Original Research Article

GGE Biplot Analysis in Mung bean genotypes under Zone-IIa in Rajasthan

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Abstract:

The objective of this research was to evaluate and to quantify the magnitude of the Genotype × environment interaction effects on mung bean seed yield and to determine the winning genotype for the test environments. Sixteen mung bean genotypes were tested at one location for over three years. The seed yield data for each year was first subjected to analysis of variance using generalized linear model. Mean seed yields of genotypes for the environments were computed to generate a genotype and environment three-way table data for the GGE Biplot analysis. The analysis revealed the presence of significant genotype x environment interactions for seed yield. Year effect explained more than 89.11% of the total seed yield variation. GGE Biplot analysis depicted the adaptation pattern of genotypes at various years at one location. RMG-1132, RMG-1139 and RMG-1147 shown to have the potential of combining high yield with stable performance, can be recommended for production in mung bean growing regions in the Rajasthan.

Keywords: GGE Biplot, Mung bean, RMG, Yield stability.

Introduction:

Mung bean (*Vigna radiate*) is a warm season annual seed legume. The optimum temperature range for good production is 27- 30°C (Imrie, 1998). Mung bean is a quick crop, requiring 75–90 days to mature. It is a useful crop in drier areas and has a good potential for crop rotation and relay cropping with cereals using residual moisture. Smallholder farmers in drier marginal environments in Rajasthan grow mung bean. However, for resource poor farmers in drier marginal environments it has been an important seed legume. These farmers need a variety that is of maximum production and stable yield in their environments. In such genotype/variety evaluation trials, Genotype × Environment Interaction (GEI) is a common phenomenon (Kang and Gauch, 1996; Yan and Kang, 2003; Ceccarelli *et al.*, 2006). GEI refers to the differential ranking of genotype among locations or years (Fernandez, 1991). It may complicate the process of selection and recommendation of superior genotypes to target environments (Magari and Kang, 1993; Ebdon and Gauch, 2002). It may also reduce the efficiency of breeding programs (Comstock and Moll, 1963). This is because in the presence of GEI, yield is less predictable and cannot be interpreted as based on genotype and environmental means alone (Ebdon and Gauch, 2002). It is also one of the main reasons for the failure of formal breeding to serve small resource-poor farmers in the marginal fragile environments (Ceccarelli *et al.,* 2006). However, scientist around the globe have been trying to exploit GEI rather than ignoring it. The use of statistical models to explain GEI and facilitate cultivar recommendations is among the strategies adopted by scientific communities. The various statistical methodologies have been extensively reviewed and published (Lin *et al.,* 1986; Becker and Leon, 1988; Crossa, 1990; Flores *et al.,* 1998; Hussein *et al.,* 2000; Ferreira *et al.,* 2006). The different methodologies have been broadly classified as univariate parametric/non-parametric and multivariate parametric. Parametric analyses are based on statistical assumptions regarding the distribution of genotypic, environmental and GEI effects. Parametric measures of phenotypic stability are mostly related to variance components or related statistics. These stability estimates are of suitable properties under certain statistical assumptions as based on the normal distribution of errors and interaction effects, but may not perform well if these assumptions are violated by such factors as the presence of outliners. The alternative, nonparametric or analytical clustering makes no specific modelling assumptions when relating environments and phenotypes. Several procedures have been proposed based on comparing the ranks of genotypes in each environment, with genotypes of similar ranking, across environments, being considered as stable (Ferreira *et al.,* 2006). The multivariate methods include Principal Component (PC), Additive Main effects and Multiplicative Interactions (AMMI) as well as Genotype plus Genotype × Environment interaction (GGE) analysis (Ferreira *et al.,* 2006, Zoble *et al.,* 1998; Gauch, 2006). Detailed accounts on different models have been given by different authors (Becker and Leon,1988; Zobel *et al.,* 1998; Gauch, 2006; Yan *et al.,*2007). More recently, GGE Biplot which show both genotypes and environments as based on Site Regression (SREG) model have been advocated to describe GEI pattern (Yan and Tinker, 2006; Yan *et al.,* 2007). GGE Biplot captures both genotype main effects and genotype x environment interaction effects, which are two important sources of variations relevant to genotype evaluation (Yan *et al.,* 2001). The objectives of this study were to evaluate and to quantify the magnitude of the GEI and describe the which-won-where pattern using GGE Biplot.

