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Research Article

Statistical analysis for stability and adaptability testing of mungbean (*Vigna radiata* (L.) Wilczek) genotypes

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Abstract :
Aimed at developing a precise and efficient parsimonious method of testing the stability of promising mungbean lines, particularly using small number of observations, this paper presents the analysis of variance of 10 mungbean lines in 4 environments for 2 years. Simultaneous varietal selection using the AMMI (additive main effects and multiplicative interaction) model along with mean deviation from maximum plot yield ,suggested single value of IPCA (interaction principal component analysis axes) scores (IPCAs)and IPCAs vs. mean yield biplot were found to be more effective for evaluating wide adaptability and stability of mungbean over diverse environments. Mungbean lines with above grand mean yield having the lowest mean deviation (D) and IPCAs scores which are close to zero are selected as the most adaptable promising lines in the multi-location trial. The AMMI1 biplot ordinate with IPCA1 captures lower percentage of genotype x environment interaction (GEI), while suggested biplot of the reference method that ordinate with IPCAs scores capture 100 % of GEI..

Key words:
AMMI model, biplot, IPCA scores, Mungbean, yield stability

Introduction

The multi location yield trials are the most important in varietal identification, especially for testing a number of genotypes in a number of environments. Therefore, statistical methods for effective analysis of yield trials have received considerable development (Gauch et al, 2008). When considering the two types of stability of a variety, in “static stability” the best genotype secures a constant yield across the environment while the yield response of each environment is always parallel to the mean response in “dynamic stability” of testing genotypes. An ideal variety should have a higher mean yield combined with a low degree of fluctuation (Tarakanovas and Rusgas, 2006). According to Abeysiriwardana et al (1991), adaptability is defined as the ability of a crop variety to perform well over diverse environment.

For analyzing the genotype x environment interaction (GEI) and the phenotypic stability of promising lines, several methods have been proposed (Tarakanovas and Ruzgas, 2006). The AMMI (additive main effect and multiplicative interaction) model is widely used in analyzing GEI. This method is effective because it captures a large portion of GEI sum of squares (Tarakanovas and Ruzgas, 2006). Gauch (2007) (Gauch,1992, Gauch and zobel,1996), explain the advantages of AMMI analysis such as (1) understanding genotype environment interaction, (2) improving the accuracy of yield estimate, which increase the probability of successful selection of genotype with high yields, (3) imputing missing data and (4)increase the flexibility and efficiency of experimental designs.

The variance involving stability measures require at least 20 observations for acceptable accuracy, such as 10 locations for 2 years or 7 locations for 3 years (Gauch et al, 2008). Even if data from less than 20 environments AMMI1 model allows to estimate the parameters in cost effective way with adequate accuracy. Consequently, principal component (PC1) scores of AMMI show consistent reproducibility for 10 or 12 environments (Gauch et al, 2008). The abscissa of an AMMI1 biplot capture 100% of Genotype (G) effect and AMMI1 ordinate with its PC1 capture as much as possible GEI (Gauch et al, 2008). The AMMI1 biplot has additional advantage for showing mean vs. stability. It is simpler to construct and to interpret because its axes are used directly, rather than needing to be rotated (Gauch et al, 2008). Also, AMMI1 separates G from GE perfectly regardless of how simple or complex a data set may be. Furthermore, the AMMI1 biplot provides

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all parameters needed to reconstruct this model's estimates of yields (Gauch et al, 2008). The results of AMMI analysis are useful in supporting breeding programme decisions such as specific adaptation and selection of environment (Gauch and Zobel, 1988).

Abeysiriwardena (2001), proposed a method to evaluate the varieties for adaptability by estimating the average superiority of a variety through calculating mean deviation from maximum plot yield and variance in deviation across locations. One of the advantages of this method is analyzing multi location yield trials with very few varieties as low as two (Abeysiriwardena, 2001). Due to this method estimate, the maximum response of varieties using the maximum plot deviation, it is difficult to reveal the actual information of G and GEI.

The purpose of this paper is to present an efficient and cost effective method of evaluating the stability of genotype across the environments using single value of IPCA scores (IPCAs) with IPCAs vs. mean yield biplot of genotypes. Application of this proposed method to the mungbean (*Vigna radiata* (L.) Wilczek) yield trial is illustrated as a modification of AMMI1 model.

