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Stability Analysis of Diverse Cytoplasm Based Pearl Millet Hybrids in Northern Dry Zones of Karnataka Using AMMI Model

A. M. Talawar[1], S. Rangaiah[2], N. Marappa[3], B. Shivanna[4] and J. Meenakshi[5]
[1,2,3&5]Department of Genetics and Plant Breeding, [4]Department of Agricultural Entomology,
College of Agriculture, UAS, GKVK, Bengaluru - 560 065
e-Mail : talawaram@gmail.com

Authors Contribution

A. M. Talawar :
Conceptualization, investigation and draft manuscript prepration ;

S. Rangaiah :
Conceptualization, editing, design and supervision;

N. Marappa and B. Shivanna :
Guidence & editing

J. Meenakshi :
Data curation and tabulation

Corresponding Author :
A. M. Talawar

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Abstract

The stability performance of thirteen pearl millet genotypes were assessed at five locations of northern dry zones of Karnataka using AMMI model. The analysis of genotypic variance was highest for grain yield followed by plant height, number of productive tillers and panicle length. The environment contributed large significant variation for plant height followed by grain yield, panicle length and number of productive tillers. While interactions between location and genotype effects was signiûcant for number of productive tillers, panicle length and grain yield. The GEI was comparatively less than location and genotype for grain yield trait. Among the three interaction principal component axes (IPCA) contributed by grain yield, the first two IPCA were significant explaining 87.34 per cent variation. Based on overall performance, AMMI bi-plot, ASV and SI score, the hybrid ICMA01555 x CPRLT-114 (G4) was considered good grain yielder and stable across five test locations. Further high yielding genotypes like Kaveri Super Boss (G2) and ICMA94222 x SGRLT-17 (G12) were exhibited least SI score but showed highly interactive with environment, hence they were considered moderately stable for grain yield. While ICMA01555 x EMRLT-139 (G9) good yielder but had higher SI and IPCA1value suggest the specific adaptability of hybrid. The population check MBP-2 was also exhibited least SI score and mean that was on par with the average yield shows little interactive with environment, hence it was said to be comparatively a good yielder with high stable genotype among all genotypes. The study also shows that highest grain yielder hybrids are moderately stable while comparatively average/less yielder hybrids have high stable for grain yield in pearl millet.

Keywords : Pearl millet, GEI, AMMI bi-plot, ASV, SI, Grain yield

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is the fourth most important cereal food crop cultivated in India after rice, wheat and maize. In India, pearl millet is occupied 6.7 million hectares area, producing 9.62 million tonnes and has a productivity of 1436 kg/ha. Karnataka occupies 0.15 million hectares area, producing 0.17 million tonnes and has a productivity of 1161 kg/ha (Anonmyous, 2022).

In Karnataka majority of area comes under northern dry part and these areas were characterized by highly variable and erratic rain fall leads to prolonged dry spells within season, present increased temperatures and drought induced heat stress affect the pearl millet yields and ultimately leads to lower productivity of the crop. It is of prime importance to develop stable, high yielding varieties and hybrids that are more adaptable against these multiple stresses associated with climate change and to produce sustainable yield in such erratic region.

In India, the identification of cytoplasmic male-sterility (CMS) system in pearl millet has significantly increased the yield of pearl millet by allowing commercial hybrid seed production. Further, a large number of hybrids have been developed and commercialized in India, largely based on the A_1 CMS system. The dependence on single cytoplasm makes important concern about the pearl millet hybrid seed industry vulnerable to disease and insect-pest epidemics.

Increased research efforts towards diversifying parental lines have resulted to the identification of several alternative cytoplasm sources in pearl millet like, A_2, A_3, A_4, A_5 and PT732A (Bellary). Amongst A_2 and A_3 sources were evaluated extensively none performed any better than the A_1 CMS system.

Hence, in the present investigation ten hybrids derived from different cytoplasmic sources (A_1, A_4 and PT732A) were selected. Further selection of hybrid for commercial cultivation in one environment are biased due to the confounding of the G x E interaction effect with the genotype performance and grain yield more affected by environment and routinely exhibit GEI. This necessitates genotype evaluation in multi-location trials (MLT) in the advanced stages of selection (Annicchiarico, 2006).

Several stability statistics used to partition genotype × environment interaction include regression analysis, multivariate analysis and cluster analysis. In recent years, stability analysis model like Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot analysis are most popular and commonly used to discriminate high yielding and stable cultivars, to determine the relationship between environments and identify ideal environments (Yan, 2001; Ajay *et al*., 2021 and Lal *et al*., 2021).

However, The AMMI and GGE-biplot methodology applied in pearl millet has revealed that it is powerful technique that allows visual examination of the GE interaction pattern of MET data and useful for evaluating the pearl millet genotypes and hybrids by Sharma *et al*. (1998), Pawar *et al*. (2012), Wedajo Gebre (2014), Narasimhulu *et al*. (2023) and Khandelwal *et al*. (2024). Therefore, in order to find suitable hybrids/varieties for the rainfed situation of northern dry regions of Karnataka, the study was undertaken to investigate the stability performance of ten improved diverse cytoplasm based pearl millet hybrids along with three recommended checks over five locations of northern dry zone of Karnataka.

MATERIAL AND METHODS

Experimental Material

The experimental material comprised of 13 pearl millet genotypes that included 10 top selected diverse cytoplasmic based hybrids, two recommended national (GHB 558) and zonal (Kaveri super boss) hybrid checks and one newly released MBP 2 as population check. The description of the genotypes included in the experiment is given in Table 1.

