RESEARCH ARTICLE

Dissecting genotype × environment interaction in advanced varietal lines of finger millet (*Eleusine coracana* L.) evaluated for seed and fodder yield across twenty environments

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Abstract

The identification of superior and stable genotypes in any crop for commercial cultivation in farmers' fields is constrained majorly by the existence of genotype × environment interaction (GEI). The current study was carried out to assess the patterns of GEI governing seed and fodder yield, identify stable and high seed and fodder yielding genotypes, besides deciphering the correlation among the them in finger millet genotypes evaluated across twenty environments (ten locations-two years combination) in India. The results revealed that the variance due to genotype, environment and GEI were highly significant (p < 0.001) for seed and fodder yield. The AMMI8 model was adequate to explain the detected variation of seed and fodder yield attributable to GEI. For obvious reasons, the check GPU 67 exhibited relatively higher mean seed and fodder yield and also showed excellent stability across all the environments based on AMMI- and BLUP-model indices. In this study, the seed and fodder yielding ability of the genotypes VR1101 and WN559 was comparable to the checks and had broad adaptation across the test environments. The most representative and discriminative environments for seed and fodder yield were E1 and E9. Seed and fodder yield revealed highly significant positive correlations indicating the possibility of simultaneous effective selection for these two traits. The identified stable and high seed and fodder yielding genotypes VR1101 and WN559 are not just worthy genetic resources, and can be recommended for commercial cultivation after further yield trials. Consequently, the genotype VR1101 is approved for commercial cultivation across South Indian states.

Keywords: GEI, finger millet, multi-environment trial, yield stability, GGE biplot.

Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn] is a member of the family of grasses Poaceae (Gramineae) and subfamily Chloridoideae. In general, self-pollination is the rule in finger millet and it is an allotetraploid (2n = 4X = 36) species whose genome is ~1.2 GB (Hittalmani *et al*. 2017; Hatakeyama et al. 2018). Among the millets, globally it ranks fourth in significance after sorghum, pearl millet and foxtail millet (Upadhyaya et al. 2007). As a consequence of finger millet being cultivated in an area of 1.17 mha in India, it is the leading producer with a production of 2 mt and average productivity of 1,661 kg/ha (ASSOCHAM 2021). Finger millet is a multi-use crop grown for food, as well as fodder and medicinal use (Oduori 2005; Phillips 1974). Due to its drought-hardy nature and nutritional significance, it is widely 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). Apparently, a major threat to current and future food security is the rate of decline in yield gains (Cairns et al. 2013;

Setimela et al. 2017), finger millet being no exception to this. The low productivity in finger millet is attributable to several

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factors including the lack of accessibility to stable and high seed and fodder yielding well-adapted cultivars tolerant to abiotic and biotic stresses.

Predominantly, finger millet varieties in cultivation especially in India are majorly through pedigree selection (55%), pure line selection (39%) from germplasm accessions (Nagaraja et al. 2022). Nonetheless, the released varieties are either longer in duration to maturity or have stagnant seed yield levels with poor fodder yielding capacity. The biomass used as animal feed is usually valued as high as seed yield and taller varieties are highly favored for this purpose. On account of these, the substitution of contemporary cultivars by identifying relatively improved finger millet genotypes with a combination of high seed and fodder yield for farmers' direct use, besides being resistant to biotic and abiotic stresses 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 identifying stable and superior cultivars that shall facilitate cultivar deployment and genetic enhancement. Such multi-environment trials (METs) aid in identifying 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.

To quantify the impact of GEI and to identify 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 in use. The major drawback of regression-based stability models is that they do not estimate mean performance and environmental index independently. The two most popular and highly effective multivariate models are used to analyze the stability, adaptability, to rank genotypes and identify mega environments (ME) are the AMMI and GGE biplots (Gauch 1992). The former is based on the analysis of variance (ANOVA) and principal component analysis (PCA), while the latter combines two important sources of variation (Genotype and GEI) of MET datasets. AMMI model combines ANOVA for main effects of the genotype and environment with principal components analysis of GE interactions (Zobel et al. 1988; Gauch and Zobel 1996). Furthermore, the AMMI model-based stability estimates derived from the first two interaction principal component scores (Yan 2001) aids in the identification of the most stable genotype/s across

environments. However, stable genotype/s may not always express a high mean seed/fodder yield. Hence, the BLUP-based stability estimates were determined. GGE biplot has been commonly used in analyzing the MET data of rice (Dwivedi et al. 2020), groundnut (Ajay et al. 2021) pigeonpea (Kumar et al. 2021), and other several commercially grown crops. Therefore, the objectives of this study were to partition GEI, evaluate the performance and stability of eleven finger millet advanced varietal lines, determine mega-environments for finger millet cultivation and assess the correlation between finger millet seed and fodder yield.

Materials and methods

Experimental material
A total of 15 finger millet genotypes (Supplementary Table S1) comprising eleven advanced varietal lines and four checks (GPU 45, GPU 67, PR 202 and VL 332) were evaluated for seed and fodder yield during the 2017 and 2018 in rainy seasons across ten Indian locations (Fig. 1 and Supplementary Table S2) in randomized complete block design with three replicates. Hereafter, both advanced varietal lines and checks are referred to as "genotypes" for the sake of simplicity. Each genotype was sown in a single row of 3m in length spaced 30cm apart. The recommended crop management practices were adopted to raise a healthy crop. Five plants were indiscriminately selected to record seed and fodder yield observations per plant (g).

