GGE Biplot Analysis in Mung Bean (*Vigna radiate*) Genotypes for Seed Yield under Zone-IIa in Rajasthan-India

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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

The goal of this research have become to assess and to quantify the significance of the Genotype × Environmental interplay effects on mung bean seed yield and to determine the triumphing genotype for the test environments. Sixteen mung bean genotypes have been examined at one region for over 3 years (2019, 2020 and 2021). The seed yield information for each year modified into first subjected to evaluation of variance the usage of generalized linear version. Mean seed yields of genotypes for the environments had been computed to generate a genotype and Environmental 3-way desk records for the GGE Biplot evaluation. The assessment located the presence of massive genotype x Environmental interactions for seed yield. Year effect described greater than 89.11% of the whole seed yield version. GGE Biplot analysis depicted the model sample of genotypes at three years at same region. RMG-1132, RMG-1139 and RMG-1147 established to have the capability of blending immoderate yield with strong basic overall performance, can be encouraged for manufacturing in mung bean developing regions inside the Rajasthan.

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1. INTRODUCTION

"Mung bean (*Vigna radiate*) is a warmness season annual seed legume. The maximum appropriate temperature variety for right manufacturing is 27- 30°C" [1]. "Mung bean is a brief crop, requiring 75–90 days to mature. Its miles a beneficial crop in drier regions and has an amazing potential for crop rotation and relay cropping with cereals the usage of residual moisture. Smallholder farmers in drier marginal environments in Rajasthan (India) expand mung bean. But, for useful resource negative farmers in drier marginal environments it's been a vital seed legume. Those farmers need a ramification that is of most manufacturing and robust yield of their environments. In such genotype/range assessment trials, Genotype × Environmental interplay (GEI) is a commonplace phenomenon" [2-4]. "GEI refers to the differential rating of genotype amongst places or years" [5]. "It is able to complicate the process of selection and recommendation of superior genotypes to goal environments" [6,7]. "It may additionally reduce the performance of breeding packages" [8]. "This is because of the fact within the presence of GEI, yield is a great deal much less predictable and can't be interpreted as based totally on genotype and environmental way by myself" [7]. "It is also one of the important reasons for the failure of formal breeding to serve small aid-horrible farmers inside the marginal fragile environments" [4]. "But, scientists around the world have been in search of to make the most GEI as opposed to ignoring it. The use of statistical fashions to offer a cause of GEI and facilitate cultivar pointers is maximum of the techniques followed through clinical corporations. The diverse statistical methodologies were significantly reviewed and published" [9-14]. "The exceptional methodologies have been extensively categorized as univariate parametric/non-parametric and multivariate parametric. Parametric analyses are primarily based on statistical assumptions regarding the distribution of genotypic, environmental and GEI effects. Parametric measures of phenotypic stability are generally associated with variance additives or related statistics. These balance estimates are of appropriate houses below sure statistical assumptions as based totally on the regular distribution of errors and interaction outcomes, however might not perform properly if these assumptions are violated through such elements because the presence of outliners. The

alternative, nonparametric or analytical clustering makes no precise modelling assumptions at the same time as touching on environments and phenotypes. Several strategies had been proposed based totally on comparing the ranks of genotypes in every surroundings, with genotypes of similar score, throughout environments, being considered as strong" [14]. "The multivariate strategies embody maximum essential detail (PC), Additive predominant outcomes and Multiplicative Interactions (AMMI) similarly to Genotype plus Genotype × environment interaction (GGE) assessment" [14-16]. Precise debts on notable fashions had been given by way of awesome authors [10,15-17]. "Greater these days, GGE Biplot which show each genotypes and environments as primarily based on web page Regression (SREG) version have been recommended to explain GEI sample" [18,19]. "GGE Biplot captures every genotype essential consequences and genotype x environmental interplay results, which might be two important resources of versions relevant to genotype evaluation" [20]. The targets of this have a look at were to assess and to quantify the significance of the GEI and describe the which-received-in which sample the use of GGE Biplot.

