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Short Communication

Stability analysis for grain yield in mung bean (*Vigna radiata* L. wilczek) grown in different agro-climatic regions

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Abstract: Plants generally showed variation in their response to changing environment. Fifteen genotypes were tested at five locations in Pakistan in the Kharif season 2006 to study their yield stability. Pooled analysis of variance and stability analysis were performed. The genotype (G) x environment (E) interaction and both variance due to genotypes and environments were significant. The partitioning of G x E interaction into linear and non-linear components indicated that both predictable and unpredictable components shared the interaction. Three stability parameters were computed to judge the stable and superior genotype. On the basis of these parameters, the top yielding genotype '2 (check) CGM-504' exhibited the stable performance over all five locations. Results also showed that the genotypes; BRM-288, NCM-257-2 and BRM-286 gave higher yield. But their performance was unstable due to high deviation from regression. Seven genotypes NCM-252-7, 2CMG-504, C1/95-3/45, BRM-286, BRM-288, NCM-257-2 and M-8 produced more grain yield than average yield. On the basis of results, 2CMG-504 was the most suitable and desirable genotype which showed stable yields at different sites.

Key words: mung bean, stability analysis, yield, interaction, environment.

تحليل الاستقرار لمحصول فول المونك (*Vigna radiata* L. wilczek) التي تنمو في عدة مناطق زراعية مناخية مختلفة

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الملخص: تظهر النباتات عادة اختلافات فى مدى استجابتها الى الظروف البيئة المختلفة. 15 صنفا تم اختيارها من خمسة مناطق مختلفة من الجمهورية الباكستانية فى خريف 2006 لدراسة مدى استقرارها من ناحية الانتاج. تم اجراء التحليل التجميعى للتباين وتحليل الاستقرار وأظهر النمط الوراثي (G) × البيئة (E) التفاعل للمتغيرين بسبب المورثات والبيئات المختلفة واظهرت تفعال اجابى ملموس. وبينت النتائج مظاهر المشاركة والتقييم لتفاعل (G × E) بواسطة المكونات الخطية واللاخطية وتبين ان كل المكونات التى يمكن التنبوء بها وعكسها التى تشارك مجتمعة. واظهرت ان ثلاثة معايير الاستقراء قد حسبت للحكم على النمط الوراثي المستقر والمتفوق وعلى اساس هذه المعايير اتضح ان الصنف ذات النمط الجينى الاعلى هو (2 (check) CGM-504) واظهر استقرارا فى الاداء فى الخمسة مناطق محل الدراسة. وبينت الدراسة ايضا الانماط الوراثية (BRM-288, NCM-257-2 و BRM-286) ذات انتاج اعلى ولكن اداءها لم يكن مستقراً بسبب الانحراف المعيارى الكلى فى الاداء الكلى وسبقه انماط وهى (NCM-252-7, 2CMG-504, C1/95-3/45, BRM-286, BRM-288, NCM-257-2) و (M-8). والتى انتجت محاصيل اعلى مقارنة بالمتوسط العام وبناء على هذه النتائج كانت صنف (2CMG-504)اكثر الانماط الوراثية استقرارا وملأمة لما اظهرته من ثبات فى الانتاج فى مختلف المناطق.

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Introduction

Mung bean (*Vigna radiata* (L.) Wilczek) is one of the most important pulses crops grown in the world. It was grown on an area of 0.246 million ha with a production of 0.178 million tons in Pakistan during 2007-08 (Anonymous, 2008). The environment is changing day by day and it is direly needed to evaluate crop genotypes at different locations to evaluate their performance for more site specific managements. Genotypes behave differently to both soil and environmental factors. The genotype-environment interaction is a challenging issue for plant breeders and plays major role in developing improved varieties. The basic and ultimate goal behind these experiments is to select stable genotypes or cultivars. Raffi et al. (2004) reported that genotype-environment interaction is of much value in the selection of better genotypes. The interaction indicates that genotypes react in different ways to variable environmental conditions. Now breeders want to develop genotypes that can withstand unpredictable transient environmental fluctuation. This concept of stability has been defined in several ways and several biometrical methods including univariate and multivariate ones, have been developed to assess stability. For studying the genotype-environment interaction, Cali´nski (1960) has proposed some methods for measuring the stability of genotypes. Finlay and Wilkinson (1963) and Eberhart and Russell (1966) have introduced kind of "stability analyses" that use a model in which the data from each genotype are regressed on an environmental productivity index, estimated as the main effect of the environment. This model has received much attention in the literature and by including further terms it has been developed into the so-called additive main effects and multiplicative interaction (AMMI) model, strongly adopted by Gauch (1992). A thorough review of the theory and applications of this model has been given by Van Eeuvijk (1996). Other statistical models discussed in the literature to study the genotype-environment interaction include Becker (1981), Kempton (1984), Lin et al. (1986), Plaisted and Peterson (1959) and Perkins and Jinks (1968). A number of research workers like Ram and Dhar (1999), Pan et al. (2001), Islam and Newaz (2001), Raffi et al. (2004), Worku et al. (2001) and Zubair et al. (2002) studied genotype-environment interaction in French bean, dry beans, maize and mash crops.