Statistical analysis
A single year and a single location combined made up twenty test environments in this study (Supplementary Table S3). The phenotypic data of seed and fodder yield collected from the fifteen finger millet test genotypes evaluated across twenty test environments was confirmed for the homogeneity of variances by the Bartlett test (Bartlett 1937). To determine the significance level of genotypes (G), environments (E) and GEI, the data was subjected to combined ANOVA using a mixed linear model (R Core Team 2020). The AMMI model was used to determine the GEI effects to assess the adaptability and stability of the finger millet genotypes across the twenty test environments. The genotypes were treated as fixed sources of variation, while the environments as random. The AMMI amalgamates ANOVA for genotype and environment main effects with PCA for the GEI with the axes of the principal components of interactions (IPCA)(Gauch 1988; Yan et al. 2007). The AMMI model used is as follows:

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

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

Y_{ij}	=	Seed/Fodder yield of the ith genotype in the jth environment
μ	=	Experimental genotype mean of seed/fodder yield
g_i and e_j	=	Genotype and environment deviations from the grand mean of seed/fodder yield
λk	=	Eigen value of the PCA analysis axis k
α_{ik} and $_{yj}k$	=	Genotype and environment principal component scores for axis k
N	=	Number of principal components retained in the model
$_{ei}j$	=	Error term

Fig. 1. Geographical map of India showing the ten testing locations in which the finger millet genotypes were evaluated for seed and fodder yield in 2017 and 2018

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 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).

Thirteen AMMI model based stability parameters were computed and the genotypes were further ranked on the basis of simultaneous selection index (SSI) for both seed and fodder yield and stability (Mahmodi *et al.* 2011) using the package 'ammistability' in R software (Ajay *et al.* 2018). The SSI, also called genotype stability index (GSI) or yield stability index (YSI), is computed by adding the ranks of stability index/parameter and mean yields. 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) were estimated. The analysis was computed using the metan package in R software version 4.2.1 (Olivoto *et al.* 2020). A correlation was examined between the seed and fodder yield of fifteen genotypes evaluated across the twenty environments. For this, corrplot package version 0.88 using the Pearson method in R software (Wei *et al.* 2021) was used. A Student's T-test procedure was used to determine the significance level for the pair of traits in the correlation matrix.

Results and discussion

The combined ANOVA showed a significant variation for genotype, environment and GEI for both seed and fodder yield (p <0.001; Table 1). The grand mean of seed and fodder yield was 3104.03 (kg/ha) and 7381.05 (kg/ha) across the twenty environments.

Additive main effect and multiplicative interaction ANOVA

The AMMI analysis of variance indicated that the genotypes, environments and GEI effects were highly significant (p <0.001) for seed and fodder yield (Table 2). The partitioning of variance components of AMMI analysis of variance highlighted that environment accounted for 62.98 and 70.06 % of the total observed variation for seed and fodder yield, respectively. This indicated that the test environments were particularly diverse and greatly impacted genotypes' potential to produce seed and fodder yield. Most often than not, the contribution of test environments is relatively higher than other variation sources in multi-environment trials (Badu-Apraku *et al.* 2012). Earlier, Gauch and Zobel (1996) and Yan *et al.* (2000) put forth that about 80% of the variation could be attributed to environment, whereas, 20% to both

Table 1. Combined analysis of variance for seed and fodder yield of fifteen finger millet genotypes across twenty environments

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	'F' value	Probability	Sum of Squares	Mean Sum of Squares	'F' value	Probability
			Seed yield				Fodder yield		
Genotype (G)	14	43284027.84	3091716.27	23.02	0.00	364623421.7	26044530.12	38.90	0.00
Environment (E)	19	426366106.3	22440321.38	167.12	0.00	3169125838	166796096.7	249.17	0.00
G × E Interaction (GEI)	266	207242274	779106.2931	5.80	0.00	989649349.4	3720486.27	5.55	0.00
E × Replication	40	8889961.50	222249.03	1.65	0.00	42780868.45	1069521.71	1.59	0.00
Residuals	560	75192059.62	134271.53			374860984.3	669394.61		

Table 2. AMMI analysis of variance for seed and fodder yield of fifteen finger millet genotypes evaluated across twenty environments

Source	Degrees of freedom	Seed yield					Fodder yield				
		Sum of Squares	Mean Sum of Squares	'F' value	Probability	Proportion (%)	Sum of Squares	Mean Sum of Squares	'F' value	Probability	Proportion (%)
Total	1165	9682167003.18	831087.30				5930689811.46	5090720.87			
Environment (E)	19	426366106.30	22440321.38	100.97	0.00		3169125838.20	166796096.75	155.95	0.00	
Genotype (G)	14	43284027.84	3091716.27	23.03	0.00		364623421.66	26044530.12	38.91	0.00	
GEI	266	207242273.96	779106.29	5.80	0.00		989649349.44	3720486.28	5.56	0.00	
Replication (E)	40	8889961.50	222249.04	1.66	0.00		42780868.45	1069521.71	1.60	0.01	
PC1	32	66130063.71	2066564.49	15.39	0.00	31.90	327216603.65	10225518.86	15.28	0.00	33.10
PC2	30	42916059.52	1430535.32	10.65	0.00	20.70	192841031.34	6428034.38	9.60	0.00	19.50
PC3	28	22716316.74	811297.03	6.04	0.00	11.00	113548384.68	4055299.45	6.06	0.00	11.50
PC4	26	19812012.47	762000.48	5.68	0.00	9.60	98212182.62	3777391.64	5.64	0.00	9.90
PC5	24	14836273.05	618178.04	4.60	0.00	7.20	67800785.48	2825032.73	4.22	0.00	6.90
PC6	22	11679274.86	530876.13	3.95	0.00	5.60	53265635.94	2421165.27	3.62	0.00	5.40
PC7	20	8570000.14	428500.01	3.19	0.00	4.10	40142579.04	2007128.95	3.00	0.00	4.10
PC8	18	6668274.37	370459.69	2.76	0.00	3.20	34938651.08	1941036.17	2.90	0.00	3.50
PC9	16	4155111.52	259694.47	1.93	0.02	2.00	18340359.16	1146272.45	1.71	0.04	1.90
PC10	14	3944080.47	281720.03	2.10	0.01	1.90	16496566.99	1178326.21	1.76	0.04	1.70
PC11	12	2657930.36	221494.20	1.65	0.07	1.30	11580951.51	965079.29	1.44	0.14	1.20
PC12	10	2202954.73	220295.47	1.64	0.09	1.10	8516459.16	851645.92	1.27	0.24	0.90
PC13	8	707934.30	88491.79	0.66	0.73	0.30	5168831.54	646103.94	0.97	0.46	0.50
PC14	6	245987.72	40997.95	0.31	0.93	0.10	1580327.25	263387.88	0.39	0.89	0.20
Residuals	560	75192059.62	134271.54				374860984.27	669394.61			

