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Identification of suitable mungbean genotypes for hilly terrains of India using GGE and AMMI biplot approaches

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Abstract

Aim : The present investigation was conducted to approximate the magnitude of genotype × environment interaction effects in mungbean crop and to identify suitable genotypes for northern hilly terrain of India.

Methodology : Thirty one promising mungbean genotypes were evaluated in three diverse environments, viz., Srinagar, Berthin and Imphal of northern hilly terrains of India. The individual genotype was planted in 5 rows of 4m length in 3 replications in randomized block design. The statistical analysis was done for Additive Main effect and Multiplicative Interaction (AMMI) and genotype main effect plus genotype-by-environment interaction (GGE) biplots analysis.

Results : ANOVA devised that the genotypes, environment and genotype × environment interactions were significant for grain yield. The first two principal components, PC1 and PC2 described 73.65 and 26.35 percent variations, respectively, of total variation. According to AMMI I, the genotypes such as Pant M 6, RMG 1092, TMB 134, CoGG 13-19, KM 2349, DGG-8, TRCM 87-6-2-1, KM 2241 and MDGGV-16 were highly stable genotypes. GGE biplot analysis revealed that Pant M 6 and TMB 134 as winning genotypes for Berthin while NMK 15-12 and MDGGV-16 were the best genotypes for Srinagar. The genotypes IPM 14-7 and GAM 5 were found best for Imphal. Overall, high yield and most stable genotype was DGG-8 for northern hilly terrains of India.

Interpretation : GGE biplot and AMMI approach could be instrumental in appraising the genotypes performance in multi-environments/locations testing for efficient selection of the stable genotypes.

Key words: AMMI plot, GGE, Mungbean, Stability

Selection of stable and high yielding mungbean
genotypes for hilly terrains of India

Multi-Environments Testing (MET)

Evaluated 31 genotypes at each location

Identified two best performing
genotypes for individual environments
using AMMI and GGE biplot analysis

Berthin	Srinagar	Imphal
• Pant M-6 • TMB 134	• NMK 15-12 • MDGGV-16	• IPM 14-7 • GAM 5

Stable genotype for all environments

AKM 12-24

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Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is an important pulse crop grown in a wide range of agro-climatic conditions of South and South-East Asia, Africa, South America and Australia (Parihar *et al.*, 2017a). It is considered as good source of easily digestible dietary protein, fibres and carbohydrate in food basket of resource poor vegetarian population (Solanki *et al.*, 2018). India is the largest producer of mungbean and the major contributing states are Rajasthan, Maharashtra, Uttar Pradesh and Madhya Pradesh. However, productivity of mungbean in the country has remained quite low as compared to other pulses (Anonymous, 2018; Parihar *et al.*, 2017b). Several biotic and abiotic stresses have constrained the productivity of this crop (Jeberson *et al.*, 2015; 2017, Parihar *et al.*, 2017a; 2017b). To avoid crop losses caused due to occurrence of various stresses, there is urgent need to develop genotypes which can perform consistently over the locations with good yield potential.

Further, there is ample scope of expansion of area under mungbean cultivation in different niches, including hilly terrains of India (Annual Report, 2016). This calls for identifying high yielding and stable genotypes for such production niches. The performance of individual genotype is generally influenced by environmental changes owing to significant genotype $\times$ environment interactions. The genotype would be less stable if more interaction between genotype and environment exists (Gauch and Zobel, 1996). At the time of evaluating the stability and adaptability of a genotype, the crucial step is approximation of GE interaction and assessment of its growth in varied environments and ecological regions (Luo *et al.*, 2015a; 2015b). It is important to understand GE interaction to ascertain the adaptability and stability of genotypes. During last decades, both techniques, i.e., AMMI (Chang *et al.*, 2006; Liu *et al.*, 2002; Tarakanovas and Ruzgas 2006; Yan *et al.*, 2007; Aketer *et al.*, 2014) and GGE biplot (Yan *et al.*, 2007; Luo *et al.*, 2009, Luo *et al.*, 2015a; 2015b, Parihar *et al.*, 2017a; 2017c) have been adopted by various researchers to elucidate GE interactions. Both AMMI and GGE biplot methods are the most popular statistical techniques for analysis of crops data of multi environmental/ locations trials (Hugh, 2006; Zhou *et al.*, 2011, Parihar *et al.*, 2018). To identify high yielding stable genotypes of mungbean for targeted environments, there is a need to assess breeding lines across locations in a specific niche. Therefore, the multi-environment yield trials were designed to screen mungbean genotypes to identify high yielding stable genotypes for northern hilly terrains of India.

