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Studies on Effects Environment on Finger Millet Genotypes for Seed and Fodder Yield Based on AMMI and BLUP Model

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***Abstract*:** The study was carried out to assess the patterns of GEI governing seed and fodder yield, identify stable and high seed and fodder yielding finger millet genotypes evaluated in ten locations in *Kharif*-2022 in India. The variance due to genotypes, environment and GEI was highly significant for seed and fodder yield. Upon comparison of different AMMI and BLUP models, BLUPg and BLUPge were the best prediction models that adequately explained the variation due to GEI for seed and fodder yield, respectively. The GGE biplot indicated that WN 577 and TNEc 1342 were the ideal genotypes for seed and fodder yield, respectively; the genotype with maximum mean and high stability was IIMR-FM-R21-8012 for seed and fodder yield. IIMR-FM-R21-8012 performed better for seed and fodder yield across maximum test locations. WN 577 and IIMR-FM-R21-8001 showed excellent stability across all the test locations based on AMMI stability indices, while IIMR-FM-R21-8012 and PR 1734 based on BLUP model stability indices for seed yield. Whereas, for fodder yield the genotypes IIMR-FM-R21-8012 and TNEc 1341 were highly stable based on AMMI- and BLUP model stability indices. Therefore, this study identified IIMR-FM-R21-8012 and PR 1734; IIMR-FM-R21-8012 and TNEc 1341 as worthy genetic resources for seed and fodder yield, respectively.

Keywords: GEI, Finger millet, Multi-environment trial, Yield stability, GGE biplot

Finger millet, *Eleusine coracana* (L.) Gaertn subsp. coracana, an annual drought-hardy and subsistence crop of small holding farmers in India and eastern Africa belongs to the subfamily Chloridoideae of the family Poaceae. Archeological records suggest that finger millet was first cultivated in Ethiopia and Uganda (Hilu and De Wet 1976). Due to its drought-hardy nature and nutritional significance, it is cultivated across arid and semiarid tropics and subtropics. However, the seed yield of finger millet is stagnant with an average of 1755 tonnes (Indiastat 2021, https://www .indiastat.com/data/agriculture). The focus on genetic improvement in finger millet was meagre resulting in use of traditional and unimproved finger millet varieties for commercial cultivation. As a result of this, both seed and fodder yielding capacity of finger millet cultivars is stagnant. Predominantly, finger millet varieties in cultivation in India are majorly through pedigree selection (55%), pure line selection (39%) from germplasm accessions (Nagaraja et al 2022). Additionally, finger millet breeding is constrained due to its pollination behavior. Hence, developing widely adaptable, stable and high seed and fodder yielding finger millet cultivars tolerant to biotic and abiotic factors to promote its production and productivity is the need of the hour. However, cultivars bred at various breeding stations have varying responses to environmental conditions. Therefore, the evaluation of the genotypes in the pipeline to be released for commercial cultivation under numerous target production environments aids in identification of stable and superior cultivars that shall facilitate cultivar deployment. Such multi-environment trials (METs) aid in the identification of stable cultivars with high seed and fodder yield potential. Most often than not, the response to selection is confounded by the genotype by environment interaction (GEI) during multi-environment trials. To effectively identify superior cultivars in the final selection cycles, while predicting their potential performance in various environments, it is imperative to quantify GEI.

MATERIAL AND METHODS

Experimental material: A total of 28 finger millet genotypes (Table 1) including twenty-three advanced breeding lines and five checks were evaluated for seed and fodder yield during *Kharif*-2022 rainy season across ten Indian locations (Table 2) in randomized complete block design in three replicates as

Table 1. Pedigree of the finger millet genotypes used in the study

Genotype	Pedigree	Centre
BUFM 19-E-1	Selection from local germplasm of Akole Tahsil, Ahmednagar	Buldana, Maharashtra
GE 6541	Selection from elite GE 6541 line from Bengaluru	Kolhapur, Maharashtra
GPU 105	GPU 28 × KMR 630 (3-1-2)	Bengaluru, Karnataka
GPU 106	GPU28 × GE 4593 (1-6)	Bengaluru, Karnataka
IIMR-FM-R21-8001	Gamma mutant from MR6 variety	Hyderabad, Telangana
IIMR-FM-R21-8006	Pedigree selection from GPU28 × GPU48	Hyderabad, Telangana
IIMR-FM-R21-8011	Pedigree selection from GPU28 × IE 990	Hyderabad, Telangana
IIMR-FM-R21-8012	Pedigree selection from PR 202 × GPU 48	Hyderabad, Telangana
KIFMG 211	Selection from germplasm accession IE 4497	Kolhapur, Maharashtra
KMR 654	Indaf 5 × IE- 2712	Mandya, Karnataka
KMR 655	Indaf 5 × GE -1409	Mandya, Karnataka
PPR 1216	Vakula × Srichaitanya	Perumallapalli, Andhra Pradesh
PPR 1272	Kalyani × PES 110	Perumallapalli, Andhta Pradesh
PR 1734	GPU 28 (ms) × PR 202	Peddapuram, Andhra Pradesh
TNEc 1341	TNEc 1228 × GE 276	Athiyandal, Tamil Nadu
TNEc 1342	KWFM × KOPN 565	Athiyandal, Tamil Nadu
VL 402	GPU 28 × VL 347	Almora, Uttarakhand
VL 409	KMR 118 × VL 347	Almora, Uttarakhand
VR 1163	VR 708 × GPU 48	Vizianagaram, Andhra Pradesh
VR 1171	PR 202 × GPU 48	Vizianagaram, Andhra Pradesh
WN 577	GPU 48 × GE 4931	Waghai, Gujarat
WN 660	Selection from germplasm accession IE 4656	Waghai, Gujarat
WN 666	Selection from germplasm accession IE 4657	Waghai, Gujarat
CFMV 1 (Check)	VL 330 × GE 532	Vizianagaram, Andhra Pradesh
CFMV 2 (Check)	Pure line selection from Dangs district	Waghai, Gujarat
GPU 67 (Check)	Selection from GE 5331	Bengaluru, Karnataka
PR 202 (Check)	Pure line selection from Mettachodiragi of Arakku valley	Peddapuram, Andhra Pradesh
VL 376 (Check)	GE 4172 × VL ragi 149	Almora, Uttarakhand