Table 3. Estimates of BLUP-based stability parameters of fifteen finger millet genotypes evaluated under twenty test environments

Genotype	HMGV		RPGV		HMRPGV	
	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield
GPU 45	2826	7254	0.96	1.05	0.95	1.05
GPU 67	3237	7439	1.09	1.08	1.09	1.07
KOPN 1059	2726	7412	0.92	1.09	0.91	1.08
ML 322	2729	6448	0.94	0.93	0.92	0.92
OEB 601	2939	6556	1.01	0.97	0.99	0.95
OEB 602	2834	6441	0.97	0.95	0.95	0.93
PR 1511	3135	7320	1.06	1.05	1.05	1.04
PR 202	3107	7139	1.05	1.04	1.04	1.03
RAuF 13	2932	6479	0.99	0.97	0.97	0.95
RAuF 15	2898	6480	1.01	0.94	0.98	0.93
VL 352	2404	5537	0.82	0.80	0.80	0.78
VR 1101	3193	7463	1.08	1.09	1.06	1.08
WN 550	2862	6774	0.98	0.97	0.95	0.97
WN 559	3081	7600	1.05	1.11	1.04	1.10
WN 585	2992	6354	1.03	0.91	1.02	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.

genotypes and GEI in wheat yield trials. While, genotypes accounted for 6.39 and 8.06 %, and GEI accounted for 30.61 and 21.87%, respectively for seed and fodder yield. The significant GEI 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, the estimates of the eight principal components were significant for both seed and fodder yield. Similar to our results, a large proportion of total variation contributed by the environment has been reported 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). The joint effect of the eight principal components of GEI accounted for 93.30 % and 93.90% of the whole effect it had on the variation for seed and fodder yield, respectively (Table 2). The first principal component accounted for 31.90% of the variation caused by the interaction, while 20.70, 11.00, 9.60, 7.20, 5.60, 4.10 and 3.20 % of the variation was caused by PC2, PC3, PC4, PC5, PC6, PC7 and PC8, respectively for seed yield (Table 5). Likewise, for fodder yield, PC1 accounted for 31.10% of the variation caused by the GEI, while 19.50, 11.50, 9.90, 6.90, 5.40, 4.10 and 3.50, of the variation was caused by PC2, PC3, PC4, PC5, PC6, PC7 and PC8, respectively for fodder yield.

Mean seed and fodder yield

The mean seed yield of the fifteen test genotypes across the twenty test environments varied from 3407.50 kg/ha

(GPU-67) to 2971.27 kg/ha (OEB602), whereas the fodder yield varied from 8206.50 kg/ha (KOPN 105) to 5992.79 kg/ha (VL352; Fig. 2). The genotypes *viz.,* GPU67 (3407.50 kg/ha), VR1101 (3354.42 kg/ha) and PR1511 (3306.75 kg/ha) were the highest seed yielders (Fig. 2). Whereas, for fodder yield the genotypes KOPN 1059(8206.59 kg/ha), VR1101 (8076.59 kg/ha) and WN559(8203.14 kg/ha) were the best performers (Fig. 2). The mean seed yield per environment varied from 4473.69 (kg/ha) in E12 to 2104.48 (kg/ha) in E19 (Fig. 3). The mean fodder yield per environment varied from 10138.17 (kg/ha) in E11 to 3690.53 (kg/ha) in E19. Maximum seed yield was obtained in the environments E12 (4473.69 kg/ha), E16(4399.00 kg/ha) and E8 (3981.20 kg/ha). While, the environments E11(10138.17 kg/ha), E15(9135.79 kg/ha) and E16 (9462.37 kg/ha) aided in producing higher fodder yield.

GGE bi-plot for interpretation of GEI

The relationship between test genotypes and test environments is presented as "grain yield *vs.* PC1 scores," *i.e.,* AMMI1 biplot (Supplementary Fig. 1). The environments E12 and E8 were farthest from the biplot origin representing strong interaction forces, while E17 and E6 had shorter vectors with weak interaction forces. The biplot depicted that the test genotypes GPU67, VR1101, PR202 had maximum seed yield and WN559 and KOPN1059 had maximum fodder yield. While, OEB601 and RAuF13 had poor seed yield, and VL352 and WN 585 had poor fodder yield, indicating their high adaptability across the environments. The environments E13 and E9 were similar in having lower main effects for fodder yield coupled with negative PC1. The AMMI2 biplot, constructed using the first two PCs, explained 51.11% and 65.41 % of the GEI for seed and fodder yield, respectively
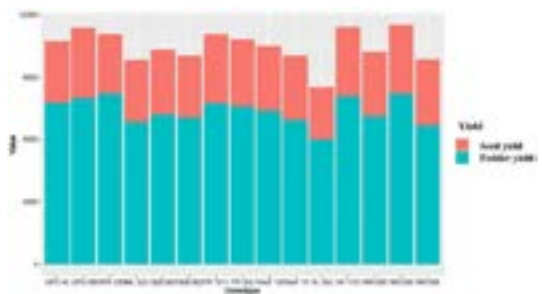

