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AMMI AND GGE BIPLOT ANALYSES FOR EVALUATION OF G×E INTERACTION IN PEARL MILLET

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Abstract

The necessary increase in agricultural production represents a huge challenge to local farming systems and must come mainly from increased yield per unit area, given the limited scope for extension of cultivated land worldwide. To meet this requirement various crop improvement programmes all over the world have been initiated. Under any crop improvement programme of important steps here is to assess the performance of improved genotypes in multi-environment trials. Often it is observed that varieties perform differently in different environments. This variation, arising from the lack of correspondence between the genetic and non-genetic effects is known as the genotype environment interaction(G×E). Based on climatic conditions, the pearl millet cultivation in India is divided in 3 major zones - A1, A and B for effective evaluation of the pearl millet breeding material. In the present study, the G×E interaction in pearl millet genotypes from zone-A1 of India have been evaluated using the techniques of AMMI and GGE biplot analysis. A new Weighted Stability Index (WSI) has been proposed for determining the high yielding and stable genotypes based on the normalized indices for grain yield and ASV indices.Three interaction principal component axes (IPCA1, IPCA2 and IPCA3) have been found to be significant in this zone. AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes while indices YSI and WI were used to find both most stable and high yielding genotypes. On the basis of ASV, genotypes MH 2091, MH 2085 and MH 2093.The Spearman's rank correlation coefficient between YSI and WSI was found to be significant at 1% level of significance indicating that the two indices have almost similar performance in determining high yielding stable genotypes.

Key words: AMMI analysis, GGE biplot analysis, G×E interaction, Stability analysis, Pearl millet and Weighted stability index.

Introduction

Pearl millet (*Pennisetum glaucum* L.) also known as bajra in Hindi, is the sixth most important rain fed cereal crop annually cultivated in arid and semi-arid areas of India. Pearl millet is a staple food for more than 90 millon farmers in arid and semi arid regions of Sub-Saharan Africa, India and South Asia. India is the largest producer of this crop, both in terms of area (7.8 mha) and production (9.25 million tons), with an average productivity of 1270kg/ha. Millet variety selection with its production environment is often challenged by the occurrence of significant genotype-by-environment interactions (GEI) in the varietal development process. In spite of millet's drought tolerance, it is largely affected by G×E interaction, making it difficult and expensive to select and recommend new millet varieties for different environments. Several statistical models have been proposed for increasing the chance of exploiting GEI and supporting breeding program decisions in variety selection and recommendation for target set of environments. Additive Main effects and Multiplicative Interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) models are among the models that effectively capture the additive (linear) and multiplicative (bilinear) components of GEI and provide meaningful interpretation of multi-environment data set in breeding programs. The AMMI model is essentially a combination of ANOVA and Principal Component Analysis (PCA). It applies PCA to the GE interaction part of the ANOVA. Because of this, the AMMI model is also called IPCA (Interaction PCA). Kempton (1984) seems to have been the first to apply AMMI to the study of GE interaction. AMMI is theoretically the most effective model to account for the GE interaction sum of squares with a minimum number of degrees of freedom. A full AMMI model (AMMI-F) equates to the ANOVA model, since all the sum of squares due to GE interaction are explained by the principal axes. AMMI with one axis is most effective, since it frequently gives the minimum predictive errors. A GGE biplot (Yan *et al*., 2000) is a biplot that displays 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 set of biplot graphs that are designed to address various research objectives when genotypes by environment two-way data are analyzed. A biplot is a scatter plot that graphically summarizes two factors in such a way that relationships among the factors and underlying interactions between them can be visualized simultaneously. To understand GEI, two types of biplot, the AMMI biplot (Crossa, 1990; Gauch, 1992) and the GGE biplot (Yan *et al*., 2000; Yan and Kang, 2003) are the most commonly used biplots. In recent literature, utility of AMMI analysis and GGE biplot analysis to visualize and interpret multilocational