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

Location	T. Max.	T. Min.	Rainfall (mm)	Latitude	Longitude	Altitude (ft.)
Bengaluru, Karnataka	28.35	19.71	43.53	12.97° N	77.59° E	3020
Berhampur, West Bengal	35.26	24.37	86.70	19.31° N	84.79° E	78
Dahod, Gujarat	30.41	22.74	72.76	22.83° N	74.26°E	984
Dapoli, Maharashtra	31.04	24.56	45.00	17°46'3.71"N	73°11'27.64"E	800
Hageri, Karnataka	36.89	25.87	28.00	15° 09' 00.89” N	76° 52' 07.05” E	226
Jagdalpur, Chattisgarh	28.13	20.85	62.09	19.08 º N	82.02 º E	1811
Nandyal, Andhra Pradesh	34.90	24.98	16.80	15°29′19″ N	78°29′11″ E	666
Perumallapalle, Andhra Pradesh	35.33	25.96	28.07	13.60° N	79.35° E	1000
Vizianagaram, Andhra Pradesh	30.78	28.75	60.10	18.10° N	83.39° E	242
Waghai, Gujarat	27.59	23.29	55.00	20.77° N	73.49° E	830

T. Max.: Maximum temperature; T. Min.: Minimum temperature part of initial varietal trial (IVT). Hereafter, both advanced breeding lines and checks are referred to as “genotypes”; location and environment are used interchangeably for the sake of simplicity. Each genotype was sown in a plot size of 3×2.25 meters (m). Therefore, the area of each plot was 6.75 square meters. Each genotype was sown in 10 rows of 3m length spaced 30cm apart. The recommended crop management practices were adopted to raise a healthy crop. Plot seed/fodder yield (kg/plot) was considered for further analysis.

Statistical analysis: The phenotypic data of seed and fodder yield collected from the twenty-eight finger millet genotypes evaluated across ten test locations was confirmed for homogeneity of variances by Bartlett test (Bartlett 1937). To determine the significance level of genotypes (G), locations (L) and GLI (genotype × location interaction), the data was subjected to combined ANOVA using mixed linear model (R Core Team 2020). The AMMI model was used to determine the GLI effects of twenty-eight finger millet genotypes to assess their adaptability and stability across the ten test locations. The genotypes were treated as fixed sources of variation, while the locations as random. The AMMI amalgamates ANOVA for genotype and location main effects with PCA for GLI with the axes of the principal components of interactions (IPCA) (Gauch 1988; Yan et al 2007). The AMMI model used is as follows:

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

Y_{ij} = Seed/Fodder yield of the ith genotype in the jth location

μ = Experimental genotype mean of seed/fodder yield

g_i and e_j = Genotype and location deviations from the grand mean of seed/fodder yield

λ_k = Eigen value of the PCA analysis axis k

α_{ik} and γ_{jk} = Genotype and location principal component scores for axis k

N = Number of principal components retained in the model

e_{ij} = Error term

In the BLUP method, the effects of genotype and GLI are considered to be random. Contrary to the AMMI model, a linear mixed model is used and the formula is as follows: $Y = X\beta + Zu + \mathcal{E}$, where β is the data vector of the fixed unknown effect (the average value of the block in each location), u is the GLI + genotype effect, X and Z represent the matrix involvingβ, u and Y and $\mathcal{E}$ is the random errors' vector. In order to better predict the AMMI and the BLUP model family, root mean square prediction difference (RMSPD) estimates were used to compare (Piepho 1994).

Genotype + Genotype × environment (GGE) bi-plot is a subjective/qualitative means to characterize patterns of GLI and assess the relative stability of test genotypes. The GGE bi-plot is constructed using the first two principal components (PC1 and PC2) derived using adjusted seed or fodder yield from ANOVA (Yan 2001, Yan 2002). The GGE bi-plot is suggestive of visual interpretation of the GLI patterns, representativeness and discriminating ability of the locations 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).

Twelve AMMI model-based stability indices *viz.,* AMMI Stability Index (ASI), AMMI stability value (ASV), AMMI Based Stability Parameter (ASTAB), Sum Across Environments of Absolute Value of GEI Modelled by AMMI (AVAMGE), Annicchiarico's D Parameter values (Da), Zhang's D Parameter (Dz), Averages of the squared eigenvector values (EV), Stability Measure Based on Fitted AMMI Model (FA), Modified AMMI Stability Index (MASI), Modified AMMI Stability Value (MASV), Sums of the absolute value of the IPCA scores (SIPC) and Absolute value of the relative contribution of IPCAs to the interaction (Za) were computed for each of the genotype for seed and fodder yield using the package 'ammistability' in R software (Ajay et al 2019). Additionally, the BLUP-based stability parameters such as harmonic mean of genotypic values (HMGV) to infer both seed/fodder yield and stability, relative performance of genotypic values (RPGV) to investigate the mean seed/fodder yield and genotypic adaptability and harmonic mean of relative performance of genotypic values (HMRPGV) to evaluate stability, adaptability and seed/fodder yield simultaneously (de Resende 2004) were also estimated. The analysis was computed using the metan package in R software version 4.2.1 (Olivoto and Lucio 2020).The Spearman's rank correlations among all the twelve AMMI stability indices was computed.

RESULTS AND DISCUSSION

Mean seed and fodder yield: The mean seed yield of the twenty-eight test genotypes across ten test locations varied from 4.19 kg/plot (IIMR-FM-R21-8012 in Nandyal) to 0.46 kg/plot (VR 1163 in Dapoli; Fig. 1a), whereas the fodder yield varied from 11.18 kg/ plot (PR 202 in Perumallapalle) to 0.59 kg/plot (VL 402 in Dapoli; Fig. 1b). The grand mean seed yield of genotypes *viz.,* IIMR-FM-R21-8012 (2.11 kg/plot) and PR 1734 (2.09 kg/plot) was the highest (Fig. 1a). Fodder yield the genotypes IIMR-FM-R21-8012 (6.17 kg/plot) and TNEc 1341(6.00 kg/plot) were the best performers (Fig. 1b). The average seed and fodder yield of all the genotypes was higher in Nandyal *i.e.,* 3.12 kg/plot and 8.54 kg/plot, respectively. There were significant variation for genotypes, locations and GLI for both seed and fodder yield (Data not shown). Similar results were reported by Kendel and Sener (2015) in wheat and Sarkar et al (2014) in Barley.