2. MATERIALS AND METHODS

Statistics analysed on this check become obtained from mung bean multiyear trial, carried out for three years in *Kharif* season (2019, 2020 and 2021) at Agricultural Reaearch Station, Fatehpur-Shekhawati, Sikar (Rajasthan)-India. It's far placed among 270 75' 04.01'' N to 270 55'43.59'' N range and 740 50 8' 47.47''E to 740 49'45.97 E longitude with an altitude of 321 to 330 meter above suggest sea diploma. The common rainfall is 300-350 mm, that is particularly received within the month of July to August. The temperature goes as immoderate as 48^{0}C in summer time and as little as -5.2^{0}C in winters. It comes to the agro-climatic zone- IIa (Transitional plains of Inland Drainage) covering geographical region of 36.9 lakh hectares unfold over Sikar, Jhunjhunu, Nagaur and some part of Churu districts (34 tehsils fall in the location), which represents 10.6 consistent with cent of the whole place of the Rajasthan, country -India. Sixteen genotypes *Viz.*, RMG-492, RMG-975, IPM-02-3, MSJ-118, RMG-1087, RMG-1094, RMG-1098, RMG-1132, RMG-1134, RMG-1137, RMG-1138, RMG-1139, RMG-1147, RMG-1148, RMG -1152 and RMG-1154 of mung bean have

been acquired from All India Coordinated Research Project on MULLaRP, RARI, Durgapur (Jaipur) Rajasthan. Every genotype changed into given in a six row plot of 4 m duration with a spacing of 30 cm among rows and 10 cm between plants. Ten plants had been determined on at random from every plot and data end up recorded on seed yield at harvesting stage in *Kharif,* 2019, 2020 and 2021 using randomized complete block layout replicated thrice instances. The applicable 4 rows have been harvested for seed yield assessment. Seed yield become adjusted for 9-10 % seed moisture earlier than conversion to kg ha^{-1} for statistical evaluation.

2.1 Statistical Analysis

The evaluation of variance end up finished the usage of a SAS PROC GLM system in SAS version nine.1 [21]. The steady impact 3-manner evaluation of Variance (ANOVA) model that consists of additive phrases for the main outcomes of replications, blocks, genotypes and year. The ANOVA version hired for an assessment of the facts is:

$$X_{ijk}=\mu+G_i+L_j+Y_k+(GL)_{ij}+(GY)_{ik}+(LY)_{jk}+(GLY)_{ijk}$$

Where in X_{ijk} is the imply yield over r replications of the ith genotype within the jth location (year), with the right hand facet of the equation giving grand mean yield μ and respective main and interplay consequences of the genotypes, one place and years. The importance of variance components changed into computed as the share of general variation to discover how the principle and interplay results explain the versions in seed yield. Endorse seed yields of genotypes for the combinations of the one place and three years, handled as three environments (as use different year environmental condition) have been computed to generate a genotype and environment - way table facts for the Biplot assessment. The GGE Biplot software [22] was employed to generate graphs displaying (i) "which-gained-wherein" sample, (ii) ranking of genotypes on the basis of seed yield and stability and (iii) an assessment of take a look at environments/years [23].

