Evaluation of G x E interaction in Pearl Millet using Proposed New Index

ABSTRACT

The challenge for plant breeders has been to establish cultivars that are stable in a wide range of environments. A particular cultivar's phenotypic performance may vary according to the environment, or several cultivars may respond differently to a given environment. The genotype-environment interaction refers to the variance that occurs as a function of its genetic makeup and the environment in which it was grown. Breeding stable genotypes aims to minimize genotype-environment interaction, making it easier to choose high-yielding and stable genotypes. AMMI and GGE biplot analyses are commonly employed to explain G×E interactions in multi-environment cultivar experiments. Pearl millet cultivation in India has been divided into three major zones based on climatic conditions, A1, A, and B, for effective evaluation of breeding material. The present study evaluated the G×E interaction in pearl millet genotypes from India's zone-B using AMMI and GGE biplot analysis. A new weighted index (WI) has been used for evaluating high-yielding and stable genotypes based on normalized grain yield and ASV indices. The three interaction principal component axes (IPCA1, IPCA2, and IPCA3) have been identified as significant for this zone. The AMMI Stability Value (ASV) and Stability Index have been applied to identify the most stable genotypes, while the indices YSI and WI have been applied to identify both the most stable and high-yield genotypes. Based on ASV, genotypes MH 2114, MH 2126, and MH 2128 have been identified as the most stable for this Zone.

KEY WORDS AND PHRASES

AMMI Analysis, GGE Biplot Analysis, G×E interaction, Pearl Millet, Stability Analysis

INTRODUCTION

Pearl millet (*Pennisetum glaucum* L.) is the fourth most common food crop cultivated after rice, wheat and maize. During 2023-24, pearl millet was grown in 6.28 million ha with an average production of 19.13 million tonnes and productivity of 3000 kg/ha. In arid and semi-arid regions of India, pearl millet is grown as a rain-fed cereal crop every year. Pearl millet is cultivated as both a food and fodder crop. Pearl millet, the 'future crop' among millets, has received little attention from policymakers despite 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 G×E interactions. Millet cultivar selection about its production environment is frequently hampered by large genotype-by-environment interactions (GEI) during the varietal development process. Several statistical models have been presented to improve the likelihood of utilizing GEI and to aid breeding program decisions in variety selection and recommendation for a target set of conditions. Additive Main Effects and Multiplicative Interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) models are examples of models that effectively capture the additive (linear) and multiplicative (bilinear) components of GEI and provide meaningful interpretation of multi-environment data sets in breeding programs. The AMMI model combines ANOVA and Principal Component Analysis (PCA). It performs PCA on the GE interaction component of the ANOVA. Because of this, the AMMI model is also known as IPCA (Interaction PCA).

Kempton (1984) was the first to use AMMI in the analysis of GE interaction. Theoretically, AMMI is the best model with the fewest degrees of freedom to explain the GE interaction sum of squares. Given that the primary axes account for all the sum of squares resulting from the GE interaction, an AMMI-F complete model is equivalent to an ANOVA model. One-axis AMMI is the most efficient since it often yields the lowest prediction errors. A GGE biplot (Yan *et al*., 2000) is a biplot that shows the genotypic main effect (G) and genotype-by-environment interaction (GE) of a genotype-by-environment dataset. GGE biplot analysis is a system that consists of a collection of biplot graphs developed to satisfy a variety of research objectives when genotypes by environment two-way data are evaluated. A biplot is a scatter plot that graphically summarizes two parameters in such a way that their relationships and underlying interactions may be shown at the same time. To understand GEI, the most widely used biplots are the AMMI biplot (Crossa, 1990 and Gauch, 1992) and the GGE biplot (Yan *et al*., 2000 and Yan and Kang, 2003). In recent research, the value of AMMI analysis and GGE biplot analysis to depict and interpret multi-environment trial data has been highly disputed (Gauch, 2006; Yan *et al*., 2007; Gauch *et al*., 2008; Yang *et al*., 2009). The measured value of each cultivar in a test environment is a sum of the genotype main effect (G), the environment main effect (E), and the GE interaction (Yan and Kang, 2003).