Additive main effect and multiplicative interaction: The AMMI analysis of variance indicated that the genotypes, locations and GLI effects were highly significant (p <0.001) for seed and fodder yield (Table 3). The partitioning of variance components of AMMI analysis of variance highlighted that locations accounted for 81.43 and 88.03 % of the total observed variation for seed and fodder yield, respectively. This indicated that the test locations were particularly diverse and greatly impacted genotypes' potential to produce seed and fodder yield. Most often than not, the contribution of test locations is relatively higher than other sources of variation in multi-environment trials (Badu-Apraku et al 2012). Earlier, Yan et al (2000) put forth that about 80% of the variation could be attributed to environment, whereas, 20% to both genotypes and GEI in wheat yield trials. While, genotypes accounted for 5.38 and 3.51 %, and GLI accounted for 13.18 and 8.44%, respectively for seed and fodder yield. A significant GLI necessitated the need to identify adaptable genotypes with consistently high seed and fodder yield (Yan and Tinker 2006) and indicated the possible existence of different mega-environments. Furthermore, four and two principal components were significant for seed and fodder yield, respectively. Similar to our results, a large proportion of total variation contributed by the environment has been reported earlier in finger millet (Adugna et al 2011, Molla et al 2013, Dagnachew et al 2014, Birhanu et al 2016, Lakew et al 2017, Seyoum et al 2019) and little millet for seed and fodder yield (Nagaraja et al. 2023). The joint effect of the four and two significant principal components of GLI accounted for 85 % and 62.10 % of the whole effect it had on the variation for seed and fodder yield, respectively (Table 3). The first principal component accounted for 34.60% of the variation caused by the interaction, while 23.70, 17.50 and 9.90% of the variation was caused by PC2, PC3 and PC4, respectively for seed yield

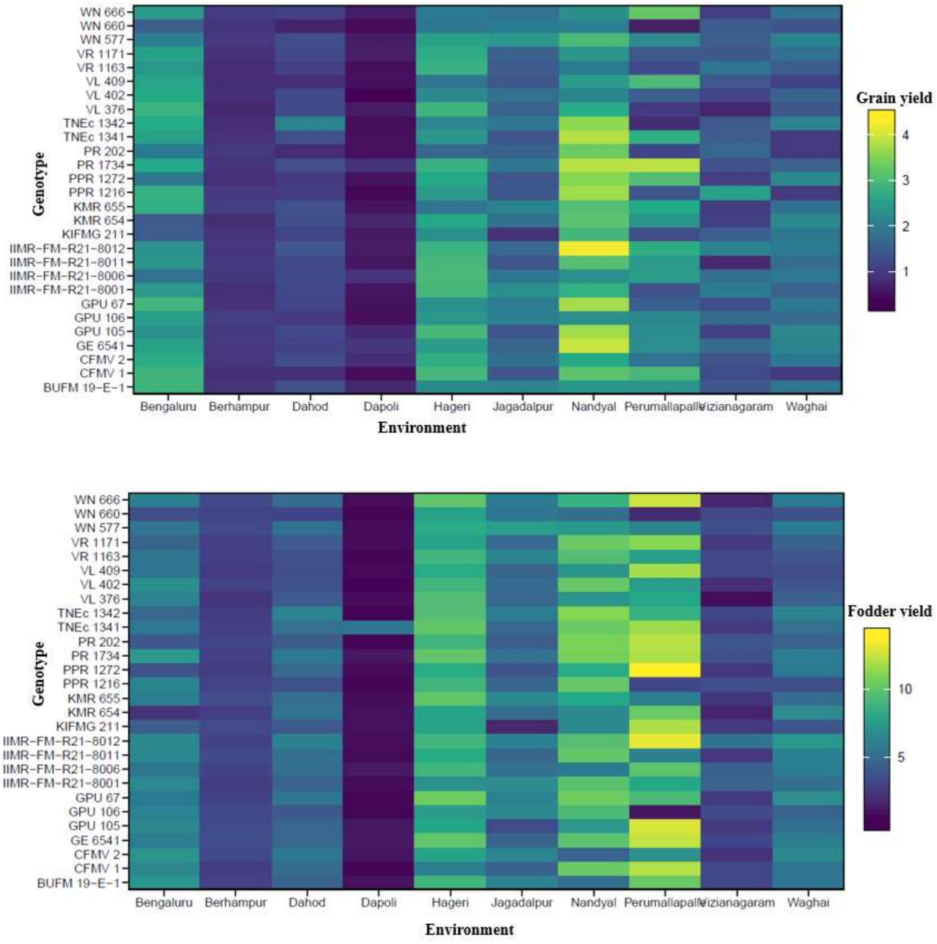

Fig. 1. Mean yield of 28 finger millet genotypes across in each of the ten locations for (a) seed yield and (b) fodder yield

(Table 3). Likewise, for fodder yield, PC1 accounted for 42.20% of the variation caused by the GEI, while 19.90 of the variation was caused by PC2 for fodder yield (Table 3).

Prediction accuracy of AMMI and BLUP Model: Root mean square prediction difference was used to predict the accuracy of AMMI and BLUP model family members for seed and fodder yield and the results are based on the average of 200 predictions of RMSPD for each test model. The model with the smallest RMSPD value is defined as the most accurate prediction and vice versa. For seed yield (Fig. 2a), BLUPg(due to genotype effects) was the most accurate prediction model among all evaluated models, while BLUPge (due to genotype and environment effects) for fodder yield (Fig. 2b). The genotypes IIMR-FM-R21-8012 and PR 1734 produced higher seed yield relatively based on BLUPg predicted values (Table 4), while IIMR-FM-R21-8012 and TNEc 1341 produced higher fodder yield relatively across the ten locations based on BLUPge predicted values (Data not shown).