Materials and Methods:

Data analysed in this study was obtained from mung bean multi location trial, conducted for three years (2019, 2020 and 2021) at Agricultural Research Station, Fatehpur-Shekhawati, Sikar (Rajasthan). It is situated between 27^0 57’ 04.01’’ N to 27^0 55’43.59’’ N latitude and

74^0 58’ 47.47’’E to 74^0 59’45.97 E longitude with an altitude of 321 to 330 meter above mean sea level. The average rainfall is 300-350mm, which is mainly received in the month of July to August. The temperature goes as high as 48^0C in summer and as low as -5.2^0 in winters. The It comes under the agro-climatic Zone IIa (*Transitional Plain of Inland Drainage*) covering geographical area of 36.9 lakh hectares spread over Sikar, Jhunjhunu, Nagaur and eastern part of Churu districts (34 tehsils fall in the zone), which represents 10.6 per cent of the total area of the Rajasthan state (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 were obtained from All India Coordinated Research Project on MULLaRP, RARI, Durgapur (Jaipur). Each genotype was given in a six row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. Ten plants were selected at random from each plot and data was recorded on seed yield during *Kharif*, 2019 to *Kharif*, 2021 using randomized complete block design replicated three times. The central four rows were harvested for seed yield assessment. Grain yield was adjusted for 9-10 % seed moisture before conversion to kg ha^{-1} for statistical analysis.

Statistical Analysis:

The analysis of variance was performed using a SAS PROC GLM procedure in SAS version 9.1 (SAS Institute, 2003). The fixed effect three-way Analysis of Variance (ANOVA) model that includes additive terms for the main effects of replications, blocks, genotypes, locations and years together with an extra additive term that accounts for all the possible interaction effects of genotype, location and year was employed. The ANOVA model employed for an analysis of the data is:

$$Xijk=\mu+Gi+Lj+Yk+(GL)ij+(GY)ik+(LY)jk+(GLY)ijk$$

where *Xijk* is the mean yield over *r* replications of the *ith* genotype in the *jth* location in year *k*, with the right hand side of the equation giving grand mean yield μ and respective main and interaction effects of the genotypes, locations and years. The magnitude of variance components was computed as the percentage of total variation to find out how the main and interaction effects explain the variations in seed yield. Mean seed yields of genotypes for the combinations of the 1 location and 3 years, treated as 3 environments were computed to generate a genotype and environment two-way table data for the Biplot analysis. The GGE Biplot software (Yan, 2001) was employed to generate graphs showing (i) “which-won-where” pattern, (ii) ranking of genotypes on the basis of mean yield and stability and (iii) an evaluation of test environments (Yan *et al.*, 2007).

Results and Discussion:

The results from analysis of variance (Table-1) revealed significant ($P < 0.05$) genotype × environment interaction. The environment effect was highly significant

($P < 0.01$). The genotypes, locations and years' main effect as well as Genotype × Year (GY) interactions were highly significant ($P < 0.01$). The interaction effects for Genotype × Location (GL) and Genotype × Location × Year (GLY) were significant ($P < 0.05$), whereas Location × Year (LY) effect was not significant. The location and year main effects explained most (up to 89.11 %) of the total variation. The contribution of genotypes' main effect as well as GL, GY, LY and GLY interaction effects appeared to be negligible. Locations' main effect by itself explained more than 70.80 % of the total seed yield variations. Moreover, the significant ($P < 0.05$) GL effects demonstrated that genotypes responded differently to different locations, confirming the importance of testing mung bean genotypes at multi-locations in Rajasthan. When genotypes are tested in multi-location yield trials, a cross over genotype by environment interaction most often occurs (Ceccarelli *et al.,* 2006). 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}).