The present research studies were conducted to know genotype-environment interaction and to identify stable and high yielding mung bean genotypes under changing environments. The results of present project may be useful both for breeders as well as farmers to select suitable genotype for sustainable mung bean production.

Materials and Methods

The yield data of fifteen genotypes of mung bean from different research institutes/stations were used in this study. Five locations (Table 1) were selected to test the yield performance of these varieties (Table 2). The locations differ significantly in climate and elevation from the sea level. The exact location is presented in Fig. 1. The experiment at each location was conducted during Kharif season 2006 in a Randomized Complete Block Design with four replications. The experimental units were a six row plot of 4 meter length. Row to row and plant-to-plant distance was kept as 30cm and 10cm, respectively, at all locations. Two and half bags of diammonium phosphate fertilizer per hectare were applied before sowing of the crop. The crop was harvested at the time of 90% pod maturity and yield data were recorded in kg ha^{-1}.

Table 1. Location of the experimental sites with climate.

Symbol	Place and climate	
L 1	Bahawalpur, Punjab 29°23′44″N 71°41′1″E	Arid climate, very hot and dry
L 2	D. I. Khan, NWFP 31.49°N 70.55°E	Arid climate with low rainfall and high temperature
L 3	Islamabad, Punjab 33°43′N 73°04′E	
L4	Fateh Jang, Punjab 33°34′8″N 72°38′16″E	Sub-humid with hot summers and cold winters
L 5	Quetta, Baluchistan 30°21′36″N, 67°1′12″E	continental arid climate