GGE bi-plot for Interpretation of GLI

Ranking genotypes relative to the ideal genotype: WN 577 (Fig. 3a) and TNEc 1342 (Figure 3b) were more

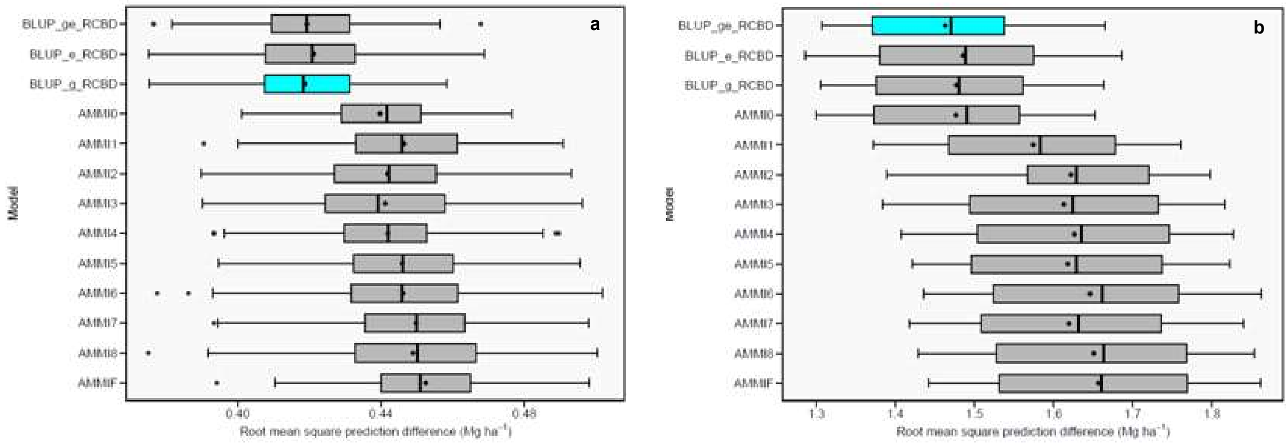

Fig. 2. Boxplot of RMSPD values for different AMMI and BLUP model family members for (a) seed yield and (b) fodder yield

Table 3. AMMI analysis of variance for seed and fodder yield of twenty-eight finger millet genotypes evaluated across ten locations

Source of variation	Degrees of freedom	Sum of squares		Mean sum of squares		'F' value		Probability		Proportion (%)	
		SY	FY	SY	FY	SY	FY	SY	FY	SY	FY
Location	9	398.89	4893.30	44.32	543.70	78.78	57.25	0.00	0.00	-	-
Replication (Location)	20	11.25	189.90	0.56	9.50	4.66	6.21	0.00	0.00	-	-
Genotype	27	26.40	195.40	0.96	7.24	8.11	4.73	0.00	0.00	-	-
GLI	243	64.52	469.50	0.26	1.93	2.20	1.26	0.00	0.00	-	-
PC1	35	22.38	197.20	0.63	5.63	5.29	3.66	0.00	0.00	34.60	42.20
PC2	33	15.37	93.19	0.46	2.82	3.86	1.84	0.00	0.00	23.70	19.90
PC3	31	11.31	55.01	0.36	1.77	3.02	1.15	0.00	0.26	17.50	11.80
PC4	29	6.39	43.92	0.22	1.51	1.82	0.98	0.00	0.49	9.90	9.40
PC5	27	4.26	41.68	0.15	1.54	1.31	1.00	0.13	0.46	6.60	8.90
PC6	25	2.94	16.67	0.11	0.66	0.97	0.43	0.50	0.99	4.50	3.60
PC7	23	1.25	12.43	0.05	0.54	0.45	0.35	0.98	0.99	1.90	2.70
PC8	21	0.56	3.87	0.02	0.18	0.22	0.12	1.00	1.00	0.90	0.80
PC9	19	0.29	3.46	0.01	0.18	0.13	0.12	1.00	1.00	0.40	0.70
Residuals	540	65.09	825.60	0.12	1.53	-	-	-		-	-
Total	1082	630.90	7041.13	-	-	-	-	-		-	-

SY: Seed yield; FY: Fodder yield

desirable for seed and fodder yield, respectively. Contrastingly, WN 660 was of course the poorest for seed and fodder yield as it was consistently the poorest. “High stability” of a genotype is worthwhile only when correlated with mean performance. WN 660 is highly “stable”, this does not mean WN 660was good; it only means that the relative performance of WN 660 was consistent. WN 660 was even poorer than the highly variable, least stable genotype KIFMG 211 for seed yield and GPU 106 for fodder yield, because KIFMG 211and GPU 106 performed reasonably well in at least some locations. This illustration, is a proof that how misleading it can be to search and select for “stability” genes alone. “Stable” genotypes are desirable only when coupled with high mean performance.

Mean performance and stability of the genotypes: The single-arrowed line in the biplot is the average-environment coordination (AEC) abscissa (or AEA); it points to higher mean seed/fodder yield across locations. PR 1734 produced highest mean seed yield, followed by IIMR-FM-R21-8012 and PPR1272; IIMR-FM-R21-8011 had mean seed yield similar to the grand mean; and WN 660 had the lowest mean seed yield (Fig. 4a). The genotype IIMR-FM-R21-8012 produced the highest mean fodder yield, followed by TNEc 1341 and GPU 67; KMR 655 produced mean fodder yield similar to the grand mean; WN 660 had the lowest mean fodder yield (Fig. 4b). The AEC ordinate is indicated by the double-arrowed line, which signifies higher variability and poor stability in either direction. Thus, TNEc 1342 was highly unstable whereas WN 577 stable for seed yield. The genotype PR 1734 was highly stable and GPU 106 unstable for fodder yield.

Table 4. Predictive value of BLUP genotype effect of seed yield

Genotype	Seed yield	Genotype	Seed yield
BUFM 19-E-1	1.80	PPR 1216	1.78
CFMV 1	1.74	PPR 1272	1.85
CFMV 2	1.86	PR 1734	2.00
GE 6541	1.82	PR 202	1.76
GPU 105	1.76	TNEc 1341	1.78
GPU 106	1.75	TNEc 1342	1.84
GPU 67	1.81	VL 376	1.68
IIMR-FM-R21-8001	1.79	VL 402	1.61
IIMR-FM-R21-8006	1.86	VL 409	1.60
IIMR-FM-R21-8011	1.74	VR 1163	1.61
IIMR-FM-R21-8012	2.01	VR 1171	1.71
KIFMG 211	1.53	WN 577	1.88
KMR 654	1.64	WN 660	1.43
KMR 655	1.77	-	-