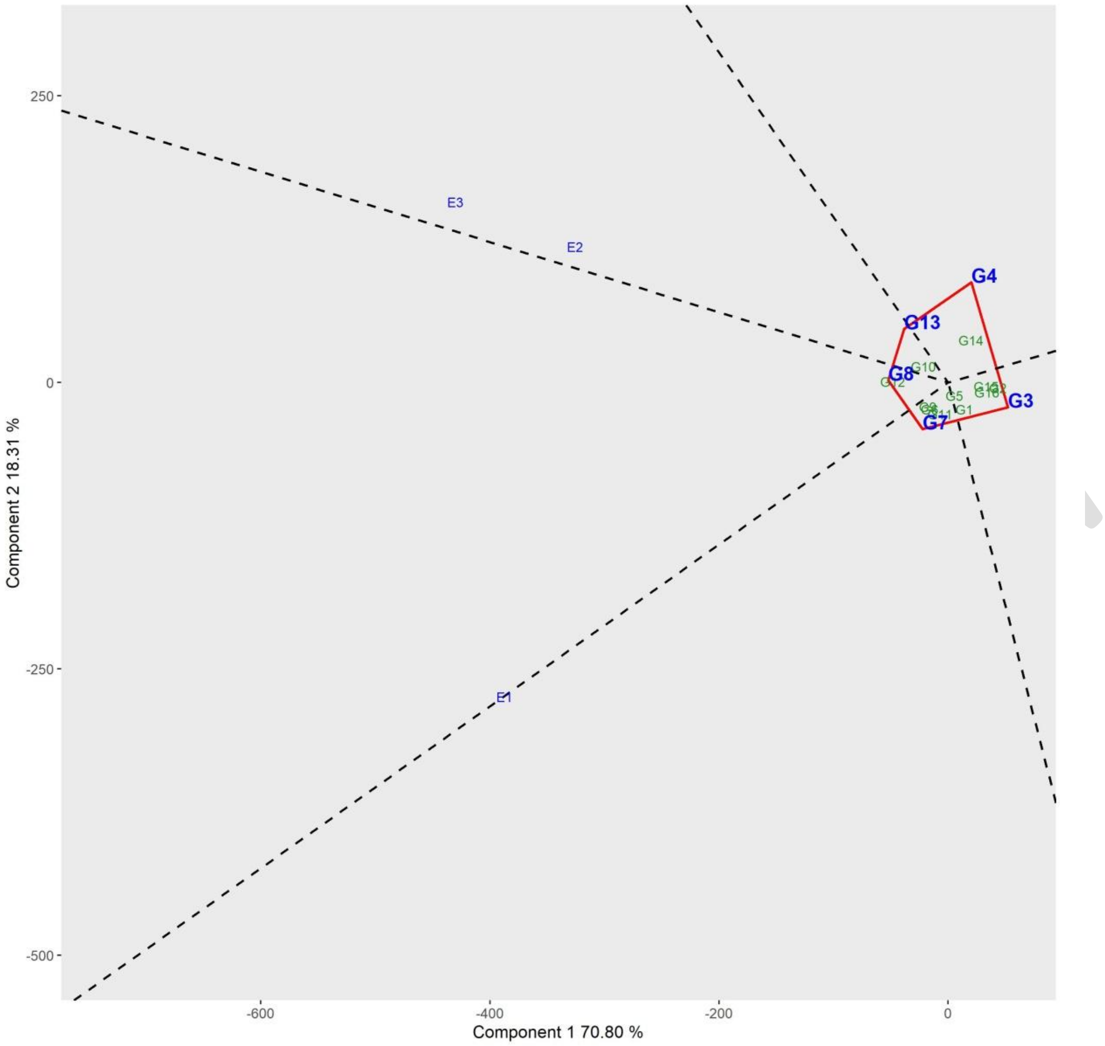
Table-1: Mean seed yield (kg ha^{-1}) of Mung bean genotypes tested at ARS, Fatehpur during *Kharif*, 2019 to 2021.

