306583.80	235.79	<0.0001	
Replication (Environment)	36	130.14	3.61	2.42	<0.0001		3252979	90360.52	1.98	<0.0001	
Genotype (G)	8	96839.04	10759.89	7231.54	<0.0001		6966008	870751.00	19.09	<0.0001	
G × E interaction (GEI)	136	49135.39	363.89	244.61	<0.0001		123965993	911514.65	19.99	<0.0001	
PC1	24	20702.71	828.10	556.56	<0.0001	42.00	65465318	2727721.57	59.82	<0.0001	53.00
PC2	22	15647.65	680.33	457.24	<0.0001	31.70	27576565	1253480.24	27.49	<0.0001	22.30
PC3	20	7935.08	377.86	253.95	<0.0001	16.10	13876588	693829.38	15.22	<0.0001	11.20
PC4	18	2580.55	135.81	91.28	<0.0001	5.20	5876552	326475.10	7.16	<0.0001	4.80
PC5	16	1314.42	77.31	51.96	<0.0001	2.70	5473620	342101.23	7.50	<0.0001	4.40
PC6	14	441.52	29.43	19.78	<0.0001	0.90	2528828	180630.55	3.96	<0.0001	2.00
PC7	12	354.68	27.28	18.34	<0.0001	0.70	1573295	131107.91	2.88	<0.0001	1.30
PC8	10	181.22	16.47	11.07	<0.0001	0.40	1104286	110428.58	2.42	<0.0001	0.90
Residuals	288	130.32	14.48	9.73		0.30	13131601	45595.84			
Total	621	428.51	1.48				633003554	1019329.40			
Fodder yield											
Environment (E)	17	3261623410	191860200.60	282.37	<0.0001		PC6	14	27057107	1932650.50	3.57
Replication (Environment)	36	24460446	679456.80	1.25	<0.0001		PC7	12	10864087	905340.50	1.67
Genotype (G)	8	630822910	78852863.70	145.62	<0.0001		PC8	10	3346012	334601.20	0.62
G × E interaction (GEI)	136	1498046976	11015051.30	20.34	<0.0001		Residuals	288	155949718	541492.10	
PC1	24	884824126	36867671.90	68.09	<0.0001	59.10	Total	621	7068526988	11382491.10	
PC2	22	265954092	12088822.40	22.33	<0.0001	17.80					
PC3	20	144008560	7200428.00	13.30	<0.0001	9.60					
PC4	18	123826208	6879233.80	12.70	<0.0001	8.30					
PC5	16	37743335	2358958.40	4.36	<0.0001	2.50					

DF: Degrees of freedom; SS:Sum of squares; MSS: Mean sum of squares

Table 6. Estimates of BLUP-based stability parameters of little millet genotypes evaluated under eighteen test environments and their ranks indicated in parenthesis

Genotype	Days to 50% flowering			Seed yield			Fodder yield		
	HMGV	RPGV	HMRPGV	HMGV	RPGV	HMRPGV	HMGV	RPGV	HMRPGV
BL6	59.00 (6)	0.86 (6)	0.85 (6)	944 (4)	1.01 (5)	0.93 (3)	5083 (2)	1.05 (3)	1.01 (4)
DHLT28-4	57.30 (7)	0.84 (7)	0.83 (7)	1048 (2)	1.08 (2)	1.03 (2)	5041 (3)	1.04 (4)	1.01 (3)
IIMRLM7162	60.605 (5)	0.90 (5)	0.89 (5)	1130 (1)	1.08 (1)	1.06 (1)	4607 (5)	1.01 (5)	0.98 (5)
JK8	47.20 (9)	0.71 (9)	0.67 (9)	867 (6)	0.91 (8)	0.72 (8)	2887 (9)	0.62 (9)	0.54 (9)
OLM203	81.40 (2)	1.24 (2)	1.20 (2)	748 (7)	0.89 (9)	0.79 (6)	5535 (1)	1.23 (1)	1.17 (1)
OLM217	81.80 (1)	1.25 (1)	1.21 (1)	566 (9)	0.96 (6)	0.64 (9)	4770 (4)	1.16 (2)	1.05 (2)
TNPSu186	57.00 (8)	0.83 (8)	0.82 (8)	1034 (3)	1.03 (3)	0.93 (4)	4493 (6)	0.97 (6)	0.93 (6)
W125	79.70 (3)	1.18 (3)	1.17 (3)	724 (8)	0.95 (7)	0.74 (7)	4184 (8)	0.95 (8)	0.91 (8)
W126	77.60 (4)	1.17 (4)	1.15 (4)	919 (5)	1.03 (4)	0.87 (5)	4189 (7)	0.96 (7)	0.91 (7)