Which-won-where: The equality line between PR 1734 and IIMR-FM-R21-8012 indicated that PR 1734 was better in Perumallapalle, Bengaluru and Hageri, whereas IIMR-FM-R21-8012 in the other locations for seed yield (Fig. 5). The equality line between IIMR-FM-R21-8012 and KIFMG 211 indicated that IIMR-FM-R21-8012 was better than KIFMG 211 across all the locations. Note that TNEc 1342 located on the line that connects IIMR-FM-R21-8012 and KIFMG 211, indicates that the rank of genotypes was IIMR-FM-R21-8012>TNEc 1342>KIFMG 211 true across all locations for seed yield. Likewise, the equality line between IIMR-FM-R21-8012 and PR 202 indicated that IIMR-FM-R21-8012 was better across most of the locations, whereas PR 202 in Perumallapalle for fodder yield (Fig. 5). TNEc 1342 and TNEc 1341 located on the line that connects IIMR-FM-R21-8012 and PR 202, indicated that the rank IIMR-FM-R21-8012>TNEc 1342>TNEc 1341>PR 202 was true in all locations for fodder yield. The equality lines divided the biplot into sectors and the winning genotype for each sector was located on the respective vertex. The ten locations fell into two sectors both for seed and fodder yield. The genotype PR 1734 was the winner in Perumallapalle, Bengaluru and Hageri, and IIMR-FM-R21-8012 across remaining locations for seed yield. The genotype PR 202 was the winner in Perumallapalle; IIMR-FM-R21-8012 for the other locations for fodder yield. This pattern suggests that the target locations may consist of two different mega-environments and that different genotypes should be selected and deployed for each.

Discriminating ability of test locations: The measure of the discriminating ability of a test location is based on the concentric circles on the biplot that assist in contemplating the length of the location vectors which is equivalent to the standard deviation within the respective location. With relatively longer location vectors, Perumallapalle and Nandyal were most discriminating and informative test locations both for seed and fodder yield (Fig. 6a and Fig. 6a). The test locations Berhampur and Dapoli with shorter vectors for seed yield and Vizianagaram for fodder yield (Fig. 6b) were non-discriminative and non-informative. They provide meagre information on the performance of the genotypes and hence shall not be useful as test locations for further seed/fodder yield trials.

Representativeness of test locations: The average location (represented by the arrow) has the average coordinates of all test locations and AEA (Average-Environment Axis) is the line that passes through the average location and the biplot origin. The test locations Berhampur and Dapoli with a smaller angle with AEA were most representative whereas, Perumallapalle and Vizianagaram

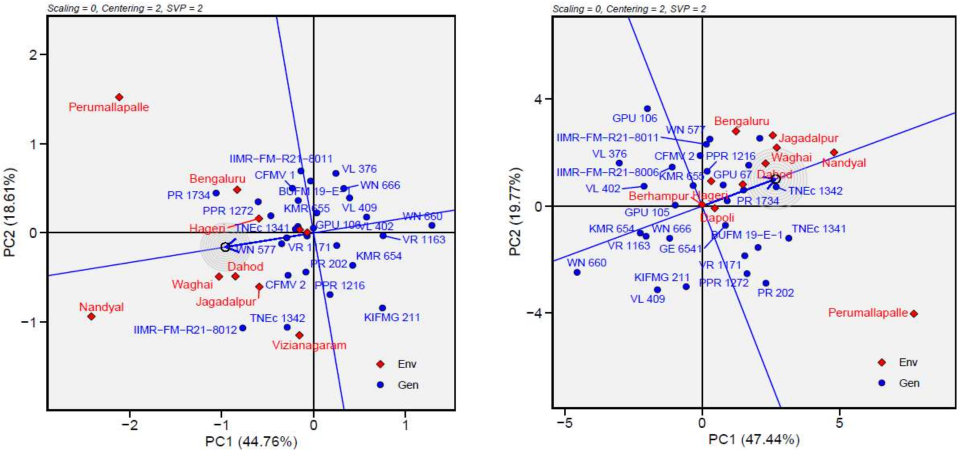

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Fig. 3. Average environment coordination view of GGE-biplot based on environment-focused scaling for the ideal genotypes of twenty-eight finger millet genotypes for (a) seed yield and (b) fodder yield

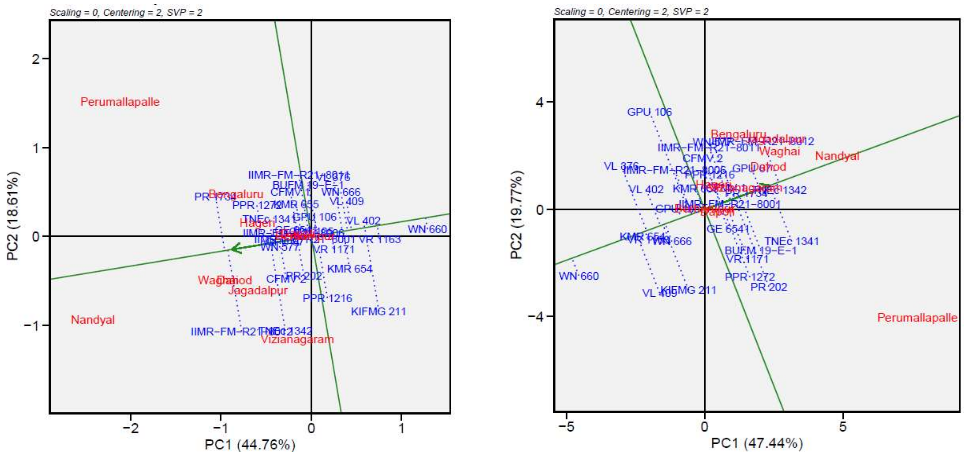

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Fig. 4. Average environment coordination view of GGE-biplot based on environment-focused scaling for the mean performance vs. stability of twenty-eight finger millet genotypes for (a) seed yield and (b) fodder yield

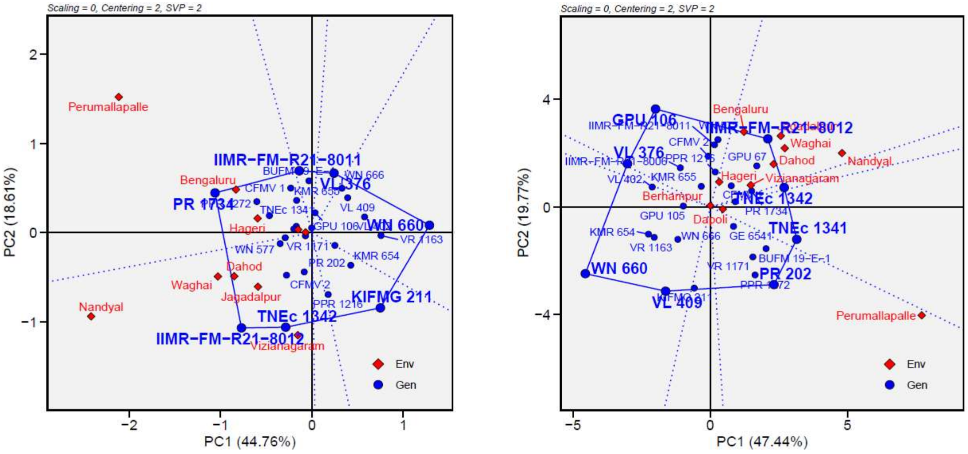

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Fig. 5. Polygon view of GGE-biplot based on the symmetrical scaling for "which won-where" pattern of twenty-eight finger millet genotypes and ten locations for (a) seed yield and (b) fodder yield

