

GENOTYPE ENVIRONMENT INTERACTION IN MUNGBEAN (*Vigna radiate* L.)

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Abstract: Five experiments were conducted in the summer of season 2002 to evaluate ten newly mungbean genotypes compared with the commercial cultivar Kawmy-1. The experiments represent a wide range of environmental conditions to assess the best genotypes to replace the commercial cultivar. The experiments were sown at Maryout in the middle of March and July; Shalakan in the middle of March and Sohag in the middle of March and July. Data of number of seeds/plant, 100 seed weight and seed yield/plant were subjected to stability analysis proposed by Eberhart and Russell (1966) and Tai (1971). The eleven genotypes showed a good performance at Shalakan and Sohag. The mean values indicated that number of seeds/plant was the major contributor to seed yield rather than seed weight. The commercial cultivar

Kawmy-1 was the best in No. of seeds/plant in all environments, however, it was the inferior in 100-seed weight. Six genotypes were unstable in number of seeds/plant and 100-seed weight and showed significant deviation from linear response (S^2d and λ), however, their b's did not differ significantly from unity and their α were small.

There was a lack of association between stability and high yielding ability. The best two unstable genotypes which are likely to candidate to replace the commercial cultivar Kawmy-1 and significantly outyielded it by 34.55 and 40.30% are No. 6 (L3740) and No. 7 (L3940). The only two stable genotypes; No. 5 (L3630) and No. 8 (L2020) outyielded the check by 13.68 and 20.40%, respectively.

Key words: genotype, environment, Mungbean.

Introduction

Mungbean (*Vigna radiate* (L.) Wilczek) is an important legume crop that traditionally grown in the tropical and sub-tropical Asia (Rachie and Roberts, 1974; Kay, 1979). This crop constitutes an important source of easily-digestible protein of low flatulence, which complements the staple rice diet in Asia. It is prepared for human consumption in many

forms such as, bean sprouts, noodles, green bean, and boiled dry beans. Besides being an excellent source of high quality protein, it contains vitamins and minerals which are necessary to human body (AVRDC, 1976 and Anon, 1978).

Mungbean has the shortest maturity span of all legume crops and can, therefore, be planted following

cereals in a number of cropping systems (Singh *et al.*, 1987).

Preliminary study of Shalaby and Rizk (1987) showed an encouraging potential of mungbean to be used in Egypt as a field crop, green vegetable or as a forage crop. Later many investigators such as Shalaby *et al.*, 1991; Hussein *et al.*, 1993; Farghaly and Hussein, 1995; Obiadalla, 1996 were succeeded to make this crop available to the Egyptian populace. Imrie and Butler (2005) evaluated thirty mungbean accessions at two sites for two years. Estimated variance due to environment exceeded that due to genotypes for seed yield, plant height and days to flower and to harvest.

The knowledge of variability for the different genotypes is important in plant breeding programs. Further, the genetic resources should be evaluated under different environmental conditions, especially the newly bred lines because the lack of information on genotype \times environment interaction. A wide range of variability among the environmental conditions for evaluation the yield production considers a prerequisite for proper selection decision. However, evaluation genotypes depending on the interaction of genotype \times environment led to unsuitable dedication for breeder to select the most stable genotype under such locations. In the same respect, Eberhart and Russell (1966) defined a specific relationship of stability

genotype which regression coefficient, b_i equal to 1 and mean square deviation from regression, S^2_{di} equal to zero.

The present study aimed to determine some stability parameters and the best genotype among ten newly bred mungbean lines compared with the commercial cultivar Kawmy-1 grown under five environmental conditions.

Materials and Methods

Five filed experiments were carried out to evaluate ten newly bred mungbean lines as well as local cultivar Kawmy-1 in a randomized complete blocks design with three replications.

Env₁: Maryout – Sowing in middle of March .

Env₂ : Maryout – Sowing in middle of July .

Env₃: shalakan - Sowing in middle of March .

Env₄: sohag - Sowing in middle of March .

Env₅: sohag - Sowing in middle of July .