Experimental Locations

The material was evaluated during *kharif* 2021 at five locations of northern dry zone of Karnataka comprising of zone 2 and 3 *viz*., Agricultural Research

TABLE 1

List of pearl millet hybrids and checks for stability studies

Sl. No.	Hybrids / Genotype	Description / sources
G1	GHB 558(NC)	National check
G2	Kaveri Super Boss (ZC)	Zonal check
G3	MBP-2(LPC)	Local population check
G4	ICMA01555 X CPRLT-114	A_4
G5	ICMA01555 X TPRLT-109	A_4
G6	PT732A X LPRLT-114	PT732A (Bellary)
G7	863A X EMRLT-33	A_1
G8	863A X EMRLT-131	A_1
G9	ICMA0555 X EMRLT-139	A_4
G10	PT732A X PDRLT-8	PT732A (Bellary)
G11	841A X PDRLT-15	A_1
G12	ICMA94222 X SGRLT-17	A_1
G13	ICMA94222 X PDRLT-2	A_1

TABLE 2

Agro-climatic characteristics of experimental locations

Sl.No	Location/ Environment	Zone	Longitude and Latitude	Altitude (>MSL)	Soil type	Avarage Rainfall (mm)
E1	ARS, Malnoor	2	16^0 28' N 76^0 28' E	383	Medium Black	726.0
E2	ZARS, Kalaburagi	2	17^0 20'N 76^0 49'E	443	Medium Black	733.0
E3	MARS, Raichur	2	16^0 7'N 76^0 79'E	411	Deep Black	696.0
E4	RARS, Vijayapur	3	16^0 49'N 75^0 43'E	593	Shallow Black	590.0
E5	ARS, Hagari	3	15^0 9'N 77^0 30'E	508	Medium Black	601.0

Station, Malnoor; Zonal Agricultural Research Station, Kalaburagi and Main Agricultural Research Station, Raichur comprising of Zone-2 and Regional Agricultural Research Station, Vijayapur and Agricultural Research Station, Hagari locations comes under Zone-3. These locations are found within altitudinal ranges of 383 to 593 m (above mean sea level) and are in the range of environments suitable for pearl millet cultivation. Since these locations are different in soil type, altitude, mean annual temperature and rainfall, they were considered as an individual environment. Description of the study locations is given in Table 2.

Experimental Design and Methods

A total of thirteen genotypes were evaluated in randomized block design (RBD) with three replications with spacing of 45 x 15cm and net plot size 4.0m x 2.7m. The recommended doses of fertilizers were applied in each experiment site. Half dose of N and full dose of P and K were applied as basal and the remaining half nitrogen was top dressed after 30 days of sowing and regular weeding was done to keep the experimental field weed free. The grain yield was obtained based on whole plot and replication yield were averaged to the plot mean and converted to quintals per hectares. The mean data were utilized for computation of statistical analysis.

Statistical Analysis

Analysis of Variance (ANOVA)

ANOVA was done for all data of each location separately as per the procedure given by Panse and Sukhatme (1984). The variance components were performed by equating mean square and significant differences, among the genotypes were detected.

Detection of Genotype × Environment Interaction (GEI)

The mean grain yield data recorded from five locations was subjected to analysis of variance to determine the contribution of genotypes, location and their interaction. The Additive Main Effects and Multiplicative Interaction (AMMI) Model (Gauch and Zobel, 1988) first fits additive effects for genotypes (G) and environment (E) by the usual additive analysis of variance (ANOVA) methods to separate the additive effects of genotypes and locations and then fits multiplicative effects for genotype by environment interaction by principal component analysis (PCA) to extract the pattern from the remaining genotype environment interaction portion of the ANOVA. The following model was used to estimate main effects of genotypes and environments and GEI effects.

$$Y_{ij}=\mu+g_i+e_j+\Sigma^{n}_{K=1}\lambda_k\alpha_{ik}\gamma_{jk}+\varepsilon_{ij}$$

Where, Y_{ij} = observed mean yield of the i^{th} genotype (i=1,….,I) in the j^{th} environment (j=1,..,J) μ = the grand mean grain yield, g_i = the mean of the i^{th} genotype as a deviation from the grand mean, e_j = the mean of the j^{th} environment deviations from the grand mean, λ_k = the square root of eigen value of the PCA axis k α_{ik} = the principal component scores for k of the i^{th}

genotypes, γ_{jk} = the principal component scores for k of the j[th] environment and 'ε_{ij}' is the residual.

The significance of the analysis was calculated by appropriate F-test at various probability levels by comparing each principal components mean squares with the pooled within environment mean square. Those PCA axes, which were not significant, were pooled into residual term (e_{ij}). The statistical analysis for ANOVA and AMMI model was done using windostat version 9.3.

Interpretation of AMMI Biplots Display

Biplot presentation was employed to show similarities both between genotypes and between environments. Integrating display of biplot and statistics of genotypic stability enable genotypes to be grouped based on similarity of performance across different environments. Genotypes with IPCA scores near zero had little interaction across and those far along the axis had high interaction. Environments and genotypes with the same sign on the IPCA axis had positive interaction and vice versa (Zobel *et al*., 1988). The closer the IPCA scores to zero, the more stable the genotypes are across their testing environments.