Fig. 2. Grand mean seed and fodder yield of fifteen finger millet genotypes evaluated across twenty environments
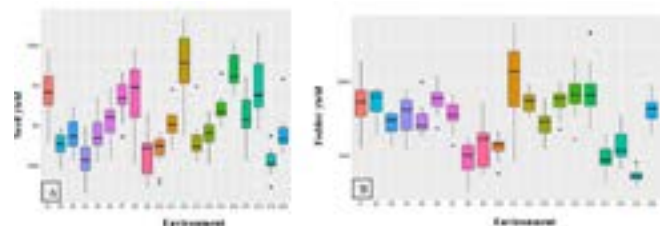

Fig. 3. Mean (A) seed yield and (B) fodder yield of fifteen finger millet genotypes in each of the twenty environment

(Supplementary Fig. 2). The AMMI2 biplot indicated that the environments E8 and E12 were discriminatory for seed yield and located far away from the biplot origin. The genotype VR1101 prevailed near the origin and proved higher stability (Supplementary Fig. 2A). The environments E11 and E16 were highly discriminating for fodder yield and the genotypes GPU45 and GPU67 were highly stable yield (Supplementary Fig. 2B). Identification of an ideal genotype is based on genotype-focused scaling that partitions the singular value decomposition into genotype eigen values and compares the genotypes to the ideal genotype. The test genotypes WN559, WN585, PR202and GPU 67 were closest to the ideal genotype in terms of their average seed yield and stability (Fig. 4A), whereas the test genotypes KOPN 1059, WN 559 and GPU67for fodder yield and stability (Fig. 4B). Conversely, VL352 was placed furthest from the vertical axis and far from the ideal genotype signifying its relatively poor performance in terms of mean seed and fodder yield and stability across the twenty environments. In the "discriminativeness *vs.* representativeness" biplot, the dotted line connecting the test environment pointing to the origin is called the environment vector. The length of the environment vectors and the angle between the respective environment vector with AEA (Average Environment Axis) helps in the identification of the discriminating ability and representativeness of the test environments. A discriminative environment is the one which has the ability to discriminate between test genotypes, while a representative environment represents an average of the twenty test environments. A lower and higher discriminative ability of the environments is indicated by a shorter and longer environment vector, respectively. The correlation between the environments is indicated by smaller and larger angles between environment vectors, respectively. The similarity and dissimilarity between the test environments is indicated by an acute and obtuse angles between the test environment vectors, respectively. In this study, the environments E8, E12, E18 and E1 had long vectors for seed yield (Supplementary Fig. 3A) and E11, E16, E9 for fodder yield (Supplementary Fig. 3B), indicative of their discriminative ability. Conversely, the environments E10 and E9 for seed yield and E19, E12 and E13 for fodder yield with relatively shorter vector lengths are indicative of the least discriminative environment; and therefore, provide little or no information about the genotypes' variability (Yan and Tinker 2006). The environments E10, E16 and E17 for seed yield and E4, E1 and E14 for fodder yield with lower angles from the AEC axis are indicative of their representative ability. Environment E1 and E9 had relatively higher discriminating ability and representativeness for seed yield and fodder yield, respectively.

In the current study, the "Which-Won-Where" biplot created a polygon with seven genotypes for seed (PR1511, KOPN 1059, VL352, RAUF13, OEB 601 WW559 and GPU 67) and fodder yield (PR1511, KOPN 1059, VR1101, OEB 601, OEB602, VL352 and ML322) at the vertices (Fig. 4A and B, respectively). The equality lines divided the polygon into seven sectors effectively both for seed and fodder yield. Therefore, the twenty testing environments were spread in four and five sectors within the biplot for seed and fodder yield, respectively. This illustrated that the test environments could be divided into mega environments (ME). The first ME (ME-I) was represented by E3, E4, E7, E8, E9, E18 and E19 with the genotypes PR1511 and GPU 67 producing the highest seed yield. The second ME (ME-II) was composed of E6, E10, E11, E13, E17 with the genotype WN 559 as the winner, the third ME (ME-III) was composed of E2, E5, E12, E15, E16, E20 and E14. The fourth ME (ME-IV) was solitary with environment E1. While, for fodder yield, ME-I was represented by E16, E8, E18, E3, E7, E19, E12 with PR1511 as the winning genotype. The ME-II was composed of the environments E9, E4, E1, E14, E5 having KOPN1059 as the winning genotype, the third ME was composed of E2, E20, E6, E17, E13, E11 with the genotype VR1101 as the winner. The fourth and fifth ME were solitary with E15 and E10, respectively. The genotype OEB 602 performed well in ME-IV. The test genotypes placed near the origin depicted consistency for seed (VR1101, GPU 45, ML322) and fodder (GPU 45, WN550 and GPU67) yield.

In this study, the "Mean *vs.* Stability" biplot AEC (Average Environment Coordinates) showed that the test genotypes GPU 67, PR1511, WN585 and WN559 had high mean seed yield (Supplementary Fig. 4) and the test genotypes KOPN1059, VR101, WN559 and GPU67 had high mean fodder yield (Supplementary Fig. 4). On the other hand, genotype VL352 produced the lowest seed and fodder yield. The test genotypes WN585, WN559 and VR1101 were most stable with high mean seed yield that had a shorter vector from average environment axis (AEA), whereas RAUF13 was the least stable having longest vector from AEC. For fodder yield, the test genotypes GPU67, GPU45, KOPN1059were most stable with higher mean. The genotype PR1511 was the least stable for fodder yield (Supplementary Fig. 4).