The experimental plot consists of three ridges 3m long and 60 cm apart. Three seeds were hand sown in each hill spaced 20 cm on one side of the ridge.

Some chemical and physical analysis of soil and irrigation water are presented in table (1).

Data of each experiment, were recorded and computed for number of seeds per plant, 100- seed weight and seed yield per plant using fifteen guarded hills of three plants each from each plot.

The phenotypic stability statistics (b_i and s^2d_i) were calculated for all the studied traits as suggested by Eberhart and Russell (1966).

Also, the genotypic stability parameters were computed according to the method of Tai (1971) by partitioning the genotype-environment interaction effect of genotype (i) into two statistical parameters, namely α_i and λ_i that measure linear response to environmental effects and the deviation from linear regression, respectively. Method of calculation with the two prediction limits of α_i and upper limits of the confidence

intervals for λ_o is given in appendix (1).

Least significant difference (LSD) was used for comparing the mean performance of the tested mungbean genotypes.

Results and Discussion

Data presented in Table (2) indicated significant differences among eleven mungbean genotypes as well as environments and genotype \times environment interaction for all traits recorded. The data also indicated that genotypes responded differently to the different environmental conditions suggesting the importance of assessment of genotypes under different environments in order to identify the best genetic makeup for each particular environment. These findings are in line with those previously obtained by Afiah and Omar (2003) in barley.

Table(2): Analysis of variance for seed yield and two of its components of 11 mungbean genotypes grown under 5 different environmental conditions.

Source of variance	d.f.	Mean squares		
		No. of seeds/plant	100-seed weight (g)	Seed yield/plant (g)
Environments (Env.)	4	13198.90**	9.152**	52.09**
Reps / Env.	10	91.82	0.047	0.152
Genotypes (G.)	10	8831.83**	8.007**	12.51**
Env. x G.	40	317.84**	0.329**	0.796**
Error	100	69.308	0.085	0.179

** Significant at 0.01 level of probability. d.f. = Degrees of freedom.

From the data illustrated in Table 3, it is clear that the average number of seeds/plant, 100-seed weight and seed yield/plant were high under Env. 3, Env. 4 and Env. 5. The genotypes No. 6 and 7 gave the highest mean values of seed yield/plant, genotypes No. 3 and 7 for 100-seed weight and genotypes No. 2 and 6 for number of seeds/plant. The mean values of the different genotypes indicated that number of seeds/plant was the major contributor to seed yield/plant rather than seed weight. Means in Table 3 indicated that the commercial cultivar Kawmy-1 exceeded significantly the other ten genotypes in number of seeds/plant under the five environmental conditions except genotype No. 2 at Env. 1 and genotype No. 9 at Env. 5. On the other hand, Kawmy-1 was the inferior in 100-seed weight. Likewise, 6, 3, 8 and 6 genotypes outyielded Kawmy-1 at Env. 1, Env. 2, Env. 3 and Env. 4, respectively. Overall environments six genotypes highly significantly outyielded the check cultivar Kawmy-1 (Table 5).

It could be noticed from Table 3 that the five environments used, represent a wide range of edafic and climatic conditions from Maryout to Sohag, and sowing mungbean in middle March was better than middle July and could be recommended for all environments.

The analysis of variance of means (Table 4) indicated highly significant mean squares for genotypes, env. + genotype x environment, env. linear and pooled deviation. Pooled deviation mean squares of most genotypes was significant indicating the importance of the unexpected deviation from regression.

The genotype x environment interaction was partitioned to phenotypic stability statistics b_i and s^2_{di} according to Eberhart and Russell (1966), and to genotypic counterparts $\hat{\alpha}$ and λ according to Tai (1971). The linear response to environmental effects was measured by b_i and $\hat{\alpha}$, and the deviation from the linear response was measured by s^2_{di} and λ . Eberhart and Russell (1969) and Brecse (1969) reported that the most important stability parameter appeared to be the minimum deviation mean squares. According to such model Table 5 show that the regression of all genotypes did not differ significantly from unity for number of seeds/plant and 100-seed weight. Also, for seed yield/plant except for genotype No. 7 ($b=0.542$) which differed significantly from unity (a stable genotype have $b_i=1$ and $s^2_{di}=0$).

