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Analysis of Pearl Millet's G x E Interaction with the Proposed New Index

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Developing cultivars that are stable in a variety of conditions has been a problem for plant breeders. The environment can have an impact on a cultivar's phenotypic performance, or different environments can have different effects on different cultivars. Variance resulting from a combination of an individual's genetic composition and the environment in which they were raised is referred to as the genotype-environment interaction. Reducing genotype-environment interaction through breeding stable genotypes facilitates selection of stable, high-yielding genotypes. In multi-environment cultivar trials, AMMI and GGE biplot analyses are frequently utilized to explain G×E interactions. In order to assess breeding material effectively, India's pearl millet agriculture has been split into three main zones, A1, A, and B, based on climatic circumstances. Using AMMI and GGE biplot analysis, the current study assessed the G×E interaction in pearl millet genotypes from Zone-B in India. Based on normalized grain yield and ASV indices, a new weighted index (WI) has been developed to assess stable and high-yielding genotypes. For this zone, the three interaction

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principal component axes (IPCA1, IPCA2, and IPCA3) have been found to be important. The indices YSI and WI have been used to identify both the high-yield and most stable genotypes, while the AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes. Based on WI, the genotypes G24 and G13 have been identified stable and high yielding genotypes for zone-B.

Keywords: Biplot analysis; food crop; multi-environment cultivar trials; phenotypic performance.

1. INTRODUCTION

The fourth most widely grown food crop, after rice, wheat, and maize, is pearl millet (*Pennisetum glaucum L*.). With an average production of 19.13 million tonnes and productivity of 3000 kg/ha, pearl millet was produced on 6.28 million hectares in 2023–2024. Pearl millet is a grain crop that is rain-fed annually in semi-arid and arid regions of India. As a crop for food and fodder, pearl millet is grown. Pearl millet is considered as the "future crop" among millets because of its superior adaptability to dry, marginal areas and capacity to withstand exceptionally harsh climatic conditions. Selecting and recommending new millet varieties for various environments is challenging and expensive due to its G×E interactions. During the varietal development process, substantial genotype-by-environment interactions (GEI) usually impede millet cultivar selection in relation to its production environment. Several statistical models have been proposed to increase the likelihood of using GEI and to assist breeding program decisions in variety selection and recommendation for a certain set of conditions. Models such as Additive Main Effects and Multiplicative Interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) effectively capture the additive (linear) and multiplicative (bilinear) components of GEI and provide meaningful interpretation of multi-environment data sets in breeding programs. Principal Component Analysis (PCA) and ANOVA are combined in the AMMI model. On the GE interaction part of the ANOVA, PCA is carried out. For this reason, the AMMI model is sometimes referred to as IPCA (Interaction PCA). The first person to apply AMMI to a GE interaction analysis was Kempton [1]. In theory, the GE interaction sum of squares can be best explained by the AMMI model, which has the fewest degrees of freedom. ANOVA and AMMI-F complete models are similar since the main axes explain all of the sum of squares that arise from the GE interaction. Since it frequently produces the lowest prediction errors, one-axis AMMI is the most effective. A biplot that displays the genotypic main effect is called a GGE biplot [2]. A genotype-by-environment dataset's genotypic main effect (G) and genotype-by-environment interaction (GE) are displayed in a biplot known as a GGE biplot [2]. When genotypes by environment two-way data are assessed, GGE biplot analysis is a system made up of a set of biplot graphs designed to meet various research aims. A scatter plot called a biplot is used to visually summarize two factors so that their correlations and underlying interactions can be seen simultaneously. The two most popular biplots for understanding GEI are the GGE biplot [2,3] and the AMMI biplot [4,5]. The usefulness of GGE biplot analysis and AMMI analysis for displaying and interpreting multi-environment trial data has been hotly debated in recent studies [6,7,8,9]. Each cultivar's measured value in a test environment is the result of adding the three primary effects of genotype (G), environment (E), and GE interaction [3].

The three main zones of pearl millet production in India-A1, A, and B—allow for the efficient assessment of pearl millet breeding materials. This work used AMMI and GGE biplot analysis to evaluate the G×E interaction in pearl millet genotypes from zone-B, India. The most stable genotypes have been determined using the AMMI Stability Value (ASV) and Stability Index, and the most stable and high-yielding genotypes have been determined using the indices YSI and WI. Based on normalized grain yield and ASV indices, a new weighted index (WI) has been developed [10] for assessing stable and high-yielding genotypes.