Material and method

The proposed method of varietal evaluation was derived from the AMMI model and mean deviation from the maximum plot yield. AMMI model for phenotypic performance of gth genotype in the eth environment can be expressed as;

$$Y_{ij}=\mu+\alpha_g+\beta_e+\sum_{n=1}^{n'}\lambda_n\gamma_{gn}\partial_{en}+\rho_{ge}$$

$$\rho_{ge} \sim N(0, \sigma^2);\ g=1,2\ldots.T;\ \ e=1,2\ldots.S.$$

Where Y_{ij} is the mean yield of gth genotype in the eth environment; μ is the grand mean; α_g is the gth genotype effect; β_e is the eth environment effect; λ_n is the eigen value of IPCA axes n; γ_{gn} and ∂_{en} are the gth genotype , eth environment IPCA scores for the IPCA axes n; ρ_{ge} is the residual; n' is the number of IPCA axes of the model (Gauch, et al, 2008).

Variety selection in multi location trials using mean deviation of the maximum plot yield and variance was proposed by Abeysiriwardena (2001), based on the concept of evaluating varietal superiority by the distance of variety's response from the maximum response of Lin and Binns (1988). The statistical model is as follows;

$$d_{ijk} = \mu+V_i+E(V)_{ji}+B(E)_{kj}+e_{ijk}$$
$$i=1\ldots.p;\ j=1\ldots n \text{ and } k=1\ldots q$$

Where d_{ijk} is the yield deviation of the ith variety in the kth block in the jth environment; μ is the grand mean of the plot yield deviation; V_i is the effect of the ith variety; $E(V)_{ji}$ is the effect of the jth environment (E) within ith variety; $B(E)_{kj}$ is the effect of kth block(B) within jth environment; e_{ijk} is the residual component.

In the present method, stability of a variety is evaluated by using AMMI analysis of variance and suggested single value of IPCA scores (IPCAs). IPCA was estimated as follows;

$$\text{IPCAs}= \sum_{n=1}^{n} A_i \times SSA_i/SSGEI$$

Where IPCAs is the single value of IPCA scores; A_i is the ith IPCA score; SSA_i is the sum of squares of the ith IPCA; SSGEI is the sum of squares of GEI of the AMMI anova.

The following mentioned statistical model was used to calculate yield deviation from the maximum response;

$$d_{ij}= \mu+V_i+E_j+ \alpha_{ji}+ +e_{ij}$$
$$i=1\ldots.p \text{ and } j=1\ldots n$$

Where d_{ij} is the yield deviation of the ith variety in the jth environment; μ is the grand mean of the plot yield deviation; V_i is the effect of the ith variety; E_j is the effect of the jth environment; α_{ji} is the combined effect of the jth environment & ith variety; e_{ij} is the residual component.

In this study, 10 mungbean lines were tested in 4 locations for two years. These 10 lines were planted in 7.2 m^2 plots using a randomized complete block design with three replicates. The spacing was 30 x 10 cm. Fertilizer application was 30 kg ha^{-1} of urea, 100 kg ha^{-1} of triple super phosphate and 75 kg ha^{-1} of muriate of potash as a basal dressing and 30 kg ha^{-1} of urea for top dressing. Recommended agrochemicals were applied to control disease. Net plot grain yield was recorded by removing border row. A combined ANOVA and AMMI analysis was preceded using statistical analyzing with open source software of MATHMODEL version 3 and CropStat version 7.2

Variety selection method

A high yielding promising stable line can be selected using the parameters of mean deviation across environments (D_i) from maximum plot yield, IPCAs scores and its biplot simultaneously. Selection criteria for selecting promising lines are considered as follows. (1) selection can be done when D_i is significantly lower when GEI of plot yield deviation is not significant and yield is above grand mean. (2) simultaneous selection can be done when D_i is significantly lower and IPCAs is close to zero, if GEI of both plot yield deviation and AMMI model is significant and yield is above grand mean. (3) if both GEI of plot yield deviation and AMMI model are not significant, all the varieties have same stability level. (4) varieties recommending only for specific area using IPCAs biplot.

RESULT AND DISCUSSION

The analysis of variance of mungbean grain yield is presented in table 1. Location, genotype , crop year x location were found to be highly significant (p=0.01) for mungbean grain yield. Crop year and location x genotype were also significant (p=0.05). Significant L x G effect revealed that the genotypes responded in different ways to the variation in environmental condition across the locations. Therefore, it is important to select more stable promising lines precisely.

The analysis of variance of plot yield deviation which is presented in table 2, shows a significant (p=0.05) interaction among genotype x location. If the G x L term was significant in plot yield deviation analysis of variance, there is a variance of varietal deviation across the environments and lowest mean deviation (D_i) indicates the stable lines (Abeysiriwardena, 2001).

According to Abeysiriwardena's (2001) proposed method mungbean lines of MIMBCP101, MIMBCP113, MIMBCP114 and MIMBCP5913 are more stable due to lowest mean deviation across environments and further consideration for selection according to variance (Table 4).