Pearl millet cultivation in India is separated into three major zones: A1, A, and B, which allow for effective evaluation of pearl millet breeding materials. This study assessed the G×E interaction in pearl millet genotypes from India's zone-B using AMMI and GGE biplot analysis. The AMMI Stability Value (ASV) and Stability Index have been employed to identify the most stable genotypes, while the indices YSI and WI have been applied to identify both the most stable and high-yielding genotypes. A new weighted index (WI) has been used (Mamata *et al*., 2019) for evaluating high-yielding and stable genotypes based on normalized grain yield and ASV indices.

MATERIAL AND METHODS

The yield data for the study were collected from the AICRP's annual report on pearl millet for the year 2015-16. Based on meteorological circumstances, the country's pearl millet cultivation has been divided into three major zones: A1, A, and B. The zone-B contains 12 pear millet-producing locations which receive less than 400mm of yearly rainfall. Data on 30 early type pearl millet genotypes have been evaluated at 12 locations: Aurangabad (ABD1), Aurangabad (ABD2), Aurangabad (ABD5), Dhule (DHL), Buldana (BUL), Pachora (PCR), Palem (PLM), Perumallapalle (PMP), Ananthapuram (APR), Malnoor (MLR), Vijayapur (VYP), and Coimbatore (CBE) in a randomized complete block design with three replications (Table 1).

Table 1: Mean grain yield (kg/ha) of thirty Pearl millet genotypes evaluated at twelve locations of Zone-B during 2015-16

ENOTYPE	ENTRY	ABD2	ABD1	ABD5	DHL	BUL	PCR	MLR	VYP	PLM	PMP	APR	CBE
G1	MH 2103	2387	3393	3594	3411	2039	2217	3921	731	1931	6078	3969	2369
G2	MH 2104	2167	3243	3812	3190	2150	2369	3534	832	1880	6698	3986	2894
G3	MH 2105	2697	2523	3555	3244	1422	2227	3022	934	1787	3462	2664	2344
G4	MH 2106	4609	3393	6044	3968	2417	3253	6376	1168	2213	4862	4066	3294
G5	MH 2107	4669	3934	5734	3744	1650	2735	6511	1127	1838	5549	3811	3442
G6	MH 2108	2312	2553	3060	2167	1056	1704	2544	735	1718	3560	2741	2578
G7	MH 2109	4072	3544	4951	3526	1611	2955	6173	996	1806	4557	2610	5217
G8	PAC 909	2558	2793	4304	3533	1222	2288	5295	933	1491	4008	2904	2361

G9	MH 2110	3745	3423	4142	3077	1272	2357	5947	909	1514	5304	3447	5089
G10	MH 2111	3410	3784	5588	4489	2000	2612	6305	858	1875	2603	3924	4317
G11	MH 2112	3103	3363	3735	2797	1394	1818	4946	739	1824	5198	3495	3522
G12	MH 2113	3564	3153	4774	3844	2233	2868	4349	1044	1731	5663	3157	2072
G13	MH 2114	3288	3423	4965	3739	1411	2624	4037	1033	1542	4681	2948	2100
G14	MH 2115	4016	3904	4087	3342	2194	2300	4553	887	1847	5600	2840	2056
G15	MH 2116	3707	3153	3888	3135	1372	1806	3303	886	1500	3700	2888	2269
G16	MH 2117	2553	3514	3397	1855	1344	1634	3503	639	1551	5179	2403	2661
G17	GHB 558	2932	2673	3247	2741	1183	2324	3161	742	1944	4666	3470	1767
G18	MH 2118	4220	3393	4479	3800	1228	2671	5352	1121	1741	5106	3531	3583
G19	MH 2119	4059	2583	4600	4207	1872	2915	3637	1223	1750	5564	2917	2578
G20	MH 2120	2700	2252	3459	2465	1222	1707	3695	928	1380	4057	2310	2250
G21	MH 2121	3907	3183	3612	2604	1667	2241	4440	1209	1532	5300	2983	1819
G22	MH 2122	4102	2823	3994	2694	1433	1480	2658	929	1560	2601	2711	2317
G23	NBH 5767	3627	3363	3640	2378	1378	2284	5327	991	1806	5652	3640	2606
G24	MH 2123	3907	3544	6102	4136	1428	3217	5454	1103	1829	5548	3658	2578
G25	MH 2124	2188	2973	3481	2691	2289	2738	2931	1134	1597	3683	2404	2733
G26	MH 2125	2824	3093	3268	2882	1194	2281	3442	908	1431	3224	2351	2339
G27	MH 2126	2601	2823	3626	2912	1706	2002	3024	926	1495	3045	2431	2039
G28	MH 2127	2425	3333	3061	3106	1144	2274	3689	888	1630	5498	2162	1672
G29	MH 2128	3521	2492	3613	2586	1378	2636	4096	909	1801	4931	2839	1867
G30	MH 2129	3060	2883	4126	3383	1867	2884	5159	876	1602	6186	3205	2528