Table 5. Estimates of AMMI-based stability parameters of twenty-eight finger millet genotypes evaluated across ten locations

Genotype	ASI		ASV		ASTAB		AVAMGE		DA		DZ		EV		FA	
	SY	FY	SY	FY	SY	FY	SY	FY	SY	FY	SY	FY	SY	FY	SY	FY
BUFM 19-E-1	0.11	0.28	0.49	1.52	0.27	0.63	1.94	3.85	0.78	2.14	0.35	0.30	0.03	0.04	0.60	4.60
CFMV 1	0.14	0.16	0.61	0.85	0.30	0.60	2.13	4.01	0.84	1.84	0.36	0.33	0.03	0.05	0.70	3.40
CFMV 2	0.06	0.19	0.25	1.01	0.26	0.40	1.80	3.96	0.70	1.62	0.37	0.25	0.03	0.03	0.49	2.64
GE 6541	0.02	0.12	0.09	0.63	0.00	0.09	0.29	1.54	0.13	0.83	0.05	0.10	0.00	0.00	0.01	0.70
GPU 105	0.01	0.12	0.04	0.65	0.10	0.12	1.12	2.27	0.42	0.94	0.25	0.13	0.01	0.00	0.18	0.89
GPU 106	0.04	0.45	0.17	2.41	0.12	1.36	1.32	5.93	0.49	3.23	0.25	0.42	0.01	0.09	0.24	10.48
GPU 67	0.07	0.08	0.32	0.47	0.23	0.12	1.55	2.03	0.63	0.86	0.37	0.14	0.03	0.01	0.40	0.74
IIMR-FM-R21-8001	0.01	0.09	0.07	0.48	0.01	0.07	0.44	1.71	0.18	0.71	0.09	0.10	0.00	0.00	0.03	0.50
IIMR-FM-R21-8006	0.04	0.22	0.18	1.19	0.41	0.30	2.05	3.68	0.79	1.55	0.51	0.19	0.06	0.01	0.63	2.42
IIMR-FM-R21-8011	0.12	0.15	0.54	0.80	0.27	0.18	1.49	0.04	0.77	1.15	0.35	0.16	0.03	0.01	0.60	1.32
IIMR-FM-R21-8012	0.14	0.02	0.61	0.13	0.49	0.00	2.38	0.51	1.02	0.24	0.48	0.04	0.05	0.00	1.06	0.05
KIFMG 211	0.19	0.17	0.38	0.89	0.44	0.16	2.41	2.59	1.04	1.15	0.42	0.14	0.04	0.01	1.09	1.33
KMR 654	0.10	0.18	0.46	0.96	0.35	0.44	2.27	4.00	0.83	1.66	0.43	0.27	0.04	0.03	0.69	2.76
KMR 655	0.08	0.09	0.34	0.51	0.11	0.06	0.97	1.64	0.49	0.68	0.24	0.08	0.01	0.00	0.24	0.46
PPR 1216	0.15	0.09	0.64	0.51	0.41	0.23	1.95	2.62	0.96	1.13	0.44	0.20	0.05	0.02	0.92	1.28
PPR 1272	0.18	0.32	0.79	1.70	0.28	0.68	2.07	4.20	0.88	2.29	0.32	0.30	0.02	0.04	0.78	5.26
PR 1734	0.23	0.13	1.01	0.72	0.45	0.23	2.76	2.94	1.12	1.21	0.40	0.19	0.04	0.01	1.25	1.47
PR 202	0.07	0.43	0.32	2.31	0.35	1.11	2.00	6.11	0.81	2.99	0.44	0.37	0.04	0.06	0.65	8.96
TNEC 1341	0.18	0.37	0.80	1.98	0.31	0.81	2.22	5.86	0.91	2.56	0.34	0.31	0.02	0.05	0.83	6.56
TNEC 1342	0.16	0.27	0.68	1.46	0.62	0.61	2.81	5.05	1.15	2.10	0.54	0.30	0.07	0.04	1.34	4.41
VL 376	0.09	0.37	0.42	1.98	0.47	1.05	2.28	5.00	0.93	2.78	0.51	0.38	0.06	0.07	0.88	7.73
VL 402	0.13	0.26	0.58	1.37	0.24	0.39	1.82	3.54	0.75	1.78	0.33	0.22	0.02	0.02	0.57	3.18
VL 409	0.08	0.14	0.35	0.74	0.19	0.50	1.38	3.89	0.61	1.67	0.32	0.30	0.02	0.04	0.38	2.80
VR 1163	0.20	0.10	0.86	0.56	0.50	0.23	2.67	2.57	1.10	1.14	0.47	0.20	0.05	0.02	1.21	1.31
VR 1171	0.07	0.29	0.33	1.54	0.07	0.50	1.07	3.94	0.42	2.01	0.17	0.25	0.00	0.03	0.17	4.06
WN 577	0.01	0.16	0.07	0.87	0.05	0.23	0.76	2.25	0.30	1.28	0.16	0.18	0.00	0.01	0.09	1.64
WN 660	0.24	0.42	1.03	2.23	0.60	2.22	3.14	9.08	1.23	3.74	0.50	0.60	0.06	0.18	1.53	14.00
WN 666	0.60	0.07	0.25	0.39	0.27	0.11	1.82	1.80	0.73	0.80	0.38	0.14	0.03	0.01	0.53	0.65

Cont...