Genotype main effect plus GIE biplot (Yan and Hunt, 2002) is used to visually identify the higher yielding genotypes for each of the environments, by connecting genotypes far away from the biplot origin with straight lines so that polygon is formed with all other genotypes included in the polygon. Perpendicular lines to the sides of the polygon are drawn, starting from the biplot origin, to divide the biplot in to quadrants each having a vertex genotype. The vertex genotype for each quadrant is the one that gave the highest yield for the environments that fall within that quadrant, so it is specifically adapted to that environment.

AMMI Stability Value (ASV)

The AMMI model does not provide measure for quantitative stability. But quantitative stability measure is crucial in order to quantify and rank genotypes according to yield stability. For this cause, AMMI stability value was calculated as:

$$ASV = \sqrt{\left[\frac{IPCA1\ sum\ of\ square}{IPCA2\ sum\ of\ square}(IPCA1\ score)\right]^2 + [IPCA2\ score\ ]^2}$$

The ASV is the distance from zero in two-dimensional scatter diagrams of IPCA1 score against IPCA2 scores. Lower the magnitude of estimates of ASV, greater in the stability of the test genotypes. The higher magnitude of ASV estimates, lower is the stability of test genotypes (Purchase *et al*., 2000).

Stability Index (SI)

The ASV measure only stability, regardless of grain yield potential of genotypes, SI was estimated to facilitate simultaneous selection of test genotypes with high stability and high mean grain yield.

The SI was estimated as SI = $R^a + R^y$ where, R^a = Rank by ASV, R^y = Rank by grain yield (Farshadfar, 2011) across five environments. The test genotypes with low SI were regarded as those with high mean grain yield and high stability.

Results and Discussion

Analysis of Variance

Analysis of variance results of individual five locations for yield and yield related traits data (Table 3) revealed that, Significant difference between genotypes was observed at all location for all studied traits, except plant height in E1, E3 and E5, productive tillers per plant in E1 and thus provide justification for their use in present investigation.

Proportion of Variance Accounted for G, E and GEI by AMMI model

Plant Height (cm)

The analysis revealed that variances due to environments is highly significant ($P<0.01$), whereas genotypes and PCA I were significant at ($p<0.05$). While genotype-environment interaction was non-significant. The main effects of Genotypes,

TABLE 3

ANOVA for four yield per se traits of pearl millet genotypes tested at five environments of North Karnataka during *kharif* 2021

Source of variation	df	Plant height (cm)					Productive tillers / plant				
		E-1	E-2	E-3	E-4	E-5	E-1	E-2	E-3	E-4	E-5
Replications	2	367.21	114.97 *	13.69	24.49	244.12	0.29	0.15	0.41 *	0.23	0.30
Treatments	12	166.37	136.28 **	86.57	157.91 **	263.48	0.37	0.17 *	0.63 **	1.03 **	0.63 **
Error	24	116.12	32.85	72.42	44.66	139.17	0.21	0.08	0.11	0.18	0.19
Source of variation	**DF**	**Panicle Length (cm)**					**Grain yield q /ha**				
		E-1	E-2	E-3	E-4	E-5	E-1	E-2	E-3	E-4	E-5
Replications	2	0.66	2.31	2.95	3.16 **	0.64	13.39	0.96	2.43	16.65	13.28 **
Treatments	12	2.62 **	20.59 **	13.33 **	11.35 **	14.37 **	73.91 **	36.84 **	34.80 **	41.75 **	70.49 **
Error	24	0.71	1.30	1.44	0.51	1.52	10.11	4.07	9.27	7.00	2.76

*Significant at 5%, **Significant at 1%

TABLE 4

Additive main effects and multiplicative interaction (AMMI) analysis of variance for plant height (cm) of 13 Pearl millet genotypes across 5 environments

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Explained SS%	Variance % PC axes
Genotypes	12	1164.33	97.03	5.52 *	14.25	-
Environments	4	2694.69	673.67	38.32 **	32.97	-
G*E Interaction	48	2078.16	43.30	2.46	25.43	-
PCA I	15	962.54	64.17	3.65 *	11.78	46.32 %
PCA II	13	498.49	38.35	2.18	6.10	23.99 %
PCA III	11	458.89	41.72	2.37	5.61	22.08 %
Pooled residual	9	158.24	17.58		1.94	7.61 %
Total	194	9688.63	49.94		100.0	100.0

*Significant at 5%, **Significant at 1%

Environments and G x E interaction accounted for 14.25, 32.97, 25.43 per cent variation, respectively of the total variation for plant height (Table 4). Even though non-significant genotype-environment interaction (GEI) by AMMI model interaction was partitioned among the first three interactions principal component axis. Further IPCA1 scores was significant, explaining 46.32 per cent and IPCA2 scores was non-significant explaining 23.99 per cent of the variability.

No. of Productive Tillers Per Plant

The AMMI analysis of variance for number of productive tillers showed that the main effects of Genotypes, Environments and G x E interaction accounted for 12.75, 15.61, 32.59 per cent variation, respectively of the total variation for number of productive tillers (Table 5).

The analysis of variance for number of productive tillers revealed that variances due to environments

TABLE 5

Additive main effects and multiplicative interaction (AMMI) analysis of variance for number of productive tillers of 13 Pearl millet genotypes across 5 environments

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Explained SS%	Variance % PC axes
Genotypes	12	3.22	0.27	3.29 *	12.75	-
Environments	4	3.93	0.98	12.07 **	15.61	-
G*E Interaction	48	8.21	0.17	2.1 *	32.59	-
PCAI	15	4.11	0.27	3.37 *	16.32	50.09 %
PCAII	13	2.47	0.19	2.33 *	9.80	30.07 %
PCAIII	11	1.01	0.09	1.13	4.02	12.34 %
Pooled residual	20	1.63	0.08	6.46	7.50 %	
Total	194	22.41	0.12		100.00	100.00

*Significant at 5%, **Significant at 1%

is highly significant (P<0.01), accounted for 15.61 per cent variation. Whereas genotypes, Genotype × Environment interaction significant at (p<0.05) accounted for 12.75 and 32.59 per cent variation, respectively.