Materials and Methods

The experiment was executed at three diverse locations namely Research Station at Berthin, Bilaspur, CSK Himachal Pradesh Agricultural University, Palampur, Himachal Pradesh (E1); Dryland Agriculture Research Station, SKUAST, Budgam, Kashmir and Research Farm, Central Agricultural University, Imphal, Manipur (E3). Given locations are true representative of

northern hill terrain of India in terms of geographical and climatic condition, these locations are significantly different from each other. Further, these locations represent a broad spectrum of agro-climatic situations with latitudes ranging from 24°49' N at Imphal to 33°98' N at Srinagar, longitude from 74°80' E at Srinagar to 93°57'E at Imphal, altitude from 375 above msl at Berthin to 1592 msl at Srinagar, minimum temperature from - 6.0°C at Srinagar to 21.4 °C at Imphal, maximum temperature from 29.7°C at Imphal to 34.6°C at Srinagar, and rainfall ranging from 706.5 mm at Imphal to 859.8 mm at Berthin, respectively.

Thirty one genotypes of mungbean were grown with recommended package of practices, viz., row to row and plant to plant spacing 30 cm and 10 cm, respectively. The individual genotype was planted in five row of 4 m length in three replications in RBD during rainy season, 2016. Rainfall at Imphal during cropping season was higher than normal but well distributed, which provided better growth for the crop. Similar situation was observed in Srinagar and Berthin also. Statistical analysis was performed for AMMI and GGE biplots analysis using SAS statistical package (Ver. 9.2, SAS Institute, 2008). The results of AMMI model analysis were interpreted from AMMI1 graph that showed main and first multiplicative axis term (PC1) of both genotypes and environments. The GGE biplot analysis was done to develop graphics which illustrate pattern and ranking of genotypes based on overall yield and stability (PBTools, 2014).

Results and Discussion

The ANOVA of AMMI model exhibited significant effects for genotype, environment and genotype by environment interaction for grain yield. The environmental effect (E) accounted maximum part of variation, followed by genotype $\times$ environment interaction (GEI) and genotypic effects (G). Further, the highest sum of squares for environments exhibited that the environment component was mainly responsible for variations in grain yield. Tadesse *et al.* (2017) reported that more than 75 percent of sum of squares of total variation contributed by environmental factors and this substantially affected the grain yield. Since in the present study, variation in grain yield account mainly due to environment component suitably justifying the identification of stable genotypes across environments and an adapted genotype in a particular environment. In the present study, the amount of GEI sum of squares was also higher than genotypes effect, demonstrating that the response of genotypes across environments was significantly different.

Therefore, according to Yan (2002) and Yan and Tinker (2006) high GEI indicates the possibility of identifying different winning genotypes at respective locations as well as different mega environments. Tarakanovas and Ruzgas (2006) and Abdipur and Vaezi *et al.* (2014) reported high GEI contribution in total variation as compared to genotypes effect in grain yield which may be due to the contribution of genes controlling varied yield attributes among environments. In addition, ANOVA also demonstrated that both the interaction principal component axis

(IPCA) were highly significant ($P < 0.001$). The AMMI analysis indicated that the first two PCs accounted for total variation. The first principal component axis (PCA1) of interaction accounted 73.65% of the interaction. Similarly, the second principal component axis further explained 26.35% of the interactions. Tadesse *et al.* (2017) described that the first two IPCA cumulatively contributed more than 88 % of the total GE interaction, while Getachew *et al.* (2015) demonstrated that first two IPCA accounted 74.40%, which also signify the use of AMMI model for the present data set and sufficiency of two IPCA for interpretation of data.