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 Analysis

The first two principal components explained 89.11% of the total Genotype plus Genotype by Environment (G+GE) variation (Figures 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 (Yan *et al.*, 2000). GGE Biplot analysis was hence used for which-won-where analysis, test environment and genotype evaluation for mung bean MET data.



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

Figure-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.

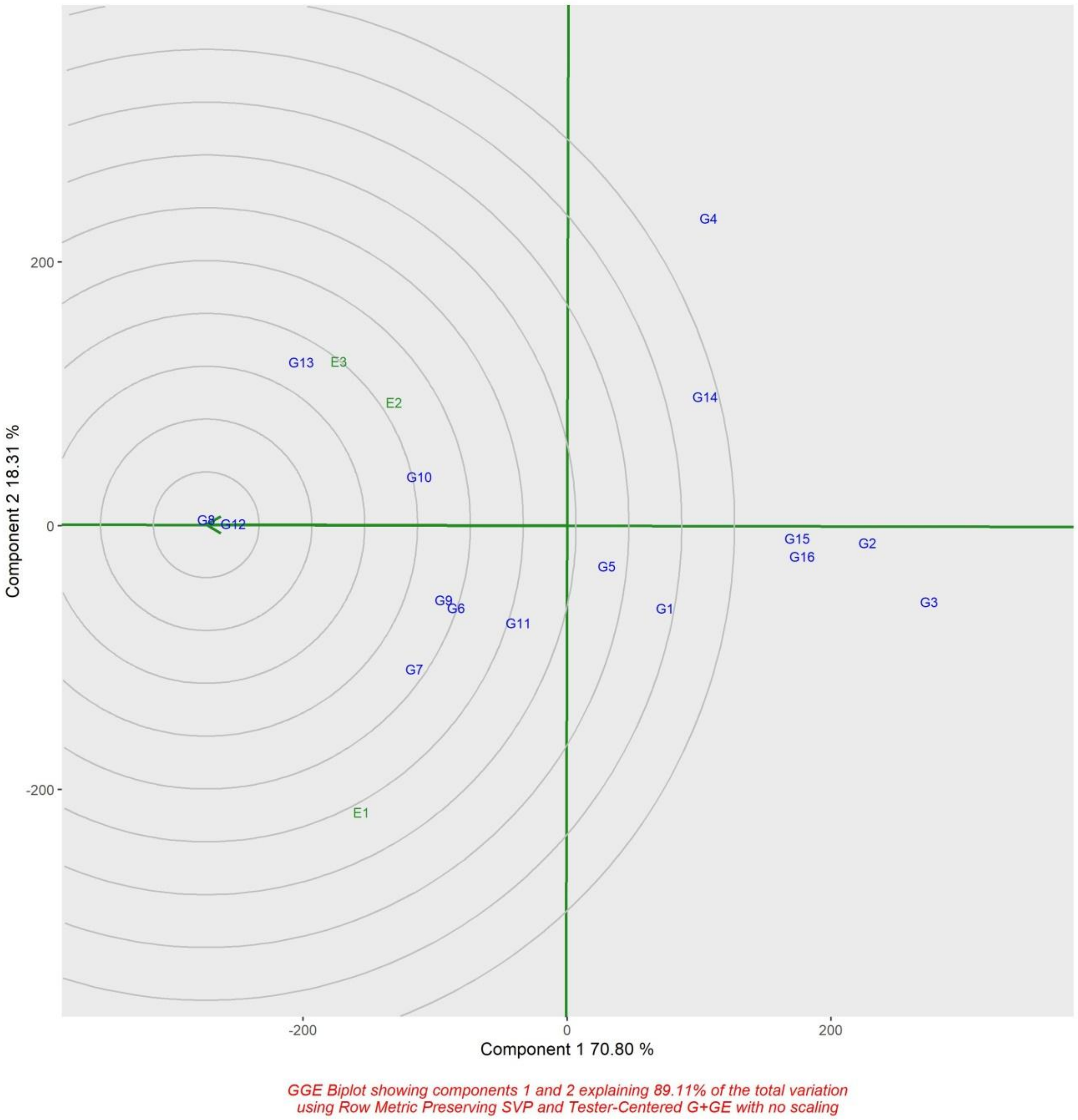


Figure-2: The “discriminating power vs. rep representativeness” view of the GGE Biplot. The data were not transformed (Transform=0), not scaled (Scaling=0) and were environment centred (Centring=2). The Biplot was based on genotype focused SPV=2. Environment and genotype name as of Figure-1.