2. MATERIALS AND METHODS

The All India Coordinated Research Project's (AICRP) annual report on pearl millet for the year 2015–16 provided the yield statistics used in this study. The nation's pearl millet crop cultivation has been split into three main zones: A1 [10], A [11] and B depending on the weather conditions. There are 12 pear millet-producing locations in zone-B that receive less than 400 mm of rain

annually. In a randomized complete block design with three replications, yield data on 30 early type pearl millet genotypes (Table 1) have been assessed at 12 locations: Aurangabad (ABD2), Aurangabad (ABD1), Aurangabad (ABD5), Dhule (DHL), Buldana (BUL), Pachora (PCR), Palem (PLM), Perumallapalle (PMP), Ananthapuram (APR), Malnoor (MLR), Vijayapur (VYP), and Coimbatore (CBE).

2.1 AMMI Analysis

Using AMMI, a hybrid of analysis of variance and multiplication effect analysis, the grain yields of pearl millet were examined. The AMMI model for *G* genotypes and *S* sites /environments/locations [12] is displayed below.

$$Y_{ij} = \mu + g_i + s_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij} \qquad (1)$$

$$\theta_{ij} \sim N(0, \sigma^2); \qquad i = 1, 2, \ldots, G;\ j = 1, 2, \ldots, S$$

where, Y_{ij} = mean grain yield of i^{th} genotype in the j^{th} site, μ = general mean, g_i = i^{th} genotypic effect, s_j = j^{th} site effect, λ_n= eigen value of the n^{th} Interaction PCA axis, α_{in} and γ_{jn} are the i^{th} genotype j^{th} site PCA scores for the axis n, n' = number of PCA axes retained in the model and θ_{ij} = error component (The PCA scores from the $N - n'$ discarded axes are combined in the error component, N = min (G-1, S-1)).

An additional limitation found in model (1) includes:

$$\sum_{i=1}^{T} \alpha^2{}_{in} = \sum_{j=1}^{S} \gamma^2{}_{jn} = 1 \ \forall\ n;\ \sum_{i=1}^{T} \alpha_{in} \alpha_{in}{}^{*} = \sum_{j=1}^{S} \gamma_{jn} \gamma_{jn}{}^{*} = 0, n \neq n^{*}\ \&\ \lambda_1 > \lambda_2 > \cdots\cdots\cdots > \lambda_{n'} > 0$$

The mean square of each axis is tested with the estimate of residual through *F*-statistics to identify the number of PCA axes to be retained [13,14]. Every PCA axis' mean sum of squares is determined by dividing each axis' degree of freedom (G+S-1-2n) by the square of the associated eigenvalue.

The singular value decomposition (SVD) in the rank two matrixes can ideally estimate the G × E data for any character. The fundamental model for creating a GGE biplot from GE interaction data is provided by with the below mentioned model notations.

$$Y_{ij} = \mu + g_i + s_j + \phi_{ij} + \theta_{ij} \qquad (2)$$

where, ϕ_{ij} represents the interaction between g_i and s_j and θ_{ij} the error component of the model associated with the genotype *i* in site *j.* The GGE (i.e., grand mean and location- centered) biplot can also be represented mathematically as:

$$Y_{ij} - \mu - \bar{Y}_j = \xi_{i1} \lambda_1 \eta_{1j} + \xi_{i2} \lambda_2 \eta_{2j} + \theta_{ij} \qquad (3)$$

Where, Y_{ij} is the mean grain yield of genotype *i* in the site *j,* $\bar{Y}_j$ is the overall mean grain yield of all genotypes in site *j,* ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, respectively for the i^{th} genotype, η_{1j} and η_{2j} are the PC1 and PC2 scores, respectively for the j^{th} site and λ_1 and λ_2 are the singular values for PC1 and PC2, respectively.