The stability per se is not considered a desirable selection criterion. In most cases, the most stable genotypes does not give the best yield performance, hence, simultaneous consideration of

grain yield and stability in a single non-parametric index is the best criteria (Purchase *et al.*, 2000). Hence, the AMMI stability value (ASV) which is a stability parameter measured in a two dimensional scatter graph of IPCA1 (interaction principal component analysis axis 1) against IPCA2 by the distance of genotypes from origin of biplot ('0'). Because, the IPCA1 score had more share in GE sum of square (Table 1), therefore, it has to be weighted by relative variation between IPCA1 and IPCA2 scores to compensate the relative fraction of IPCA1 and IPCA2 in total GE. The ASV discriminated genotypes namely AKM 12-24 (G12), KM 2349(G15), KM 2241 (G16), COGG 13-19 (G9) and SKNM 12-06 (G2) as stable genotypes based on low stability value. Bhartiya *et al.* (2017) also discriminated the genotypes for adaptability considering stability value in rice, while Darai *et al.* (2017) recommended stable genotypes of lentil based on stability

Table 1 : Stability parameters for 31 genotypes of mungbean evaluated at three locations/environments

Genotypes/code	Grain Yield (GY)	IPCA1	IPCA2	ASV
Pusa 0672 (G1)	6.37	0.66	0.36	1.89
SKNM 12-06 (G2)	5.91	-0.14	-0.02	0.39
IPM 14-7(G3)	9.50	1.51	-0.67	4.27
GGG-1(G4)	6.58	0.27	-0.07	0.76
DGG-8(G5)	7.12	0.38	-0.57	1.21
Pant M 6(G6)	7.91	-1.29	-1.22	3.80
VGG 15-030(G7)	5.11	-0.86	0.39	2.42
PM 11-25(G8)	5.69	-0.67	-0.48	1.92
COGG 13-19(G9)	6.42	-0.10	-0.02	0.27
TRCM-351-2-1(G10)	5.92	-0.68	0.31	1.92
NBPGR 150(G11)	5.23	-0.71	0.60	2.08
AKM 12-24(G12)	5.72	0.09	-0.03	0.25
IGKM 06-26-5(G13)	4.56	-0.18	0.90	1.03
PM 11-26(G14)	6.13	0.27	0.16	0.76
KM 2349(G15)	6.68	-0.08	-0.01	0.22
KM 2241(G16)	7.09	-0.10	-0.23	0.36
NDMK 15-513(G17)	6.92	0.80	-0.01	2.23
RMG 1092(G18)	6.61	-0.51	0.23	1.46
Pusa 1672(G19)	4.14	-0.85	0.80	2.51
NMK 15-12(G20)	5.01	0.08	0.40	0.46
TRCM 87-6-2-1(G21)	7.09	-0.09	-0.63	0.68
MH 1142(G22)	6.02	-0.21	0.23	0.63
SML 1811(G23)	6.60	0.68	-0.06	1.91
RMG 1087(G24)	6.64	0.11	-0.59	0.66
AKM 12-14(G25)	6.62	0.19	-0.14	0.55
Pusa 1671(G26)	5.90	-0.15	-0.14	0.44
IGKM 05-18-2(G27)	6.29	-0.46	-0.19	1.31
TMB 134(G28)	7.18	-0.29	-0.49	0.96
MDGGV-16(G29)	5.41	0.45	0.80	1.49
GAM 5(G30)	6.70	1.22	0.37	3.44
IPM 312-9(G31)	7.26	0.65	0.02	1.83
Berthin(E1)	5.99	-1.92	-1.55	5.58
Srinagar(E2)	4.35	-0.78	2.06	2.99
Imphal(E3)	8.66	2.69	-0.51	7.55