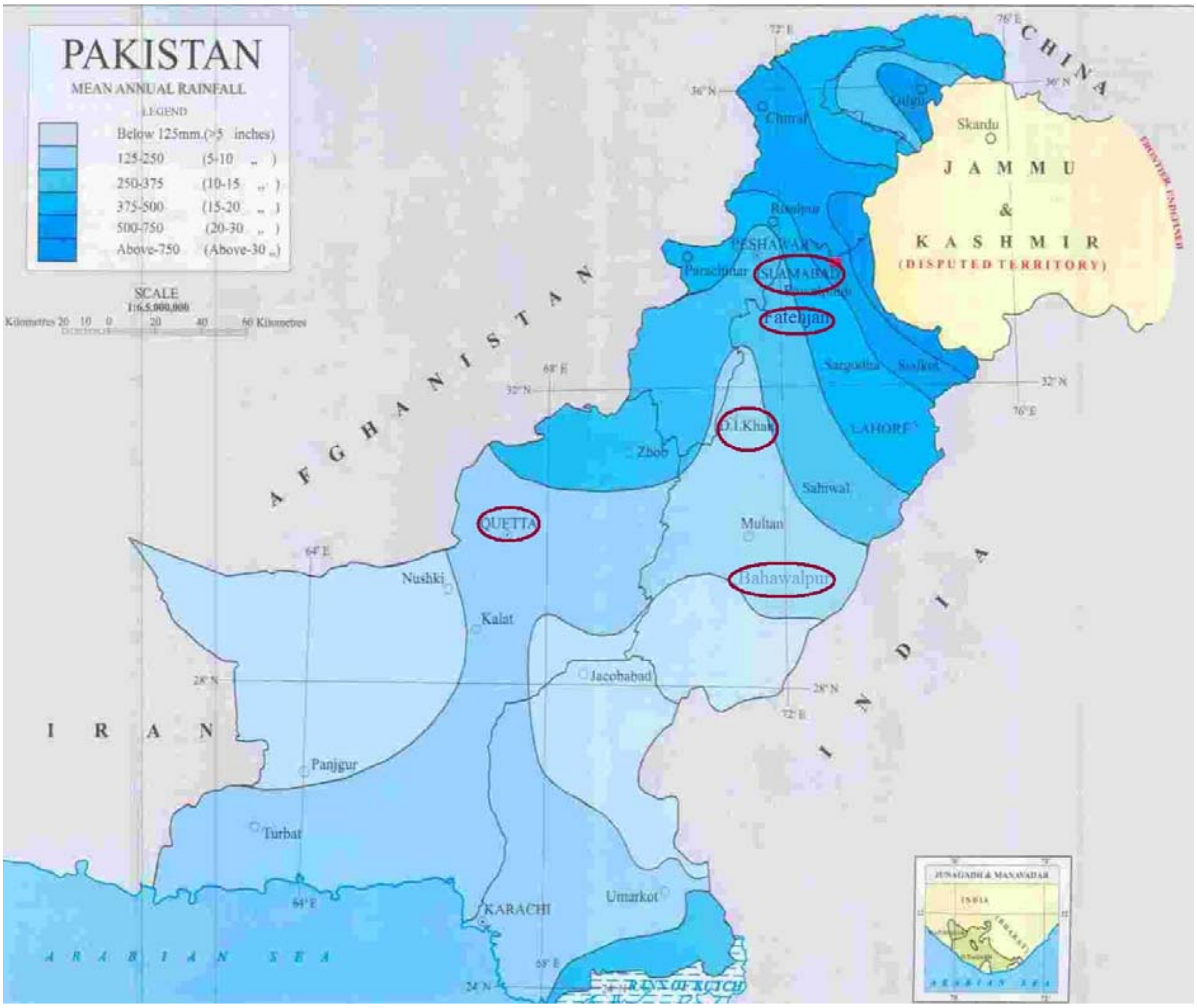

Figure 1. Geographical location of five experimental sites in Pakistan according to precipitation (http://www.mofa.gov.pk/Maps).

Table 2. Mean grain yield, regression coefficient (b_i) and mean square of deviation of mung bean genotypes grown in 5 environments.

Genotypes	Mean (kg ha^{-1})	Ranks	b_i	S^2d_i
DM-2	455.6	13	0.86±0.568	9033.72**
NCM-252-7	518.2	7	0.78±0.817	22705.93**
2CMG-504	626.8	1	1.15±0.171	-2558.21
C1/95-3/45	543.1	5	1.05±0.841	24276.68**
BRM-286	554.3	4	1.36±0.338	810.72**
2CMG-501	471.2	12	0.53±0.790	20994.84**
BRM-288	598.3	2	1.54±0.521	7026.20**
NCM-209	492.9	10	1.03±0.750	18537.62**
L1P5/5/89	497.8	9	1.30±0.350	1289.32**
AZRI M-06	388.5	15	1.10±0.487	5674.94**
AEM-6/20	447.4	14	1.35±0.418	3211.58**
NM-4	509.0	8	-0.36±0.964	33075.85**
NCM-257-2	567.6	3	0.91±0.817	22691.99**
NM-98	484.7	11	1.01±0.439	3905.04**
M-8	524.9	6	1.40±0.293	-322.82**
Mean	512.0		1.00	11357.0

‡ = No regression coefficient is significantly different from unity, ** = significant at the 1 % and 5% levels, respectively.

Statistical procedure

For the statistical analysis each of the five environments was considered as an independent environment. To identify the genotype and environment interaction from replicated multi-location trials a most commonly used method is combined analysis of variance. Mathematically for a trial in which the yield of G genotypes is measured in E environments each with R replicates is modeled as

$$Y_{ij} = u + G_i + E_j + GE_{ij} + e_{ij} \ldots\ldots\ldots\ldots\ldots\ldots(1)$$

Where u is the overall mean, G_i ,E_i, and GE_{ij} represents the effect of the genotype, environment, and the genotypes and environments interaction. Whereas e_{ij} is the average of the random errors associated with the r^{th} plot that receives the i^{th} genotype in the j^{th} environment. After removing the replicate effect when combining the data, the GE observations are partitioned into two sources: (a) additive main effect for genotypes and environments and (b) non-additive effects due to genotypes and environments interaction.

One of the main deficiencies of the combined analysis of variance of multi-location trials is that it does not explore any underlying structure within the observed nonadditivity (GEI). The analysis of variance fails to determine the pattern of response of genotypes and environments. The valuable information contained in (*G-1*) (*E-1*) degrees of freedom is particularly wasted if no further analysis is done. If the genotype and environment interaction variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s). Stability analysis provides a general summary of the response patterns of genotypes to environmental change. The Eberhart & Russel (1966) approach is used for stability analysis. Eberhart and Russell (1966) proposed pooling the sum of squares for environments and genotype and environment interaction (GEI) and subdividing it into a linear effect between environments (with 1 df), a linear effect for genotype x environment (with *E-2* df). In effect the residual mean squares from the regression model across environments is used as an index of stability, and a stable genotype is one in which the deviation from regression mean squares is small.