AMMI-based stability parameters to identify stable genotypes

The AMMI model does not make provision for a quantitative stability measure which is essential to quantify and rank the genotypes accordingly. Therefore, various AMMI-model-based stability measures were estimated for seed and fodder yield of each genotype. The lower the score, the more stable a genotype is with respect to any stability parameter and vice versa. The genotype GPU 45 with the least estimates for ASTAB, DZ, EV, FA, MASV and SIPC was the most stable, while the genotype PR 202 was highly stable based on ASI, ASV and MASI for seed yield (Supplementary Table S4). For fodder yield, the genotype GPU 45 was highly stable based on ASTAB, ASI, ASV, AVAMGE, DA, FA and MASV, whereas, the genotype WN550 was the most stable based on MASI, SIPC,

ZA and WAAS (Supplementary Table S4). Similar results were reported by Anuradha et al. (2021) in finger millet using the same set of stability indices. Further, the SSI for yield and stability was computed for each of the thirteen measures of stability (Mahmodi et al. 2011). Stability alone by itself is not a desirable selection criterion as these stable genotypes may not be high-yielders, for which simultaneous consideration of seed yield and stability in a single nonparametric index is essential (Mohammadi et al. 2007; Mohammadi and Amri 2008; Mahmodi et al. 2011). Thus, including phenotypic trait and stability in a single selection index is necessary. The least SSI is considered the most stable with high yield, whereas high SSI is the least stable with low yield. In the present study, SSI computed using all the AMMI-based stability measures identified genotypes GPU 67, PR 202 and WN 559 as most stable and high seed yielders, whereas genotypes GPU 45, GPU 67 and WN 559 as most stable and high fodder yielders.

BLUP-based stability parameters to identify stable genotypes

The BLUP-based stability parameters were also estimated for reasons justifying the estimation of SSI. 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 seed yield, the genotypes GPU 67 and VR1101 were the top two rankers in that order (Table 3). For fodder yield, the genotype WN559 was the top
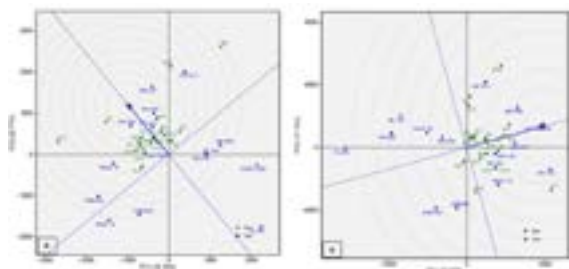

Fig. 4. GGE-biplot showing the ideal finger millet genotypes based on mean (A) seed yield and (B) fodder yield performance across twenty environments

Fig. 5. Polygon view of GGE-biplot based on the symmetrical scaling for "which won-where" pattern of fifteen finger millet genotypes and twenty environments for (A) seed yield and (B) fodder yield

ranker based on all the three BLUP-based stability estimates, followed by the genotype KOPN 1059 based on RPGV and HMRPGV, and VR 1101 based on HMGV (Table 3). Although the studied stability parameters were applied to various crops to estimate the stability and adaptability, only one study by Anuradha *et al.* (2021) was reported on finger millet.

Correlation among seed and fodder yield

A positively significant correlation between seed and fodder yield (r=0.36***; P <0.001; Supplementary Fig. 5) was observed in this study implying that the selection for high seed yield positively affects the fodder yield levels as evident in the genotypes GPU 67 and VR1101. The same was reflected in the performance of the genotypes as well. For example, GPU 67 and VR1101 produced a higher seed and fodder yield.

Authors'contributions

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

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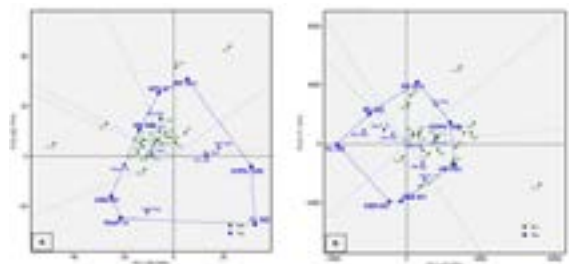
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Supplementary Table S1. Pedigree details of the finger millet genotypes used in the study

Sl. No.	Genotype	Centre	Pedigree
1	WN 550	Waghai	Local collection from Subir Taluka, Dangs Dist. Of Waghai
2	WN 585	Waghai	Local Collection from Waghai Taluka, Dangs District
3	OEB 601	Berhampur	Indaf 5 x Bhairabi
4	VR 1101	Vizinagaram	VL 330 × GE 532
5	PR 1511	Peddapuram	PR 1045 × PR 202
6	WN 559	Waghai	Local Collection from Waghai Taluka, Dangs District
7	OEB 602	Berhampur	AKP 7 x Purnea
8	RAuF 15	Dholi	RAU 8 x GPU 28
9	RAuF 13	Dholi	RAU 8 x GPU 28
10	ML 322	MAS, Bengaluru	IE 1012/I.5
11	KOPN 1059	Kolhapur	Selection from 4129 germplasm
12	GPU 45	PC, Unit, Bangalore	GPU 26 x L5
13	VL 352	Almora	VR 708 x VL 149
14	GPU 67	PC, Unit, Bangalore	Selection from GE 5331
15	PR 202	Peddapuram	Pure line selection from Mettachodi ragi of Arakku valley