Additive main effect and multiplicative interaction analysis of variance show that the GEI is significant at the probability level 0.05 (table 3). GEI capturing percentage of IPCA1 is 70.67%, IPCA2 is 21.77% and IPCA3 is 7.56% in the mungbean yield trials. But suggested new scores of IPCAs capture the 100% of GEI. Therefore, the IPCAs vs. mean yield biplot explain the maximum information of G and GEI.

Space of the graph fig.1 and fig.2 are divided into 4 quadrants as lower yielding environments in quadrants I & IV and high yielding quadrants II & III. The biplot of IPCAs explained how they achieved the average yield. According to the biplots MIMB101, MIMB113, MIMB114, MIMBCP5913, MIMB5913, MIMB539-17 and MI6 showed higher grand mean yield and stability across the environments by being close to the zero of IPCA scores (Fig. 1 & Fig. 2). Genotype MIMBCP101 showed higher yield above the grand mean yield but it is less stable than ANMB16 and MIMBCP113 which are close to zero of IPCAs. The check variety MI6 shows low yield than the MIMBCP101, MIMBCP113, MIMBCP114, and MIMBCP5913. (Fig.1).

When considering both IPCA scores and mean yield deviation, MIMBCP101, MIMBCP113, MIMBCP114, and MIMBCP5913 can be considered as more stable lines due to their significantly lower mean deviation with higher yield over grand mean. (Table 4, 5 and Fig.1).

This proposed method of selecting stable promising lines through IPCAs scores and its biplot along with mean deviation from maximum plot yield can be used to evaluate small number of even two varieties due to the mean maximum response. In addition, this method can be used to evaluate the promising lines across the mega environment with higher precision due to using of AMMI analysis of variance. New IPCAs biplot explain 100% of G effect as well as 100% GEI effect.

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Table 1. Analysis of variance of grain yield for 10 mungbean lines grown in 4 locations in 2008-2009.

Source	***DF***	***SS***	***MS***
Replication	2	0.055	0.028
Crop-year (Y)	1	0.596	0.596*
Location (L)	3	17.871	5.957**
Genotype (G)	9	2.604	0.289**
YxL	3	17.356	5.786**
LxG	27	4.418	0.164*
YxG	9	0.541	0.06

*, ** significant at 0.05 and 0.01 probability levels respectively. *DF*= degree of freedom, *SS*= sum of squares. *MS*= Mean sum of squares square.

Table 2. Analysis of variance of plot yield deviation for 10 mungbean lines grown in 4 locations in 2008-2009.

Source	***DF***	***SS***	***MS***
Replication	2	0.055	0.028
Crop-year (Y)	1	0.923	0.923**
Location (L)	3	15.431	5.144**
Genotype (G)	9	2.604	0.289**
YxL	3	10.793	3.598**
LxG	27	4.418	0.164*
YxG	9	0.541	0.06

*, ** significant at 0.05 and 0.01 probability levels respectively.

Table 3. Additive main effect and multiplicative interactions analysis of variance for mungbean grain yield (t ha^{-1}) of 10 mungbean genotypes grown in 4 environments

Source	***DF***	***SS***	***MS***
Genotype (G)	9	1.302	0.319*
environment(E)	3	8.936	2.979**
ExG	27	2.209	0.082*
IPCA1	11	1.561	0.142**
IPCA2	9	0.481	0.054
IPCA3	7	0.167	0.024
RxG residual	0	0	

*, ** significant at 0.05 and 0.01 probability level respectively.
¶ Explained percentage of IPCA1=70.67%, IPCA2=21.77% & IPCA3=7.56%

Table 4. Mean yield and mean deviation (D_i) and stability parameter (V_i^2) for 10 mungbean lines grown in 4 locations

Variety	Mean yield (t ha^{-1})*	D_i*	V_i^2
MIMBCP101	1.777a	0.549c	0.261
MIMBCP113	1.716a	0.609c	0.184
MIMBCP114	1.711a	0.617c	0.381
MIMBCP116	1.651ab	0.675bc	0.269
MIMBCP5913	1.71a	0.616c	0.171
MIMB539-17	1.697ab	0.629bc	0.146
MIMBCP604	1.496bc	0.829ab	0.204
ANMB16	1.669ab	0.657bc	0.196
MI6	1.692ab	0.634bc	0.392
MI5	1.420c	0.906a	0.364

* The same letters are not significantly different at 5% probability level of DMR test.