AMMI(Additive Main Effect Multiplicative Interactions)

The grain yields of pearl millet were analyzed using AMMI, a combination of analysis of variance and multiplication effect analysis. The AMMI model (Rao & Prabhakaran, 2005) for *G* genotypes and *L* environments/locations is shown below.

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

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

where, Y_{ij} = mean yield of i^{th}genotype in the j^{th} environment/location, μ = general mean,g_i= i^{th}genotypic effect, e_j= j^{th} location effect, λ_n= eigen value of the nth IPCA axis, α_{in} and γ_{jn} are the i^{th}genotype j^{th} environment PCA scores for the axis *n*, θ_{ij} = residual and *n'* = number of PCA axes retained in the model.

The residual combines the PCA scores from the *N* - *n*' discarded axes, where *N* = min (*G*-1, *L*-1). The other constraints in the model (1) are;$\sum_{i=1}^{T} \alpha^2_{in} = \sum_{j=1}^{S} \gamma^2_{jn} = 1 \; \forall n; \sum_{i=1}^{T} \alpha_{in} \alpha_{in}{}^{*} = \sum_{j=1}^{S} \gamma_{jn} \gamma_{jn}{}^{*} = 0, n \neq n^{*}$and $\lambda_1 > \lambda_2 > \ldots\ldots\ldots > \lambda_{n'} > 0$

For many practical situations, the number of PCA axes to be retained is determined by testing the mean square of each axis with the estimate of residual through *F*-statistics (Gollob, 1968 and Gauch, 1988). The mean sum of squares of each PCA axis is equal to the ratio of the square of the corresponding eigenvalue and the degree of freedom of each axis obtained as *G*+*L*-1-2*n*.

Further, the G × E data for any character can be optimally approximated by SVD in the rank two matrixes. With the above notations, the basic model for constructing a GGE biplot from GE data is given by

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

where, ϕ_{ij} = interaction between g_i and $e_j$and θ_{ij} the residual of the model associated with the genotype *i*in environment *j*. The GGE (i.e., grand mean and environment- cantered) biplot can also be represented mathematically as

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

where, Y_{ij} is the average yield of genotype *i*in environment *j*, $\bar{Y}_j$ is the average yield over all genotypes in environment *j*, λ_1 and λ_2 are the singular values for PC_1 and PC_2 respectively and ξ_{i1} and ξ_{i2} are the PC_1 and PC_2 scores, respectively for genotype *i*, η_{1j} and η_{2j} are the PC1 and PC2 scores, respectively for environment *j*

To display PC_1 and PC_2 in a biplot, the equation (3) is rewritten as

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

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

GGE biplot is generated by plotting ξ^*_{i1} and η^*_{1j} against ξ^*_{i2} and η^*_{2j}. Though *k* may take an infinite number of values between 0 and 1, only three values 0, 1 and 0.5 are common in use.

Stability Indices:

The AMMI model does not make provision for a quantitative stability measure, such a measure is essential in to quantify and rank genotypes according to their yield stability.

AMMI Stability Value (ASV)

The AMMI stability value (ASV) proposed by Purchase *et al*. (2000) is a useful measure to quantify and rank genotypes according to their yield stability. In the ASV method, a genotype with the least ASV score is the most stable.