Supplementary Table S2. 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, Tamil Nadu	35.52	26.63	18.94	34.57	26.58	18.3	12.07° N	78.99° E	561
Berhampur, Odisha	35.55	24.35	69.72	35.26	24.37	86.70	19.31° N	84.79° E	78
Dahod, Gujarat	32.25	23.15	37.69	30.41	22.74	72.76	22.83° N	74.26°E	984
Hanumanamatti, Karnataka	31.75	21.75	63.75	32.75	21.5	64.25	14.66º N	75.56º E	1912
Jagdalpur, Chattisgarh	30.78	22.88	74.91	28.13	20.85	62.09	19.08 º N	82.02 º E	1811
Mandya, Karnataka	31.52	19.42	1.75	23.44	19.51	20.85	12.52 º N	76.89 º E	2224
Peddapuram, Andhra Pradesh	33.72	26.06	37.54	33.13	25.68	31.24	17.07° N	82.13° E	114
Perumallapalle, Andhra Pradesh	34.72	25.75	44.88	35.33	25.96	28.07	13.60° N	79.35° E	1000
Vizianagaram, Andhra Pradesh	30.55	27.83	39.88	30.78	28.75	60.1	18.10° N	83.39° E	242
Waghai, Gujarat	31.42	24.28	126.8	27.59	23.29	55	20.77° N	73.49° E	830

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

Supplementary Table S3. Description and combination of a single year and a single location making up twenty test environments

Environment code	Year	Environment code	Year	Location
E1	2017	E11	2018	Peddapuram, Andhra Pradesh
E2	2017	E12	2018	Perumallapalle, Andhra Pradesh
E3	2017	E13	2018	Vizianagaram, Andhra Pradesh
E4	2017	E14	2018	Jagdalpur, Chattisgarh
E5	2017	E15	2018	Dahod, Gujarat
E6	2017	E16	2018	Waghai, Gujarat
E7	2017	E17	2018	Hanumanamatti, Karnataka
E8	2017	E18	2018	Mandya, Karanataka
E9	2017	E19	2018	Behrampur, Odhisha
E10	2017	E20	2018	Athiyandal, Tamil Nadu

Supplementary Table S4. Estimates of AMMI-based stability parameters of fifteen finger millet genotypes evaluated under twenty test environments and their ranks of simultaneous selection index (SSI) indicated in parenthesis

Genotype	ASTAB		ASI		ASV		AVAMGE	
	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield
GPU 45	1003.94 (13)	1605.87 (6)	2.47 (14)	3.51 (6)	11.92 (14)	17.98 (6)	5999.71 (14)	10576.18 (6)
GPU 67	1161.12 (3)	3096.21 (11)	3.39 (5)	5.30 (9)	16.37 (5)	27.16 (9)	5381.84 (2)	14392.51 (10)
KOPN 1059	1717.68 (26)	4544.75 (16)	8.16 (26)	8.89 (9)	39.44 (26)	45.59 (9)	7621.36 (26)	15374.96 (10)
ML 322	1632.94 (22)	2464.39 (17)	5.18 (20)	13.33 (26)	25.02 (20)	68.34 (26)	6628.09 (18)	14907.47 (20)
OEB 601	1491.79 (14)	3368.50 (17)	9.75 (23)	9.13 (17)	47.09 (23)	46.82 (17)	7400.49 (18)	16190.48 (19)
OEB 602	1499.74 (18)	4415.97 (24)	8.00 (22)	11.02 (22)	38.64 (22)	56.51 (22)	7384.48 (20)	18839.12 (24)
PR 1511	1635.04 (14)	3835.49 (16)	6.93 (12)	10.62 (17)	33.47 (12)	54.45 (17)	7760.20 (17)	17510.59 (18)
PR 202	1443.07 (11)	2343.24 (9)	1.69 (7)	8.28 (12)	8.17 (7)	42.45 (12)	6290.30 (9)	11794.87 (9)
RAuF 13	1895.18 (23)	2926.90 (14)	9.11 (22)	9.53 (17)	43.99 (22)	48.85 (17)	8753.21 (23)	14284.30 (13)
RAuF 15	1650.87 (18)	2704.43 (17)	7.29 (16)	4.09 (16)	35.22 (16)	20.94 (16)	7317.88 (15)	12702.23 (16)
VL 352	1730.75 (28)	5587.62 (30)	2.49 (18)	17.05 (30)	12.01 (18)	87.42 (30)	7164.80(22)	21131.93 (30)
VR 1101	2388.55 (17)	4096.53 (15)	7.42 (12)	14.26 (17)	35.83 (12)	73.11 (17)	9408.16 (17)	20427.61 (17)
WN 550	1416.28 (14)	2230.18 (12)	9.17 (24)	3.65 (13)	44.30 (24)	18.73 (13)	7467.00 (21)	11156.92 (12)
WN 559	1513.69 (11)	3964.73 (11)	3.68 (8)	3.62 (3)	17.77 (8)	18.58 (3)	6394.79 (7)	15799.91 (10)
WN 585	1319.67 (8)	4006.13 (25)	4.90 (11)	11.73 (26)	23.66 (11)	60.13 (26)	6773.25 (11)	17627.98 (26)

ASTAB=AMMI-based stability parameter; ASI= AMMI stability index; ASV= AMMI stability value and AVAMGE= Absolute value of GEI modeled by AMMI

Supplementary Table 4. Cont..