3. RESULTS AND DISCUSSION

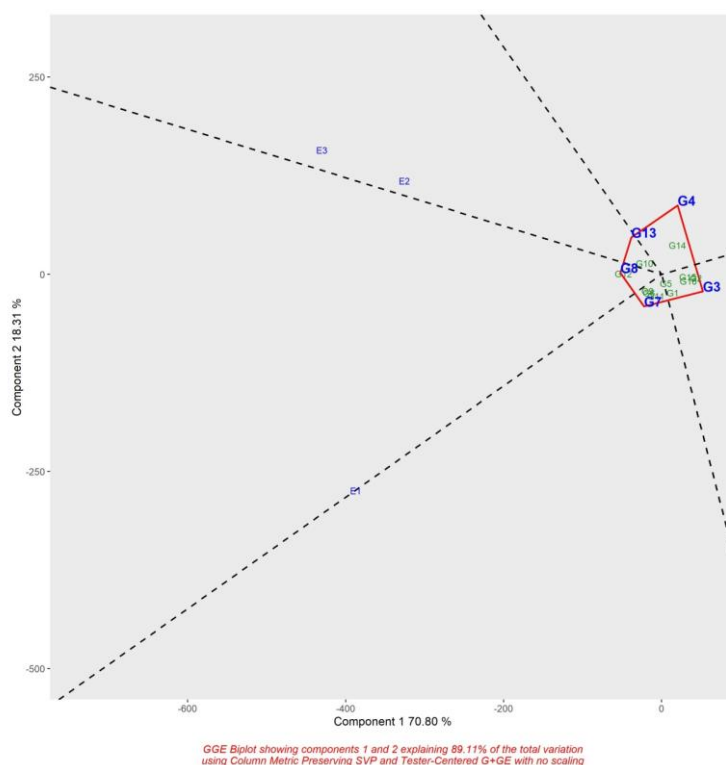The effects from assessment of variance (Table 1) located out huge (P< zero.05) genotype x environment interplay. The surroundings impact emerges as rather considerable (P< 0.01). The genotypes, location and years' predominant impact as well as Genotype x Year (GY) interactions had been pretty good sized (P< 0.01). The interaction consequences for Genotype x location (GL) and Genotype x Location x Year (GLY) had been considerable (P< zero.05), whereas location x year (LY) impact become not full-size. The place and year main results described maximum (as plenty as 89.11 %) of the whole model. The contribution of genotypes' number one impact in addition to GL, GY, LY and GLY interaction results regarded to be negligible. Location fundamental impact via itself explained greater than 70.80 % of the whole seed yield versions. Furthermore, the huge (P< 0.05) GL effects demonstrated that genotypes responded differently to location, confirming the importance of testing mung bean genotypes at multi-years in Rajasthan. When genotypes are tested in multi-year yield trials, a cross over genotype by environment interaction most often occurs [4]. Such an interaction results from changes in relative ranking of genotypes from one environment to another. This complicates cultivar recommendation in breeding programs. The significance of main and interaction effects for majority of the sources of yield variations in mung bean revealed the importance of further analysis for adaptation pattern, genotypes response and their stability for better exploitation of the genotype by environment interaction. Mean yield levels of different genotypes at three environments for 2019, 2020 and 2021 are depicted in Table 1. Relatively better yield was obtained in 2019 as compared with 2020 & 2021. The highest yield across environments obtained from by RMG-113 (1053 kg ha^{-1}) followed by RMG-1139 (1043 kg ha^{-1}) and RMG-1147 (1015 kg ha^{-1}).

3.1 GGE Biplot Analysis

The first two principal components explained 89.11% of the total Genotype plus Genotype by Environment (G+GE) variation (Figs. 1-3). "This demonstrated a Biplot constructed by plotting the first Principal Component (PC1) scores of genotypes and the environments against their respective scores for second Principal Component (PC2) scores adequately capturing the environment-centred data. Moreover, the large yield variation due to location justified the selection of Site Regression (SREG) analysis model for Multi- Environment (MET) data" [24]. GGE Biplot analysis was hence used for which-won-where analysis, test environment and genotype evaluation for mung bean MET data.