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trials data is being widely debated (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 cumulative measure of genotype main effect (G), environment main effect (E) and the GE interaction (Yan and Kang, 2003). The application of AMMI and GGE biplot analyses in evaluation of G×E in pearl millet (Mamata *et al*., 2019). The pearl millet cultivation in India is divided in 3 major zones-A1, A and B for effective evaluation of the pearl millet breeding material. In the present study, the G×E interaction in pearl millet genotypes from zone-A of India have been evaluated using the techniques of AMMI and GGE biplot analysis. AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes while indices YSI and WI have been used to find both the most stable and high yielding genotypes. A new weighted index (WI) have been proposed for determining the high yielding and stable genotypes based on the normalized indices for grain yield and ASV indices.

Materials and Methods

The yield data for the present study were obtained from the annual report of AICRP on pearl millet for the year of 2015-16. Based on climatic conditions, the pearl millet cultivation in the country is divided in 3 major zones-A1, A and B. The zone-A1 includes 9 pearl millet growing locations which receive less that 400mm of annual rainfall. For this study, data on 24 early type genotypes of pearl millet evaluated at 9 locations Mandor (MDR), Jodhpur (JDR), Bikaner (BKR), Lalawas (LWS), Jaipur (JPR), Kothara (KTR), S.K. Nagar (SKN), Hisar (HSR), Bawal (BWL) in a randomized complete block design with three replications have been used (Table 1).

AMMI and GGE Biplot Models: The AMMI analysis is a combination of analysis of variance and multiplication effect analysis. The AMMI model (Rao and Prabhakaran, 2005) for *G* genotypes and *L* environments is below.

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

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

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.

a_{in}=and g_n are the i^{th} genotype j^{th} environment PCA scores for the axis *n*

q_{ij}= residual

n' = number of PCA axes retained in the model

The residual combines the PC 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 $\lambda_1 > \lambda_2 > \cdots\cdots > \lambda_{n'} > 0$

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 square of the corresponding eigen value 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 rank two matrix. With above notations, the basic model for constructing a GGE biplot from GE data is given by

$$Y_{ij} = \mu + g_i + e_j + \phi_{ij} + \theta_{ij}$$

Where,f_{ij} interaction between g_i and e_j and q_{ij} the residual of the model associated with the genotype *i* in enjronment *j*. The GGE (i.e. grand mean and environment centered) biplot can also be represented mathematically as

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

Where,

Y_{ij} is the average yield of genotype *i* in environment *j*

Y_j is the average yield over all genotypes in environment *j*

l_1 and $_2$ are the singular values for PC_1 and PC_2 respectively

z_{i1} and z_{i2} are the PC_1 and PC_2 scores, respectively for genotype *I*

h_{1j} and h_{2j} are the PC1 and PC2 scores, respectively for environment *j*

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

Where,

$$z^*_{in} = l_n^{\,k} z_{in} \text{ and } h^*_{nj} = l_n^{\,1-k} h_{nj} \text{ with } n = 1, 2$$

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

Weighted Stability Index (WSI): The AMMI model does not provide a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according to their yield stability. 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 ASV method, a genotype with the least ASV score is the most stable and is given by

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

An index for determining high yielding and stable genotypes, called yield Stability Index (YSI) is given by

$$YSI = R(ASV)_i + R(GY)_i \qquad (6)$$

Where, $R(ASV)_i$ is the rank of the AMMI stability value of i^{th} genotype and $R(GY)_i$ is the rank of the mean grain yield of i^{th} genotype across environments. The Yield stability value (YSI) incorporates both mean yield and stability in a single criterion. Low value of YSI parameter show desirable genotypes with high mean yield and stability.