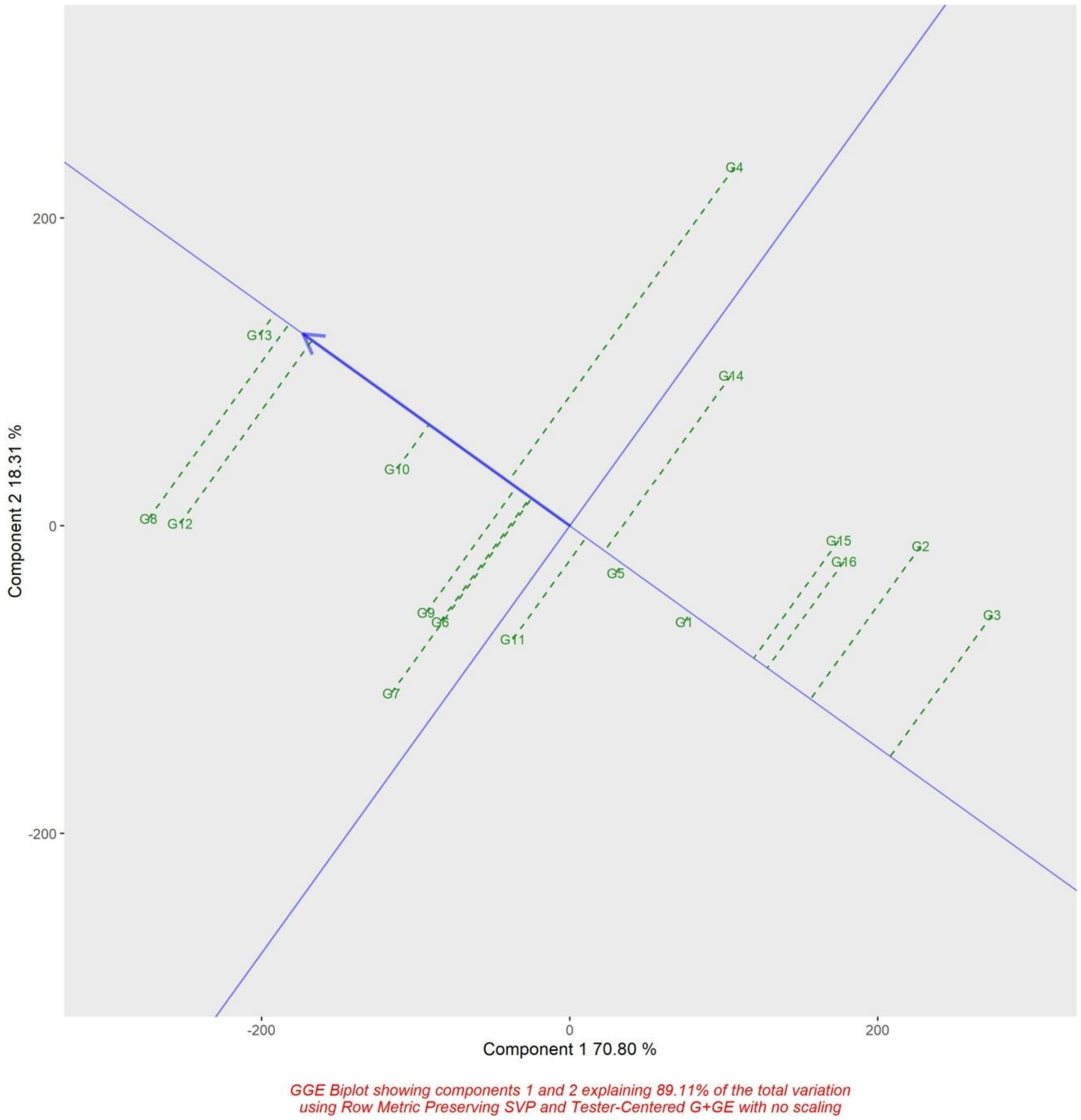


Figure-3: The "mean vs. stability" view of the GGE Biplot as based on genotype focused SPV=1. The data were not transformed (Transform=0), not scaled (Scaling=0) and were environment centred (Centring=2). An ideal cultivar is at the centre of the innermost circle. Environment and genotype name as of Figure-1.