Table 1. Mean seed yield (kg ha^{-1}) of Mung bean genotypes tested at ARS, Fatehpur-Shekhawati, Sikar during *Kharif,* 2019 to 2021

Mung bean Genotypes	2019	2020	2021	Mean
1.RMG-492	981	648	740	790
2.RMG-975	852	574	675	700
3.IPM-02-3	861	505	647	671
4.MSJ-118	722	731	859	771
5.RMG-1087	981	671	791	814
6.RMG-1094	1074	569	960	868
7.RMG-1098	1130	782	798	903
8.RMG-1132	1130	1000	1028	1053
9.RMG-1134	1074	907	808	930
10.RMG-1137	1009	727	943	893
11.RMG-1138	1055	695	809	853
12.RMG-1139	1120	1016	994	1043
13.RMG-1147	991	1047	1007	1015
14.RMG-1148	833	671	808	771
15.RMG-1152	880	676	655	737
16.RMG-1154	889	533	750	724
Mean	974	735	830	846
C.D.	227.846	95.392	99.468	154.214
SE(m)	78.509	32.869	34.273	53.137
SE(d)	111.028	46.484	48.47	75.148
C.V.	13.963	7.751	7.156	10.88

GGE Biplot showing components 1 and 2 explaining 89.11% of the total variation using Column Metric Preserving SVP and Tester-Centered G+GE with no scaling

Fig. 1. GGE Biplot based on environment focus SPV=2 showing "which –won-where"
The environments (years) are indicated as E1 for 2019, E2 for 2020 and E3 for 202. Genotypes are denoted by G1 to G16 where G1= RMG-492, G2= RMG-975, G3= IPM-02-3, G4= MSJ-118, G5= RMG-1087, G6= RMG-1094, G7= RMG-1098, G8= RMG-1132, G9= RMG-1134, G10= RMG-1137, G11= RMG-1138, G12= RMG-1139, G13= RMG-1147, G14= RMG-1148, G15= RMG -1152 and G16= RMG-1154
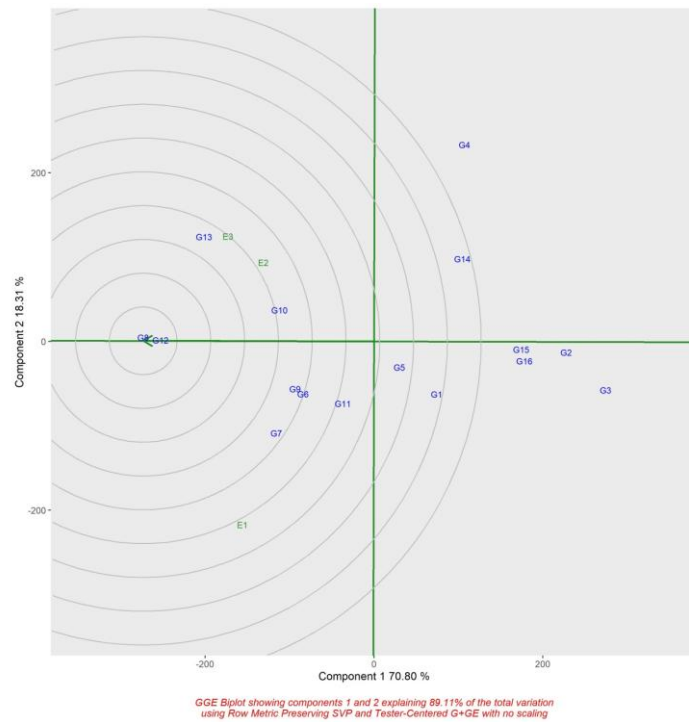
Fig. 2. The "discriminating power vs. Rep representativeness" view of the GGE Biplot.
The data were not transformed (Transform=0), not scaled (Scaling=0) and was environment centred (Centring=2). The Biplot was based on genotype focused SPV=2. Environment/year and genotype name as of Fig. 1
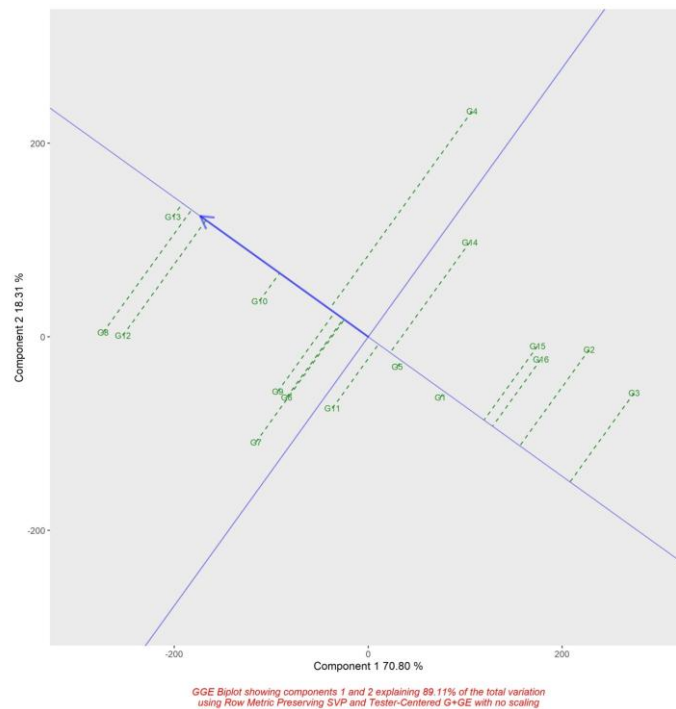
Fig. 3. The "mean vs. Stability" view of the GGE Biplot as based on genotype focused SPV=1
The data were not transformed (Transform=0), not scaled (Scaling=0) and was environment centred (Centring=2). An ideal cultivar is at the centre of the innermost circle. Environment and genotype name as of Fig. 1