Table(4): Analysis of variance of means for yield and some yield components of 11 mungbean genotypes grown under five different environmental conditions.

Source of variance	d.f.	Mean squares		
		No. of seeds/plant	100- seed weight (g)	Seed yield /plant (g)
1- Total	54	949.55	0.802	2.255
2- Genotypes (G.)	10	2943.93**	2.670**	4.171**
3- Env. + G. x Env.	44	496.28**	0.377**	1.820**
a- Env. Linear	1	17598.40**	12.200**	69.45**
b- G. x Env. linear	10	71.09	0.120	0.222
c- Pooled deviation	33	106.89**	0.094**	0.255**
Genotype -1	3	45.17	0.116**	0.192*
Genotype -2	3	251.00*	0.174**	0.224**
Genotype -3	3	37.27	0.047	0.300**
Genotype -4	3	55.20	0.019	0.094
Genotype -5	3	77.53*	0.054	0.015
Genotype -6	3	102.17**	0.015	0.546**
Genotype -7	3	3.70	0.214**	0.201*
Genotype -8	3	2.53	0.095**	0.079
Genotype -9	3	80.60*	0.035	0.322**
Genotype -10	3	437.40**	0.105**	0.591**
Genotype -11	3	83.13*	0.173**	0.236**
4- Pooled error	110	23.78	0.027	0.059

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

- Pooled deviation mean squares was used to test the significance of genotypes, Env+GxEnv., Env.linear, and GxEnv.linear .
- Pooled error mean squares was used to test the significance of pooled deviation and deviation mean squares of individual genotypes .

Respect to number of seeds/plant, all the genotypes were stable (Table 5) and showed b's did not differ from unity, except genotypes No. 2 and 10 which showed s^2_d highly significantly deviated from zero. However, the genotypic stability parameters of tai (Table 5 and Fig. 1) indicated the instability of genotypes No. 2, 5, 6, 9, 10 and 11 because of the significant deviation from linear