Further the significance of regression coefficient (b_i) and deviations from regression (S^2d_i) were tested using t-test and F-test respectively. According to Eberhart & Russel (1966), a genotype is said to be stable when it has a regression co-efficient of unity ($b_i = 1$) and a minimum deviation from the regression ($S^2d_i = 0$). So a stable genotype had a high mean yield and satisfying the above requirements for stability. MSTAT-C and Spread sheet 2007 computer programmes were used for analysis of variance and stability analysis, respectively.

Results and discussion

Pooled analysis of variance of mung bean yield data across the five locations of Pakistan was performed (Table 3). The results showed highly significant differences among the genotypes. The results also revealed that difference among genotypes and locations were also highly significant indicating the presence of genetic variability among the genotypes as well as the environments under study (P<0.01).

Table 3. Combined analysis of variance for grain yield of mung bean genotypes.

Source	D.F	MS
Genotypes (G)	14	18671.4^{**}
Environment + (G × E)	60	46829.7^{**}
Environment (Linear)	1	261399.65^{**}
GXE (Linear)	14	133588.13^{**}
Pooled Deviation	45	15067.97^{**}
Pooled error	225	14844.29

The sums of squares due to environments and genotype x environment are partitioned into environments (linear), genotype x environment (linear) and deviations from the regression model. The significance of both these components showed that both predictable and unpredictable components shared G x E interaction. The G × E (Linear) interaction was highly significant (tested against pooled deviation) which demonstrated that genotypes respond differently to variation in environmental conditions. Further the variation in stability of different cultivars performance was mainly due to genotypes by environment interaction. The results are similar with the finding of Chaudhary et al. (1994) in field pea, Arshad et al. (2003) in chick pea and Worku et al. (2001) in maize. In practice the scientists usually relay on least significant difference test (LSD) and Duncan's Multiple Range test (DMR) for grouping the varieties of similar average means. But these tests do not show the performance of the genotypes across all distinct environments. To make the stability statements for average yield on all different locations, stability analysis based on environmental index was performed.

In Table 2 the stability parameters according to the model of Eberhart & Russell are given. The first parameter was the mean of grain yield over the five locations. This column revealed that the genotype '2CMG-504' gave the highest yield (626.8 kg ha^{-1}) and was most favourable over all locations. Whereas the genotypes ‘AZRI M-06’ with yield (388.5 kg ha^{-1}) gave the poor performance over all the environments. The performance of all other genotypes was moderately well in all environments. On the bases of mean yield ranking, four genotypes namely: 2CMG-504, BRM-288, NCM-257-2 and BRM-286 were the top yielding genotypes across all the five distinct environments of Pakistan.

According to Finlay and Wilkson (1963), the genotypes with slope greater than one (>1) are specifically adapted to high yielding environments while genotypes with slope less than one (<1) are insensitive to change in environment and are therefore, better adapted to poor environments. Also there exists a positive association between linear response and mean yield performance (Finlay and Wilkinson, 1963; Perkins and Jinks, 1968; Perkins and Jinks, 1968). On the other hand many researchers (Eberhart and Russell, 1966; Paroda and Hayes, 1971; Westerman, 1971; Gautam, 1974; Saxena, 1975) suggested that both linear (bi) and non-linear (S^2di) components of G x E interaction should be considered as the criterion of stability of a particular genotype.

The estimates of b_i (Table 2) ranged from -0.36 to 1.54. The results indicated that most of the genotypes had average responsiveness to environments. The major variation in responsiveness favors higher grain production.

All the genotypes had a significant deviation mean square from linear regression except ‘2CMG-504’ (Table 2). This implies that all the genotypes were unstable and unpredictable across all five environments. The high yielding genotype ‘2CMG-504’ had non-significant regression coefficient above unity (b_i) indicating its average responsiveness to the high yielding environments. In addition the mean grain yield more than grand mean which indicates its superior performance over all the genotypes. This implied that among all genotypes, the genotype ‘2CMG-504’ is suited to all environments.

Other genotypes: ‘DM-2, 2CMG-501, NCM-209, LIP5/5/89, AZRIM-06, AEM-6/20, NM-4 and NM-98 was poor and produce below average grain yield. In addition all these genotypes had high deviation from regression indicating that these genotypes were unstable. These genotypes cannot be recommended due to their overall performance.

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