Let GY_i denote the value of the mean grain yield of i^{th} genotype for all the locations ($i = 1, 2,\ldots,G$), then normalized index by Hooda et al. (2017) of i^{th} genotype for all the locations may be obtained as

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

Where, *GYi* is the mean grain yield of the *i*th genotype in all the locations and *Max* (*GYi*) and *Min* (*GYi*) are taken for *i*th genotype.

Also, let *ASVi* denote the value of the AMMI Stability Value of *i*th genotype for all the locations ($i = 1, 2,\ldots, G$) 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 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, we propose the following weighted stability index (WSI) for determining the high yielding and stable genotypes

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

Here, ($0 \le W_1, W_2 \le 1$ and $W_1 + W_2 = 1$) are the weights associated with the *NGY* and *NASV* and the weights W_1 and W_2 are given by as

$$W1 = \frac{s_2}{s_1 + s_2} \text{ and } W2 = \frac{s_1}{s_1 + s_2}$$

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 used for stability of genotype. 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) was calculated by using ranks of respective YSI and WI to demonstrate the similarity of inference drawn from the proposed index WI and index YSI.

Results and Discussion

The AMMI ANOVA (Table 2) indicates that maximum contribution towards variation (76.51%) was made by environment effect followed by G×E interaction (16.50%) and genotypic variation (6.77%). The axes IPCA1, IPCA2 and IPCA3 were found significant using the Gollob's F-test. These axes accounted for 31.98 percent, 20.16 percent and 14.11 percent of the interaction sum of squares, respectively.

Based on the yield stability values (Table 3), the genotype G6 was found to be the most stable genotype with high yield followed by genotype G3 on the basis of stability index. Based on YSI value, the most stable genotypes with higher grain yield were found to be G23 and G12. Similarly, based on weighted index (WI), G23 was found to be most stable genotype with higher yield followed by genotype G5. On the basis of SI values, only two groups of stable genotypes were found. Very low SI (%) was recorded in Genotypes G3, G7, G8, G16, G21 and G22 whereas low SI (%) in G1, G2, G4, G5, G6, G9, G10, G11, G12, G13, G14, G15, G17, G18, G19, G20, G23 and G24.

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 0.918 which was significant at 1% level of significance. It shows that the two indices have almost equal performance in determining high yielding stable genotypes.

Graphical presentation of stability and high grain yield of genotypes for Zone A1

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 x-axis and NASV taken along y-axis. This scatter plot represents most stable, high yielding and most stable with high yielding genotype. It also observed that G6 was most stable (on the basis of NASV), G20 was high yielding (on the basis of NGY) and G23 was most stable with high yielding.

GGE biplots for Zone A pearl millet genotypes included the following major three aspects:

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

Mega-environment analysis for Zone A1

Visualisation of the "which-won-where" pattern of MEYT's data is important for studying the possible existence of different mega-environments (ME) in a region. Since the mega-environment is defined as group of environment that consistently share the best set of genotypes across environments. Figure 2 represents column metric preserving GGE biplot. The data indicates genotype environment yield data.

In "which-won-where" (Figure 2) biplot, a polygon was drawn between the genotype vector farthest from origin, and lines drawn perpendicularly from the biplot origin to each sides of polygon. Now if perpendicular lines on the side of polygon are imagined as virtual environment then the two genotypes over which the perpendicular line *i.e.* virtual environment has been drawn perform equally since they have equal projections on the virtual environment. Any deviation in environment from this virtual line or environment makes one of winner genotype interact more than other towards which we lean the environment. The additional information about both the genotypes and environments was obtained by division of 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. One or more environments located within one of the sectors formed by the perpendicular lines, the genotype which share that sector perform better in that particular sector, and the best performing genotypes were located at the vertices of these sectors. So, the total environment got divided into different sectors which have their own superior genotypes which are known as winner genotypes. Likewise, genotypes without environment were not expected to perform better in any of the tested environments and the poorest performing genotypes were located at the vertices of these sectors. The "which won where" biplot (Figure 2) for Zone A1 pearl millet data identified LWS, SKN and JPR forming one mega environment, KTR, MDR, HSR, BWL and JDR forming second mega environment and BKR forming third mega environment. The genotypes G8 (MH2087), G20 (MH2098) and G1 (MH2081) have been observed to be the winner genotypes in the respective mega environments.