To represent PC1 and PC2 in a biplot, the equation (3) is rewritten as

$$Y_{ij} - \mu - \bar{Y}_j = \xi^{*}{}_{i1}\, \eta^{*}{}_{1j} + \xi^{*}{}_{i2}\, \eta^{*}{}_{2j} + \theta_{ij} \qquad (4)$$

where,

$\xi^{*}_{in} = \lambda_n^{k}\, \xi_{in}$ and $\eta^{*}_{nj} = \lambda_n^{1-k}\, \eta_{nj}$ with n = 1, 2.

GGE biplots are created by graphing ξ^{*}_{i1} and η^{*}_{1j} against ξ^{*}_{i2} and η^{*}_{2j}. Although k can take an infinite number of integers between 0 and 1, only three are commonly used: 0, 1, and 0.5.

2.1.1 The stability indices

A quantitative stability measure is needed to quantify and rank genotypes based on their yield stability, but the AMMI model does not provide one.

2.2 The AMMI Stability Value (ASV)

A valuable measure for quantifying and ranking genotypes based on yield stability is the AMMI stability value (ASV), which was introduced by Purchase et al. [15]. According to the ASV approach, the most stable genotype is the one with the lowest ASV score.

$$ASV = \sqrt{\left[\frac{IPCA1_{sum\ of\ square}}{IPCA2_{sum\ of\ square}} (IPCA1_{score})\right]^2 + (IPCA2_{score})^2} \qquad (5)$$

Table 1. Thirty pearl millet genotypes' mean grain yield (kg/ha) studied at twelve locations in Zone-B during 2015-16

Genotype	ENTRY	ABD2	ABD1	ABD5	DHL	BUL	PCR	PLM	PMP	APR	MLR	VYP	CBE
G1	MH 2103	2387	3393	3594	3411	2039	2217	1931	6078	3969	3921	731	2369
G2	MH 2104	2167	3243	3812	3190	2150	2369	1880	6698	3986	3534	832	2894
G3	MH 2105	2697	2523	3555	3244	1422	2227	1787	3462	2664	3022	934	2344
G4	MH 2106	4609	3393	6044	3968	2417	3253	2213	4862	4066	6376	1168	3294
G5	MH 2107	4669	3934	5734	3744	1650	2735	1838	5549	3811	6511	1127	3442
G6	MH 2108	2312	2553	3060	2167	1056	1704	1718	3560	2741	2544	735	2578
G7	MH 2109	4072	3544	4951	3526	1611	2955	1806	4557	2610	6173	996	5217
G8	PAC 909	2558	2793	4304	3533	1222	2288	1491	4008	2904	5295	933	2361
G9	MH 2110	3745	3423	4142	3077	1272	2357	1514	5304	3447	5947	909	5089
G10	MH 2111	3410	3784	5588	4489	2000	2612	1875	2603	3924	6305	858	4317
G11	MH 2112	3103	3363	3735	2797	1394	1818	1824	5198	3495	4946	739	3522
G12	MH 2113	3564	3153	4774	3844	2233	2868	1731	5663	3157	4349	1044	2072
G13	MH 2114	3288	3423	4965	3739	1411	2624	1542	4681	2948	4037	1033	2100
G14	MH 2115	4016	3904	4087	3342	2194	2300	1847	5600	2840	4553	887	2056
G15	MH 2116	3707	3153	3888	3135	1372	1806	1500	3700	2888	3303	886	2269
G16	MH 2117	2553	3514	3397	1855	1344	1634	1551	5179	2403	3503	639	2661
G17	GHB 558	2932	2673	3247	2741	1183	2324	1944	4666	3470	3161	742	1767
G18	MH 2118	4220	3393	4479	3800	1228	2671	1741	5106	3531	5352	1121	3583
G19	MH 2119	4059	2583	4600	4207	1872	2915	1750	5564	2917	3637	1223	2578
G20	MH 2120	2700	2252	3459	2465	1222	1707	1380	4057	2310	3695	928	2250
G21	MH 2121	3907	3183	3612	2604	1667	2241	1532	5300	2983	4440	1209	1819
G22	MH 2122	4102	2823	3994	2694	1433	1480	1560	2601	2711	2658	929	2317
G23	NBH 5767	3627	3363	3640	2378	1378	2284	1806	5652	3640	5327	991	2606
G24	MH 2123	3907	3544	6102	4136	1428	3217	1829	5548	3658	5454	1103	2578
G25	MH 2124	2188	2973	3481	2691	2289	2738	1597	3683	2404	2931	1134	2733
G26	MH 2125	2824	3093	3268	2882	1194	2281	1431	3224	2351	3442	908	2339
G27	MH 2126	2601	2823	3626	2912	1706	2002	1495	3045	2431	3024	926	2039
G28	MH 2127	2425	3333	3061	3106	1144	2274	1630	5498	2162	3689	888	1672
G29	MH 2128	3521	2492	3613	2586	1378	2636	1801	4931	2839	4096	909	1867
G30	MH 2129	3060	2883	4126	3383	1867	2884	1602	6186	3205	5159	876	2528