IPCA= Interaction principal component analysis axis; ASV=AMMI stability value

Fig.1: Illustration of 31 mungbean genotype performance evaluated in three environments using: (a) which-won-where view of GGE biplot; (b) AMMI-1 biplot; (c) AMMI-2 biplot. Codes correspond to genotypes as listed in Table 1. Environments are: E1, Berthin; E2, Srinagar; E3, Imphal.

and mean values for grain yield, since both stability and mean yield play crucial role in identification of best performing genotypes with wider adaptability. The AMMI 1 biplot considered both main effect of grain yield and IPCA 1 scores for discrimination of genotypes stability and yield. As a result, Fig. 1 showed different groups of genotypes viz., Pusa 1672 (G19), VGG 15-030 (G7) and NBPGR 150 (G11) which were less stable and low yielding. The genotypes PM 11-26 (G8) and TRCM-351-2-1 (G21) were less stable with moderate yield. Genotypes IGKM 06-26-5 (G13) and Pusa 1671 (G26) were moderate by stable with low yield. Genotypes, NMK 15-12 (G20), AKM-12-24 (G12), MH 1142 (G22) and PM 11-25 (G8) were moderate yielder, however,

stable in all environments. The genotypes IGKM 05-26-5 (G13), RMG 1092 (G18) and TMB 134 (G28) had moderate yield and stability. COGG 13-19 (G9), KM 2349 (G15), Pusa 1671 (G26), RMG 1087 (G24), AKM 12-14 (G12), GGG-1 (G4), DGG-8 (G5), Pusa 0672 (G1) and SML 1811 (G23) were moderate yielders and stable genotypes. Genotypes, NDMK 15-513 (G17), IPM 312-9 (G31) and GAM 5 (G30) were unstable genotypes with moderate yield. Although, IPM 14-7 (G3) and Pant M 6 (G6) were unstable genotypes with highest yield, but suitable for favorable environments. The AMMI1 biplot revealed that 31 mungbean genotypes varied from each other in terms of mean yield and interaction effects. Similarly, the interactions characterized by

IPCA 1 scores witnessed that the entries AKM-12-24 (G12), NMK-15-12 (G20), AKM-12-14 (G25), RMG 1087 (G24), GGG-1(G4) and DGG-8 (G5) had minimal interactions due to low IPCA1 scores (Table 1) and these comparatively showed stable genotypes with broad adaptation in all the studied locations. Genotypes such as IPM-14-7 (G3) and GAM 5 (G30) had high IPCA scores were unstable at all locations.

The differences present in the genotypes may be due genetic as well as environmental effects. AMMI analysis has been used to estimate the stability of genotypes on the basis of mean performance as well as magnitude of IPCA1 scores in soybean (Zobel *et al.*, 1988) and chickpea (Zali *et al.*, 2011). Both the parameters assume importance in deciding the stability of genotypes. The AMMI 2 biplot explaining the extent of interaction of individual genotypes with environments, accordingly entries which are located close to each other are similar in mean yields in all the locations and entries which are located far differed in the mean yields. Hence, the genotypes which were located farthest from the origin in AMMI biplot 2 (Fig. 1) were more sensitive to the environment interaction while nearer were less interactive. In the present investigation, the genotypes AKM-12-24 (G12), Pusa 1671(G26), MH 1142 (G22), KM 2241(G16), GGG-1(G4) and DGG-8 (G5) were located near to the origin seemed to be less

interactive to the environments, but others were located farthest to the environments, so they interacted strongly to the environments. Similar way, environments also located distant from the origin indicates that they were strongly interacting with the genotypes. Rashidi *et al.* (2013) described the extent of interaction of individual genotypes and environments in chickpea using AMMI 2 biplot and recommended stable and environment specific genotypes. Similarly, Akter *et al.* (2014) identified two rice genotypes as more interactive being farthest from the origin while four genotypes which were situated near to the origin of biplot were less responsive to environments. Darai *et al.* (2017) reported that lentil genotypes which were close to ordinate displayed stability, while the genotypes observed farthest from ordinate demonstrated suitability to particular environment. Therefore, the genotypes which were less interactive with the environments were stable and vice versa. Genotypes demonstrated positive interaction in an environment indicating suitability of genotypes to a particular environment.