Test-environment evaluation for Zone A1

The relationship among the environments is evaluated by correlation value measured by the cosine of the angle between them as shown in Figure 3. So, for evaluation of representativeness, target environment is depicted as arrow on AEC by taking average of all environments and angle between target and test environment is representativeness of one another. The discriminating property is observed by the variance of the variable (environment). More the variance of environment more is the discriminating power of environment for genotypes. It was observed that MDR highest representativeness of the trial while JPR had the highest discriminating power. BKR had low representativeness as well as low discriminating power. The environment MDR was observed to be the most fruitful trial while BKR the least fruitful trial.

Genotype evaluation for Zone A1

Breeding programs have main focus on enhancement of agricultural production and search of superior genotypes. Varieties are evaluated not only by performances in a mega-environment but also by mean yield of genotypes along with their stability for general recommendation of cultivar in experimental region. For general release as a breed, evaluation of a genotype is performed with respect to average performance and stability of all genotypes.

The test environment evaluation axis (Figure 4) is helpful in evaluation of genotypes. The axis passing through this virtual environment is called average environment axis (AEA) while a perpendicular axis is also overlaid on biplot which is called average coordination axis (AEC). 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 Fig 4 indicates that the genotypes G12 (MH2091) and G17 (MH2095) were favourable for the trial region in view of both average yield and stability of genotypes. In contrast, G8 (MH2087) and G2 (MH2082) were least stable genotypes.

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Table 1: Mean grain yield (kg/ha) of twenty four Pearl millet genotypes evaluated at nine locations of Zone A1 during 2015-16

Genotype	Entry	MDR	JDR	BKR	LWS	JPR	KTR	SKN	HSR	BWL
G1	MH 2081	2755	2620	1605	3667	1464	1241	1239	3911	3877
G2	MH 2082	2902	3370	1424	4222	1828	1213	1933	6353	3586
G3	MH 2083	1477	1594	1261	4333	939	1106	1351	3032	2222
G4	MH 2084	2968	2728	822	3444	1661	1514	1340	4543	3938
G5	RHB 177	2924	2029	843	4611	2028	1995	2325	4518	3846
G6	MH 2085	2625	1941	789	3111	900	1102	1343	2947	1704
G7	MH 2086	2264	1486	1225	5333	1422	1454	1817	3265	1858
G8	MH 2087	3275	233	1288	5944	2333	2083	3207	4962	3691
G9	MH 2088	3139	2807	1499	3500	2239	1824	3204	4878	3173
G10	MH 2089	3216	2919	1520	3833	1450	1583	3433	5541	3401
G11	MH 2090	3292	2775	1055	3611	2125	1875	2610	4359	2914
G12	MH 2091	3338	2466	572	4611	1944	1699	2109	4269	3920
G13	MH 2092	2951	2437	876	4667	2214	1569	2778	4926	2475
G14	HHB 67	2676	2313	608	3611	1556	1287	2338	3670	3191
G15	MH 2093	3183	2736	788	4056	1717	1551	2526	3849	3124
G16	MH 2094	3000	2179	611	5222	2097	1278	2555	5403	2173
G17	MH 2095	2852	3430	599	4444	2122	1435	3242	3292	3648
G18	MH 2096	2903	2860	437	5833	2028	1912	2102	4178	3994
G19	MH 2097	3391	2865	578	5556	2450	1620	3107	4593	3019
G20	MH 2098	3380	3485	668	4444	2672	1935	2814	5934	4537
G21	MH 2099	2414	3951	451	4667	1267	1593	2478	4669	3821
G22	MH 2100	3074	2672	518	5778	1836	1278	2428	4306	2852
G23	MH 2101	3597	3604	1430	5222	1783	1778	2058	4984	3370
G24	MH 2102	2706	2365	1673	4889	850	1208	1356	3583	4167