Table 5. IPCA scores and suggested single value of IPCA scores (IPCAs) of the 10 mungbean lines grown in 4 locations

Genotype	mean yield (t/ha)	IPCA1	IPCA2	IPCA3	IPCAs¶
MIMBCP101	1.777	-0.14466	-0.25825	-0.23809	-0.176457012
MIMBCP113	1.716	0.12281	0.01517	0.2042	0.105524934
MIMBCP114	1.711	0.32094	-0.07959	-0.07219	0.204005804
MIMBCP116	1.651	0.20434	0.04341	-0.23441	0.136128782
MIMBCP5913	1.71	-0.42022	0.04341	-0.05506	-0.291660584
MIMB539-17	1.697	-0.39406	0.27288	-0.04064	-0.222118271
MIMBCP604	1.496	-0.10937	-0.29397	0.22192	-0.124520371
ANMB16	1.669	-0.1195	-0.12564	0.13279	-0.10176388
MI6	1.692	0.40541	0.02388	0.00587	0.292128375
MI5	1.42	0.13432	0.38448	0.0756	0.184352014

¶ IPCAs=IPCA1x0.707+IPCA2x0.218+IPCA3x0.076 for these 10 mungbean genotypes grown at 4 locations.

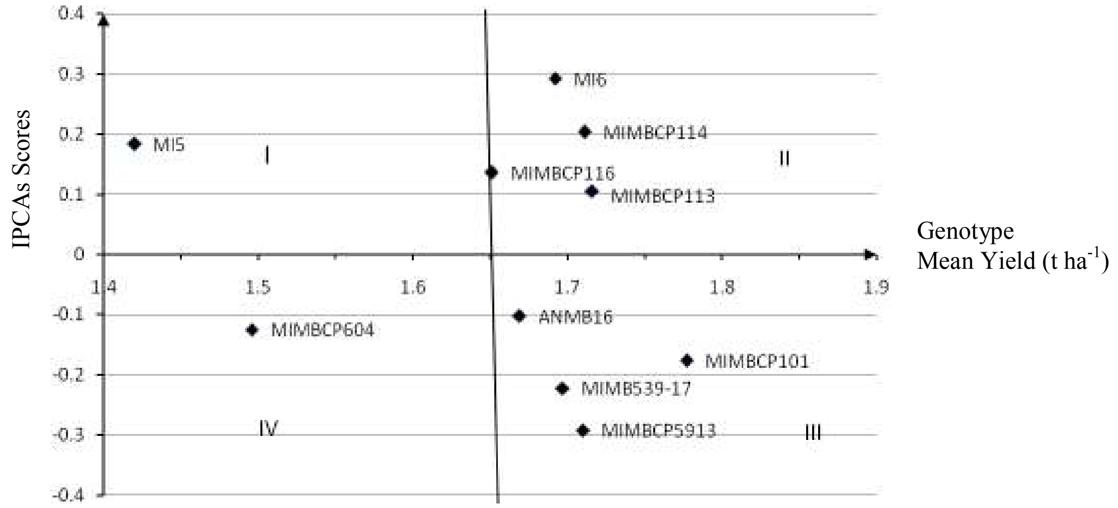

Fig1. Suggested biplot of single value of IPCA scores (IPCAs) for mean grain yield (t ha^{-1}) of 10 mungbean lines in 4 locations.

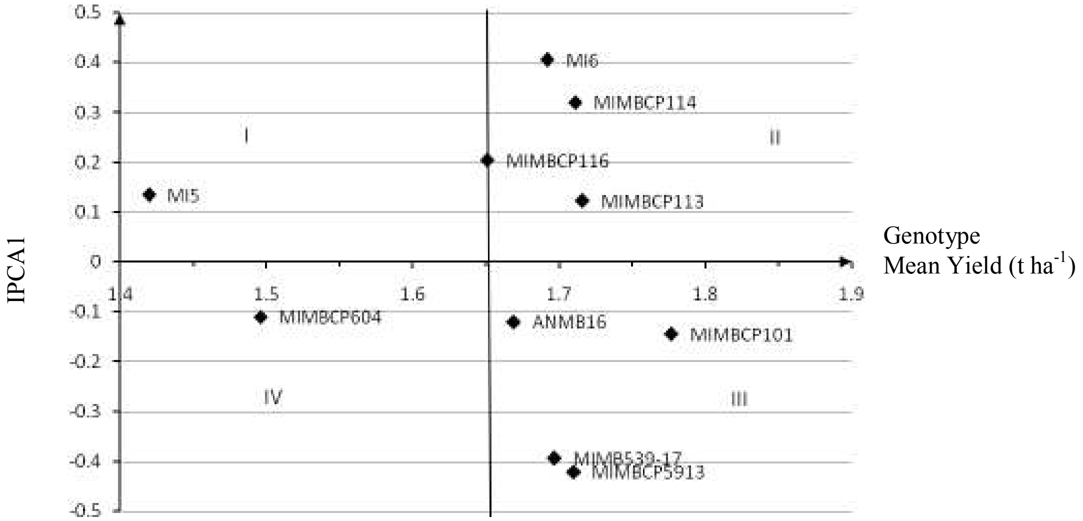

Fig2. AMMI1 biplot for mean grain yield (t ha^{-1}) of 10 mungbean lines in 4 locations.