2.3 The Yield Stability Index (YSI)

YSI index used to identify genotypes with high yield and stability. The following equation used to calculate the YSI as follows:

$$YSI_i = R_i(ASV) + R_i(GY) \quad (6)$$

Where, YSI_i is the yield stability index for i^{th} genotype in all the sites, $R_i(GY)$ is the rank of the genotype's mean grain yield in all sites, and $R_i(ASV)$ is the genotype's ASV value. Mean yield and stability are combined into a single criterion, which is the YSI. The genotype with a high mean yield and stability is with a low YSI value.

2.4 The Weighted Index (WI)

2.4.1 Normalized index for AMMI stability value

Let ASV_i represents the value of the ASV of i^{th} genotype for all the sites (i = 1, 2,..., G) where lower the ASV more stable is the genotype, then normalized index [16] for i^{th} genotype for all the sites written as:

$$NASV_i = \frac{MAX(ASV_i) - ASV_i}{MAX(ASV_i) - Min(ASV_i)} \quad (7)$$

Where, $NASV_i$ is the normalized index for ASV and $Max(ASV_{ik})$ and $Min(ASV_{ik})$ are the ASV values taken for the i^{th} genotype in all the sites.

The higher the value of NASV more stables the genotype.

2.4.2 Normalized index for mean grain yield

Let GY_i represent the mean grain yield of the i^{th} genotype for all sites (i = 1, 2,..., G). The normalized index of the i^{th} genotype for all sites written as:

$$NGY_i = \frac{GY_i - Min(GY_i)}{MAX(GY_i) - Min(GY_i)} \quad (8)$$

where, NGY_i is the normalized index of mean grain yield for the i^{th} genotype and $Max\ (GY_i)$ and $Min\ (GY_i)$ are the GY_i taken for i^{th} genotype in all the sites.

The normalized index values are ranging from 0 and 1. Lower the value of Normalized index indicates lesser stability and higher values indicates higher stability.

The WI for determining high-yielding and stable genotypes given by:

$$WI_i = W_1 NGY_i + W_2 NASV_i \quad ; \quad i = 1, 2, \ldots, G \quad (9)$$

Where, ($0 \le W_1, W_2 \le 1$ & $W_1 + W_2 = 1$) are the weights associated with the NGY_i and $NASV_i$ and W_1 and W_2 is calculated as

$$W1 = \frac{s_2}{s_1 + s_2} \quad \& \quad W2 = \frac{s_1}{s_1 + s_2}$$

where, s_1 is the standard deviation of NGY_i and s_2 is the standard deviation of $NASV_i$.

The range of the weighted index is zero to one. To assess genotype stability, a simple ranking based on WI is applied. The genotype with the highest WI index is the most stable and produces the highest yield. The rank-based YSI and WI were generated using Spearman's rank correlation coefficient to demonstrate the similarity of the inference taken from the suggested index WI and index YSI.

2.5 The Sustainability Index (SI)

Babarmanzoor et al. [17] proposed the following formula for calculating the sustainability index (SI):

$$SI = \left[\frac{\bar{Y}_i - s_i}{\max\ (Y_{i1}, Y_{i2}, \ldots\ldots, Y_{iS})}\right] X100 \quad (10)$$

where, $\bar{Y}_i$ is the mean performance of a particular genotype, s_i is the standard deviation and $\max\ (Y_{i1}, Y_{i2}, \ldots\ldots, Y_{iS})$ the value of the best genotype in any site.