Table 2: AMMI analysis of variance for Zone A1 pearl millet grain yield (kg/ha) data

Source	D.F	Sum of squares	Mean square	F_{cal}	Sum of squares (%)
Genotype	23	25393273.25	1104055.70	3.282**	6.77
Environment	8	287615207.50	35951900.93	106.90**	76.71
G×E interaction	184	61881151.24	336310.60	1.61**	16.50
IPCA1	30	19790994.70	659699.82	3.16**	31.98
IPCA2	28	12479717.12	445704.18	2.135**	20.16
IPCA3	26	8737159.37	336044.59	1.610*	14.11
Residual	100	20873280.03	208732.80		
Total	215	374 889632	1743672.70		

Table 3: Yield-stability indices for Zone A1

Genotype	GY	ASV	YSI	I	WI	SI(%)	SIG
G1	2487(20)	28.05(18)	38(21)	656770.3(5)	0.50(20)	34.46	Low
G2	2981(6)	31.73(22)	28(16)	787423.8(19)	0.64(16)	21.17	Low
G3	1924(23)	22.75(14)	37(19)	508152.8(2)	0.36(23)	18.81	Very low
G4	2551(18)	29.84(20)	38(22)	673760.9(7)	0.51(19)	27.86	Low
G5	2791(10)	6.36(4)	14(3)	737181(15)	0.81(3)	32.64	Low

G6	1829(24)	6.01(2)	26(14)	483119.4(1)	0.49(21)	30.35	Low
G7	2236(22)	41.68(23)	45(24)	590590(3)	0.29(24)	17.27	Very low
G8	3002(4)	57.23(24)	28(17)	792853.1(21)	0.40(22)	20.77	Very low
G9	2918(7)	21.87(12)	19(8)	770754.5(18)	0.71(10)	39.25	Low
G10	2988(5)	25.80(16)	21(10)	789331.4(20)	0.69(11)	29.93	Low
G11	2735(15)	15(8)	23(13)	722419.2(10)	0.71(9)	40.24	Low
G12	2770(12)	5.55(1)	13(2)	731575.6(13)	0.81(2)	30.90	Low
G13	2766(13)	19.07(9)	22(11)	730548.4(12)	0.68(12)	29.47	Low
G14	2361(21)	9.11(6)	27(15)	623635.4(4)	0.64(14)	35.53	Low
G15	2614(17)	6.26(3)	20(9)	690547.7(8)	0.75(7)	37.62	Low
G16	2724(16)	30.54(21)	37(20)	719543(9)	0.56(17)	20.38	Very low
G17	2785(11)	10.56(7)	18(5)	735566.8(14)	0.77(5)	35.78	Low
G18	2916(8)	19.96(10)	18(6)	770284.9(17)	0.73(8)	22.98	Low
G19	3020(3)	20.40(11)	14(4)	797636.8(22)	0.76(6)	27.87	Low
G20	3319(1)	27.30(17)	18(7)	876581.6(24)	0.79(4)	29.80	Low
G21	2812(9)	22.65(13)	22(12)	742815.5(16)	0.66(13)	27.29	Low
G22	2749(14)	22.95(15)	29(18)	726116.8(11)	0.64(15)	20.35	Very low
G23	3092(2)	7.63(5)	7(1)	816624.6(23)	0.90(1)	32.14	Low
G24	2533(19)	29.01(19)	38(23)	669035.8(6)	0.51(18)	22.80	Low