The IPCA 1 and PCA II significant at (p<0.05) explained 16.32 and 9.80 per cent of the GEI sum of squares. The GEI presence also clearly demonstrated by the AMMI model when the interaction was partitioned into the first two interaction PC axes (IPCA). IPCA 1 and IPCA 2 scores were significant, explaining 50.09 and 30.07 per cent of the variability, respectively.

Panicle Length (cm)

The AMMI analysis of variance for panicle length of 13 genotypes tested in five environments showed that the main effects of Genotypes, Environments and G x E interaction accounted for 8.70, 26.44, 30.83 per cent variation, respectively of the total variation for Panicle length (Table 6).

The analysis revealed that variances due to environments, Genotype × Environment interaction, PCA I and PCA II is highly significant (P<0.01), whereas significant (p<0.05) for genotypes. The IPCA 1 & 2 explained 16.61 and 11.02 per cent of interaction sum of squares.

The presence of GEI was also clearly demonstrated by the AMMI model when the interaction was partitioned into the first two interaction PC axes (IPCA) (Table 6). IPCA 1 and IPCA 2 scores were significant, explaining 53.89 and 35.74 per cent of the variability, respectively.

Grain Yield (q/ha)

The AMMI analysis of variance for grain yield (q/ha) of 13 genotypes tested in five environments revealed that variances due to genotypes and environments is highly significant at (P<0.01) accounted for 41.57 and 32.45 per cent, respectively. Whereas, Genotype × Environment interaction was significant at (*p*<0.05) accounted for 12.74 per cent variation of the total variation for grain yield (q/ha) (Table 7).

The interactions principal component axis IPCA 1 and IPCA 2 axes declared significant by an F test and explained 7.09 and 4.05 per cent interaction sum of squares and variability of 55.67 and 31.77 per cent, respectively.

The present combined analysis of variance results revealed significant genotypic and environment effects for agronomic traits studied. The genotypic variance was highest for grain yield followed by plant height, number of productive tillers and panicle length. The high genotypic effect for grain yield traits shows

TABLE 6

Additive main effects and multiplicative interaction (AMMI) analysis of variance for panicle length of 13 Pearl millet genotypes across 5 environments

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio		Explained SS%	Variance % PC axes
Genotypes	12	54.37	4.53	4.53	*	8.70	
Environments	4	165.26	41.31	41.34	**	26.44	
G*E Interaction	48	192.70	4.01	4.02	**	30.83	
PCAI	15	103.84	6.92	6.93	**	16.61	53.89 %
PCAII	13	68.87	5.30	5.3	**	11.02	35.74 %
PCAIII	11	13.30	1.21	1.21		2.13	6.90 %
Pooled residual	20	19.99	1.00	0.74		3.20	3.47 %
Total	194	466.85	2.41			100.00	100.00

*Significant at 5%, **Significant at 1%

TABLE 7

Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (q/ha) of 13 genotypes across five environments

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Explained SS%	Variance % PC axes
Genotypes	12	604.22	50.35	63.23 **	41.57	
Environments	4	471.63	117.91	148.06 **	32.45	
G*E Interaction	48	185.20	3.86	4.85 *	12.74	
PCAI	15	103.10	6.87	8.64 *	7.09	55.67 %
PCAII	13	58.84	4.53	5.68 *	4.05	31.77 %
PCAIII	11	16.09	1.46	1.84	1.11	8.69 %
Pooled residual	9	7.17	0.80	1.00	0.49	3.87 %
Total	194	1629.85	8.40		100	100

*Significant at 5%, **Significant at 1%

flexibility of genotypes across locations (Sanjana Reddy *et al.*, 2021). However, it was noticed that environment contributed large significant variation for plant height followed by grain yield, panicle length and number of productive tillers indicated that the environments were diverse with large difference among locations means causing most of the variation. The interactions between location and genotype effects exhibited significant differences for the agronomic traits such as number of productive tillers, panicle length and grain yield.

This finding indicated that changes in environmental conditions had a greater influence on the majority of traits. Khandelwal *et al.* (2024) reported most of the characters indicated considerable genotype-environment interactions (GEIs) in a joint analysis of variance except productive tillers per plant and plant population at harvest. Gangashetty *et al.* (2023) reported the highest genotypic and comparable interaction effects between location-genotype variance for plant height, panicle length, days to flowering and grain yield. Sanjana Reddy *et al.* (2021) also reported significant results for all the agronomic traits of pearl millet studied using the AMMI model.

The presence of GEI for grain yield clearly demonstrated by the AMMI model when the interaction was partitioned into the first two interaction IPCA 1 and IPCA 2 scores were significant and explained the variability of 55.67 and 31.77 per cent, respectively. This suggested the IPCA I axis contributed to the majority of the variance fallowed IPCA II. Therefore, AMMI I and II biplot were created for grain yield trait to investigate IPCA I and II the results outcome for grain yield traits discussed below.