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

Yield Stability Index (YSI)

An index for determining high-yielding and stable genotypes

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

where, $R_i(ASV)$ is the rank of the AMMI stability value of i^{th} genotype and $R_i(GY)$ is the rank of the mean grain yield of i^{th}genotype across all the environments. The Yield stability value incorporates both mean yield and stability in a single criterion. The low value of YSI is desirable for genotypes with high mean yield and stability.

Weighted Index (WI)

Normalized Index for mean grain yield

Let GY_idenote the value of the mean grain yield of i^{th}genotype for all the locations (i = 1, 2, ….., T), then normalized index by Hooda *et al.* (2017) of i^{th} genotype for all the locations may be obtained as follows:

$$NGY_i = \frac{GY_i - Min(GY_i)}{MAX(GY_i) - Min(GY_i)} \quad (7)$$

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

Normalized Index for AMMI Stability Value:

Let ASV_idenote the value of the AMMI Stability Value of i^{th}genotype for all the locations (i = 1, 2, ….., T) where lower the ASV more stable in the genotype then normalized index Hooda *et al.* (2017) of i^{th} genotype for all the locations may be obtained as follows:

$$NASV_i = \frac{MAX\,(ASV_i) - ASV_i}{MAX\,(ASV_i) - Min\,(ASV_i)} \quad (8)$$

where, $NASV_i$ is the normalized index of AMMI stability value, where the higher the value of NASV more stable the genotype; ASV_i is the AMMI stability value of the i^{th} genotype in all the locations and $Max(ASV_{ik})$ and $Min(ASV_{ik})$ are taken for i^{th} genotype.

The normalized values indices also lie between 0 and 1 and increase or decrease in the direction of the stability i.e. lower values imply lesser stability and higher values imply higher stability.

From the matrix of the normalized indices for grain yield and ASV indices, we propose WI for determining the high-yielding and stable genotypes given by:

$$WSI_i = w_1 NGY_i + w_2 NASV_i; i = 1, 2, \ldots T \quad (9)$$

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

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

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

The weighted index lies between zero to one. A simple ranking of genotypes based on WI is used for the stability of genotypes. Genotype with maximum WI index is most stable with high yielding. By using Spearman's rank correlation coefficient, the rank based Yield Stability Value (YSI) and Weighted Index (WI) were calculated by using ranks of respective YSI and WI to demonstrate the similarity of inference drawn from the proposed index WI and index YSI.

Sustainability Index (SI)

The sustainability index (SI) was calculated as suggested by Babarmanzoor*et al.* (2009):

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

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

On the basis of SI values, genotypes are classified into five categories as very low stability(upto 20%), low stability(21% to 40%), moderate stability(41% to 60%), high stability(61% to 80%) and vey high stability(above 80%).

Stability Index (I)

The stability Index was computed to identify their yield stability (Bajpai & Prabhakaran, 2000)

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

where,$\bar{Y}_i$is the mean performance of the i^{th} genotype,$\bar{Y}$ is the overall mean,s_i^2 is Shukla's stability variance (Shukla, 1972) of the i^{th} genotype and$S$ is the number of environments.

RESULTS AND DISCUSSIONS

In AMMI ANOVA, it was found (Table 2) that the maximum contribution towards variation (71.24%) was made by environment effect followed by G ×E interaction (14.66%) and genotypic variation (10.80%). The axes IPCA1, IPCA2 and IPCA3 were found significant

using the Gollob's *F*-test. These axes accounted for 35.19 percent, 25.42 percent and 14.66 percent of the interaction sum of squares, respectively.

Table 2: AMMI analysis of variance for Zone B pearl millet grain yield (kg/ha) data

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		

Based on the yield stability values in Table 3, G6 was found to be the most stable genotype with high yield followed by genotype G20 based on the stability index. Based on YSI value, the most stable genotypes with higher grain yield were genotypes G24 and G12. Similarly, based on a weighted index (WI), genotype G24 was found to be the most stable genotype with a higher yield followed by genotype G13. Based on observations recorded on SI (%), two groups of stable genotypes were found. Low SI (%) was recorded in Genotype G21 whereas moderate SI (%) in 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 where as moderate SI (%) G3, G15, G25, G26 and G27.