Genotypes are categorized into five groups based on SI values: very low stability (SI≥20%), low stability (21%≤ SI≤40%), moderate stability (41 ≤ SI≤ 60%), high stability (61% ≤ SI≤ 80%), and very high stability (SI≥80%).

2.6 The Stability Index (I)

According to Bajpai and Prabhakaran [18], the stability index was calculated to determine their yield stability.

$$I_i = \left(\frac{\bar{Y}_i}{\bar{Y}} + \frac{1}{{s_i}^2}\right) / \left[\frac{1}{S}\sum\left(\frac{1}{{s_i}^2}\right)\right] \quad (11)$$

where, I_i is the Stability index for i^{th} genotype in all the sites, S is the number of environments, $\bar{Y}_i$ is the average performance of the i^{th} genotype in

all the sites, $\bar{Y}$ is the overall mean, s_i^2 is Shukla's stability variance [19] of the i^{th} genotype in all the sites.

3. RESULTS AND DISCUSSION

In AMMI analysis of variance (ANOVA), it was discovered (Table 2) that the environment effect contributed the most variance (71.24%) followed by the G × E interaction (14.66%) and genotypic variation (10.80%). Using the Gollob's *F*-test, the axes IPCA1, IPCA2 and IPCA3 were determined to be significant. The IPCA1, IPCA2 and IPCA3 axes were accounted 35.19%, 25.42% and 14.66% to the interaction sum of squares, respectively.

The results in Table 3 shows that the highest grain yield was recorded for the genotype G4 followed by G5, based on the ASV values the genotype G6 was found most stable followed by genotype G20 whereas on the basis of stability index values the genotype G6 was found to be most stable with highest yield followed by G20. The genotypes G24 and G12 were the most stable genotypes based on YSI value. Based on WI value the genotype G24 was found to be most stable and high yielding genotype followed by genotype G13. Similarly, based on SI (%) two groups of stable genotypes were found i.e., low and moderate stable genotype groups. The genotype G21 was recorded under low stable genotype group, whereas the genotypes G1, G2, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G16, G17, G18, G19, G20, G21, G22, G23, G24, G28, G29 and G30 were recorded under moderate stable genotype group.

In parenthesis are the genotype ranks according to mean grain yield and several stability parameters. At the 1% level of significance, the Spearman's rank correlation coefficient between the YSI and WSI was determined to be 0.935, indicating statistical significance. It demonstrates that when it comes to identifying stable genotypes with high yields, the two indices perform nearly equally.

3.1 Graphical Representation of Genotypes' Stability and High Grain Yield in Zone B

An instant understanding of stable genotypes with high yields may be obtained from the basic scatter plot of the Normalized *ASV* values (*NASV*) and Normalized Grain Yield (*NGY*). The scatter plot of *NGY* along the x-axis and *NASV* along the y-axis is shown in Fig. 1. The genotype that yields the highest yields and is the most stable is represented by this scatter plot. Additionally, it was noted that G20 had the highest level of stability (based on *NASV*), G4 had the most yielding (based on *NGY*), and G24 had the highest level of stability and yielding.

3.2 The GGE Biplots for Zone B

The three main areas of investigation for genotypic environment data, was as follows:

i. A genetic link between location and the which-won-where pattern is used to analyze mega-environments.
ii. Assessment of test locations according to their representativeness and capacity for discrimination.
iii. Evaluation of genotypes according to their average stability and performance in a mega-environment.

Table 2. AMMI ANOVA for pearl millet grain yield (kg/ha) data in Zone-B

Source	D.F	Sum of squares	Mean square	F_{cal}	Sum of squares (%)
Genotype	29	66106925.6	2279549.15	6.62**	10.80
Environment	11	435812536.86	39619321.53	115.11**	71.24
G × E interaction	319	109797337.53	344192.28	2.63**	14.66
IPCA1	39	38639180.01	990748.20	7.59**	35.19
IPCA2	37	27911974.09	754377.67	5.78**	25.42
IPCA3	35	16097008.53	459914.52	3.52**	14.66
Residual	208	27149174.88	130524.87		
Total	359	611716800	1703946.51		