Mean Performance and Stability Visualized through Genotype Main Effect Plus GEI AMMI Biplot Display for Grain Yield Trait

The mean grain yield (q/ha) value of genotypes (Table 8) averaged over environments indicated that the genotypes Kaveri S Boss (ZC) (G2) and ICMA94222 x PDRLT-2 (G 13) had the highest (31.01) and the lowest (19.32) grain yielder (q/ha), respectively. The environments mean of grain yield (q/ha) ranged from for E1 28.98 to 20.99 for E5 and averaged grain yield (q/ha) over environments and genotypes is 24.60.

On the basis of environmental index value, ZARS, Kalaburagi (E2) and ARS, Hagari (E5) are poor and ARS, Malnoor (E1), MARS, Raichur (E3) and RARS, Vijayapur (E4) are rich environment. Within the genotypes Kaveri S Boss (ZC) (G2), ICMA01555 x CPRLT-114 (G4), ICMA01555 x

TABLE 8

Mean performance and stability parameters for grain yield (q/ha) of 13 Pearl millet genotypes tested at five environments during *kharif* 2021

Genotype	ARS, Malnoor (E1)	ZARS, Kalaburagi (E2)	Raichur (E3)	RARS, vijayapur (E4)	ARS, Hagari (E5)	Var.µ	Var index	PCAI	PCAII	G*E Res SS
GHB 558(NC) (G1)	25.85	22.63	27.09	26.28	20.77	24.52	-0.08	-1.21	-0.04	-0.13
Kaveri Super Boss(ZC) (G2)	38.51	29.54	31.37	30.25	25.40	31.01	6.41	0.96	-0.83	0.18
MBP 2(LPC) (G 3)	30.22	21.62	25.23	24.76	20.40	24.45	-0.16	0.33	-0.26	0.04
ICMA01555 x CPRLT 114 (G4)	32.70	28.57	29.88	29.40	22.70	28.65	4.05	-0.20	-0.87	-0.33
ICMA01555 x TPRLT 109 (G5)	26.50	20.13	21.92	20.98	17.90	21.49	-3.12	0.31	0.03	-0.04
PT732A x LPRLT 114 (G6)	24.88	19.94	23.75	21.39	19.53	21.90	-2.70	-0.40	0.53	0.41
863A x EMRLT 33 (G 7)	26.92	22.23	22.48	22.98	20.67	23.05	-1.55	0.12	0.54	-0.69
863A x EMRLT 131 (G8)	26.89	23.09	29.93	26.65	19.43	25.20	0.60	-1.40	-0.84	0.82
ICMA01555 x EMRLT 139 (G9)	35.05	26.16	25.51	27.70	23.47	27.58	2.98	1.20	-0.26	-1.00
PT732A x PDRLT 8 (G10)	31.13	21.30	23.33	19.12	20.57	23.09	-1.51	1.52	0.45	1.19
841A x PDRLT 15 (G 11)	27.63	20.49	23.11	22.11	23.10	23.29	-1.32	0.31	1.35	0.03
ICMA94222 x SGRLT 17 (G12)	30.87	24.02	28.12	28.24	20.17	26.28	1.68	-0.33	-1.07	-0.20
ICMA94222 x PDRLT 2 (G 13)	19.59	17.22	20.90	20.15	18.77	19.32	-5.28	-1.20	1.27	-0.27
Env. Mean	28.98	22.84	25.59	24.62	20.99	GM=24.60				
Env. Index	4.38	-1.76	0.98	0.01	-3.61					
PCAI	2.54	0.12	-1.45	-1.26	0.05					
PCAII	-0.77	-0.28	-0.59	-0.81	2.45					
PCAIII	0.24	-0.44	1.48	-1.25	-0.03					
G*ERes.SS	0.51	5.31	0.02	1.20	0.13	7.18				

Fig. 1 : Graph showing significant difference among the genotypes for grain yield (q/ha) tested at five locations during *kharif* 2021

EMRLT-139 (G9), ICMA94222 x SGRLT-17 (G12) and 863A x EMRLT-131 (G8) have highest average grain yielder (q/ha) than grand mean, while genotypes GHB 558(LC) (G1), MBP-2(LPC) (G3),841A x PDRLT-15 (G 11), PT732A x PDRLT-8 (G 11), 863A x EMRLT-33 (G 7), PT732A x LPRLT-114 (G 6), ICMA01555 x TPRLT-109 (G 5) and ICMA94222 x PDRLT-2 (G13) have exhibited less grain yield (q/ha) than average.

AMMI 1 Biplot Display

Distribution of genotype points in the AMMI biplot at Fig. 2, revealed that the genotypes, Kaveri Super Boss (ZC) (G2) and ICMA01555 x EMRLT - 139 (G9) had higher mean yield compared to average yield (q/ha) with high main (additive) effects showing high positive IPCA 1 score, indicating highly interactive nature. Furthermore, they were