3.2 Which-Won-Where

The "which-won-where" pattern of the GGE Biplot [17] is the most suitable tool for mega-environments analysis in variety trials [23]. The "which-won-where" pattern of MET data is represented by a polygon formed by connecting the markers of genotypes that are further from a biplot origin and a set of lines drawn from the biplot origin perpendicular to each side of the polygon. "The perpendicular lines to the polygon sides divide the polygon sectors, each having its own winning cultivar which is the vertex genotype for that sector" [22]. Five out of the sixteen genotypes located in the vertex formed a five-sided polygon having five possible sectors (Fig. 1). The vertex genotype for each sector is the one that yielded the highest for the environments filling within that sector. The environments fell into three sectors delineated by years 2019, 2020 and 2021 with different winning genotypes. Environment-2 (Year, 2020) stood as intermediate between the two sectors indicating the existence of one mega location classification repeatable over years for mung bean. Genotype G8 (RMG-1132) was the winning genotype at all year at one location in the suitable year 2019, 2020 and 2021. Genotype G13 (RMG-1147) was the winner genotype in cropping year 2019, 2020 and 2021.The vertex genotypes G3 (IPM-02-1), G4 (MSJ-118) and G7 (RMG-1098) had no environment in their sector. "The three genotypes were not the highest yielding ones at any of the test year as environments. G5 (RMG-1087) is located near to the plot origin and hence was less responsive than the vertex genotypes. The genotypes within the polygon and located nearer to plot origin are less responsive than vertex genotypes" [24]. "The mung bean MET data did not strongly indicate the presence of different mega-environments, which is defined as the group of location/year that consistently share the most suitable set of genotypes across years" [18]. Yan et al. [23] stressed "the need for data from multiple years to decide whether the target region can be divided into different environments at one location. It would therefore be impossible for our data set to confirm the existence of environment or years".

3.3 Test Environment/year Evaluation

"An ideal environment should be both discriminating of the genotypes and representative of the mega-environment" [23]. Fig. 2 is a GGE biplot which is based on environment-focused scaling [18], with the singular values entirely partitioned into the environment scores (SVP= 2) making it appropriate for studying the relationships among test environment. In the biplot, the line that connects the environment marker to the biplot origin is proportional to the standard deviation of the genotype mean in the environment when the data is not standardized (Scaling= 0). Environments with longer vectors are more discriminating of the genotypes whereas environments with very short vectors are little or not.