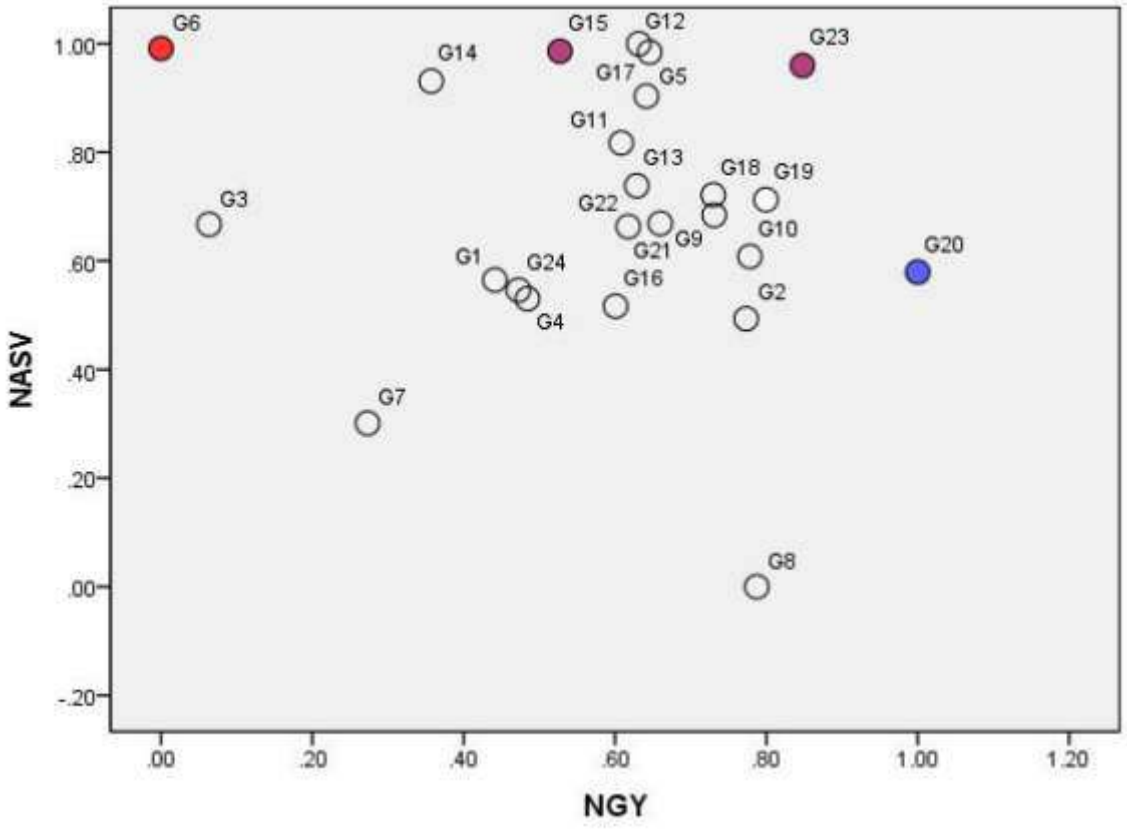

Figure 1: Graphical presentation of stability and high grain yield of genotypes for Zone A1