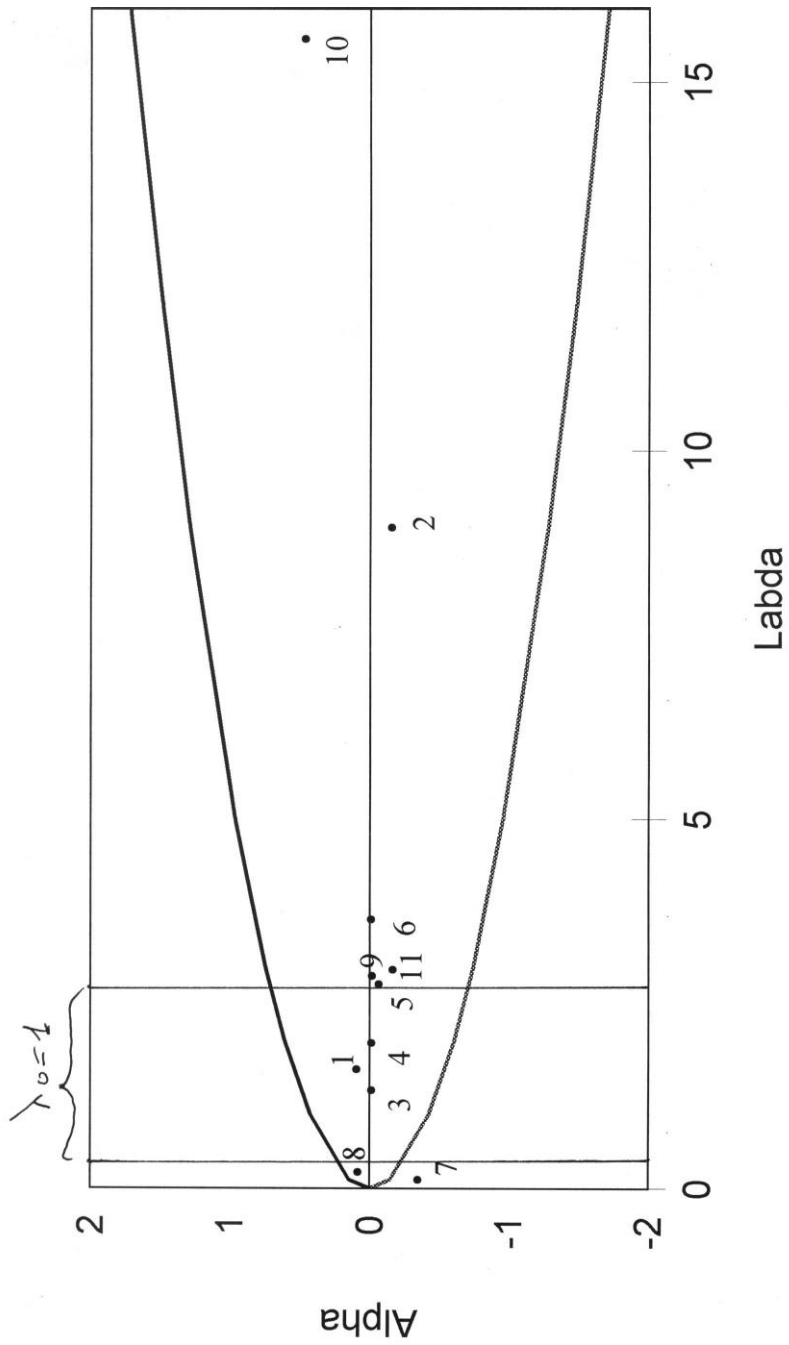


Fig. (1): Distribution of estimated of genotype stability parameters of No. of seeds / plant

response (λ). However, both analyses (Table 5 and Fig. 2) show significant deviation from linear response for genotypes No. 1, 2, 7, 8, 10 and 11 in 100-seed weight.