Genotype	DA		DZ		EV		FA	
	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield
GPU 45	1591.45 (14)	2679.53(6)	0.66 (13)	0.68(7)	0.04(13)	0.05(7)	2532708.46 (14)	7179869.72 (6)
GPU 67	1538.10 (2)	3930.46 (9)	0.83 (9)	0.82(12)	0.07(9)	0.07(12)	2365755.23 (2)	15448492.40 (9)
KOPN 1059	2332.02 (26)	5254.94(14)	0.79 (20)	0.92(16)	0.06(20)	0.08(16)	5438295.94 (26)	27614363.09 (14)
ML 322	1961.71 (20)	4441.91(21)	0.91 (26)	0.65(14)	0.08(26)	0.04(14)	3848291.51 (20)	19730552.31 (210
OEB 601	2337.26 (21)	4417.71(16)	0.71 (12)	0.89(19)	0.05(12)	0.08(19)	5462781.49 (21)	19516171.34 (16)
OEB 602	2288.16 (21)	5432.30(24)	0.69 (14)	0.89(22)	0.05(14)	0.08(22)	5235678.91 (21)	29509866.48 (24)
PR 1511	2198.06 (13)	5214.38(18)	0.81 (11)	0.77(13)	0.06(11)	0.06(13)	4831446.35 (13)	27189719.00 (18)
PR 202	1690.52 (9)	3813.20(10)	0.89 (18)	0.68(9)	0.08(18)	0.05(9)	2857867.38 (9)	14540465.56 (10)
RAuF 13	2546.95 (23)	4254.29(14)	0.83 (18)	0.75(12)	0.07(18)	0.06(12)	6486953.14 (23)	18098977.76 (14)
RAuF 15	2160.67 (15)	3520.96(15)	0.88 (18)	0.84(21)	0.08(18)	0.07(21)	4668475.10 (15)	12397169.14 (15)
VL 352	1952.16 (21)	6584.20(30)	0.92 (29)	0.92(30)	0.09(29)	0.08(30)	3810927.91 (21)	43351711.42 (30)
VR 1101	2690.23 (17)	5569.97(17)	0.94 (17)	0.81(10)	0.09(17)	0.07(10)	7237330.06 (17)	31024586.95 (17)
WN 550	2292.70 (21)	3055.26(12)	0.68 (12)	0.76(15)	0.05(12)	0.06(15)	5256494.18 (21)	9334602.91 (12)
WN 559	1914.98(8)	4603.01(10)	0.85 (13)	0.89(13)	0.07(13)	0.08(13)	3667143.45 (8)	21187746.04 (10)
WN 585	1855.35 (9)	4980.96(24)	0.79 (10)	0.90(27)	0.06(10)	0.08(27)	3442339.84 (9)	24809965.85 (24)

DA= Annicchiarico's D parameter; DZ= Zhang's D parameter; EV= Averages of the squared eigenvector values and FA= Fitted AMMI model

Supplementary Table 4. Cont…

| Genotype	MASI		MASV		SIPC		ZA		WAAS	
	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield	Seed yield	Fodder yield
GPU 45	3.71 (15)	4.48 (7)	41.83 (13)	48.44 (6)	73.57 (13)	101.14 (7)	0.14 (14)	0.11 (7)	8.07 (14)	9.45 (7)
GPU 67	3.66 (3)	6.28 (8)	46.51 (3)	77.80 (10)	88.28 (4)	116.65 (8)	0.15 (4)	0.15 (8)	8.19 (4)	12.13 (8)
KOPN 1059	8.49 (25)	10.24 (11)	58.73 (26)	94.16 (12)	91.01 (18)	179.78 (17)	0.22 (23)	0.26 (15)	13.79 (23)	21.98 (14)
ML 322	5.64 (20)	13.38 (26)	53.48 (19)	79.06 (20)	106.53 (24)	108.46 (16)	0.19 (19)	0.18 (19)	10.60 (19)	16.77 (21)
OEB 601	9.86 (23)	9.28 (16)	56.75 (16)	85.39 (180	95.21 (16)	136.93 (17)	0.23 (18)	0.19 (18)	14.20 (18)	17.03 (18)
OEB 602	8.56(23)	11.19 (21)	51.99 (15)	108.23 (25)	79.50 (13)	150.40 (21)	0.21 (19)	0.21 (21)	13.34 (19)	18.40 (21)
PR 1511	7.29 (12)	11.19 (18)	59.67 (17)	98.55 (19)	118.14 (18)	155.43 (18)	0.26 (17)	0.25 (19)	15.09 (16)	22.01 (20)
PR 202	2.90 (7)	8.84 (12)	49.38 (9)	70.36 (9)	92.14 (11)	135.12 (13)	0.13 (7)	0.19 (13)	6.98 (7)	16.37 (12)
RAuF 13	9.33 (23)	10.04 (16)	68.59 (23)	77.05 (13)	100.12 (18)	130.46 (13)	0.26 (23)	0.19 (16)	16.13 (24)	16.69 (15)
RAuF 15	7.64 (16)	5.47 (15)	55.45 (14)	72.43 (16)	114.46 (20)	130.91 (18)	0.24 (18)	0.14 (15)	14.28 (18)	11.53 (15)
VL 352	3.86 (19)	17.77 (30)	58.53 (26)	116.25 (30)	101.20 (25)	169.44 (28)	0.17 (20)	0.29 (30)	9.16 (19)	27.20 (30)
VR 1101	7.87 (12)	14.84 (17)	79.26 (17)	95.45 (14)	126.51 (17)	169.50 (17)	0.27 (17)	0.28 (17)	15.34 (15)	25.56 (17)
WN 550	9.29 (23)	4.29 (11)	58.00 (19)	57.90 (12)	94.96 (17)	93.94 (11)	0.25 (22)	0.11 (11)	15.45 (24)	8.53 (11)
WN 559	4.64 (8)	6.44 (6)	53.03 (8)	81.90 (9)	107.94 (15)	147.56 (26)	0.20 (10)	0.17 (6)	11.00 (10)	13.62 (6)
WN 585	5.15 (11)	12.18 (26)	58.11 (15)	100.53 (27)	94.14 (11)	166.70 (10)	0.17 (9)	0.24 (25)	9.34 (10)	20.80 (25)