Interestingly, in 'mean versus stability' GGE biplot (Fig. 2) it is easy to devise both stability and mean yield performance at a glance through graphical presentation. An average tester coordinate (ATC) axis passes horizontally through the biplot origin and the average location and the oval show the positive end

Fig. 2: The "mean vs. stability" view of the GGE biplot as based on genotype focused Singular Value Partitioning (SVP= 1). The data were not transformed (Transform= 0), not scaled (Scaling =0), but environment-centered (Centering= 2). An ideal cultivar is at the center of the innermost circle. Codes correspond to genotypes as listed in Table 1.

of the ATC horizontal axis. The average yield of genotype was estimated by projections of their marks on to the ATC horizontal axis (Karimmizadeh *et al.*, 2013). The farthest position of the genotypes from origin over ATC axis indicated highest mean performance and vector projection on the ATC axis indicated the stability. The mean performance displayed that the genotype IPM 14-7 (G3) was the highest yielding and Pusa 1672 (G19) was the lowest yielding genotypes. Stability of each of them was assessed by its projection onto the ATC vertical axis, where absolute length of projection of a genotype was small it was found as more stable one and vice versa. Thus, the genotypes Pant M6 (G6), IPM 14-7 (G3) and GAM 5 (G30) were least stable and IGKM 06-26-5 (G13), AKM 12-24 (G12), KM 2349 (G15), DGG 8 (G5), GGG-1(G4) were highest stable, other genotypes showed moderate stability. Considering mean yield and stability, the genotypes GGG-1(G4), DGG-8 (G5), RMG 1087(G24) and AKM 12-14 (G25) were identified to be most stable at all environments. Farshadfar *et al.* (2011) have identified high yielding and stable genotypes of chickpea based on position of genotypes and vector projection on ATC axis, respectively, using mean versus stability GGE biplot. Likewise, Parihar *et al.* (2018) suggested rust resistant stable genotypes in lentil using GGE biplot techniques. On the basis of yield and stability, Jeberson *et al.* (2018) recommended four genotypes of lentil with best performing genotypes adapted to a wide range of ecological conditions. Hence, the identified stable and high yielding genotypes in the present study can also be recommended for cultivation in northern hilly terrain of India.

The GGE biplot visually displays G + GE which are instrumental in identifying suitable stable genotypes and mega environment (Yan *et al.*, 2000). The two dimensional polygon view of GGE biplot of MET data was constructed using environment standardized data which displayed complex interaction between genotypes and environments. The biplot portrayed first two principal components which accounted 97.1 of total variation (G=63.9% and G x E=33.2%). The genotypes positioned at vertices of polygon contributed highest to the interactions, since they had lowest and highest values. The vertex genotypes were Pant M6 (G6), IPM 14-7(G3), GAM 5 (G30), MDGGV-16 (G29), IGKM 06-26-5 (G13) and Pusa 1672 (G19). Since these genotypes were at great distance from the origin of biplot, therefore, they were considered as the best or poorest performing genotypes at few or all locations. Besides, all three environments produced three distinct mega-environments (Fig. 1). Berthin (E1) had best performing genotypes, i.e., PM 11-25 (G8), IGKM 06-26-5 (G13), TMB 134 (G28), TRCM 87-6-2-1(G21), KM 2241(G16), RMG 1092 (G18), KM 2349 (G15) and CoGG 13-19 (G9), with the entry Pant M 6 (G6) was the best. Similarly, the location Srinagar (E2) had best performing genotypes namely TRCM-351-2-1(G10), VGG 15-030 (G7), NBPGR 150 (G11), Pusa 1671(G26), SKNM 12-06 (G2), MH 1142 (G22), AKM 12-24 (G25) and NMK 15 -12 (G20) with winning genotype MDGGV-16 (G29). The Imphal (E3) location had genotype such as IPM 14-7 (G3) and GAM 5 (G30) as the winning genotype along with other elite genotypes, i.e., RMG 1087(G24), DGG 8 (G5), AKM 12-14 (G25),