Table 5. Estimates of AMMI-based stability parameters of twenty-eight finger millet genotypes evaluated across ten locations

Genotype	MASI		MASV		SIPC		ZA	
	SY	FY	SY	FY	SY	FY	SY	FY
BUFM 19-E-1	0.11	0.28	0.79	1.52	0.70	1.10	0.10	0.13
CFMV 1	0.15	0.16	0.84	0.85	0.91	0.93	0.14	0.08
CFMV 2	0.08	0.19	0.75	1.01	0.89	0.89	0.11	0.09
GE 6541	0.02	0.12	0.13	0.63	0.15	0.38	0.02	0.04
GPU 105	0.04	0.12	0.45	0.65	0.50	0.50	0.05	0.05
GPU 106	0.06	0.45	0.55	2.41	0.48	1.53	0.06	0.19
GPU 67	0.08	0.08	0.55	0.47	0.75	0.47	0.09	0.04
IIMR-FM-R21-8001	0.02	0.09	0.20	0.48	0.19	0.38	0.02	0.04
IIMR-FM-R21-8006	0.07	0.22	0.68	1.19	0.94	0.67	0.10	0.09
IIMR-FM-R21-8011	0.13	0.15	0.76	0.80	1.01	0.60	0.15	0.07
IIMR-FM-R21-8012	0.15	0.02	1.05	0.13	1.08	0.13	0.14	0.01
KIFMG 211	0.19	0.17	0.99	0.89	1.02	0.42	0.18	0.06
KMR 654	0.12	0.18	0.82	0.96	1.14	0.91	0.15	0.09
KMR 655	0.08	0.09	0.46	0.51	0.66	0.31	0.09	0.04
PPR 1216	0.16	0.09	0.96	0.51	1.23	0.53	0.18	0.05
PPR 1272	0.18	0.32	0.80	1.70	0.68	1.10	0.13	0.13
PR 1734	0.23	0.13	1.01	0.72	0.76	0.67	0.15	0.07
PR 202	0.10	0.43	0.83	2.31	1.03	1.21	0.12	0.16
TNEC 1341	0.18	0.37	0.84	1.98	0.80	1.00	0.15	0.14
TNEC 1342	0.17	0.27	1.19	1.46	1.25	1.10	0.17	0.13
VL 376	0.12	0.37	0.94	1.98	1.26	1.42	0.15	0.17
VL 402	0.14	0.26	0.71	1.37	0.94	0.74	0.14	0.10
VL 409	0.09	0.14	0.58	0.74	0.85	0.81	0.11	0.07
VR 1163	0.20	0.10	1.02	0.56	1.33	0.60	0.20	0.05
VR 1171	0.08	0.29	0.40	1.54	0.43	0.86	0.07	0.11
WN 577	0.03	0.16	0.34	0.87	0.33	0.68	0.04	0.08
WN 660	0.24	0.42	1.13	2.23	1.35	0.07	0.22	0.22
WN 666	0.09	0.07	0.81	0.39	0.83	0.42	0.11	0.04

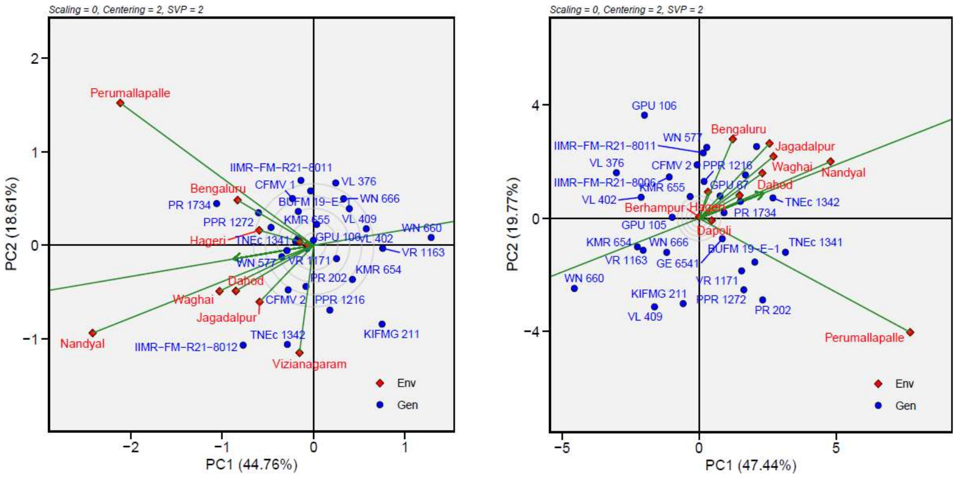
ASI= AMMI stability index; ASV= AMMI stability value; ASTAB=AMMI-based stability parameter; AVAMGE= Absolute value of GEI modeled by AMMI; DA= Annicchiarico's D parameter; DZ= Zhang's D parameter; EV= Averages of the squared eigenvector values and FA= Fitted AMMI model; MASI=Modified AMMI Stability Index; MASV= Modified AMMI Stability Value; SIPC= Sums of absolute value of the IPC scores; ZA= Absolute value of the relative contribution of IPCs to the interaction and WAAS= Weighted average of absolute score; SY: Seed yield; FY: Fodder yield

with a greater angle with AEA were least representative for seed yield. For fodder yield, Nandyal was most representative while, Perumallapalle and Bengaluru were least.Nandyal was both discriminating and representative location both for seed and fodder yield indicating its potential in identifying generally adapted genotypes. Perumallapalle was discriminating but non-representative test location for seed and fodder yield signifying its use selecting specifically adapted genotypes.

Association among different stability parameters: Various AMMI-based stability indices such as ASI, ASV, ASTAB, AVAMGE, DA, DZ, EV, FA, MASI, MASV, SIPC and Za were computed both for seed and fodder yield (Table 5). The lower the score of the stability index, higher is the stability of the genotype and vice versa. The scores of EV were close to 0, followed by Za. The genotypes WN 577, IIMR-FM-R21-8001and GE 6541 were highly stable based on all the estimated stability indices for seed yield. Subsequently, the genotypes IIMR-FM-R21-8012 and WN 666 were highly stable for fodder yield. The order of the rank of these genotypes varied for each of the stability index. These differences may be attributable to the variation in estimation methods that consider the first two or all the significant PCs. Nevertheless, a similar trend in identifying stable genotypes was observed for all the stability indices. Similar results were reported in by Cheloei et al (2020) in rice and Anuradha et al (2022) in finger millet using AMMI stability indices.