The ranks of the genotypes as per various stability indices and mean grain yield are given in parentheses. The Spearman's rank correlation coefficient between YSI and WSI was found to be 0.935 which was significant at a 1% level of significance. It shows that the two indices have almost equal performance in determining high-yielding stable genotypes.

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

Graphical presentation of stability and high grain yield of genotypes for Zone B

A quick idea about high-yielding stable genotypes can be had from the simple scatter plot of the Normalized Grain Yield (NGY) and Normalized ASV values (NASV). Figure-1 gives the scatter plot of NGY taken along the x-axis and NASV taken along the y-axis. This scatter plot represents the most stable, high-yielding and most stable with high-yielding genotype. It also observed that G20 was the most stable (on the basis of NASV), G4 was high yielding (on the basis of NGY) and G24 was most stable with high yielding.

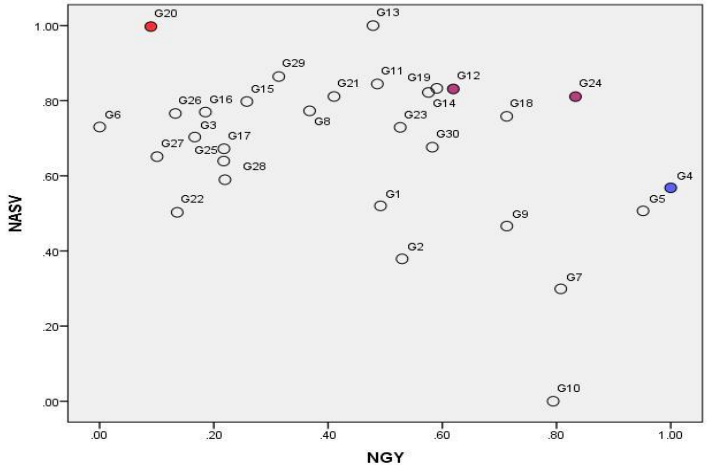

Figure 1. Graphical presentation of stability and high grain yield of genotypes for Zone B

GGE biplots for Zone B

The analysis of genotypic environment data (*i.e.* MET data) included the following major three aspects:

i) Mega-environment analysis based on genetic correlation between location and the which-won-where pattern.
ii) Test location evaluation based on their discriminating ability and representativeness.
iii) Genotype evaluation based on their mean performance and stability across a mega-environment.

Mega-environment analysis for Zone B

In this biplot (Figure 2), a polygon is drawn between the genotype vector farthest from the origin (where zero interacts with the x and y axes) and lines are drawn perpendicularly from the biplot origin to each of the sides of polygon. The additional information is about both the genotypes and environments by division of the total trial area into homogeneous groups with respect to genotype performance. An irregular convex polygon has been formed such that all genotypes come inside the polygon. When one or more environments are located within one of the sectors formed by the perpendicular lines, genotypes which share that sector perform better there, and the best-performing genotypes are located at the vertices of these sectors. So, the total environment was divided into different sectors which have their superior genotypes. The superior genotype is called the winner genotype in the respective sector. Likewise genotypes without environment in their sector are not expected to perform better in any of the tested environments and the poorest performing genotypes will be located at the vertices of these sectors.

The "which won where" biplot (Figure 2) for Zone B pearl millet data identified PMP forming one mega environment, PLM, APR, ABD1, BUL, CBE, MLR, PCR, DHL ABD5 and ABD2forminga second mega environment and VYP forming third mega environment. The genotypes G1 (MH2103), G4 (MH2106) and G19 (MH2119) have been observed to be the winner genotypes in the respective mega environments.