discriminative and representative environments (Yan and Kang 2002). It helps to cull out the inferior genotypes from the superior ones. A discriminative environment has the ability to discriminate between test genotypes, while a representative environment represents an average of the eighteen test environments. A lower and higher discriminative ability of the environments is indicated by a shorter and longer environment vector, respectively. The most and least representative environments are indicated by smaller and larger angles between environment vectors, respectively (Yan and Tinker 2006). The environments with long vectors like E3, E12 and E9 for days to 50% flowering (Fig. 5a), while E13, E18 and E14 for seed yield (Fig. 5b) and E9, E6 and E18 for fodder yield (Fig. 5c) were most discriminating. Whereas, the environments E17, E2 and E1 for days to 50% flowering while, E12, E1 and E15 for seed yield and E17, E14 and E1 for fodder yield were nearer to the average environment indicating their representativeness. The environment E1 was representative for days to 50% flowering, seed yield and fodder yield. The environments E9, E13 and E6 were most discriminating and representative for days to 50% flowering, seed yield and fodder yield, respectively. Therefore, these environments can be used jointly as discriminative environments during early-generation testing. On the other hand, the environments that were, being discriminating and non-representative are useful for selecting specifically adapted genotypes.

Which-won-where and mega-environment identification: Polygon of the fodder yield is relatively well distributed than the polygon for days to 50% flowering and seed yield, hence making its biplot most informative as it could discriminate environments more effectively (Fig. 6c). With fewer vertices, the polygons for days to 50% flowering (Fig. 6a) and seed yield (Fig. 6b) depicted that the environments were not well separated and hence, being less informative are not discussed further. The polygon of fodder yield has genotypes JK8, WV125, OLM217, DLM203 and BL6 at the vertices. The equality lines divided the seed and fodder yield polygon into five sectors effectively, while four sectors for days to 50% flowering. Therefore, the eighteen testing environments were spread in two, four and three MEs for days to 50% flowering, seed yield and fodder yield, respectively. The ME-I of fodder yield, included the environments E9 and E18 with OLM217 as the winner, while the ME-II encompassed the environments E6, E5, E15, E14, E10, E11, E17, E1, E2, E7 and E16 with the genotype OLM203 as the winner. The third ME had the environments E13, E12, E8, E3 and E4 with BL6 as the winner. Although, METs are conducted in numerous environments, evaluation in one or two representatives of mega-environments also shall give the same results, thereby reducing the cost incurred in conducting METs. The genotypes present in a sector devoid of any environment, signified that these genotypes are not productive in any environment for any of the trait evaluated.

BLUP-based stability parameters to identify stable genotypes: The BLUP-based stability parameters such as HMGV, RPGV, and HMRPGV further represent robust statistical approaches for predicting stability coupled with adaptability and higher trait mean (Pires et al 2011; Anuradha et al 2022). An attempt was made to identify stable high seed and fodder yielding, preferably early flowering types using BLUP-based stability indices. The chief advantage of biometric approaches, such as HMGV, RPGV and HMRPGV is to disclose the randomness of the genotypic effects and to allow the ranking of genotypes in relation to their performance based on the genetic effects (Resende et al 2001). Based on all three BLUP-based stability estimates (HMGV, RPGV and HMRPGV) for both days to 50% flowering and fodder yield the genotypes OLM217 and

OLM203 were the top rankers (Table 5), whereas for seed yield, the genotype IIMRLM7162 was the top ranker, followed by DHLT28-4 (Table 5), as evident by the results of biplots and high mean performance in the field across the environments. Although the BLUP-based stability parameters were applied to various crops to estimate the stability and adaptability, but none in little millet.

CONCLUSIONS

The current study deciphered the effects of genotype × environment interaction for days to 50% flowering, seed yield and fodder yield in little millet advanced lines and checks. Identified the most stable and high seed and fodder yielding genotypes that were also early in flowering, discerned the representativeness and discriminativeness of eighteen environments for the traits evaluated. The environment and genotype × environment interaction components significantly affected the days to 50% flowering, seed yield and fodder yield. For obvious reasons, the check OLM203 produced higher seed and fodder yield but was late flowering. We recommend DHLT28-4 as an early flowering and most stable with high seed and fodder yielding ability that could be commercialized in India and can be a potential substitute for contemporary cultivars. The environments E9, E13 and E6 were both most representative and discriminative for days to 50% flowering, seed yield and fodder yield, respectively and hence can be used to recognize superior early flowering genotypes with high seed and fodder yielding adapted to specific agro-ecologies.

CONTRIBUTION OF AUTHORS

SB and NC performed data compilation and analysis. TEN, SGP, DNV and IST drafted the manuscript.

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