Which-Won-Where

The "which-won-where" pattern of the GGE Biplot (Yan *et al.*, 2000) is the most suitable tool for mega-environments analysis in variety trials (Yan *et al.*, 2007). 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 (Yan *et al.*, 2000). Five out of the sixteen genotypes located in the vertex formed a five-sided polygon having five possible sectors (Figure1). 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 locations in the favourable 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 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 (Yan *et al.,* 2001). The mung bean MET data did not strongly indicate the presence of different mega-environments, which is defined as the group of locations that consistently share the most suitable set of genotypes across years (Yan and Rajcan, 2002). Yan *et al.* (2007) stressed the need for data from multiple years to decide whether the target region can be divided into different mega-environments. It would therefore be impossible for our data set to confirm the existence of mega environments.

Test Environment Evaluation

An ideal environment should be both discriminating of the genotypes and representative of the mega-environment (Yan *et al.,* 2007). Figure-2 is a GGE biplot which is based on environment-focused scaling (Yan, 2002), with the singular values entirely partitioned into the environment scores (SVP= 2) making it appropriate for studying the relationships among test environments. 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 (Yan, 2002; *Yan et al.,* 2007). 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 (Yan and Tinker, 2006;

Yan *et al.,* 2007). 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.

Genotype Evaluation

An ideal genotype should possess both high mean performance and high stability within a mega-environment (Yan *et al.,* 2007). In Figure-1, the grouping of the test locations for mung bean yield delineate the locations by years. Year 2020 was the average environment of the trial (Figure-2) suggesting the three locations could be considered as one mega-environment. The mean performance and stability across environments were presented in Figure-3. For such an evaluation Yan *et al.,* 2000 and 2001 indicated the high correlation (r> 0.95) between genotypes' yield (averaged over environments) and their PC1 scores as a requirement. Such near-perfect correlations between genotypes mean yield and PC1 scores may not be always met. In such instances Yan and Rajcan (2002) proposed an alternative, the use of a mean environment coordinate system created by drawing a mean environments' axis line that passes through the biplot origin and the mean environment marker for evaluation of both genotypes and environments. The projections of the genotype markers on the average environment axis are proportional to the rank-two approximation of the genotype means representing the main effects of the genotypes. The arrow shown on the axis of the Average Environment Coordinate (AEC) abscissa points in the direction of higher mean performance of the genotypes (Figure-3) and, consequently ranks the genotypes with respect to mean performance (Yan *et al.,* 2007).Yield ranking of the genotypes as based on position relative to the end of the mean-environmental axis was 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 increasing absolute difference between genotype marker and AEC axis was 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 yield with stable performance was qualified as the most suitable genotype among the others, evaluated for production in mung bean growing regions in the Rajasthan.

Conclusions:

Mung bean is important seed legume in semi-arid region of Rajasthan. It is mostly grown by vulnerable and risk-averse smallholder farmers in the Rajasthan. Breeding programs should deliver these farmers robust germplasm that fit their wide range of environmental conditions. This requires testing of genotypes for quantification of the importance of G × E interaction, mainly genotype x location, genotype x year and genotype × location × year as well as a determination of the winning genotypes for the test environments. Several statistical methods have been proposed for increasing the chance of exploiting positive G×E interaction and supporting the breeding program decision in variety selection and recommendation. GGE biplot is among the many that effectively quantifies G×E interaction and provides meaningful interpretation of multi-environmental trial data. The application of GGE biplot to mung bean multi-environmental seed yield trial facilitated the visual comparison and identification of the winning genotype in relation to the Zone-IIa (Rajasthan) environment.

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