Informative on the genotype difference [18,23]. "Accordingly, environment first (2019) and Environment third (2021) provided more information regarding the genotype differences whereas environment second (2020) provided little information concerning the genotype differences. Representativeness of the test environment is visualized by the angle formed between the environment vector and abscissa of average environment axis (the line passing through the biplot origin and the average environmental coordinate). The smaller the angle, the more representative the environment is" [20,23]. The most representative location for mung bean seed yield was 2019 & 2021. The ideal test environment (characterized by the combined ability of a location to discriminate among genotypes in the study and to represent other locations in the overall environment of interest) was not very much clear with the present MET data indicating the need for more multi-location sites and annual data.

3.4 Genotype Evaluation

"An ideal genotype should possess both high mean performance and high stability within a mega-environment" [23]. In Fig. 1, the grouping of the test locations for mung bean seed yield delineate the locations by years. Year 2020 was the average environment of the trial (Fig. 2) suggesting the three years could be considered as one mega-environment. The mean performance and stability across environments/years were presented in Fig. 3. For such an evaluation Yan et al. [18] and [24] indicated the high correlation (r> 0.Ninety five) amongst genotypes' yield (averaged over environments) and their PC1 rankings as a demand. Such near-excellent correlations among genotypes seed yield and PC1 ratings might not be always met. In such times Yan and Rajcan [18] proposed an alternative, using an average surroundings coordinate device created with the

aid of way of drawing an average environments' axis line that passes thru the biplot foundation and the suggest surroundings marker for assessment of each genotypes and environments/years [25-27]. The projections of the genotype markers at the common surroundings axis are proportional to the rank-two approximation of the genotype manner representing the primary consequences of the genotypes. The arrow proven at the axis of the common environment Coordinate (AEC) abscissa points inside the direction of better suggest ordinary overall performance of the genotypes (determine-three) and, therefore ranks the genotypes with respect to intend overall performance [23]. Seed yield ranking of the genotypes as based totally on role relative to the cease of the seed-environmental axis changed into recorded as: G13 (RMG-1147), G8 (RMG-1132), G12 (RMG-1139), G10 (RMG-1137), G4 (MSJ-118), G9 (RMG-1134), G6 (RMG-1094), G7 (RMG-1098), G11 (RMG-1138), G14 (RMG-1148), G5 (RMG-1087), G1 (RMG-492) G15 (RMG-1152), G16 (RMG-1154), G2 (RMG-975) and G3 (IPM-02-3). The projection of genotype marker onto the AEC approximates the genotype stability. The stability ranking of the genotypes based on the developing absolute distinction among genotype marker and AEC axis have become G13 (RMG-1147), G8 (RMG-1132), G12 (RMG-1139), G10 (RMG-1137), G9 (RMG-1134), G6 (RMG-1094) G7 (RMG-1098), G11 (RMG-1138), G5 (RMG-1087), G1 (RMG-492), G4 (MSJ-118), G14 (RMG-1148), G15 (RMG-1152), G16 (RMG-1154), G2 (RMG-975) and G3 (IPM-02-3). RMG-1147, RMG-1132 and RMG-1139 combining a high mean seed yield with strong performance became qualified because the most suitable genotype a few of the others, evaluated for manufacturing in mung bean developing regions inside the Rajasthan-India.

4. CONCLUSIONS

Mung bean is crucial seed legume in semi-arid area of Rajasthan. It is by means of and large grown with the resource of prone and danger-averse smallholder farmers within the Rajasthan. Breeding applications have to deliver those farmers strong germplasm that in shape their wide sort of environmental conditions. This calls for attempting out of genotypes for quantification of the importance of G × E interplay, especially genotype x environmental in addition to a will power of the triumphing genotypes for the test environments. Numerous statistical strategies were proposed for growing the danger of

exploiting fine G×E interplay and helping the breeding application preference in variety choice and recommendation. GGE biplot is the diverse many that successfully quantifies G×E interaction and gives tremendous interpretation of multi-year trial information. The software of GGE biplot to mung bean multi-year seed yield trial facilitated the visible contrast and identification of the triumphing genotype in relation to Zone-IIa (Rajasthan-India) environments.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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