Table 3. Yield-stability indices for zone B

Genotype	GY	ASV	YSI	I	WI	SI(%)	SIG
G1	3003(14)	29.60(24)	38(21)	95247.42(17)	0.51(20)	26.93	Low
G2	3063(12)	36.98(28)	40(22)	97136.95(19)	0.44(25)	23.94	Low
G3	2490(25)	20.02(17)	42(25)	78970.5(6)	0.47(23)	47.36	Moderate
G4	3805(1)	27.09(23)	24(9)	120679.3(30)	0.75(3)	35.74	Low
G5	3729(2)	30.30(25)	27(11)	118250.5(29)	0.70(8)	31.18	Low
G6	2227(30)	18.62(15)	45(28)	70637.6(1)	0.42(27)	39.83	Low
G7	3502(4)	41.16(29)	33(17)	111046.1(27)	0.52(18)	31.14	Low
G8	2808(18)	16.39(11)	29(13)	89037(13)	0.60(15)	28.40	Low
G9	3352(6)	32.41(27)	33(18)	106310.2(25)	0.57(16)	29.02	Low
G10	3480(5)	56.79(30)	35(19)	110377.4(26)	0.34(30)	30.08	Low
G11	2995(15)	12.64(4)	19(6)	94967.52(16)	0.69(9)	31.45	Low
G12	3204(8)	13.33(6)	14(2)	101622.2(23)	0.74(4)	33.05	Low
G13	2983(16)	4.51(1)	17(4)	94589.76(15)	0.78(2)	34.28	Low
G14	3136(11)	13.81(7)	18(5)	99439.14(20)	0.72(7)	31.94	Low
G15	2634(20)	15.09(10)	30(15)	83532.11(11)	0.56(17)	41.28	Moderate
G16	2519(24)	16.54(12)	36(20)	79900.68(7)	0.52(19)	24.70	Low
G17	2571(22)	21.66(19)	41(24)	81531.38(9)	0.48(22)	32.21	Low
G18	3352(7)	17.14(14)	21(7)	106308(24)	0.74(5)	36.25	Low
G19	3159(9)	13.25(5)	14(3)	100176.4(22)	0.73(6)	33.67	Low
G20	2369(29)	4.65(2)	31(16)	75124.03(2)	0.61(14)	34.01	Low
G21	2875(17)	14.39(8)	25(10)	91169.79(14)	0.64(11)	30.32	Low
G22	2442(26)	30.50(26)	52(30)	77440.03(5)	0.34(29)	35.66	Low
G23	3058(13)	18.68(16)	29(14)	96970.64(18)	0.64(10)	28.57	Low
G24	3542(3)	14.40(9)	12(1)	112330.6(28)	0.82(1)	31.38	Low
G25	2570(23)	23.36(21)	44(27)	81510.04(8)	0.46(24)	50.25	Moderate
G26	2436(27)	16.74(13)	40(23)	77268.6(4)	0.49(21)	45.96	Moderate
G27	2386(28)	22.74(20)	48(29)	75664.25(3)	0.41(28)	44.52	Moderate
G28	2574(21)	25.96(22)	43(26)	81615.82(10)	0.43(26)	23.69	Low
G29	2722(19)	11.60(3)	22(8)	86338.92(12)	0.63(13)	31.56	Low
G30	3147(10)	21.44(18)	28(12)	99790.56(21)	0.64(12)	26.98	Low