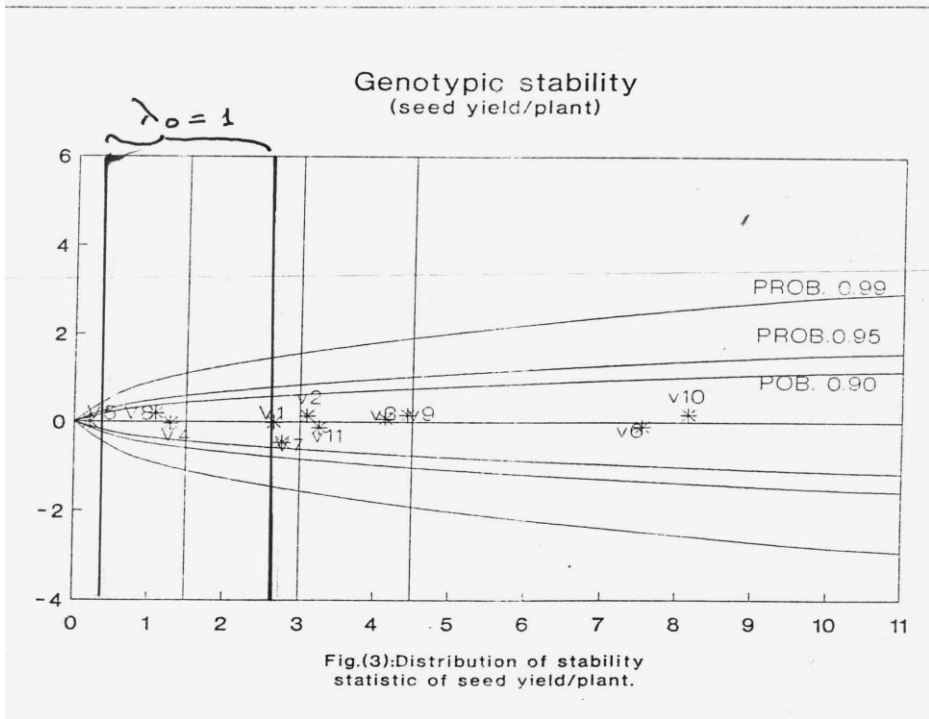
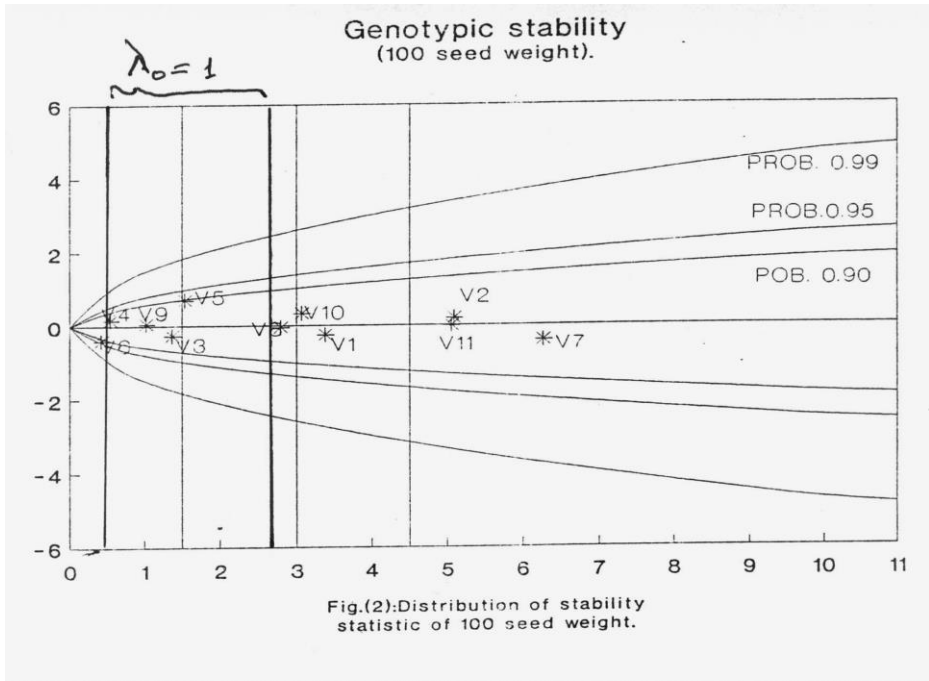
Concerning seed yield/plant all the genotypes showed insignificant differences of b's from unity, and estimates of α were very small (Fig. 3). However, the genotypes No. 1, 2, 3, 6, 7, 9, 10 and 11 gave s^2d significantly differed from zero. Therefore, these genotypes considered unstable. Furthermore, λ estimates coincides with s^2d for all genotypes except genotype No. 1 (Table 5). Two stable genotypes No. 5 (4.57 g) and No. 8 (4.84 g) outyielded the commercial cultivar Kawmy-1 (4.02 g). however, the two best cultivar in seed yield/plant; genotypes No. 6 and 7 were not stable.

It could be concluded that several genotypes were better in yield than the check cultivar Kawmy-1. There was a lack of association between stability and high yielding ability. The best two genotypes which are likely to be candidates to replace the commercial cultivar Kawmy-1 and significantly outyielded it at all environments are genotypes No. 6 and 7 (Table 3). The main cause of the instability of these two elite genotypes could be due to delay planting at Maryout. The two unstable genotypes No. 6 and 7 also outyielded the two stable genotypes; No. 5 and 8. Overall environments

the genotype No. 6 (L3740) and No. 7 (L3940) highly significantly outyielded the check cultivar Kawmy-1 by 39.55 and 40.30%, respectively. Whereas, the two stable genotypes No. 5 (L3630) and 8 (L2020) highly significantly outyielded the check by 13.68 and 20.40%, respectively. It is of interest to indicate that the four genotypes No. 5, 6, 7 and 8 outyielded the check cultivars at the individual environments (Table 3).

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Appendix (1): Details of calculation for Tai (1971) method with the two prediction limits of α_i and upper limits of the confidence intervals for λ_o .