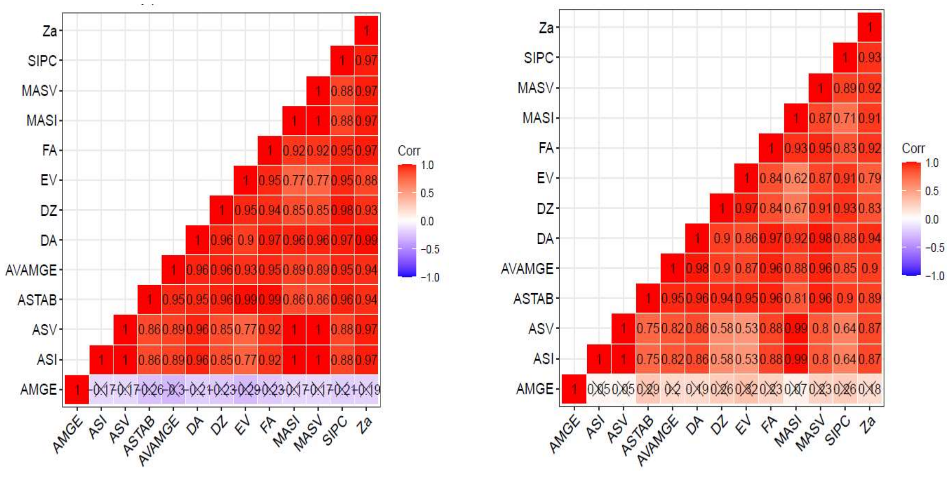
In an effort to disclose the relationship between each of the AMMI stability indices, Spearman's rank correlation uncovered strong association among almost all the estimated AMMI-based stability indices. The stability indices, ASI and ASV were significantly associated in positive direction for seed yield (Fig. 7a). The stability index AMGE was not significantly associated with any other stability index in positive direction both for seed and fodder yield (Fig. 7a and 7b). Significant association of MASV with all the stability parameters at a relatively higher magnitude in positive direction except AMGE. It was ascertained that ASI and ASV; MASV and ASI; MASV and ASV; MASV and MASI; MASI and ASI; MASI and ASV were 100% associated for fodder yield (Fig. 7b).

BLUP-based stability parameters to identify stable genotypes: Based on all three BLUP-based stability estimates for seed yield, the genotypes IIMR-FM-R21-8012 and PR 1734 were the top two rankers in that order (Table 6). The genotypes IIMR-FM-R21-8012 and TNEc 1341 were highly stable and produced maximum fodder yield. Although the BLUP-based stability indices were applied to various crops to estimate the stability and adaptability, only one study by Anuradha et al (2021) was reported in finger millet.



a b

Fig. 6. Discriminative vs. representativeness view of GGE biplot for (a) seed yield and (b) fodder yield of twenty-eight finger millet genotypes evaluated across ten locations



a b

Fig. 7. Correlation between different AMMI stability parameters estimated for (a) seed yield and (b) fodder yield

Table 6. Estimates of BLUP-based stability parameters of fifteen finger millet genotypes evaluated under twenty test environments

Genotype	HMGV		RPGV		HMRPGV	
	SY	FY	SY	FY	SY	FY
BUFM 19-E-1	1.50	3.79	1.05	1.09	1.04	1.08
CFMV 1	1.39	3.33	0.98	1.02	0.97	1.02
CFMV 2	1.56	3.51	1.08	1.04	1.08	1.04
GE 6541	1.51	3.51	1.05	1.04	1.05	1.04
GPU 105	1.48	3.10	1.02	0.96	1.01	0.96
GPU 106	1.40	3.04	0.99	0.97	0.99	0.97
GPU 67	1.45	3.85	1.03	1.11	1.03	1.10
IIMR-FM-R21-8001	1.46	3.51	1.03	1.04	1.03	1.04
IIMR-FM-R21-8006	1.61	3.22	1.10	0.99	1.09	0.98
IIMR-FM-R21-8011	1.38	3.54	0.98	1.05	0.97	1.05
IIMR-FM-R21-8012	1.71	4.36	1.19	1.20	1.18	1.18
KIFMG 211	1.18	2.46	0.84	0.89	0.83	0.88
KMR 654	1.35	2.15	0.93	0.85	0.92	0.82
KMR 655	1.45	3.26	1.02	1.00	1.02	1.00
PPR 1216	1.45	3.32	1.02	1.02	1.01	1.02
PPR 1272	1.49	3.49	1.05	1.04	1.05	1.04
PR 1734	1.69	3.80	1.17	1.09	1.17	1.08
PR 202	1.41	3.50	1.00	1.05	0.99	1.05
TNEC 1341	4.41	4.38	1.01	1.18	1.00	1.15
TNEC 1342	1.50	3.88	1.06	1.11	1.05	1.11
VL 376	1.33	2.00	0.94	0.84	0.92	0.80
VL 402	1.25	2.25	0.89	0.87	0.89	0.84
VL 409	1.24	2.38	0.88	0.88	0.87	0.86
VR 1163	1.25	1.97	0.90	0.85	0.89	0.80
VR 1171	1.39	3.40	0.97	1.03	0.97	1.02
WN 577	1.56	3.70	1.09	1.08	1.09	1.07
WN 660	1.10	0.79	0.78	0.75	0.77	0.53
WN 666	1.24	2.62	0.88	0.91	0.88	0.90

HMGV= Harmonic mean of genotypic values; RPGV= Relative performance of the genotypic values and HMRPGV= Harmonic mean of the relative performance of genotypic values; SY: Seed yield; FY: Fodder yield

CONCLUSION

The current study deciphered the effects of genotype×environment interaction for seed yield and fodder yield in finger millet genotypes. The seed yield and fodder yield was significantly affected by environment and genotype × environment interaction. While, BLUPg and BLUPge prediction models amply explained the variation due to GEI for seed and fodder yield, respectively. This study identified IIMR-FM-R21-8012 and PR 1734; IIMR-FM-R21-8012 and TNEc 1341 as worthy genetic resources for seed and fodder yield, respectively. They can be further tested across multi-locations and further released for commercial cultivation across farmers fields.

AUTHORS CONTRIBUTIONS

Conceptualization of research (TEN, SB, CN, S and GKN); Designing of the experiments (SB, CN, S and GKN); Contribution of experimental materials (TEN, SB, CN, S and GKN); Execution of field/lab experiments and data collection (SB, CN, S and GKN); Analysis of data and interpretation (TEN and GPS); Preparation of the manuscript (TEN and GPS).

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