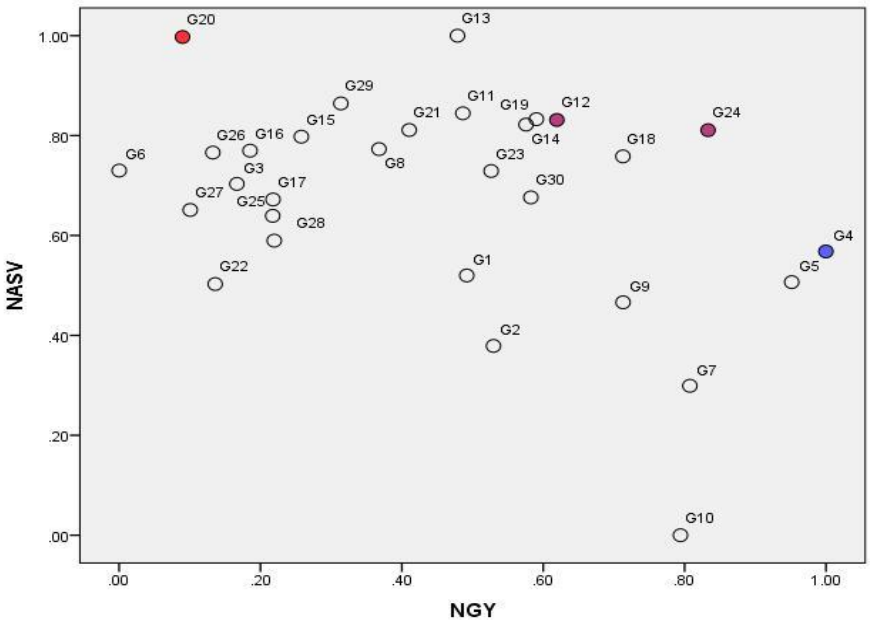

Fig. 1. Graphical representation of genotypes' stability and high grain yield in Zone B

3.2.1 Zone B mega-environments analysis

The genotype vector that is furthest from the biplot origin (where zero interacts with the x and y axes) is displayed as a polygon in Fig. 2, and lines are drawn perpendicularly from the biplot origin to each of the polygon's sides. By dividing the entire trial area into homogeneous groups based on genotype performance, more information is obtained about the environments as well as the genotypes. All genotypes are contained inside an irregular convex polygon that has been created. The genotypes that share a sector formed by the perpendicular lines perform better there when one or more environments are found within it, and the genotypes that perform best are found at the vertices of these sectors. The entire environment was thus split into different sectors which have their superior genotypes. The superior genotype is referred to as the winning genotype in the given sector. Similarly, genotypes lacking an environment in their sector are unlikely to perform better in any of the tested environments, and the poorest performing genotypes will be found at the vertices of these sectors.

The Zone B pearl millet data's "which won where" biplot (Fig. 2) showed that PMP formed one mega environment, APR, BUL, CBE, MLR, PCR, DHL ABD5, ABD2, PLM and VYP formed a second mega environment. It has been noted that the genotypes G1 (MH2103), G4 (MH2106), and G19 (MH2119) are the superior genotypes in their respective mega environments.

3.2.2 Evaluation of the test environment for Zone B

The breeding program's overarching goal is to gather ever-more data regarding environments and genotypes. It is always important to keep in mind that trials must be conducted in appropriate locations and in sufficient numbers to be conducted effectively. To increase the effectiveness of the experiment, the environments in which the trials are conducted are assessed for their representativeness and discriminativeness.

As seen in Fig. 3, the relationships between the environments were assessed using correlation, or the angle between them. Therefore, the angle between the target and test environments shows how representative the experiment was. The target environment was displayed by taking an average of all sites. The variance of the variable (environment) was used to measure the discriminating characteristic; the greater the variance of the environment, the greater its ability to discriminate across genotypes.

As illustrated in Fig. 3, ABD5 had the strongest discriminating power and MLR the highest trial representativeness. While CBE had low discriminating power, VYP had low representativeness. The most productive was MLR.