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 scores
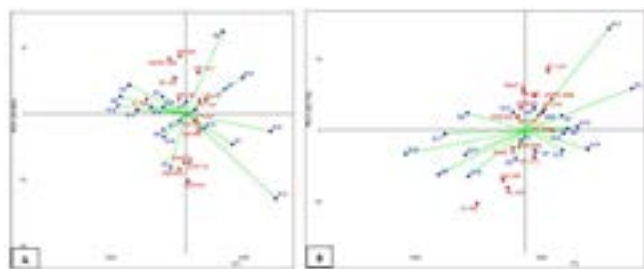
Supplementary Fig. 1. AMMI1 biplot plotted against (A) seed yield and (B) fodder yield of fifteen finger millet genotypes evaluated across twenty environments
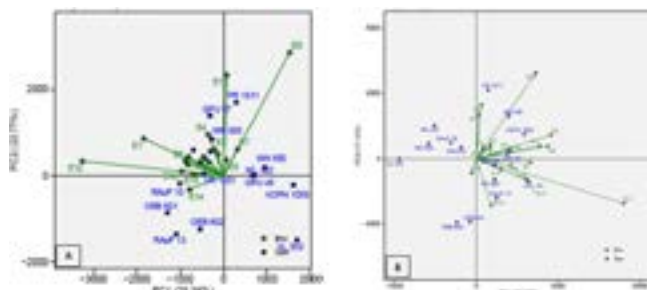

Supplementary Fig. 2. AMMI2 biplot of the fifteen finger millet genotypes and twenty environments for (A) seed yield and (B) fodder yield
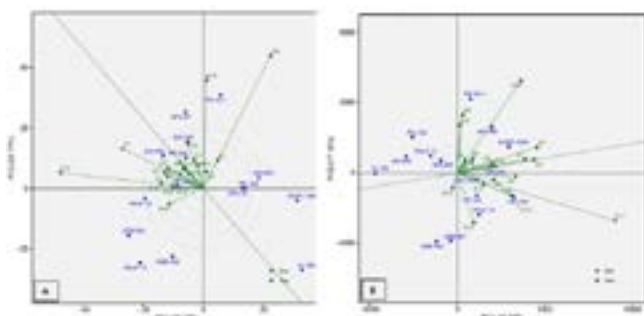
Supplementary Fig. 3. Discriminative vs. representativeness view of GGE biplotfor (A) seed yield and (B) fodder yield of fifteen finger millet genotypes evaluated across twenty environments
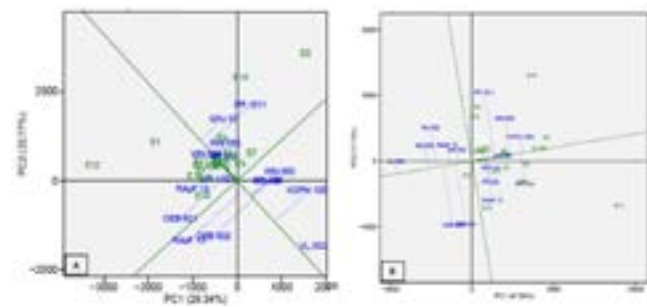
Supplementary Fig. 4. Average environment coordination view of GGE-biplot based on environment-focused scaling for the mean performance vs. stability of fifteen finger millet genotypes for (A) seed yield and (B) fodder yield
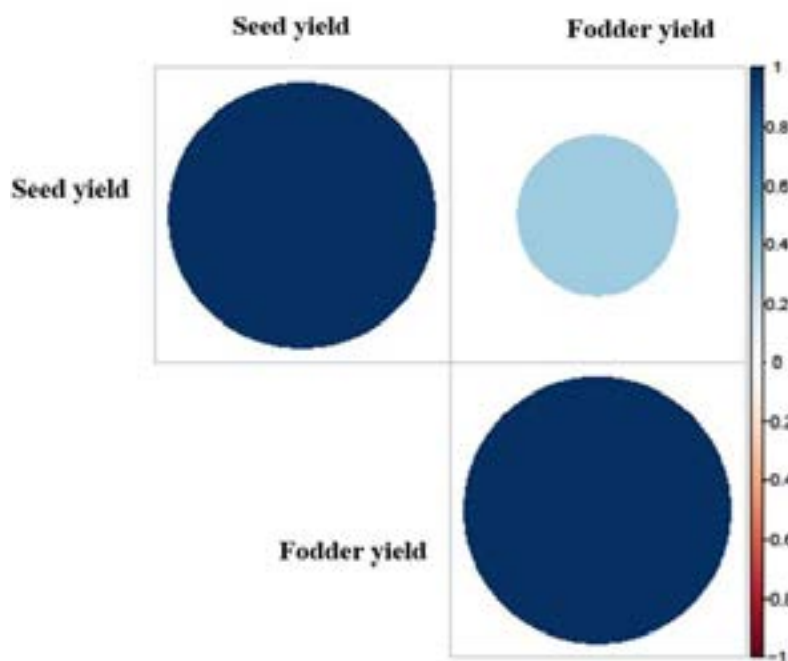
Supplementary Fig. 5. Correlation coefficient plot for (A) seed yield and (B) fodder yield in fifteen finger millet genotypes