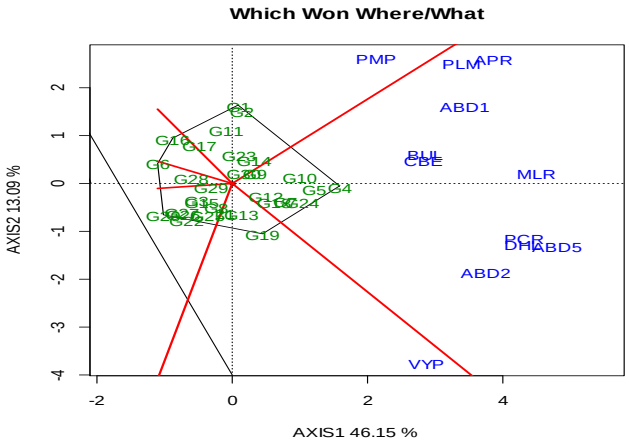

Figure 2. Mega-environments analysis for zone B

Test-environment evaluation for Zone B

The main motto of the breeding program is to extract more and more information about genotypes and environments. It remains always in mind that the trials are conducted are in proper environment and in sufficient numbers for efficient conduction of experiment to improve the efficiency of the experiment the environments where trials are conducted are evaluated in terms of their representativeness and discriminativeness.

The relationship among environments was evaluated by correlation i.e. by angle between them as examined in Figure 3. So for evaluation of representativeness, the target environment was plotted by taking an average of all environments and the angle between the target and test environment indicates the representativeness of the experiment. The discriminating property was observed by the variance of the variable (environment), the more the variance of environment more the discriminating power of environment for genotypes. Figure 3 showed that MLR had the highest representativeness of the trial while ABD5 had the highest discriminating power. VYP had low representativeness while CBE had low discriminating power. MLR was the most fruitful.

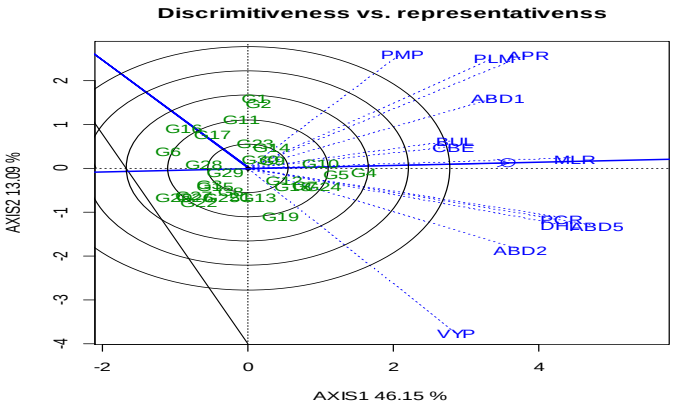

Figure 3. Test-environment evaluation for Zone B

Genotype evaluation for Zone B

For the general release of a breed evaluation of a genotype is compared with respect to the average performance and stability of the genotype. The test environment evaluation axis as formed in Figure 4 was useful in the search for such properties. The axis passing through the virtual environment is called the average environment axis (AEA) while a perpendicular axis is also overlaid on the biplot which is called the average coordination axis (AEC).

Projections of a genotype on the AEA and AEC axes are the mean yield and stability of the genotype respectively. The arrow shown on the axis of the AEC abscissa points in the direction of higher mean performance of the genotypes and consequently ranks the genotypes with respect to mean performance. Unless the genotypic effect (G) is too small to be meaningful, the ranking of the genotypes on the AEC abscissa is always perfectly or highly correlated with G. The above analysis suggested that genotypes G4 (MH2106) and G10 (MH2111) were favorable for the trial region considering both average yield and stability of genotypes. In contrast, G1 (MH2103) and G19 (MH2119) were the least stable genotypes.