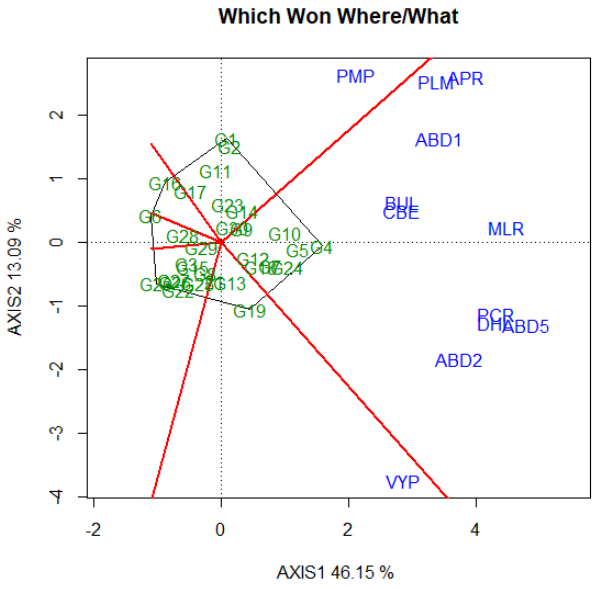

Fig. 2. Zone B mega-environment analysis

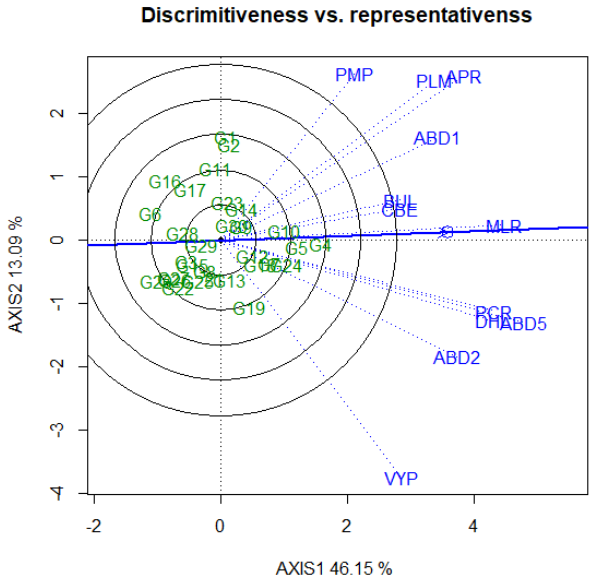

Fig. 3. Evaluation of the test environment for Zone B

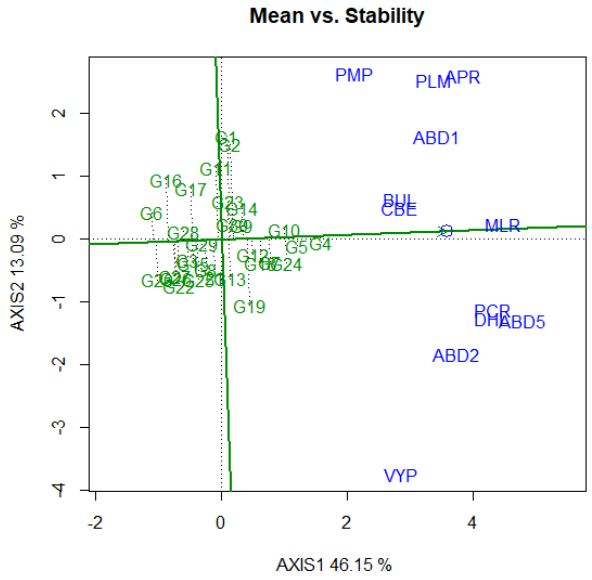

Fig. 4. Assessment of Zone B's genotype

3.2.3 Assessment of zone B's genotype

A genotype's evaluation is compared to its average performance and stability prior to the breed's general release. The evaluation axis of the test environment, as shown in Fig. 4, proved helpful in searching for these attributes. The average environment axis (AEA) is the axis that runs through the virtual environment, and the average coordination axis (AEC) is the axis that is superimposed on the biplot at a right angle [20,21].

The mean yield and stability of a genotype are projected on the AEA and AEC axes, respectively. The genotypes are ranked according to their mean performance, with the arrow on the axis of the AEC abscissa pointing in the direction of higher genotype mean performance. The ranking of the genotypes on

the AEC abscissa is always perfectly or highly linked with the genotypic effect (G), unless G is too minor to be significant.

Based on average yield and genotype stability, the study above indicated that genotypes G4 (MH2106) and G10 (MH2111) were advantageous for the trial region. The least stable genotypes were G1 (MH2103) and G19 (MH2119).

4. CONCLUSION

In pearl millet yield studies conducted in a variety of environments, the AMMI model proved useful for evaluating GEI. A significant result and a strong correlation were seen in the stability measures YSI and WI. The indices YSI and WI have been used to identify both the high-yield and most stable genotypes, while the ASV and Stability Index have been used to find the most stable genotypes. Based on ASV value the genotype G13 (MH2114) was recorded as most stable genotype whereas genotype G6 (MH2108) was observed as most stable and high yielding genotype on the basis of stability index. Based on YSI and WI the genotype G24 (MH2123) was found to be most stable and high grain yielding genotype whereas on the basis of GGE Biplot the genotype G4 (MH2106) was found to be most stable genotype. The present study is quite general it can be applied to any related studies.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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