$\alpha_i = [S_l(gl)i] / [(MSL-MSB) / vr.]$, and $\lambda_i = [S^2(gl)i - \alpha_i S_l(gl)i] / [(v-1)MSE/vr.]$, where:

α_i = The linear response of the i^{th} genotypes to the environmental effects,

λ_i = The deviation from the linear response of the i^{th} genotypes to the environmental effects,

I = The environmental effects,

(gl)i; The interaction effect for i^{th} genotypes,

$S^2(gl)i$ = The sample variance of the interaction effects of the i^{th} genotypes to the environmental effects,

$S_l(gl)i$ = The sample covariance between the environmental and interaction effects,

MSL = Mean squares for environments,

MSB = Mean squares for replicates within environments,

MSE = Mean squares for error,

Denoting: 1) the tabulated t-value at the probability level $\alpha=1-p$ with $(n-2)$ degrees of freedom as t_a , the two prediction limits for α_i corresponding to $\alpha_i = 0$ can be shown to be:

$$\pm t_a = ([\lambda_i (v-1)MSE.MSL] / \{(MSL-MSB)[(n-2)MSL - (t_a + n - 2)MSB]\})^{0.5}$$

2) the confidence interval for λ_o can be constructed by means of an F distribution with; $n_1 = n-2$, and $n_2 = n(v-1) (r-1)$ degrees of freedom, where:

n = number of environments,

v = number of varieties (genotypes), and

r = number of replicates.

For $\lambda_o = 1$; the interval at the probability level (p) is:

$$F_a (n_1, n_2) \geq \lambda_i \geq F_a [1/ (n_1, n_2)]$$

and for the estimating the upper limits of the confidence intervals for $\lambda_o > 1$

$F_a (n^*, n_2) \geq \lambda_o \geq 1/\lambda_o F_a (n^*, n_2)$; where: $o = 2, 3, \dots$, and

$$n^* = n_1 \lambda_o / 2 \lambda_o - 1.$$

التفاعل بين التركيب الوراثى والبيئة فى فول المانج *Vigna radiate* L.

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أجريت خمسة تجارب فى صيف 2002 لتقييم 10 تراكيب وراثية جديدة من فول المانج مقارنة بالصنف التجارى Kawmy-1 . والتجارب تمثل تباين واسع للظروف البيئية لتحديد أفضل التراكيب الوراثية التى يمكن أن تحل محل الصنف التجارى . زرعت تجربتان فى مريوط فى منتصف مارس ومنتصف يوليو وتجربة فى شلقان فى منتصف مارس وتجربتين فى سوهاج فى منتصف مارس ومنتصف يوليو . أخذت البيانات لعدد البذور للنبات ووزن 100 بذرة ومحصول النبات الفردى وأجرى عليها تحليل الثبات الخاص بـ Eberhart & Russell (1996), Tai (1971) . وأظهر الاحدى عشر تركيب وراثى أداء جيداً فى شلقان وسوهاج .

وتوضح النتائج أن عدد البذور للنبات هو أهم مكون للمحصول أكثر من وزن البذرة . وكان الصنف التجارى Kawmy-1 أفضلها جميعاً فى كل البيئات فى عدد البذور للنبات ، فى حين أنه كان أقلها فى وزن 100 بذرة . وأظهرت ستة تراكيب وراثية عدم ثبات لعدد البذور للنبات ووزن 100 بذرة وأظهرت انحراف معنوى عن الأداء الخطى وعن قيم λ ، ولكن لم يختلف معامل الانحدار فيها عن الوحده وكانت قيم α صغيرة .

وكانت العلاقة بين الثبات والمحصول العالى ضعيفة . وأظهرت النتائج أن تركيبين وراثيين لم يظهرأ ثباتاً وراثياً ولكنهما تفوقا معنوباً بمقدار 34.55% (L3740) ، 40.30% للتركيب (L3940) . والتركيبان الوحيدان اللذان أظهرأ ثباتاً وراثياً هما (L3630) ، (L2020) وتفوقا معنوباً فى المحصول عن الصنف التجارى بمقدار 13.68 ، 20.40% على الترتيب . وينصح بأن يحلا محل الصنف التجارى .