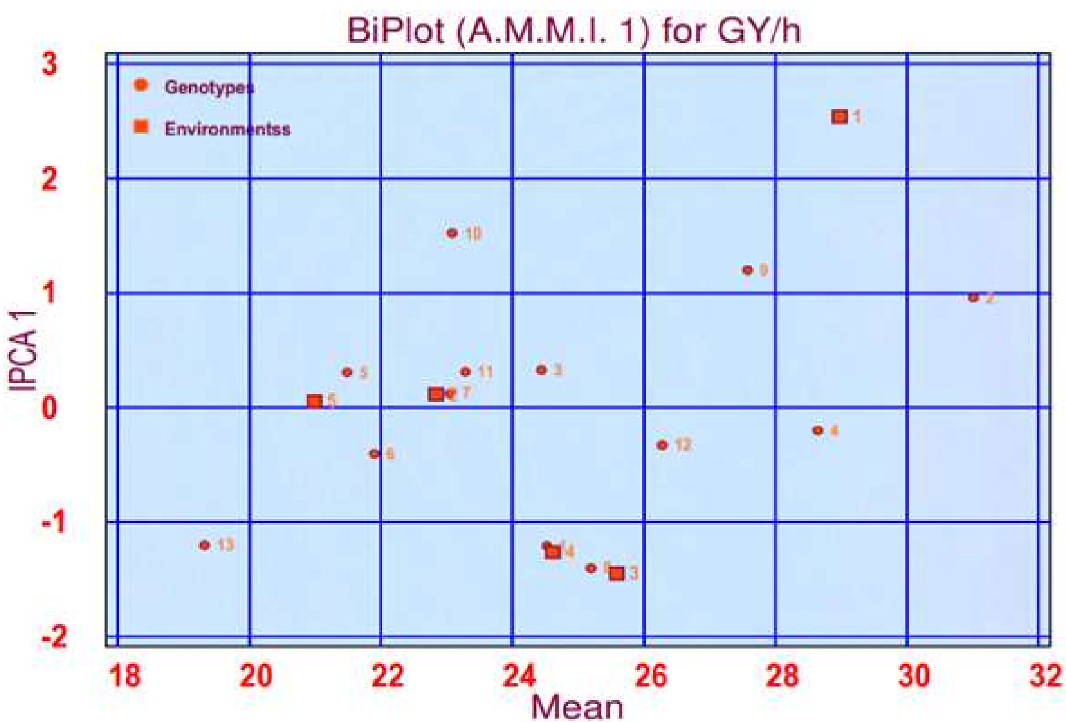

Fig. 2 : AMMI 1 Biplot for grain yield (q/ha) of 13 Pearl millet genotypes (G) and five environments (E) using genotypic and environmental scores

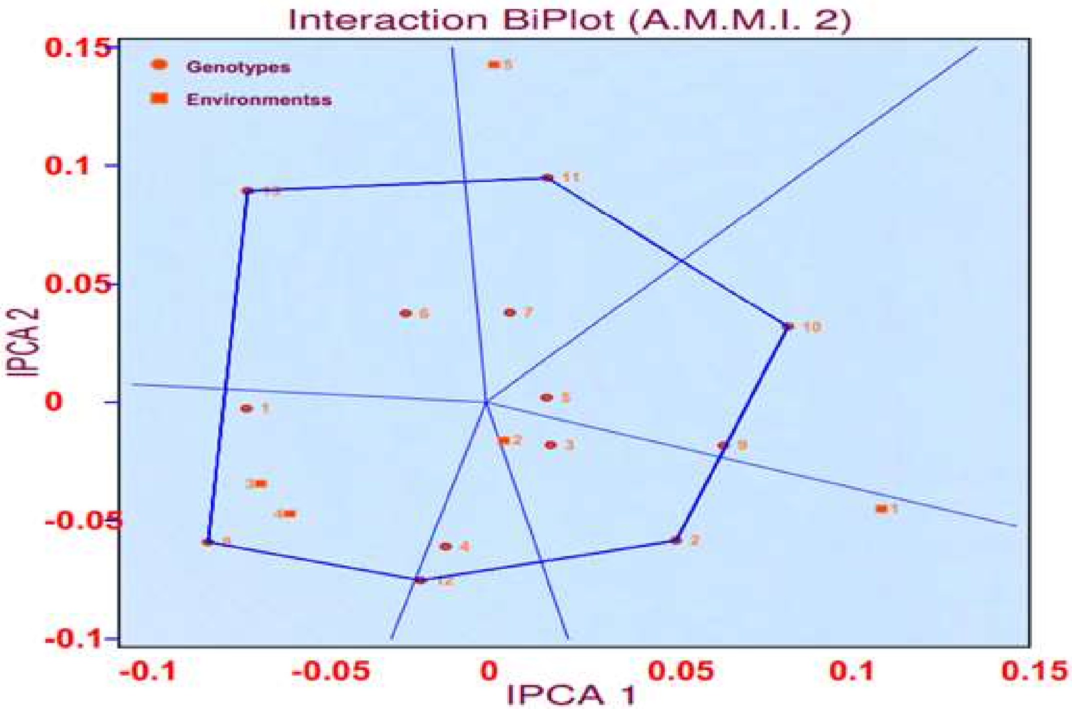

Fig. 3 : AMMI 2 Biplot for grain yield (q/ha) showing the interaction of IPCA 2 against IPCA 1 scores of 13 Pearl millet genotypes (G) in five environments (E)

specifically adapted to rich environment like ARS, Malnoor (E1) as evident by their placement along the IPCA I line in the AMMI I biplot (Table 5 and Fig. 2).

The genotype ICMA01555 x CPRLT-114 (G4), ICMA94222 x SGRLT-17 (G12) and 863A x EMRLT-131 (G8) though having highest grain yield (q/ha), but recorded negative IPCA 1 score indicating its environment sensitivity. But the genotype ICMA01555 x CPRLT-114 (G4) and ICMA94222 x SGRLT-17 (G12) had near-zero negative IPCA I value with high means for grain yield and the genotype MBP-2 (LPC) (G3), 841A x PDRLT - 15 (G11), 863A x EMRLT - 33 (G7) and ICMA01555 x TPRLT - 109 (G5) had low positive IPCA1 score with below average grain yield (q/ha) indicating relatively less GE and their moderate stability over locations.