GGG-1(G4), PM 11-26 (G14), IPM 312-9 (G31), SML 1811(G23), NDMK 15-513 (G17) and Pusa 0672 (G1). Whereas the poorest genotypes IGKM-06-26-5 (G13) and Pusa 1672 (G19) which were situated at two corners and at a greater distance from all testing environments, indicated poor performance of these at each environment (Fig.1). Farshadfar *et al.* (2011) identified three mega-environments and specific genotypes for particular environment in chickpea using GGE analysis. In addition, they also identified the best representative location to discriminate genotypes. Similarly, Segherloo *et al.* (2010) suggested four mega-environments for chickpea along with winning genotypes at particular environment using which-won-where biplot. Nzuve *et al.* (2013) identified three mega environments along with suitable genotypes for each environment. Gedif and Yigsaw (2014) recommended an ideal testing location as well as ideal genotype for Amhara region in Ethiopia for potato using GGE biplot. Therefore, this technique can be successfully used to identify suitable genotypes and mega environments for mungbean production.

Graphical illustration of AMMI analysis demonstrated the main effect means on the abscissa and IPCA-1 scores of both entries as well as locations, simultaneously on the ordinate (Fig. 1). The illustration also describes the differential interaction of genotypes to the most discriminating environmental variable (Bose *et al.*, 2014). The IPCA1 was highly significant and explained the interaction pattern better than other axis. Genotypes with IPCA-1 scores close to zero had small interactions, and hence show wider adaptation (Carbonell *et al.*, 2004; Akter *et al.*, 2014). A large genotypic IPCA-1 score with either positive or negative value had high interaction and thus reflects more specific adaptation to the environments with IPCA-1 values of same sign. The environments showed difference for both main effects and interactions (Fig. 1).

The Imphal high potential environment can be seen in quadrant-II, with minimum interaction effects, high positive IPCA-1 and minimal IPCA-2 scores. Similarly, the low potential environments Berthin and Srinagar were distributed in quadrant-IV, the Berthin had negative IPCA-1 score to medium negative IPCA-2 scores. The Srinagar was the second highest yielding environment as it compounds the negative IPCA-1 and high positive IPCA-2 scores (Table 1; Fig. 1). Thus, the biplot identified Imphal as the highest yielding environment and Srinagar as the lowest yielding environment for mungbean. Akter *et al.* (2014) recognized two environments as most stable locations for hybrid rice improvement for grain yield based on lowest IPCA score. Correspondingly, Getachew *et al.* (2015) using IPCA scores also identified stable environments with least GEI and high yield. Therefore, IPCA1 score is useful in recognizing ideal environment for selecting genotypes with specific adaptability. The genotypic and environmental scores of first two AMMI components were used to construct AMMI 2 biplot (Fig.1). The IPCA 1 versus IPCA 2 biplot described the magnitude of interaction of each genotype and environment. Distances from the origin (0, 0) are pinpointing towards the amount of interaction that was exhibited by genotypes over environments or vice-versa (Vargas and Crossa, 2000; Thangavel *et al.*, 2011). The

genotypes and environments that are farthest from the origin are considered unstable. Genotypes and environments that fall into the same sector interact positively (Osiru et al., 2009). In AMMI 2 biplot the location scores are connected to the origin by vector which is a one side arrow lines. The lines with short and long spokes exert weak and strong interactive forces, respectively (Pabale et al., 2010; Akter et al., 2014). All the three environments such as E1, E2 and E3 had long spokes which indicate strong interaction. The results of present investigation revealed that in mungbean genotypes grain yield was highly influenced by the environmental factors followed by genotypic and G x E effects. Further, the AMMI and GGE biplots can be considered as an effective tool for identification of stable and high yielding genotypes across environments.

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