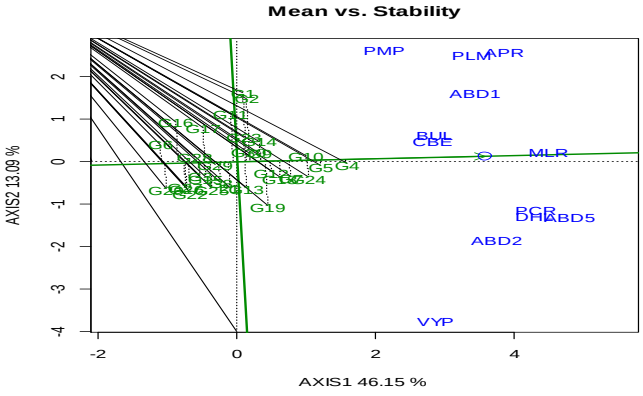

Figure 4. Genotype evaluation for Zone B

Conclusion

The AMMI model was effective for assessing GEI in pearl millet yield tests across multiple environments. The stability measurements YSI and WI showed a strong correlation and significant outcome. The AMMI Stability Value (ASV) and Stability Index have been applied to identify the most stable genotypes, while the indices YSI and WI have been applied to identify both the most stable and high-yield genotypes. Based on ASV, genotypes MH 2114, MH 2126 and MH 2128 have been identified as the most stable for Zone B.

REFERENCES

Bajpai, P.K. and Prabhakaran, V.T. 2000. A new procedure of simultaneous selection for high yielding and stable crop genotypes. *Indian Journal of Genetics and Plant Breeding*, **60**(2): 141-146.

Barbarmanzoor, A., Tariq, M.S., Ghulam, A. and Muhammad, A. 2009. Genotype x environment interaction for seed yield in Kabuli Chickpea (*Cicer arietinum* L.) genotypes developed through mutation breeding. *Pakistan Journal of Botany*, **41**: 1883-1890.

Cornelius, P.L., Seyedsadr, M. and Crossa, J. 1992. Using the shifted multiplicative model to search for "separability" in crop cultivar trials. *Theoretical and Applied Genetics*, **84**: 161-172.

Crossa, J. 1990. Statistical analyses of multilocation trials. *Advances in Agronomy*, **44**: 55–85.

Gauch, H.G. Jr. 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. *Elsevier*, Amsterdam.

Gauch, H.G. Jr. 2006. Statistical analysis of yield trials by AMMI and GGE. *Crop Science*, **46**: 1488-1500.

Gauch, H.G., Piepho, H.P. and Annicchiarico, P. 2008. Statistical analysis of yield trials by AMMI and GGE: further considerations. *Crop Science*, **48**: 866–889.

Gauch, H.G.Jr. 1988. Model selection and validation of yield trials with interaction. *Biometrics*, **44**: 705-715.

Gollob, H.F. 1968. A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, **33**: 73-115.

Hooda, E., Hooda, B.K. and Manocha, V. 2017. Dynamics of inter-district developmental disparities in Haryana. *Journal of Applied and Natural Science*, **9**(2): 983-991.

Kempton, R.A. 1984.The use of biplots in interpreting variety by environment interactions. *Journal of Agricultural Science*, **103**: 123-135.

Kumar, B. 2017. Biplots and Their Application in Multi-environment Trials Data Analysis. M.ScThesis (unpublished) submitted to the Chaudhary Charan Singh Haryana Agricultural University, Hisar.

Mamata, Hooda, B.K. and Hood, E. 2019. A new index for evaluation of G×E interaction in pearl millet using AMMI and GGE biplot analyses. *Indian Journal of Agricultural Research*, **53**(5): 529-535.

Purchase, J.L., Hatting, H. and Van, D.C.S. 2000. Genotype x Environment interaction of winter wheat (T. aestivum) in South Africa: stability analysis of yield performance. *South African Journal of Plant and Soil*, **17**: 101-107.

Rao, A.R. and Prabhakaran, V.T. 2005. Use of AMMI in Simultaneous Selection of Genotypes for Yield and Stability. *Journal of Indian Society of Agricultural Statistics*, **59**(1): 76-82.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype environmental components of variability. *Heredity*, **29**: 237-245.

Yan, W. and Kang, M.S. 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton.

Yan, W., Hunt, L.A., Sheng, Q. and Szlavnics, Z. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Science*, **40**: 597–605.

Yan, W., Kang, M.S., Ma, B.L., Woods, S. and Cornelius, P.L. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science*, **47**: 643–653.

Yang, R.C., Crossa, J., Cornelius, P.L. and Burgueno, J. 2009. Biplot analysis of genotype environment interaction: proceed with caution. *Crop Science*, **49**: 1564–1576.