Among them as evident by their placement along the IPCA I line MBP 2 (LPC) (G3) had on par mean yield compared to average yield (q/ha) with low positive IPCA 1 score near to zero and the genotype ICMA01555 x CPRLT - 114 (G4) and ICMA94222 x SGRLT 17 (G12) they were located on the right side of the overall mean line with low negative IPCA 1 score near to zero (Fig. 1) indicating their wider stability over location compared other genotypes. While 863A x EMRLT 131 (G8) with high negative IPCA 1 score was presumed to had specific adaptability.

The hybrid GHB 558 (LC) (G1) had relatively better yield, while PT732A x LPRLT 114 (G6) and ICMA94222 x PDRLT 2 (G13) had below average grain yield (q/ha) with negative IPCA1 score indicating that these varieties were more influenced by the environments.

In environment analysis, all the testing environments occupied different positions in the biplot analysis. The testing environments namely ARS Malnoor (E1), MARS, Raichur (E3) and RARS Vijayapur (E4) occupied the position above the average grain yield values signifying favourable environments for high yield. On other hand environments ARS, Malnoor had positive IPCA 1 score above zero and Raichur (E3) and RARS, Vijayapur (E4) had negative IPCA 1 score below zero indicating the more interaction effect on the genotype, among all environments.

AMMI 2 Biplot Display

Whereas, environments ZARS, Kalaburagi (E2) and ARS, Hagari (E5) occupied under the position below the average grain yield presented very near mid value indicating low yielding said to be an average environment and had positive IPCA1 score near zero hence had less interaction effects on the genotypes.

While ARS Malnoor (E1) (2.54) had positive IPCA1 above zero hence had large interaction effects and which is favourable environment for the genotypes Kaveri S Boss (ZC) (G2) and ICMA01555 x EMRLT - 139 (G9). When IPCA1 was plotted against IPCA2 the biplot representing a polygon view (Fig. 3) having some vertex hybrids while the rest are inside the polygon. These vertex hybrids are supposed to be the most responsive since they have they are farthest from the biplot origin. Responsive hybrids are either better or the poorest at one or all locations.

In present study hybrids., ICMA01555 x TPRLT-109 (G5), MBP - 2 (LPC) (G3) and GHB 558 (LC) (G1) were found closer or at proximity to the centre of the biplot compared to other genotypes hence they were non-sensitive to environmental interactive forces. Similarly, the hybrids ICMA94222 x PDRLT-2 (G 13), 841A x PDRLT - 15 (G11), PT732A x PDRLT - 8 (G10), ICMA01555 x EMRLT - 139 (G9), Kaveri S Boss (ZC) (G 2), ICMA94222 x SGRLT - 17 (G12) and 863A x EMRLT - 131 (G8) had more responsive since they were away from the origin. While 863A x EMRLT - 33 (G7), PT732A x LPRLT-114 (G6) and ICMA01555 x CPRLT-114 (G4) they were present little away from origins relatively less sensitive to environmental interactive forces.

It is worthwhile to note that, although hybrids G2 and G9 achieved the highest and better mean yield compared others but it exhibited the highest interaction and more responsive with the environments (IPCA 1 score), sinking the reliability of its stability performance. On the other hand, hybrids G5, G7, G4 and population MBP-2 (LPC) (G3) exhibited almost no or less interaction with the environments (IPCA 1 score) convincing the reliability of its performance. Among all Genotype ICMA01555 x CPRLT-114 (G4) had second highest mean grain yielder and relatively closer to average environment axis and near-zero IPCA 1 score so it could be considered as relatively stable with high yielder.

In the present study, whereas the genotypes ICMA01555 x TPRLT-109 (G5), MBP-2 (LPC) (G3) and GHB 558 (LC) (G1) were close to the origin and hence they were non-sensitive to environmental interactive forces and were considered as stable with low yielder. Among the environment ZARS, Kalaburagi (E2), MARS, Raichur (E3) and RARS, vijayapur (E4) were near to the origin and they did not exert strong interactive forces compared to ARS, Malnoor (E1) and ARS, Hagari (E5).

Based on the GGE biplot analysis, five environments fell into three different sectors with different high yielding hybrids (Fig. 3). The E1 and E2 were part of similar clusters with marginal variation as E1 was more productive site for grain yield testing it is also evident from earlier findings of (Mamata and Hooda, 2024) ARS, Malnoor (MLR) was highest trial representativeness and most productive location among B zone of pearl millet trial testing location of India. The E3 and E4 fell in similar cluster indicating the performance of hybrids in these locations not much different. Whereas, E5 formed separate clusters. Similarly, many researchers in several study identified high yielding stable cultivars and ideal environments by AMMI biplot approach (Sharma *et al.*, 1998; Pawar*et al.,* 2012; Wedajo Gebre, 2014 and Narasimhulu *et al.*, 2023) in pearl millet and (Kuchanur *et al.*, 2015) in maize.