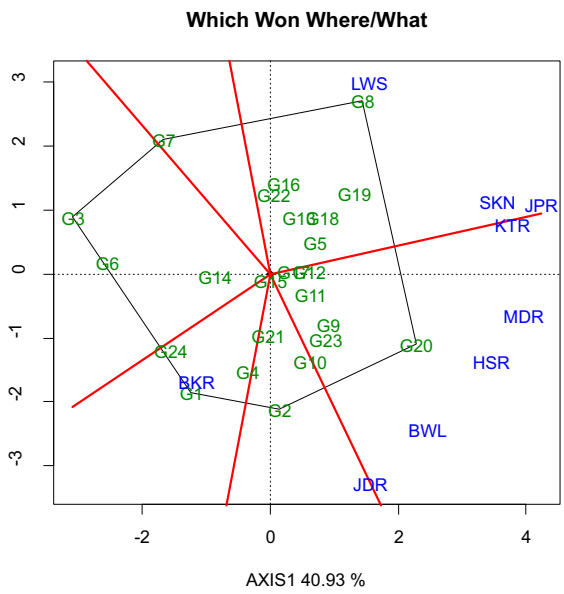

Figure 2: Mega-environment analysis for Zone A1

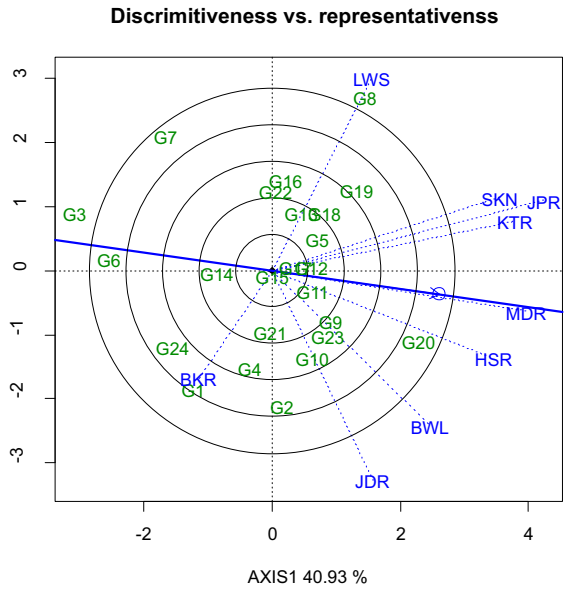

Figure 3: Test-environment evaluation for Zone A1

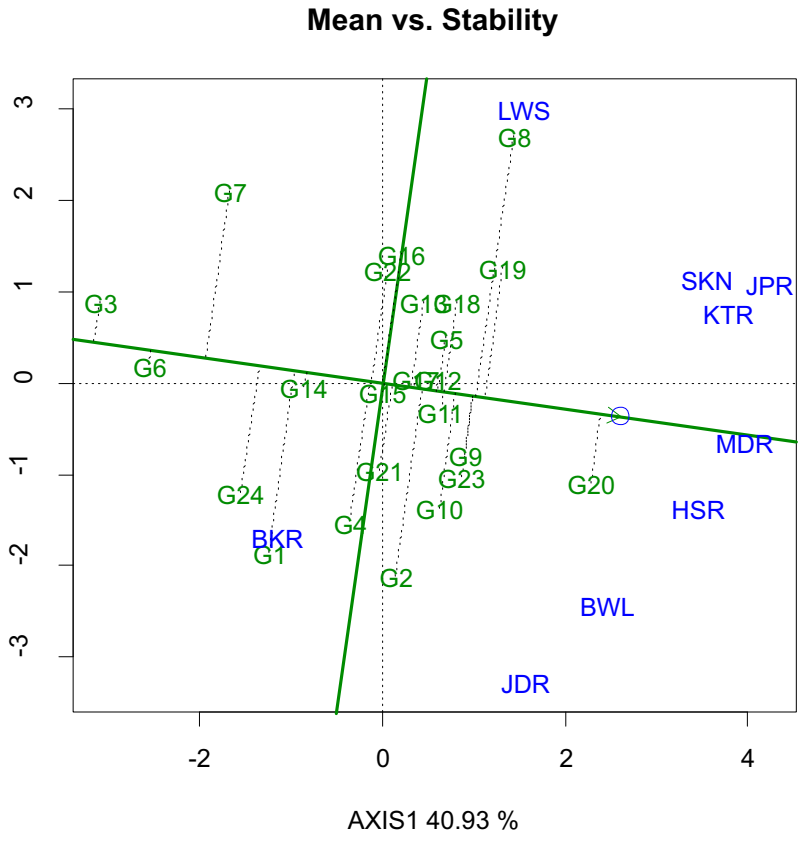

Figure 4: Genotype evaluation for Zone A1