AMMI Stability Value (ASV)

AMMI stability value of grain yield is presented in Table 9. According to these results, ICMA01555 x TPRLT 109 (G5) 863A x EMRLT 33 (G7) and PT732A x LPRLT 114 (G6) were found stable for

TABLE 9

Mean grain yield (q/ha) and yield stability indices of 13 Pearl millet genotypes tested at five environments during *kharif* 2021

Genotypes	Mean	R^Y	AMMI stability value (ASV)	R^A	Stability Index (SI)
GHB 558 (NC) (G1)	24.52	6	2.12	10	16
Kaveri Super Boss(ZC) (G2)	31.01	1	1.88	8	9
MBP 2 (LPC) (G 3)	24.45	7	0.63	3	10
ICMA01555 x CPRLT 114 (G4)	28.65	2	0.94	5	7
ICMA01555 x TPRLT 109 (G5)	21.49	12	0.54	1	13
PT732A x LPRLT 114 (G6)	21.90	11	0.88	4	15
863A x EMRLT 33 (G 7)	23.05	10	0.58	2	12
863A x EMRLT 131 (G8)	25.20	5	2.59	12	17
ICMA01555 x EMRLT 139 (G9)	27.58	3	2.12	9	12
PT732A x PDRLT 8 (G10)	23.09	9	2.70	13	22
841A x PDRLT 15 (G 11)	23.29	8	1.46	7	15
ICMA94222 x SGRLT 17 (G12)	26.28	4	1.22	6	10
ICMA94222 x PDRLT 2 (G 13)	19.32	13	2.46	11	24
Mean	24.60				
SEm	0.75				
CD@5%	2.11				
CD@1%	2.79				

R^Y : Rank of the test genotype based on mean grain yield, R^A : Rank of the test genotype based ASV

their grain yield with low yielder rank of 12th, 10th and 11th, respectively. The best high yielding ICMA01555 x CPRLT 114 (G4) and ICMA94222 x SGRLT 17 (G12) were also found relatively stable with ASV rank of 5th and 6th, respectively. Among them genotype (G4) was best because it had little IPCA1 implies they had no interaction with locations, *i.e.,* was stable. The highest yielding genotype Kaveri Super Boss (ZC) (G2) and ICMA01555 x EMRLT 139 (G9) had large IPCA1 implies they had large interaction *i.e.,* were less stable. While genotype MBP 2 (LPC) (G3) had 3rd ASV and 7th mean grain yield rank and have relatively small IPCA 1 implies they had small interaction with locations hence said to be relatively good yielder with more stable. Earlier research by using same criteria identified stable grain yielder in Pearl millet (Wedajo Gebre, 2014).

Stability Index (SI)

Stability index which takes into account of both mean grain yield and stability in a single criterion helps in simultaneous selection of genotypes based on yield and stability. In terms of the Stability Index, the genotypes with low SI are regarded as those with high grain yield and stability. In the present study, ICMA01555 x CPRLT 114 (G4) had implied lower magnitude of SI (7) fallowed by Kaveri Super Boss (ZC) (G2) and ICMA 94222 x SGRLT 17 (G12) and MBP-2 (LPC) (G3) (9 and 10, respectively). Further G4 and G12 were regarded as the best genotypes with high grain yield and stability. Similarly, (Narasimhulu *et al.,* 2023) and Mamata and Hooda (2024) has also identified high grain yield and stable genotypes in pearl millet using modified AMMI stability indices and (Kiran kumar *et al.*, 2023) in Horse gram based on stability index.

With respect grain yield stability of hybrids using AMMI model revealed that analysis of variance had highly significant differences among genotypes and locations. The GE interaction was significant though comparatively less than genotype and location effects. The hybrids ICMA01555 x CPRLT 114 (G4), ICMA01555 x EMRLT 139 (G9), ICMA94222 x SGRLT 17 (G12) and 863A x EMRLT 131 (G8) were found superior among all the hybrids and over national check GHB 558 and on par with zonal check Kaveri Super Boss (Plate 1 and 2).

Based on overall performance, AMMI bio-plot display, ASV and SI score, the genotype ICMA01555

G1 - GHB 558 (NC) | G2 Kaveri Super Boss (ZC) | G4 - (ICMA01555 x CPRLT 114) | G12 - (ICMA94222 x SGRLT 17)

Plate 1 : Ear head size and shape of top performed stable hybrids in comparison with checks

G1 - GHB 558 (NC) | G2 - Kaveri Super Boss (ZC) | G8 - (863A x EMRLT 131) | G9 - (ICMA01555 x EMRLT 139)

Plate 2 : Ear head size and shape of top performed stable hybrids in comparison with checks

x CPRLT 114 (G4) was considered as stable grain yielder across all five test locations. Further high yielding genotypes Kaveri Super Boss (ZC) (G2) and ICMA94222 x SGRLT 17 (G12) were exhibited least SI score (9 and 10, respectively) but showed highly interactive with environment hence they were considered moderately stable for grain yield. Kavya and Rangaiah (2019) have also identified Black gram genotypes stable across different sowing season using AMMI bio-plot display, ASV and SI score. However, ICMA01555 x EMRLT 139 (G9) had higher IPCA 1 value was specifically adapted to ARS, Malnoor location (E1).

It is worthwhile to note that population check MBP 2 also exhibited least SI score (10) and mean that was on par with the average yield showed little interactive with environment and hence it was comparatively a good yielder with high stable genotype among all. It is a known fact that populations in pearl millet would have more stable yields and they are more widely adapted than hybrids, and are less vulnerable to pests and diseases (Charyulu *et al*., 2014 and Narasimhulu *et al*., 2023). The study clearly indicates that the highest grain yielder hybrids are moderately stable while comparatively average/less yielder hybrids are highly stable for grain yield in pearl millet. However greater scope for development of promising OPVs in pearl millet having better stability across all the environment as compared to hybrids.

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